Supplementary Appendix

Related to *ARMC5* Mutations in Macronodular Adrenal Hyperplasia with Cushing's Syndrome

From Guillaume Assié,* M.D.,Ph.D, Rossella Libé,* M.D., Stéphanie Espiard,* M.D., Marthe Rizk-Rabin,* Ph.D., Anne Guimier, M.D., Windy Luscap, M.Sc., Olivia Barreau, M.D., Lucile Lefèvre, M.Sc., Mathilde Sibony, M.D., Laurence Guignat, M.D., Stéphanie Rodriguez, M.Sc., Karine Perlemoine, Fernande René-Corail, Franck Letourneur, Ph.D., Bilal Trabulsi, M.D., Alix Poussier, M.D., Nathalie Chabbert-Buffet, M.D., Ph.D., Françoise Borson-Chazot, M.D., Ph.D, Lionel Groussin, M.D., Ph.D., Xavier Bertagna, M.D., Constantine A Stratakis, M.D., Ph.D., Bruno Ragazzon, ° Ph.D., Jérôme Bertherat, ° M.D., Ph.D.

For the purpose of clarity, the sample names have been changed to numbers in the manuscript, but not in the supplemental appendix.

The correspondence between the two nomenclatures is provided below:

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sample numbers	sample names
1	H10
2	H11
3	H12
4	H14
5	H44
6	H5
7	H60
8	H63
9	H6
10	H7
11	H9
12	H24
13	H20
14	H21
15	H23
16	H61
17	H15
18	H25
19	H3
20	H27
21	H4
22	H8
23	H58
24	H2
25	H1

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Table of contents

SUPPLEMENTAL METHODS 2
1. SNP Array Analysis 2
2. Microsatellite Analysis 5
3. Whole Genome Sequencing 5
4. Sanger Sequencing of *ARMC5* 6
5. Microarray Experiments and Analyses 6
6. siRNA Experiments: siRNA Sequences 7
7. Reverse Transcription Quantitavite Polymerase Chain Reaction (RT-qPCR) Experiments: Primer Sequences 8
8. Western Blot Experiment: Antibodies 8
9. Immunohistochemistry 9
10. Fluorescence Immunostaining 9
Figure S1: Flowchart of the SNP Chips (Affymetrix SNP6) Data Analysis 10
Figure S2: Flowchart of the Whole Genome (Complete Genomics) Data Analysis 11
Figure S3: Chromosomal Alterations in ACTH-Independent Macronodular Adrenal Hyperplasia Nodules Identified with SNP Arrays 12
Figure S4: Location of the *ARMC5* Mutations 13
Figure S5: Germline Microdeletion in a Patient Including the *ARMC5* Locus 14
Figure S6: the *ARMC5* Mutations are Present on two Different Alleles 15
Figure S7: Sequencing *ARMC5* in Inter-Nodular Regions 16
Figure S8: Unsupervised Hierarchical Clustering of the ACTH-Independent Macronodular Adrenal Hyperplasia Transcriptome 17
Figure S9: Immunohistochemistry of ARMC5 18
Figure S10: Expression of ARMC5 in HeLa Cells 19
Figure S11: Decreased Apoptosis Associated with *ARMC5* Mutations 20
Table S1: Patients Characteristics 21
Table S2. SNP6_CNLOH_ChrArm: Alterations in Chromosome Arms 22
Table S3. SNP6_CNLOH_segments: Alterations in Large Chromosome Segments (but Smaller than a Chromosome Arm) 23
Table S4. SNP6_CNnoLOHinfo_segments: Alterations in Small Chromosomal Segments 26
Table S5: Microsatellite Analysis of 16p 27
Table S6 : Whole Genome Sequence Samples 28
Table S7 : List of Small Somatic Variants Identified by Whole Genome Sequencing. 29
Table S8 : List of Genes Impacted by a Junction, Related to a Somatic Structural Variant. 37
Table S9 : Exome Variants Server (EVS) Allelic Frequencies of the *ARMC5* Variants Identified in the ACTH-Independent Macronodular Adrenal Hyperplasia Patients. 40
Table S10: List of Genes with a HIGH Expression in *ARMC5*-Mutated Compared with *ARMC5* Wild-Type ACTH-Independent Macronodular Adrenal Hyperplasia 41
Table S11: List of Genes with a LOW Expression in *ARMC5*-Mutated Compared with *ARMC5* Wild-Type ACTH-Independent Macronodular Adrenal Hyperplasia 798

SUPPLEMENTARY METHODS

1. SNP Array Analysis

The aim was to identify the chromosomal alterations (gains, losses and copy-neutral loss-of-heterozygosity) occurring in adrenal nodules of patients with ACTH-independent macronodular adrenal hyperplasia.

SNP Array Experiments

500 ng of genomic DNA from adrenal nodules and leucocytes were hybridized to Affymetrix SNP6 chips according to the manufacturer recommendations at the Genomic Platform of the Cochin Institute (Paris, France). The chips were scanned with the Affymetrix GeneChip Scanner 3000 and the Affymetrix GeneChip Command Console Scan Controle 3.2.3.1515. The raw data and normalized data can be downloaded at the Gene Expression Omnibus website (www.ncbi.nlm.nih.gov/geo) under the GSE42171 accession number.

Generation of a Normalized aAnd Filtered B-Allele Frequency from Affymetrix SNP6

The genotype of each SNP is the combination of two alleles, arbitrarily called A and B. A SNP genotype can either be provided as a discrete value (genotypes "AA", "AB" or "BB"), or as a quantitative value called the B-allele frequency (BAF). The B-allele frequency is the proportion of the B allele in a given genotype, with a value measured around 0 for SNPs AA, around 1 for SNPs BB, and around 0.5 for heterozygous SNPs AB. The quantitative genotypes provided by the B-allele frequency are important for the sensitive detection of chromosomal regions with loss-of-heterozygosity in tumors[19].

B-allele frequencies were generated for each SNP with the allele-specific intensities ("signal A" and "signal B" from the Affymetrix Genotyping Console 4.0) and the discrete genotypes ("AA", "AB" or "BB") provided by the Affymetrix Genotyping Console 4.0 (Birdseed V2). For that aim, the genotype of each SNP was expressed in Cartesian coordinates from its signal A and its signal B, and then transformed into polar coordinates θ using the arctangent function (as shown in Figure S1, in the "Signal transformation" box of the "i. Calling LOH" panel). The "Signal transformation" box (Fig. S1) shows one SNP, each dot corresponding to the SNP genotype measured in one of our samples (adrenal nodules and leucocytes). For each SNP, the median centroid of each genotype in this Cartesian representation (black crosses named AA, AB and BB) and the origin of the plot define three reference directions, one for each genotype (θ_{AA}, θ_{AB} and θ_{BB}).

A noise reduction was then applied, to filter out the SNPs with the lowest ability to discriminate the different genotypes --this is important because SNPs within a somatic chromosomal alteration will show intermediate θ values, that are neither θ_{AA}, θ_{AB} nor θ_{BB}. For that aim, for any SNP with θ_{AB}- θ_{AA} lower than 0.45 radians, all the genotypes with θ lower than θ_{AB} were discarded, and for any SNP with a θ_{BB}- θ_{AB} lower than 0.45, all the genotypes with θ higher than θ_{AB} were discarded (approximately half of the genotypes were discarded).

Normalized B-allele frequencies were obtained by converting θ values to values between 0 and 1. For that aim, any genotype with θ lower than θ_{AA} was affected to 0, and any genotype with $\theta \geq \theta_{BB}$ was affected to 1. θ values between θ_{AA} and θ_{AB}, were transformed into values between 0 and 0.5 by linear interpolation. In a similar manner, θ values between θ_{AB} and θ_{BB}, were transformed into values between 0.5 and 1.

Detection of Somatic Chromosomal Alterations

Somatic loss-of-heterozygosity (LOH) and copy number (CN) alterations were identified using the SOMATICs method[19], following the general flow-chart presented in Figure S1. Briefly, two information were combined: the SNP genotypes, used for calling regions with loss-of-heterozygosity (see Fig. S1, "i. Calling LOH" panel), and the DNA copy number measured for each SNP, used for calling regions with copy-number alterations (see Fig. S1, "ii. Calling CN" panel).

Somatic loss-of-heterozygosity calls were based on the B-allele frequency (BAF), with detection of patterns of allelic imbalance. Indeed, when plotting the B-allele frequencies of heterozygous SNPs in chromosomal regions with allelic imbalance, the single band centered on 0.5 is replaced by two bands, as shown in the "Calling LOH segments" box and the "Filtering" box of the "i.Calling LOH" panel of Figure S1, and as described previously[19].

Copy number alteration calls (gains or losses) were based on the DNA copy number, quantified by the Log2Ratio.

Three detection algorithms were applied, depending on the size of the events to be detected:

a- For whole chromosome arms, patterns of allelic imbalance were automatically detected, easily confirmed visually on plots presenting the B-allele frequency of the SNPs along the genome. Losses were called when the mean Log2Ratio of the chromosome arm reached -0.1 or less. Gains were called when the mean Log2Ratio of the chromosome arm reached 0.1 or more. Otherwise, a copy-neutral loss-of-heterozygosity was called. The full set of altered chromosome arms is provided in the Table S2 ("SNP6_CNLOH_ChrArm") of this Supplementary appendix.

b- For large chromosome segments (but smaller than chromosome arms), allelic imbalance was first detected, based on the specific two-band pattern of allelic imbalance when plotting the B-allele frequencies along the genome (an example is provided in Fig. S1, in the "i. Calling LOH" panel, the "Calling LOH segments" box). These chromosome segments were then tested for potential copy number alterations. Calling a "loss" or a "gain" required a significant shift of the DNA copy number (an example is provided in the Fig. S1, in the "ii. Calling CN" panel, the "Calling CN segments" box), with a shift of the mean of Log2Ratios of at least 0.1, and with a t-test $p<0.05$ versus a normal chromosome. A copy-neutral loss-of-heterozygosity was called otherwise. To confirm the somatic origin of the alteration (and rule out a germline copy number variation), the chromosomal segment was tested in the corresponding leucocyte sample (when available), for the absence of allelic imbalance and of any significant shift in the DNA copy number. The full set of large chromosome segments with an alteration (somatic loss, gain or copy-neutral LOH) is provided in the Table S3 ("SNP6_CNLOH_segments") of this Supplementary appendix.

c- Small chromosome segments, were defined as those with insufficient informative SNPs (<10 heterozygous SNPs). For these segments, the allelic imbalance patterns detection could not be applied, and copy number alterations calls were based only on DNA copy number. For that aim, segments were first defined using a smoothed DNA copy-number value called the "CNState" (Affymetrix Genotyping Console V4.0). Any stretch of consecutive markers with a CNState differing from 2 copies of DNA was considered. Because this detection is far too sensitive, more stringent filters were then applied: the shift of the Log2Ratio had to reach a t-test $p<1e-10$ versus a normal chromosome, with no significant shift in the log2ratio for the same segment in the corresponding leucocyte DNA. When no matched leucocyte sample was available, a mean Log2ratio between 0.1 and 0.3 (for losses), and 0.1 and 0.2 (for gains) was requested. These values correspond to the mean Log2Ratios of large segments and chromosome arms with a somatic loss or a gain in our dataset. The full set of small chromosome segments with an alteration (somatic loss, gain or copy-neutral LOH) is provided in the Table S4 ("SNP6_CNnoLOHinfo_segments") of this Supplementary appendix.

Bioinformatics

These analyses were performed using R 2.15.0 and custom scripts derived from the SOMATICs method[19]. These scripts can be provided on request.

2. Microsatellite Analysis

Loss-of-heterozygosity on chromosome 16p was tested using 10 microsatellite markers (D16S521, D16S3024, D16S3134, D16S3082, D16S475, D16S3065, D16S3027, D16S423, D16S3135 and D16S3108). Primer sequences and PCR conditions were those provided by the National Center for Biotechnology Information (NCBI) *uniSTS* (STS stands for Sequence Tagged Sites) website (www.ncbi.nlm.nih.gov/unists). Fluorescent-labeled primers were used (Sigma-Aldrich Proligo, Saint Quentin Fallavier, France). Polymerase Chain Reactions (PCR) were performed using the Taq Gold (Applied Biosystems, Courtaboeuf, France). PCR products were migrated on a Beckman Ceq™ 8800 sequencer (Beckman Coulter, Fullerton, CA). Allelic peak heights were read with the Beckman Genetic Analysis System version 8.0 software. For each marker, the allelic ratios were determined in the leucocyte and in the adrenal nodules. A normalized ratio was obtained by dividing the allelic ratios of the leucocyte and of the adrenal nodule. Loss-of-heterozygosity was called for normalized ratios <0,6 or >1,66.

3. Whole Genome Sequencing

Five ACTH-independent macronodular adrenal hyperplasia nodules and their paired leucocyte were sequenced by Complete Genomics[20], starting from 10 µg of genomic DNA. The samples were processed through the Cancer Sequencing Service pipeline version 2.0.2.26, which includes an increased sequencing depth for the tumor samples, and a paired analysis with the matched leucocytes. Two types of variants called by Complete Genomics for each tumor were used for subsequent analysis, following the general flow-chart presented in Figure S2 of this Supplementary Appendix:

- the small variations (the "masterVar" file provided by Complete Genomics): this matrix reports all the SNPs, small deletions, insertions and more complex variations including only a few bases compared to the reference genome (NCBI built 37.2). Several filters were applied (Fig. S2), including the quality of the calls, the impact on proteins (variations that impact the protein only, including non-synonymous variations within the coding sequence, and splice-sites variations), and the compartment (somatic).
- the structural variants (the "somaticHighConfidenceJunctions" file provided by Complete Genomics): this file reports all the large deletions, inversions, translocations and other more complex structural variants called at the somatic level (in comparison to the germline sample). Only the junctions occurring within genes were considered. In addition, any junction that had already been identified in the 69 reference genomes sequenced with the same technique

(http://www.completegenomics.com/public-data/69-Genomes/) were discarded, because of the high probability of false positive call.

4. Sanger Sequencing of *ARMC5*

ARMC5 coding and flanking intronic sequences were amplified by PCR from tumor and leukocyte DNA. The following primers and conditions were used.

Exons	Amplicon	Primers sequence: forward (above), reverse (below)	annealing temperature	PCR product size
Exon 1	Amplicon 1a	GATTCTCCCTCGCCTCTTCT	60	491
		GAGCTTCTCACGCCTACCTC		
Exon 1	Amplicon 1b	GTCGGACTTCTGGGCTGTTC	60	456
		CTCAGGGGTGTCTCGTTGGT		
Exon 1	Amplicon 1c	TTTCCCTGTCTTCCAGTTCC	56	655
		ACGTTATTCCGGGATAGGAC		
Exon 2	Amplicon 2	AGGGGTAGAACCCTCACAAG	60	204
		CACTCAAGCCTTTCTTCTGC		
Exon 3	Amplicon 3a	GTAAGAGGCTGTGAGGTTGG	58	507
		TCATCTACCAGCACCTCCAC		
Exon 3	Amplicon 3b	GATCCTCGCCAACCTGTGT	60	500
		CACTGCTCACCCTCCCAAG		
Exon 4	Amplicon 4a	TTGGCTCTGGGTTCAGTCTC	64	629
		GAGTGGGAAGGTGAGGTTCT		
Exon 4	Amplicon 4b	GGCCTGCTGACCTATGTGAC	60	669
		CAGAAGGGCTCCTTGGTCTA		
Exon 5	Amplicon 5	GTCTCACTCACCCCACCTGT	60	441
		ACAGTGGGAGACACCAGGTC		
Exon 6	Amplicon 6a	ACACCCGCTCTTCCTCTTCT	60	481
		CTCTTCCAGCTCCTCCTCCA		
Exon 6	Amplicon 6b	CTGCTGGCCGTTTCCTACTG	60	632
		GAACAAGACCCTGCTTGGTG		

5. Microarray Experiments and Analyses

Each tumor was snap frozen immediately after surgery and kept in liquid nitrogen until use. RNA extraction was performed as previously described[21] from 10 ACTH-independent macronodular adrenal hyperplasia tumor samples. Microarray experiments were performed as previously described, using Affymetrix U133 Plus 2.0 chips[21]. The full dataset can be found at Array Express (http://www.ebi.ac.uk/arrayexpress, experiment E-TABM-311). The accession numbers are CIT-HS-ACT-EC-AIMAH1, CIT-HS-ACT-EC-AIMAH5, CIT-HS-ACT-EC-AIMAH9, CIT-HS-ACT-EC-

AIMAH10, CIT-HS-ACT-EC-AIMAH11, CIT-HS-ACT-EC-AIMAH27, CIT-HS-ACT-EC-AIMAH74, CIT-HS-ACT-EC-AIMAH75, CIT-HS-ACT-EC-AIMAH76, and CIT-HS-ACT-EC-AIMAH77, corresponding to the samples H1, H5, H9,H10, H11, H27, H74, H75, H76 and H77 respectively.

All the transcriptome analyses were carried out using "R" (www.r-project.org). The transcriptome data was normalized using the Robust Multi-array Analysis (RMA) method (Affy package, www.bioconductor.org). Unsupervised hierarchical clustering was generated with the "hclust" function, using the "Euclidean" metrics and the "Ward" method, considering the top 1871 genes with the highest variation among the nodules of adrenal hyperplasia (coefficient of variation 0.2 or higher). The Linear Models for Microarray Data (LIMMA) test was used for the supervised group comparison of *ARMC5* mutated versus *ARMC5* non-mutated ACTH-independent macronodular adrenal hyperplasia (LIMMA R package, www.bioconductor.org). Multiple testing was corrected with the Benjamini-Hodgeberg false discovery rate assessment for all tests. The functional annotation of the differentially expressed gene (selected as those with an adjusted p-value <0.1) was performed with the Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7 (http://david.abcc.ncifcrf.gov/), using Gene Ontology annotations (http://www.geneontology.org/).

6. siRNA Experiments: siRNA Sequences

The following sequences were used:

siRNA		sequence
ARMC5	siARMC5-1	GACAGACAGCATCCAGAAC
	siARMC5-2	CTTAGCCATGGAACCTGAG
	siARMC5-3	GGATGAATTGGCTGTGAAG
	siARMC5-4	CCATTCTGATCCTCGCCAA
Control	siCtr	GCGAGCAACCGAACCTAAA

7. Reverse Transcription Quantitavite Polymerase Chain Reaction (RT-qPCR) Experiments: Primer Sequences

The following sequences were used:

Gene		Primers	annealing temperature	PCR product size
ARMC5	Forward	CTCGGAGGCATACTCCCTTT	60	68
	Reverse	GTTCGGTTCTGGATGCTGTC		
NR5A1	Forward	AGCAGAAGAAGGCACAGATTCG	60	110
	Reverse	CTGGGAGGCAGCACGTAGTC		
NR0B1	Forward	CAAATGCTGGAGTCTGAACATCA	60	116
	Reverse	ACTGGAGTCCCTGAATGTACTTCAC		
MC2R	Forward	GCCCAGAAAGTTCCTGCTTCAG	64	157
	Reverse	TCTCCTGCTTGTGGTTAAGGCG		
CYP17A1	Forward	GCCCCATCTATTCGGTTCGTA	60	169
	Reverse	GAGTCAGCGAAGGCGATACCC		
CYP21A2	Forward	CCTTCGGAGACAAGATCAAGGA	60	109
	Reverse	TCACGTCCACAATTTGGATGG		
CYP11A1	Forward	TGTATGAGATGGCACGCAACC	58	227
	Reverse	CAGTGTCTTGGCAGGAATCAT		

8. Western Blot Experiment: Antibodies

The following antibodies were used:

Antibodies			
Antibodies	dilution		reference
	Western-blot	IHC	
anti-GAPDH	1/2500		SC-25778 (Santa Cruz)
anti-Cleaved LAMIN A/C	1/1000		2032S (Cell Signalling)
anti-β-ACTIN	1/2500		A-2066 (Sigma-Aldrich)
anti-cleaved-caspase3		1/200	D9661 (cell signalling)
anti-ARMC5	1/1000	1/25	Abnova PAB23822
anti-Flag M2		1/200	F-1804 (Sigma-Aldrich)
anti-CYP11A1		1/750	sc-18040 (Santa Cruz)
peroxydase-conjugated anti-rabbit	1/5000		7074S (cell signalling)
peroxidase-conjugated anti-mouse	1/5000		SC-2005 (Santa Cruz)
alexia fluor 488 goat anti-rabbit		1/400	A11008 (Life technology)
alexia fluor 568 goat anti-mouse		1/400	A11004 (Life technology)

9. Immunohistochemistry

Immunohistochemistry was performed on serial sections of the same tissues. Sections were deparaffinized in xylene and rehydrated through 100% ethanol. For antigen unmasking, the slides were incubated in citrate buffer pH6 for 40 min at 99° C. Endogenous peroxidases were inhibited by incubation in 3% hydrogen peroxide (Sigma-Aldrich, St. Louis, MO) in water for 5 min. Primary antibodies against ARMC5(1:25) and CYP11A1(1:750) were incubated overnight at 4 C. Bond Polymer Refine Detection (ref DS9800 - Ménarini-Leica) was used for antigen detection. Sections were washed; incubated 10 min with Post Primary IgG linker reagent localizes mouse antibodies. Than with Poly-HRP IgG reagent localizes rabbit antibodies for 10 min. The slides were developed using diaminobenzidin and counterstained with hematoxilin (Sigma) and blue in saturated Lithium carbonate for 20 seconds.

10. Fluorescence Immunostaining

Culture cells were fixed in chilled methanol/acetone solution (vol/vol) for 10 min followed by 5 min permeabilization with 0.2% Triton™ X-100 (Sigma, MO, USA). Blocking was performed at room temperature for 30 min with 10% horse serum. Samples were incubated in primary antibodies , cleaved caspase 3 Ab (1/200), Flag Ab (1/200) ON at°C and secondary antibodies , Alexia fluor 568 goat anti mouse (1/400, Life thecnology), alexia fluor 488 goat anti rabbit (1/400, Lifetechnonoly) for 1h at room temperature. Every time after incubation with antibody, the samples were washed three times with phosphate buffered saline. The nuclei were stained with DAPI and after mounting with Fluoromount G™ (DAKO), images were taken with a fluorescence microscope (BX-41; Olympus, Japan).

Figure S1: Flowchart of the SNP Chips (Affymetrix SNP6) Data Analysis

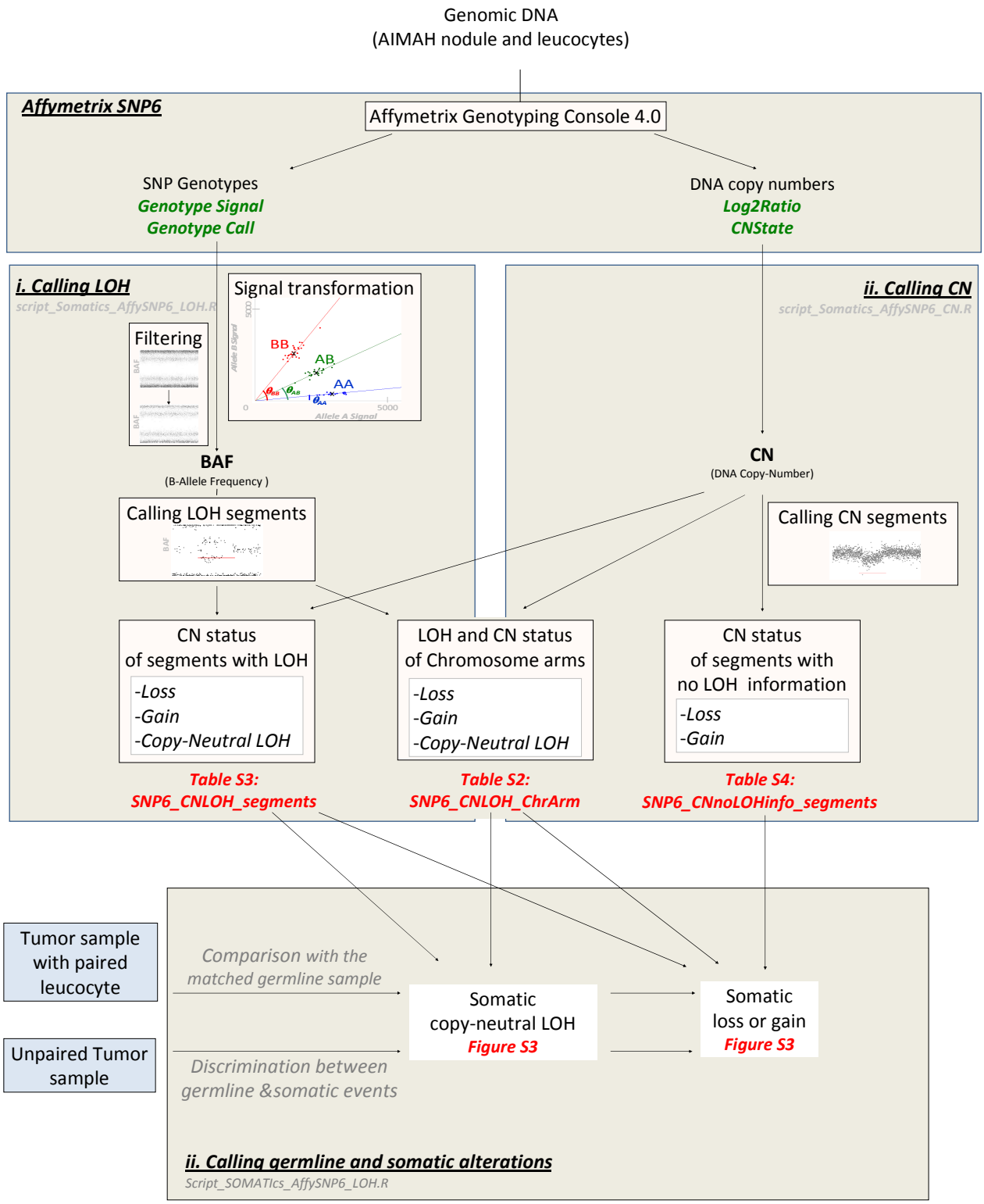
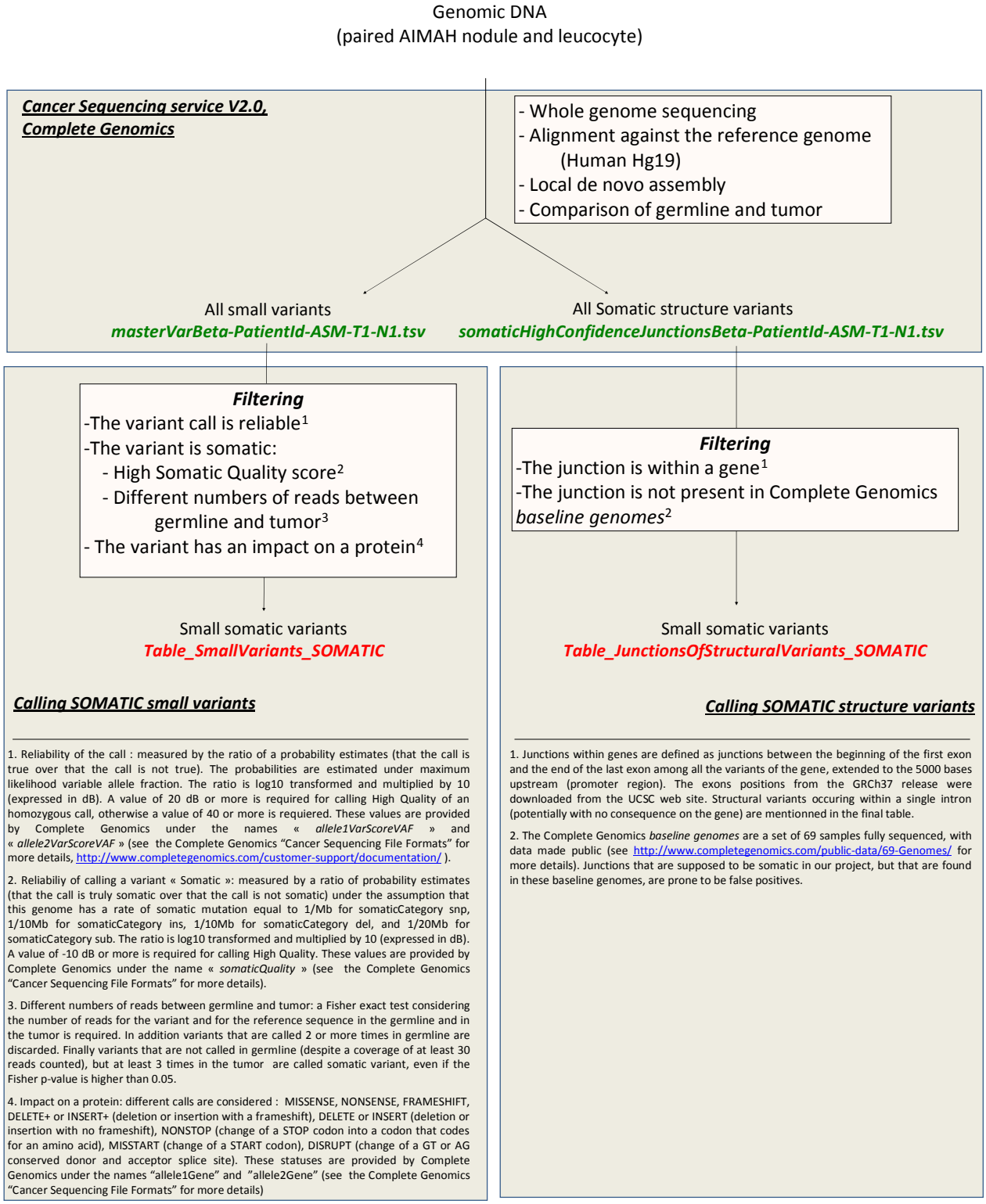


Figure S2: Flowchart of the Whole Genome (Complete Genomics) Data Analysis



1. Reliability of the call : measured by the ratio of a probability estimates (that the call is true over that the call is not true). The probabilities are estimated under maximum likelihood variable allele fraction. The ratio is log10 transformed and multiplied by 10 (expressed in dB). A value of 20 dB or more is required for calling High Quality of an homozygous call, otherwise a value of 40 or more is requiered. These values are provided by Complete Genomics under the names « *allele1VarScoreVAF* » and « *allele2VarScoreVAF* » (see the Complete Genomics "Cancer Sequencing File Formats" for more details, http://www.completegenomics.com/customer-support/documentation/).

2. Reliabiliy of calling a variant « Somatic »: measured by a ratio of probability estimates (that the call is truly somatic over that the call is not somatic) under the assumption that this genome has a rate of somatic mutation equal to 1/Mb for somaticCategory snp, 1/10Mb for somaticCategory ins, 1/10Mb for somaticCategory del, and 1/20Mb for somaticCategory sub. The ratio is log10 transformed and multiplied by 10 (expressed in dB). A value of -10 dB or more is required for calling High Quality. These values are provided by Complete Genomics under the name « *somaticQuality* » (see the Complete Genomics "Cancer Sequencing File Formats" for more details).

3. Different numbers of reads between germline and tumor: a Fisher exact test considering the number of reads for the variant and for the reference sequence in the germline and in the tumor is required. In addition variants that are called 2 or more times in germline are discarded. Finally variants that are not called in germline (despite a coverage of at least 30 reads counted), but at least 3 times in the tumor are called somatic variant, even if the Fisher p-value is higher than 0.05.

4. Impact on a protein: different calls are considered : MISSENSE, NONSENSE, FRAMESHIFT, DELETE+ or INSERT+ (deletion or insertion with a frameshift), DELETE or INSERT (deletion or insertion with no frameshift), NONSTOP (change of a STOP codon into a codon that codes for an amino acid), MISSTART (change of a START codon), DISRUPT (change of a GT or AG conserved donor and acceptor splice site). These statuses are provided by Complete Genomics under the names "allele1Gene" and "allele2Gene" (see the Complete Genomics "Cancer Sequencing File Formats" for more details)

1. Junctions within genes are defined as junctions between the beginning of the first exon and the end of the last exon among all the variants of the gene, extended to the 5000 bases upstream (promoter region). The exons positions from the GRCh37 release were downloaded from the UCSC web site. Structural variants occuring within a single intron (potentially with no consequence on the gene) are mentionned in the final table.

2. The Complete Genomics *baseline genomes* are a set of 69 samples fully sequenced, with data made public (see http://www.completegenomics.com/public-data/69-Genomes/ for more details). Junctions that are supposed to be somatic in our project, but that are found in these baseline genomes, are prone to be false positives.

Figure S3: Chromosomal Alterations in ACTH-Independent Macronodular Adrenal Hyperplasia Nodules Identified with SNP Arrays

Panel A shows the chromosomal gains (pink), losses (blue) and copy-neutral loss-of-heterozygosity (yellow) along the genome in each ACTH-independent macronodular adrenal hyperplasia nodule. For some patients (1,17, 6 and 44), several nodules were included. Chromosomal losses in 1p, and 18q, gains in 1q and copy-neutral loss-of-heterozygosity in 16p are the most frequent events. Panel B shows for each region of the genome the number of patients having a chromosomal alteration in at least one of their ACTH-independent macronodular adrenal hyperplasia nodules. The most common event is the copy-neutral loss-of-heterozygosity in 16p, found in seven of 26 patients. Panels C to L show the chromosome 16 of the ACTH-independent macronodular adrenal hyperplasia nodules with a copy-neutral loss-of-heterozygosity in 16p. The upper part of each panel shows the genotypes of the SNPs expressed as the proportion of minor allele B in the genotype (B-allele frequency or BAF): SNPs of genotype "AA", "BB" and "AB" have a BAF of 0, 1 and 0.5, respectively. In the yellow regions (16p), the normal band of heterozygous SNPs "AB" has been lost, and has been replaced by two bands with BAF values in the 0 to 0.5 and 0.5 to 1 intervals, corresponding to loss-of-heterozygosity (LOH) events. The lower part of each panel shows the DNA copy-number along the chromosome 16, expressed in log-scale (logR), with the red line corresponding to two copies of DNA. In the regions with loss-of-heterozygosity, the DNA copy number is not altered (two copies remain), showing that the loss-of-heterozygosity is copy-neutral.

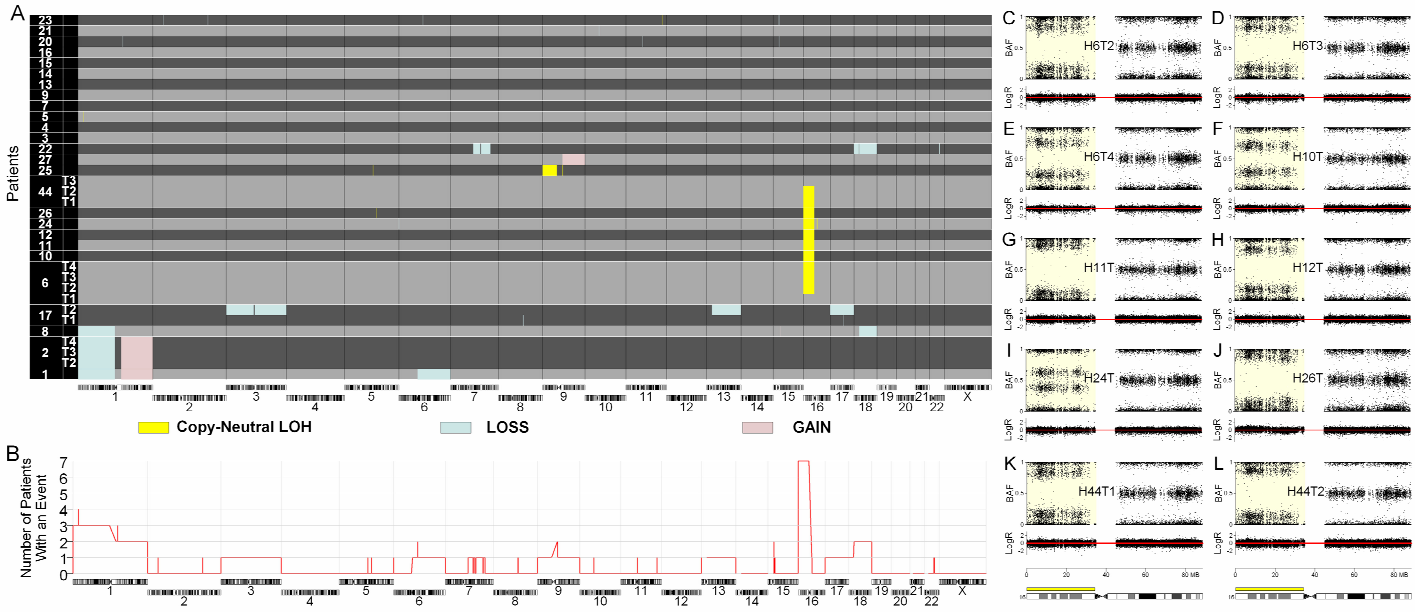


Figure S4: Location of the *ARMC5* Mutations

The sites in the ARMC5 protein of the various genetic alterations found on the tumor DNA are shown.

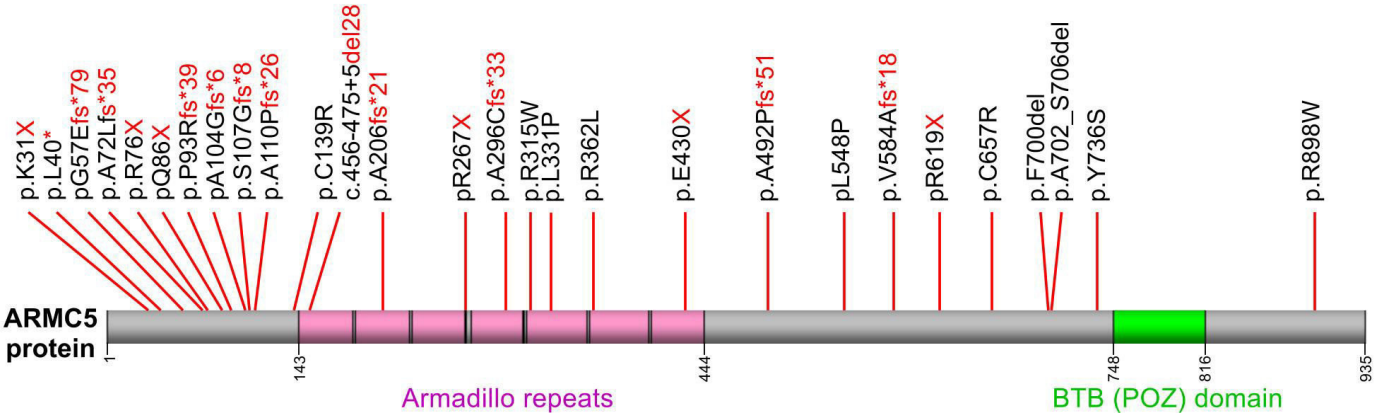


Figure S5: Germline Microdeletion in a Patient Including the *ARMC5* Locus

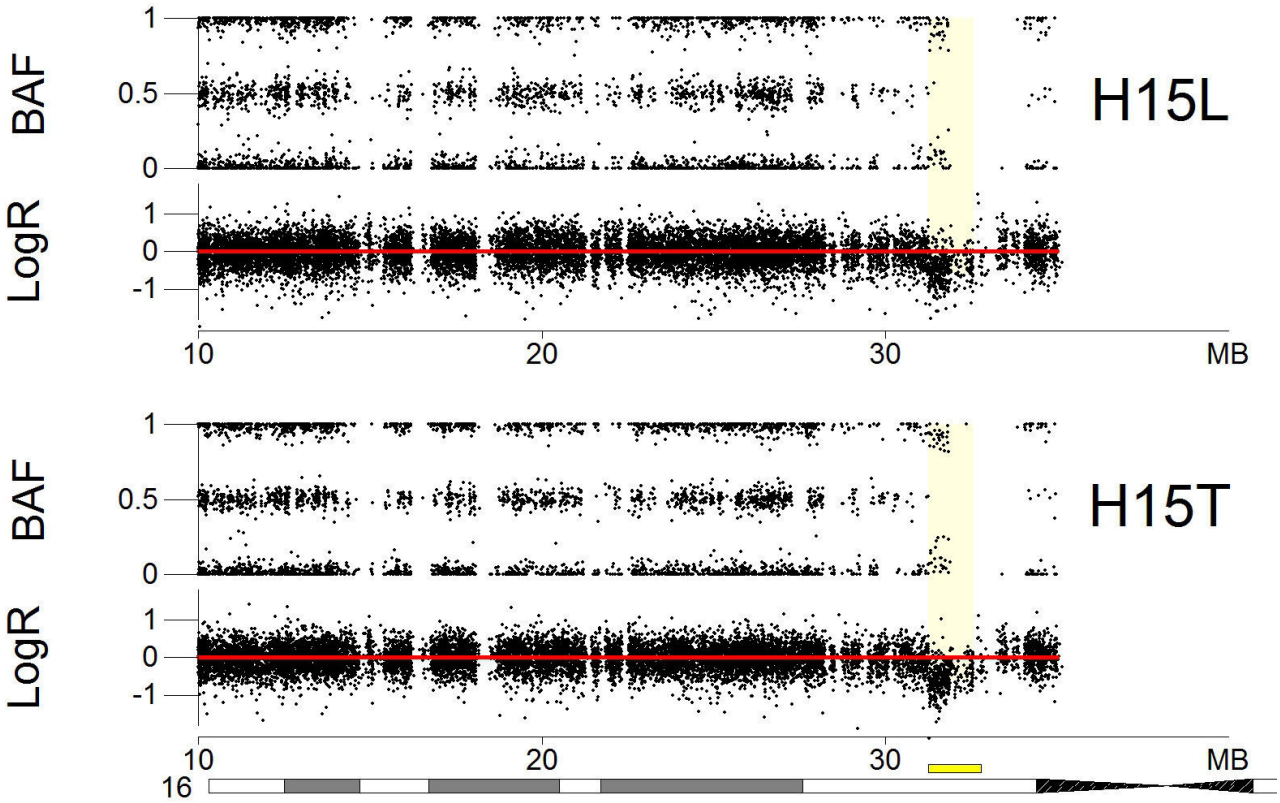


Figure S6: the *ARMC5* Mutations are Present on two Different Alleles

For two tumors H7T and H25T, the two mutations were close enough to belong to the same amplicon. In order to determined if the mutations were present on the two different alleles, PCR products were cloned in the pGEM-T-Easy vector (Promega) and transformed in DH5 bacteria (Life Technologies). Ten clones were sequenced for each tumor, showing that the two mutations were present on two different alleles.

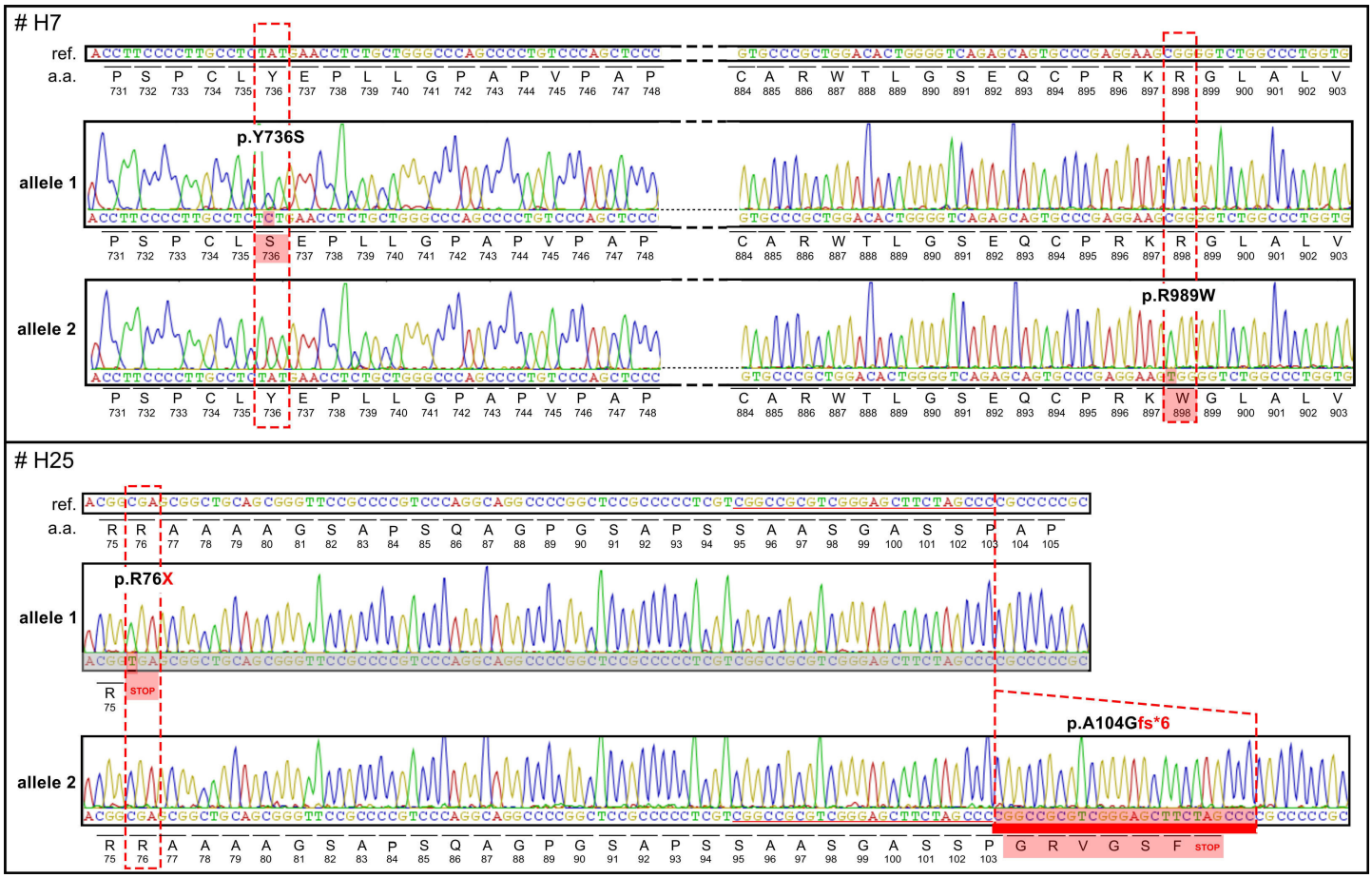


Figure S7: Sequencing *ARMC5* in Inter-Nodular Regions

The coding and flanking intronic sequences of *ARMC5* were sequenced in inter-nodular regions of 4 different AIMH from patient with *ARMC5* mutation.

Only the germline mutation was found. No somatic second hit could be identified, and the heterozygous status of each mutant indicates the abscence of loss-of-heterozygosity as a second event.

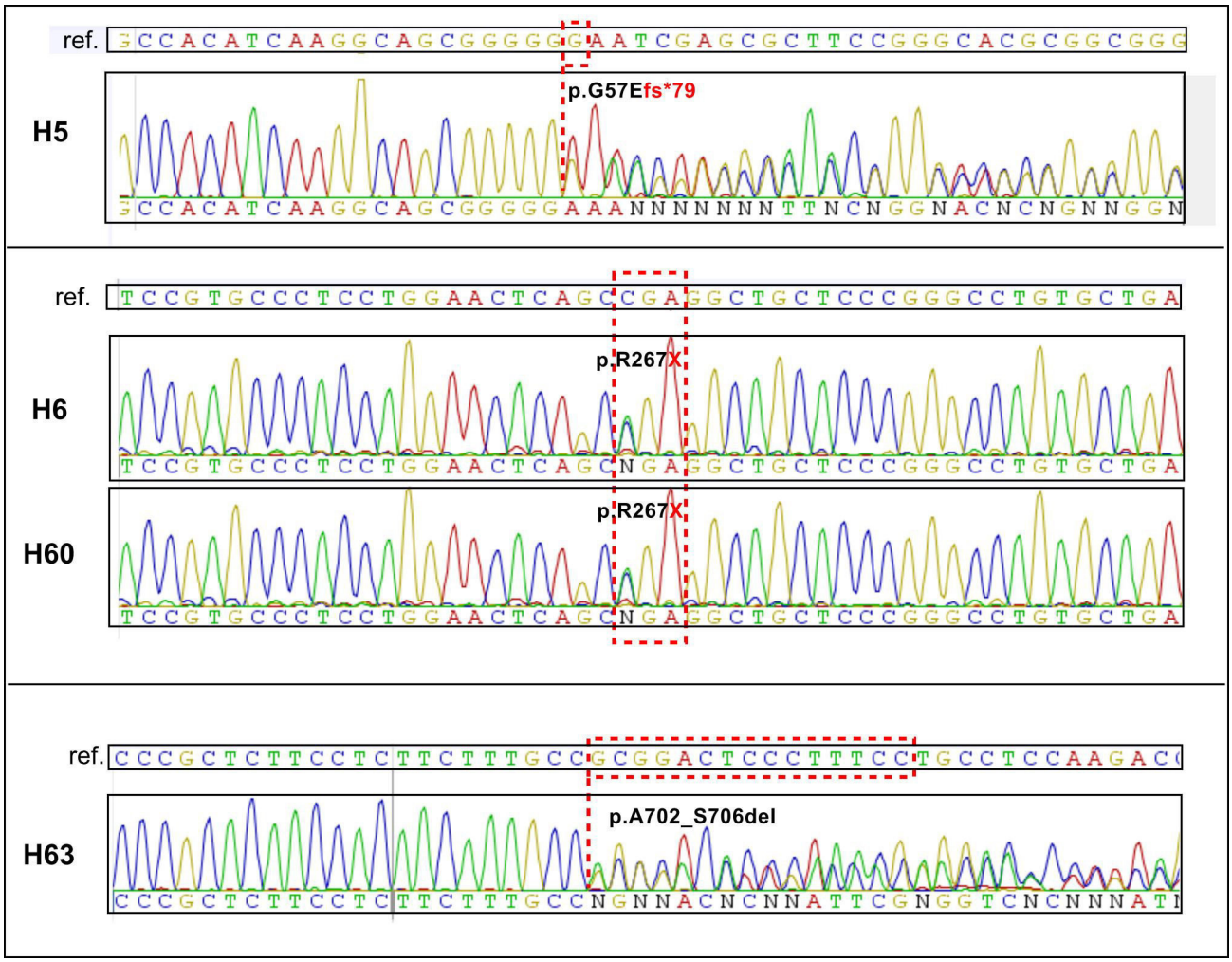


Figure S8: Unsupervised Hierarchical Clustering of the ACTH-Independent Macronodular Adrenal Hyperplasia Transcriptome

Unsupervised hierarchical clustering of the ACTH-independent macronodular adrenal hyperplasia transcriptome (performed blind to the *ARMC5* mutation status). The patients are separated into two groups, with *ARMC5* mutations (M) in one, and the wild type (WT) *ARMC5* in the other.

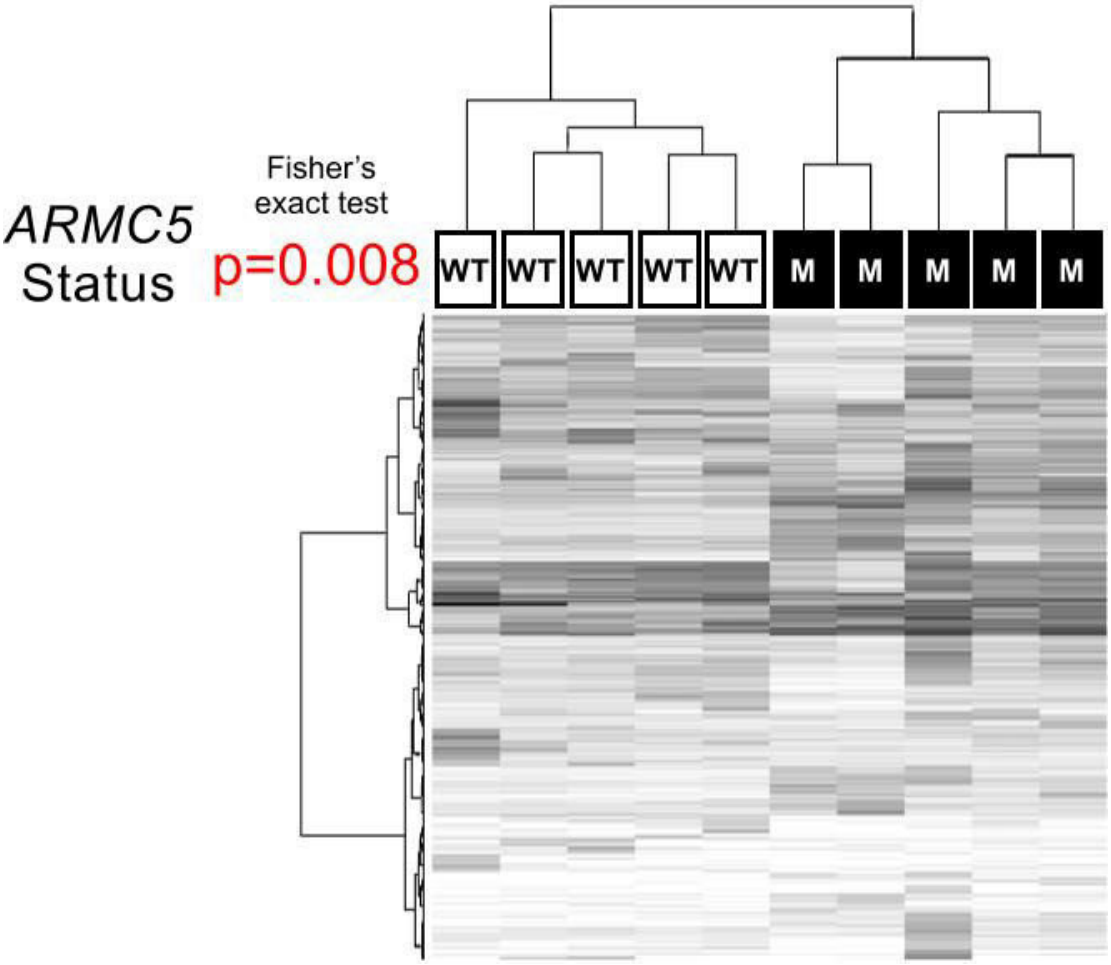


Figure S9: Immunohistochemistry of ARMC5

Panel A: Immunohistochemistry of ARMC5 (middle panel) and CYP11A1 (right panel) proteins, shows expression a membranous and cytoplasmic expression of ARMC5 and CYP11A1 in the normal adrenal cortex and in an ACTH-independent macronodular adrenal hyperplasia nodule with no *ARMC5* mutation, contrasting with a decreased expression of ARMC5 and CYP11A1 in an ACTH-independent macronodular adrenal hyperplasia nodule with a germline *ARMC5* nonsense mutation. Panel B : Immunocytochemistry of ARMC5 in H295R and Hela cell lines shows a membranous and cytoplasmic expression. Panel C: The expression of CYP11A1 is decreased at the mRNA level after *ARMC5* inactivation by siRNA in the adrenocortical H295R cells .

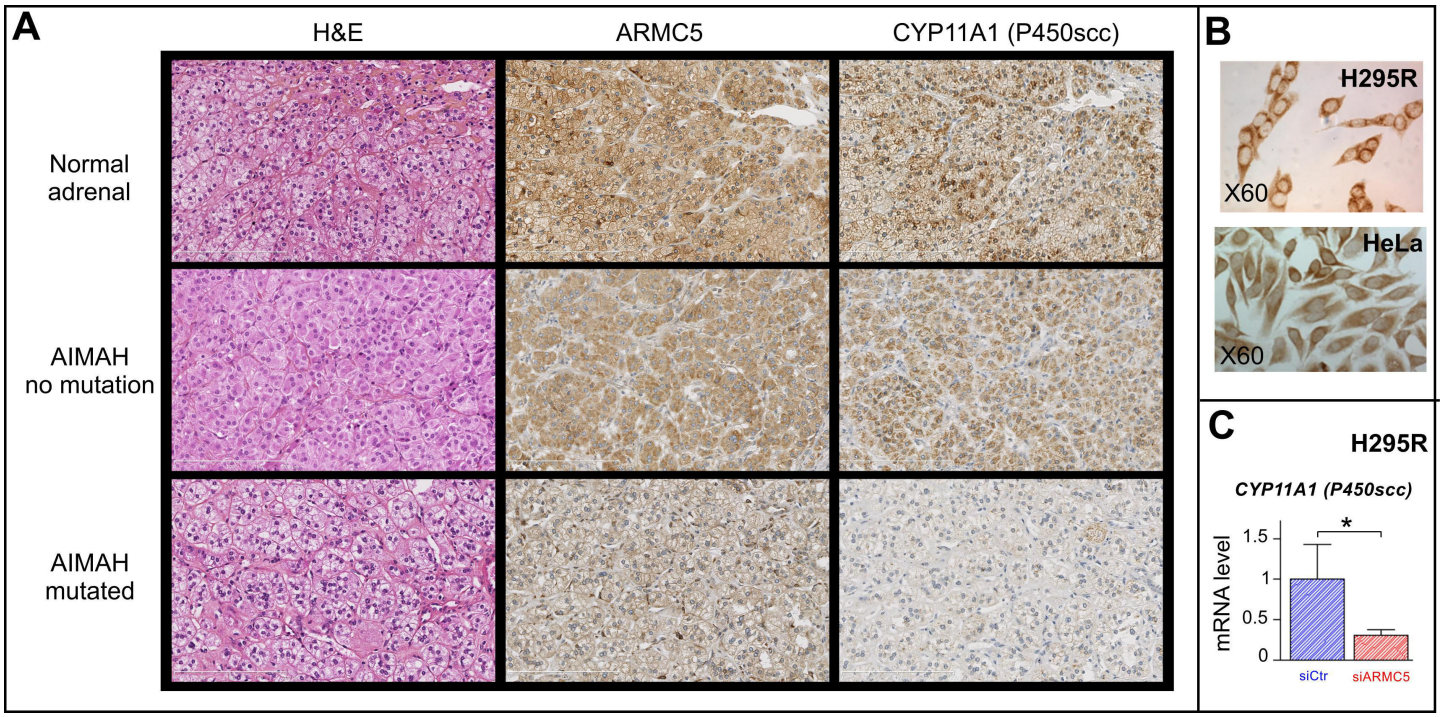


Figure S10: Expression of ARMC5 in HeLa Cells

Immunofluorescence staining of transfected HeLa cells with different flagged ARMC5 constructs [a wild-type and two missense mutants : p.R898W and p.L548P]. Red staining corresponds to the Flag antibodies (targeting the ARMC5 constructs), green staining to the cleaved-caspase3 antibodies (detection of apoptosis), and blue staining to dapi (detection of cells nuclei). After 6 hrs the cells expressing the ARMC5 construct (both the wild type and the mutants) have a normal morphology. After 14 hrs, the cells expressing the wild type ARMC5 construct (indicated by the white arrows) are apoptotic, as suggested by the co-expression of the cleaved-caspase 3, and by the altered cell morphology with condensed nuclei. By contrast, the cells expressing the missense ARMC5 constructs (p.R898W and p.L548P) do not co-express cleaved-caspase, nor present any altered morphology.

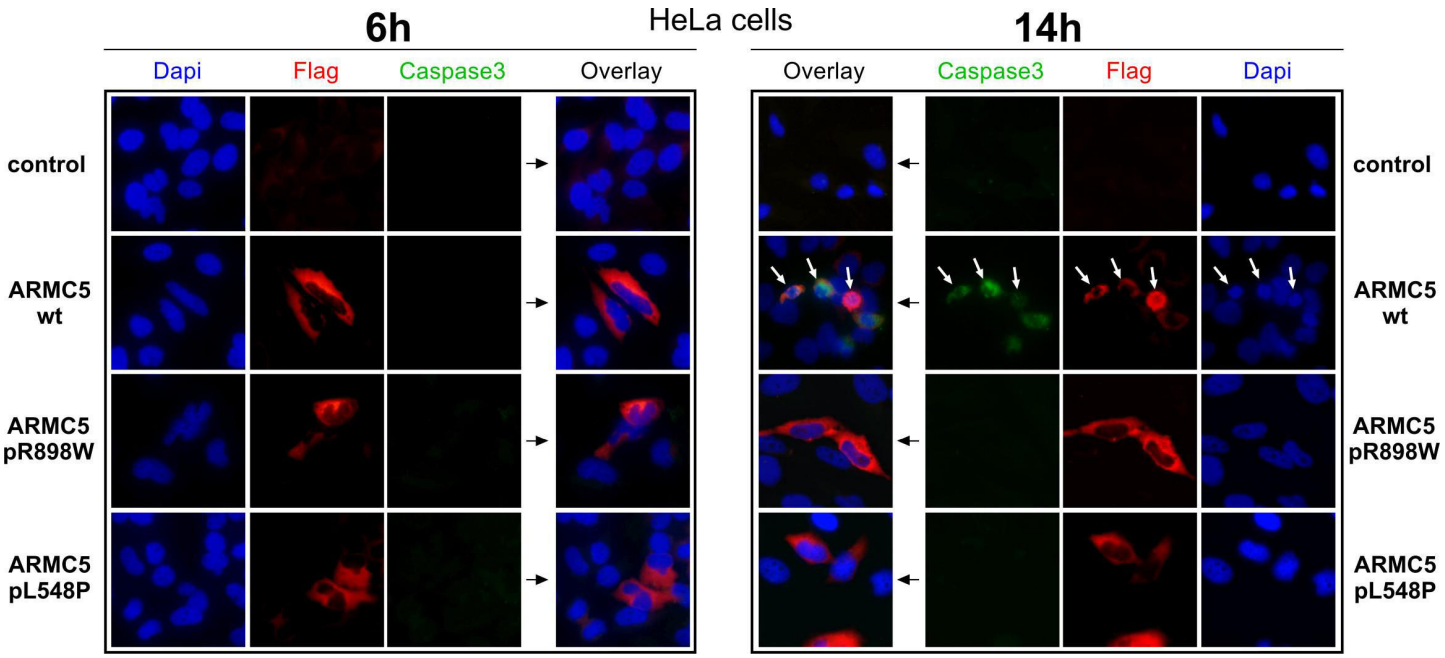


Figure S11: Decreased Apoptosis Associated with *ARMC5* Mutations

Western blot of H295R cells tranfected with the empty control vector, wild type ARMC5 and the two ARMC5 mutants pR898W and pL548P. The expression of the wild type ARMC5 increased the cleaved-PARP and cleaved-Lamin A/C levels, suggesting induction of apoptosis, while the mutants did not.

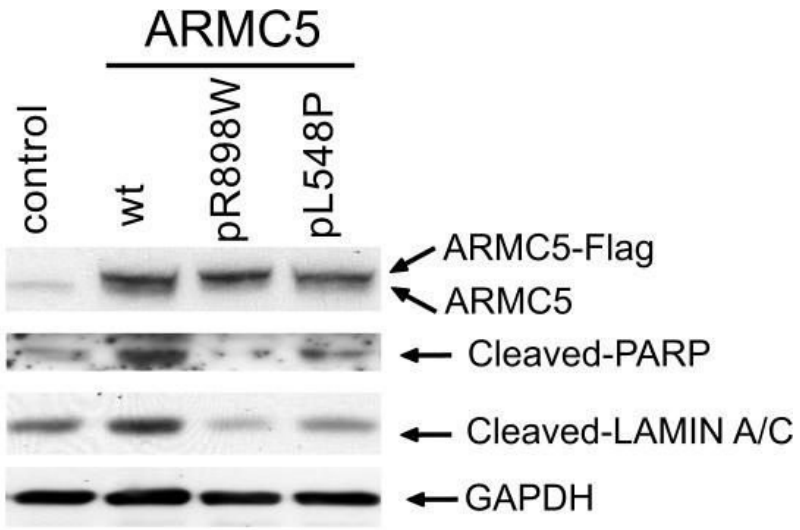


Table S1: Patients Characteristics

This table includes the clinical data of Table 1 with more detailed endocrine characteristics, including the illegitimate responses, the mineralocorticoid and the androgene profiles of each patient.

*** p<0.05**
 # quantitative variables are expressed as mean and 95% confidence interval; qualitative variables are expressed as numbers of patients
¶ CC: clinical Cushing's syndrome; SubC C: subclinical Cushing's syndrome
~ NA: not available
§ comparison was performed only in female patients
& 4 values of renin and aldosterone were removed because of interfering treatments
Cells in red: abnormal value

	Patient	Sex	Age (yr)	Glucorticoid function						Adrenal Weight~ (g)			Illegitimate Response~				Mineralocorticoid function		Androgens and precursors				
				ACTH (pg/ml)	Cortisol (µg/dl)	Cortisol after Corticotropin stimulation (µg/dl)	Plasma Cortisol / DXM 1mg~ (µg/dl)	Urinary Cortisol£ (µg/24 hrs)	Clinical Cushing¶	Right	Left	Total	Upright posture	Food	GnRH	Metoclo-pramide	aldosterone (pmol/l)	renin (µU/L)	17OHP (nmol/l)	17OHP after Corticotropin stimulation(nmol/l)	DHEA-S (µmol/l)	testosteone (nmol/l)	androstene-dione (nmol/l)
ARMC5-mutated	H10	F	34	<5	15,8	59,2	23,6	373	CC	40	26	66	Yes	No	No	Yes	332	9	0,4	7,5	1,7	7,3	2,4
	H11	F	41	<5	NA	NA	NA	NA	CC	30	94	124	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	H12	M	64	6	NA	NA	27,2	866	CC	39	118	157	Yes	No	NA	NA	205	70,2	0,9	NA	0,5	1,4	2,4
	H14	F	40	<5	NA	NA	18	233	CC	NA	NA	NA	NA	NA	NA	NA	NA	NA	3,0	NA	3,0	1,0	6,6
	H44	F	30	<5	16,3	57,4	26,1	458	CC	52	67	119	No	No	No	No	219	12,6	3,0	9,0	0,5	1,7	7,3
	H5	F	48	<5	21,1	49,9	27,4	118	CC	34	50	84	Yes	No	No	No	526	1120	1,5	21,2	0,8	1,7	4,2
	H60	F	51	<10	26,5	58,3	22,4	248	CC	45	64	109	NA	NA	NA	NA	235	16,2	1,2	30,3	0,5	1,7	1,7
	H63	M	45	<10	34,0	81,3	36,7	1463	CC	48	71	119	Yes	No	No	No	64	72	1,8	29,7	0,8	2,1	1,7
	H6	F	70	<5	14,4	46,4	16	122	CC	21	60	81	Yes	No	No	Yes	58	7,2	21,8	25,8	0,5	0,3	2,8
	H7	M	41	<5	NA	NA	29	394	CC	65	121	186	NA	NA	NA	NA	127	12,6	NA	NA	1,6	11,1	2,4
	H9	M	46	<5	NA	NA	18	204	CC	34	46	80	NA	NA	NA	NA	83	5,58	1,5	NA	6,5	5,2	1,5
	H24	M	55	<5	13,2	40,8	3,6	135	SubC C	42	30	72	No	No	No	No	704	19,8	2,7	22,8	0,3	5,9	5,9
	H20	M	63	8	NA	NA	22,9	302	CC	35	50	85	Yes	No	No	No	596	1,8	NA	NA	NA	NA	NA
	H21	M	53	<5	27,2	76,0	25,1	293	CC	65	77	142	Yes	No	No	Yes	512	28,8	4,2	41,8	0,5	24,6	3,1
	H23	M	56	<5	NA	NA	NA	107	CC	56	110	166	Yes	No	No	NA	NA	NA	2,7	NA	NA	NA	NA
	H61	M	51	<5	NA	NA	NA	NA	CC	NA	NA	NA	Yes	No	No	No	NA	NA	NA	NA	NA	NA	NA
	H15	F	52	<5	NA	NA	8,9	37	SubC C	24	29	53	NA	NA	NA	NA	720	14,4	NA	NA	NA	NA	NA
	H25	F	73	<5	NA	NA	15	NA	SubC C	21	34	55	Yes	No	No	No	NA	NA	NA	NA	NA	NA	NA
	Total#	F: 9 M: 9	51 [27-74]	6 [<5-9]	21 [6 to 36]	59 [31 to 87]	21,3 [4.7-38.0]	357 [0-1089]	CC: 15 SubC C: 3	41 [13-69]	65* [3-128]	106* [25-188]	Yes: 10* No: 2	Yes: 0 No: 12	Yes: 0 No: 11	Yes: 3 No: 7	225& [0 to 628]	25& [0 to 78]	5§ [0 to 22]	24 [1 to 46	1§ [0 to 3]	2§ [0 to 7]	4§ [0 to 9]
ARMC5-wild-type	**Total#**	F:12 M:3	52 [31-74]	8 [<5-18]	13 [0 to 30]	47 [0 to 112]	14,6 [0-32.5]	362 [0-1466]	CC: 11 SubC C: 3	27 [0-75]	38 [0-88]	55 [0-144]	Yes: 3 No: 6	Yes: 3 No: 6	Yes: 1 No: 7	Yes: 3 No: 5	116 [0 to 309]	10 [0 to 24]	3 [0 to 8]	42 [0 to 185]	3 [0 to 13]	2 [0 to 4]	6 [0 to 14]
reference values				10 to 60	10 to 21	>21	<1.8	<90									55 to 360	9 to 72	M: 4.5 to 8.5 F: 0.9 to 9.4		M: 4.0 to 13.5 F: 1.0 to 7.3	M: 6.6 to 34.5 F: 0.17 to 1.7	M: 2.8 to 7.4 F: 0.7 to 4.9

Table S2. SNP6_CNLOH_ChrArm: Alterations in Chromosome Arms

Chromosome gains, losses and copy-neutral loss-of-heterozygosity (LOH) are provided at the chromosome arm level.

[1]. Mean of the B-allele frequency of the heterozygous SNPs in the region with loss-of-heterozygosity. Values between 0.5 and 1 are transformed to fit the 0 to 0.5 interval by the formula 1-BAF.

[2]. Number of SNPs detected as heterozygous by Somatics.

[3]. The p-value is generated by a two-sided Student T-test comparing the Log2Ratio of the markers in the segment with loss-of-heterozygosity and the Log2Ratio of the markers in the reference (e.g. unaltered) chromosome from the same sample. In this study, the chromosome 2 was chosen for all tumors as the reference chromosome.

Sample	Chromosome	Arm	Start_Marker	End_Marker	Start_posGRCh36	End_posGRCh36	Start_posGRCh37	End_posGRCh37	BAF of heterozygous SNPs[1]	Number of heterozygous SNPs[2]	Log2Ratio	Number of markers	Log2Ratio p-value vs reference chromosome[3]	Status of the chromosome arm
H1T	1	p	CN_473963	CN_003665	51586	121184490	61723	121482967	0.22	10890	-0.33	73285	0	LOSS
H2T2	1	p	CN_473963	CN_003665	51586	121184490	61723	121482967	0.20	10070	-0.41	73285	0	LOSS
H2T3	1	p	CN_473963	CN_003665	51586	121184490	61723	121482967	0.20	9505	-0.39	73285	0	LOSS
H2T4	1	p	CN_473963	CN_003665	51586	121184490	61723	121482967	0.21	8800	-0.39	73285	0	LOSS
H8T	1	p	CN_473963	CN_003665	51586	121184490	61723	121482967	0.22	10251	-0.39	73285	0	LOSS
H1T	1	q	SNP_A-8682618	CN_479920	142693888	247190999	144007037	249224376	0.35	7615	0.21	68063	0	GAIN
H2T2	1	q	SNP_A-8682618	CN_479920	142693888	247190999	144007037	249224376	0.36	6401	0.27	68063	0	GAIN
H2T3	1	q	SNP_A-8682618	CN_479920	142693888	247190999	144007037	249224376	0.36	6234	0.25	68063	0	GAIN
H2T4	1	q	SNP_A-8682618	CN_479920	142693888	247190999	144007037	249224376	0.36	6570	0.26	68063	0	GAIN
H17T2	3	p	CN_1037129	CN_1027289	35333	90568640	60333	90485950	0.40	7369	-0.14	60562	0	LOSS
H17T2	3	q	CN_254643	CN_243384	95002156	199380402	93519466	197896106	0.40	6967	-0.14	63394	0	LOSS
H1T	6	q	CN_1182727	CN_1175224	61944387	170824447	61886428	171050993	0.32	10180	-0.21	70117	0	LOSS
H25T	9	p	SNP_A-8451753	CN_1320237	36587	47006984	46431	47217164	0.27	2553	-0.01	31202	6.37E-02	CNLOH
H27T	9	q	SNP_A-8360464	CN_1306207	65336138	140211203	65616959	141091382	0.41	3921	0.15	47904	0	GAIN
H17T2	13	q	SNP_A-8712632	CN_638458	17943628	114126487	19045720	115108385	0.39	7795	-0.14	64071	0	LOSS
H6T2	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.16	1588	-0.02	20506	3.10E-03	CNLOH
H10T	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.28	2271	-0.03	20506	5.93E-12	CNLOH
H11T	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.12	2125	-0.03	20506	5.52E-06	CNLOH
H12T	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.17	1759	-0.03	20506	7.41E-04	CNLOH
H6T3	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.17	1620	-0.01	20506	1.66E-02	CNLOH
H6T4	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.23	1689	-0.02	20506	1.84E-04	CNLOH
H24T	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.36	1972	-0.03	20506	6.12E-20	CNLOH
H26T	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.14	1785	0.11	20506	0	CNLOH
H44T1	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.16	1879	-0.01	20506	9.40E-01	CNLOH
H44T2	16	p	CN_724789	CN_713390	765	35140715	60765	35283214	0.13	2549	-0.03	20506	8.28E-06	CNLOH
H17T2	17	p	CN_758857	SNP_A-8387602	514	22159777	514	22235650	0.41	1326	-0.13	12854	3.41E-304	LOSS
H17T2	17	q	CN_734553	SNP_A-8656409	22294526	78643088	25270399	81049726	0.40	3309	-0.14	32034	0	LOSS
H22T	18	p	SNP_A-8496414	CN_738309	1543	15391751	11543	15401751	0.31	1339	-0.28	10329	0	LOSS
H8T	18	q	CN_738353	SNP_A-8448011	16795645	76116029	18541647	78015057	0.24	7157	-0.36	40132	0	LOSS
H22T	18	q	CN_738353	SNP_A-8448011	16795645	76116029	18541647	78015057	0.30	5255	-0.28	40132	0	LOSS

Table S3: SNP6_CNLOH_segments: Alterations in Large Chromosome Segments (but Smaller than a Chromosome Arm)

Chromosome alterations (gains, losses and copy-neutral loss-of-heterozygosity) are provided at the level of chromosome segments smaller than a chromosome arm. These alterations are identified by a loss-of-heterozygosity, with or without copy number alteration.

[1]. Mean of the B-allele frequency of the heterozygous SNPs in the region with loss-of-heterozygosity. Values between 0.5 and 1 are transformed to fit the 0 to 0.5 interval by the formula 1-BAF.

[2]. Number of SNPs detected as heterozygous by Somatics.

[3]. The p-value is generated by a two-sided Student T-test comparing the Log2Ratio of the markers in the segment with loss-of-heterozygosity and the Log2Ratio of the markers in the reference (e.g. unaltered) chromosome from the same sample. In this study, the chromosome 2 was chosen for all tumors as the reference chromosome.

[4]. The CopyNumber State (CN_State) is the mean of DNA copy number estimates at each marker provided by Affymetrix Genotyping Console

[5]. The same segment is measured in the germline sample paired with the tumor (when available), to ensure that the alteration is not present in germline.

Sample	Chromosome	Start_Marker	End_Marker	Start_posGRCh36	End_posGRCh36	Start_posGRCh37	End_posGRCh37	BAF of heterozygous SNPs[1]	Number of heterozygous SNPs[2]	Log2Ratio	Number of markers	Log2Ratio p-value vs reference chromosome[3]	Status CopyNumber State[4]	Log2Ratio Mean Germline[5]	Log2Ratio p-value in Germline_vs reference chromosome[3,5]	Status CNState in Germline[4,5]	Gene Symbols	RefSeq	Paired_Leucocyte	CN_Status	Compartment
H5T	1	SNP_A-2105728	SNP_A-2113650	17620614	18036509	17748027	18163922	0.36	12	-0.01	233	9.95 E-01	2				rcc2 arhgef10l arhgef10l actl8	nm_018715 nm_018125 nm_001011722 nm_030812	NO	CNLOH	SOMATIC
H23T	2	SNP_A-2224136	SNP_A-8488069	181766773	181847753	28439	182139420	0.36	8	-0.12	60	1.91 E-02	2						NO	LOSS	SOMATIC
H25T	5	SNP_A-2138253	SNP_A-4254661	95043287	95182213	95017531	95156457	0.34	10	-0.02	94	5.91 E-01	2				spata9 rhobtb3 glrx	nm_031952 nm_014899 nm_002064	NO	CNLOH	SOMATIC
H26T	5	SNP_A-8468011	SNP_A-4278463	107306669	107344762	107278770	107316863	0.40	9	-0.07	34	2.82 E-01	2				fbxl17	nm_022824	NO	CNLOH	SOMATIC
H1T	6	SNP_A-8667015	SNP_A-8688252	102117705	102804623	102011012	102697930	0.18	51	-0.23	412	6.63 E-28	1.79	0.00	0.58	2	grik2	nm_021956 nm_175768	YES	LOSS	SOMATIC
H1T	6	SNP_A-2254158	SNP_A-2069063	111721479	112606760	111614786	112500067	0.19	60	-0.25	560	1.51 E-40	1.68	-0.02	0.73	2	rev3l traf3ip2 fyn fyn wisp3 wisp3 wisp3 tube1 loc619208 lama4	nm_002912 nm_147200 nm_147686 nm_153047 nm_002037 nm_153048 nm_003880 nm_198239 nm_130396 nm_016262 nm_001033564 nm_001105206 nm_001105207 nm_002290	YES	LOSS	SOMATIC
H22T	7	SNP_A-4196039	SNP_A-2177485	75124953	92091908	75287017	92253972	0.32	1242	-0.26	10556	0	1.4991 5				hip1 ccl26 ccl24 rhbdd2 por tmem120a styxl1 mdh2 flj37078 hspb1 ywhag srcrb4d zp3 dtx2 dtx2 upk3b pomzp3 kiaa1505 fgl2 loc54103 ptpn12 rsbn1l tmem60 phtf2 magi2 gnai1 gnat3 cd36 cd36 sema3c hgf hgf hgf cacna2d1 pclo pclo sema3e sema3a sema3d grm3 kiaa1324l dmtf1 c7orf23 crot abcb4 abcb1 rundc3b slc25a40 dbf4 adam22 sri steap4 znf804b mgc26647 steap1 steap2 steap2 steap2 flj21062 gtpbp10 cldn12 pftk1 fzd1 mterf akap9 cyp51a1 krit1 ankib1 gatad1 pex1 dkfzp564o0523 fam133b cdk6	nm_005338 nm_006072 nm_002991 nm_001040456 nm_001040457 nm_000941 nm_031925 nm_016086 nm_005918 nm_001039212 nm_001540 nm_012479 nm_080744 nm_007155 nm_001102594 nm_001102595 nm_020892 nm_001102596 nm_030570 nm_182684 nm_012230 nm_152992 nm_020879 nm_006682 nm_017439 nm_002835 nm_198467 nm_032936 nm_020432 nm_012301 nm_002069 nm_001102386 nm_001001547 nm_000072 nm_001001548 nm_006379 nm_000601 nm_001010932 nm_001010931 nm_001010933 nm_001010934 nm_000722 nm_033026 nm_014510 nm_012431 nm_006080 nm_152754 nm_000840 nm_152748 nm_021145 nm_024315 nm_021151 nm_000443 nm_018849 nm_018850 nm_000927 nm_138290 nm_018843 nm_006716 nm_004194 nm_021721 nm_016351 nm_021722 nm_021723 nm_003130 nm_198901 nm_024636 nm_181646 nm_152706 nm_012449 nm_152999 nm_001040665 nm_001040666 nm_001039706 nm_001042717 nm_033107 nm_012129 nm_012395 nm_003505 nm_006980 nm_147166 nm_005751 nm_147171 nm_147185 nm_000786 nm_004912 nm_001013406 nm_194454 nm_194455 nm_194456 nm_019004 nm_021167 nm_000466 nm_032120 nm_001040057 nm_152789 nm_001259	NO	LOSS	SOMATIC
H22T	7	SNP_A-1990585	SNP_A-8601241	92662815	97312277	92824879	97474341	0.32	324	-0.26	2879	0	1.5915 2				loc253012 ccdc132 calcr tfpi2 gngt1 gng11 bet1 col1a2 casd1 sgce peg10 ppp1r9a pon1 pon3 pon2 asb4 pdk4 dync1i1 slc25a13 shfm1 dlx6 dlx5 acn9 tac1	nm_198151 nm_001039372 nm_024553 nm_017667 nm_001742 nm_006528 nm_021955 nm_004126 nm_005868 nm_000089 nm_022900 nm_001099400 nm_001099401 nm_003919 nm_001040152 nm_015068 nm_017650 nm_000446 nm_000940 nm_000305 nm_001018161 nm_145872 nm_016116 nm_002612 nm_004411 nm_014251 nm_006304 nm_005222 nm_005221 nm_020186 nm_003182 nm_013996 nm_013997 nm_013998	NO	LOSS	SOMATIC

H22T	7	SNP_A-8612101	SNP_A-2298460	101016140	124860589	101229420	125073353	0.32	1559	-0.27	14230	0	1.50267				mylc2pl cutl1 cutl1 cutl1 sh2b2 prkrip1 orai2 alkbh4 dkfzp434k1815 polr2j polr2j3 mgc119295 rasa4 polr2j2 fbxl13 lrrc17 lrrc17 armc10 nape-pld pmpcb zrf1 psmc2 slc26a5 slc26a5 reln orc5l orc5l lhfpl3 mll5 srpk2 pus7 rint1 atxn7l1 flj23834 sypl1 pbef1 flj36031 pik3cg prkar2b hbp1 cog5 gpr22 dus4l bcap29 slc26a4 cbll1 slc26a3 dld lamb1 lamb4 nrcam pnpla8 thap5 dnajb9 loc154907 immp2l lrrn3 dock4 znf277p ifrd1 ifrd1 c7orf53 tmem168 flj31818 gpr85 ppp1r3a foxp2 mdfic tfec tes tes cav2 cav1 met capza2 st7 wnt2 asz1 cftr cttnbp2 lsm8 ankrd7 kcnd2 tspan12 ing3 flj21986 wnt16 wnt16 fam3c loc392979 ptprz1 aass fezf1 cadps2 rnf133 rnf148 tas2r16 slc13a1 iqub ndufa5 asb15 lmod2 wasl hyal4 spam1 loc392982 gpr37 pot1	nm_138403 nm_001913 nm_181500 nm_181552 nm_020979 nm_024653 nm_032831 nm_017621 nm_152892 nm_006234 nm_001097615 nm_001031618 nm_001079877 nm_006989 nm_032959 nm_145032 nm_005824 nm_001031692 nm_031905 nm_198990 nm_004279 nm_014377 nm_002803 nm_206883 nm_206884 nm_206885 nm_198999 nm_005045 nm_173054 nm_002553 nm_181747 nm_199000 nm_018682 nm_182931 nm_182691 nm_182692 nm_019042 nm_021930 nm_152749 nm_152750 nm_182715 nm_006754 nm_005746 nm_175884 nm_002649 nm_002736 nm_012257 nm_006348 nm_181733 nm_005295 nm_181581 nm_001008405 nm_018844 nm_001008406 nm_001008407 nm_000441 nm_024814 nm_000111 nm_000108 nm_002291 nm_007356 nm_001037133 nm_001037132 nm_005010 nm_015723 nm_182529 nm_012328 nm_001024607 nm_032549 nm_001099658 nm_001099660 nm_018334 nm_014705 nm_021994 nm_001007245 nm_001550 nm_182597 nm_022484 nm_152556 nm_018970 nm_002711 nm_014491 nm_148898 nm_148899 nm_199072 nm_001018058 nm_012252 nm_015641 nm_152829 nm_001233 nm_198212 nm_001753 nm_000245 nm_006136 nm_021908 nm_018412 nm_003391 nm_130768 nm_000492 nm_033427 nm_016200 nm_001077708 nm_019644 nm_012281 nm_012338 nm_198267 nm_019071 nm_024913 nm_016087 nm_057168 nm_001040020 nm_014888 nm_001085391 nm_002851 nm_005763 nm_001024613 nm_001009571 nm_017954 nm_139175 nm_198085 nm_016945 nm_022444 nm_178827 nm_005000 nm_080928 nm_207163 nm_003941 nm_012269 nm_153189 nm_003117 nm_001085395 nm_005302 nm_001042594 nm_015450	NO	LOSS	SOMATIC
H22T	7	SNP_A-2288985	SNP_A-1991309	125532152	131634215	125744916	131983675	0.32	421	-0.27	3666	0	1.39825				grm8 znf800 gcc1 arf5 fscn3 pax4 snd1 c7orf54 lrrc4 lep rbm28 impdh1 hig2 mettl2b fam137b fam137a calu opn1sw ccdc136 flnc atp6v1f irf5 irf5 irf5 tnpo3 tspan33 smo kiaa0828 fam40b nrf1 nrf1 ube2h zc3hc1 kiaa0265 flj14803 c7orf45 cpa2 cpa4 cpa5 cpa1 tsga14 mest mest mest copg2 tsga13 klf14 mkln1 podxl plxna4	nm_000845 nm_176814 nm_024523 nm_001662 nm_020369 nm_006193 nm_014390 nm_014411 nm_022143 nm_000230 nm_018077 nm_000883 nm_001102605 nm_183243 nm_001098786 nm_013332 nm_018396 nm_001012454 nm_032599 nm_001219 nm_001708 nm_022742 nm_001458 nm_004231 nm_002200 nm_001098628 nm_001098629 nm_001098630 nm_032643 nm_001098631 nm_001098627 nm_012470 nm_178562 nm_005631 nm_015328 nm_020704 nm_005011 nm_001040110 nm_003344 nm_182697 nm_016478 nm_014997 nm_032842 nm_145268 nm_001869 nm_016352 nm_080385 nm_001868 nm_018718 nm_177524 nm_177525 nm_002402 nm_012133 nm_052933 nm_138693 nm_013255 nm_001018111 nm_005397 nm_020911	NO	LOSS	SOMATIC
H17T1	8	SNP_A-2265313	SNP_A-8522256	81219894	82004083	81057339	81841528	0.20	18	-0.14	397	1.06E-10	1.85139	-0.03795	0.19614768	2	zbtb10 loc389672 znf704	nm_001105539 nm_023929 nm_001089588 nm_001033723	YES	LOSS	SOMATIC
H23T	11	SNP_A-8298100	SNP_A-8457851	120011981	120227667	120506771	120722457	0.31	8	-0.04	175	0.17866497	2				grik4	nm_014619	NO	CNLOH	SOMATIC
H24T	16	CN_717836	SNP_A-1828684	45021271	45559127	46463770	47001626	0.37	13	-0.08	205	0.00119437	2				shcbp1 vps35 orc6l mlck loc388272 gpt2 dnaja2	nm_024745 nm_018206 nm_014321 nm_182493 nm_001001436 nm_133443 nm_005880	NO	CNLOH	SOMATIC
H17T1	17	SNP_A-8500120	SNP_A-2191701	43923154	44118402	46568155	46763403	0.18	11	-0.19	88	3.13E-05	1.95455	-0.04575	0.42257326	2	hoxb1 hoxb2 hoxb3 hoxb4 hoxb5 hoxb6 hoxb7 hoxb8 hoxb9	nm_002144 nm_002145 nm_002146 nm_024015 nm_002147 nm_018952 nm_004502 nm_024016 nm_024017	YES	LOSS	SOMATIC
H22T	22	SNP_A-2031292	SNP_A-8536659	32263520	33699903	33933520	35369903	0.32	169	-0.24	1354	8.36E-145	1.42614				large	nm_004737 nm_133642	NO	LOSS	SOMATIC

Table S4: SNP6_CNnoLOHinfo_segments: Alterations in Small Chromosomal Segments

Chromosome alterations (gains and losses) are provided at the level of small chromosome segments (defined as showing less than 10 informative heterozygous SNPs). These alterations are identified by copy number alterations only (no loss-of-heterozygosity can be called).

[1,2,3,4,5]: See Supplemental Table 3 legend.

Sample	Chromosome	Start_Marker	End_Marker	Start_posGRCh36	End_posGRCh36	Start_posGRCh37	End_posGRCh37	BAF of heterozygous SNPs[1]	Number of heterozygous SNPs[2]	Log2Ratio	Number of markers	Log2Ratio p-value vs reference chromosome[3]	Status CopyNumber State[4]	Log2Ratio Mean Germline[5]	Log2Ratio p-value in Germline_vs reference chromosome[3,5]	Status CNState in Germline[4,5]	Gene Symbols	RefSeq	Paired_Leucocyte	CN_Status	Compartment
H20T	1	SNP_A-2078169	CN_441332	147306690	147456930	149040066	149190306		2	-0.36	74	8.77E-12	1						NO	LOSS	SOMATIC
H42T	1	SNP_A-2078169	CN_441332	147306690	147456930	149040066	149190306		1	-0.38	74	1.51E-12	1						NO	LOSS	SOMATIC
H23T	2	SNP_A-8320969	SNP_A-8462753	34552819	34594531	53271	34740787		0	-0.38	52	2.13E-13	1						NO	LOSS	SOMATIC
H23T	6	CN_1206812	CN_330453	79025772	79091892	78969053	79035173		1	-0.38	108	2.25E-24	1						NO	LOSS	SOMATIC
H24T	6	SNP_A-1816135	CN_1179771	182215	239825	237215	294825		3	-0.39	49	9.96E-11	1				dusp22	nm_020185	NO	LOSS	SOMATIC
H21T	10	CN_558701	CN_524337	46401289	46514638	46981283	47094632		6	-0.39	93	3.01E-13	1				gprin2 ppyr1	nm_014696 nm_005972	NO	LOSS	SOMATIC
H20T	11	CN_587570	CN_589649	55133062	55210140	55376486	55453564		2	-0.36	54	3.91E-11	1				or4c11 or4p4 or4s2 or4c6	nm_001004700 nm_001004124 nm_001004059 nm_001004704	NO	LOSS	SOMATIC
H43T	11	SNP_A-8602821	CN_574527	4924693	4930593	4968117	4974017		0	-0.77	25	5.75E-13	1	-0.19	2.49E-02	2	or51a4	nm_001005329	YES	LOSS	SOMATIC
H8T	15	SNP_A-2272623	CN_695993	22966261	23048398	25415168	25497305		5	0.36	59	1.40E-14	3	0.07	7.67E-02	2			YES	GAIN	SOMATIC
H20T	15	CN_117462	CN_680783	19852349	20232428	22350985	22681064		6	-0.38	101	9.16E-17	1				or4m2 or4n4 loc650137	nm_001004719 nm_001005241 nm_001080841	NO	LOSS	SOMATIC
H23T	15	CN_680690	CN_680783	19787121	20232428	22285757	22681064		8	-0.36	116	2.13E-21	1				or4m2 or4n4 loc650137	nm_001004719 nm_001005241 nm_001080841	NO	LOSS	SOMATIC

Table S5: Microsatellite Analysis of 16p

Short allele: peak height of the short allele (values are fluorescence intensities).

Long allele: peak height of the long allele (values are fluorescence intensities)

Ratio: normalized ratio, obtained by dividing the allelic ratios (short allele over long allele) of the leucocyte and the tumor. The normalized ratios >0.6 or <1.6 are highlighted in yellow.

MSI: incalculable (because of microsatellites instability)

NA: not available

HOMO: homozygous marker

The normalized ratios >0.6 or <1.6 are highlighted in yellow.

	S521			S3024			S3134			S3082			S475			S3065			S3027			S423			S3135			S3108		
	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio	Short allele	Long allele	Ratio
H57L	85889	53622	1	NA	NA	NA	NA	NA	NA	122672	90650	1.02	172033	-	HOMO	160385	1E+05	1.1	66896	61324	0.9	2E+05	-	HOMO	171037	2E+05	0.72	158426	-	HOMO
H57T	133185	82902		NA	NA		NA	NA		158334	1E+05		172647	-		163825	1E+05		1E+05	96821		2E+05	-		165839	1E+05		146924	-	
H58L	172605	2E+05	MSI	NA	NA	NA	NA	NA	NA	162303	1E+05	MSI	162649	93200	MSI	99086	1E+05	MSI	2E+05	2E+05	MSI	2E+05	169234	MSI	126982	-	MSI	157576	-	MSI
H58T	74519	46310		NA	NA		NA	NA		159214	2E+05		167294	2E+05		157204	2E+05		1E+05	1E+05		1E+05	76369		156123	1E+05		166028	2E+05	
H59L	163202	-	HOMO	NA	NA	NA	2807	2483	1.04	171742	63177	1.19	59461	45054	0.98	144206	1E+05	1	29519	14646	1.2	69719	-	HOMO	88936	2E+05	1.04	154963	1E+05	1.22
H59T	5808	-		NA	NA		4044	3719		167774	73728		117868	87793		14599	10957		26811	15379		76754	-		92212	2E+05		168159	1E+05	
H60L	88385	61367	2	NA	NA	NA	NA	NA	NA	83711	45060	1.99	47893	19907	0.43	62734	44446	1.5	25622	14710	0.5	2E+05	-	HOMO	131991	-	HOMO	156956	-	HOMO
H60T	19738	27369		NA	NA		NA	NA		89119	95642		43997	7941		128779	1E+05		76565	19884		2E+05	-		149155	-		153904	-	
H62L	117347	80763	1	2238	2037	0.9	21666	-	HOMO	122335	-	HOMO	22570	19585	0.96	146756	1E+05	1	25033	17473	0.9	2E+05	145066	0.73	60518	19019	0.88	132145	96411	0.98
H62T	60833	42048		1518	1481		8394	-		88464	-		32049	26664		41545	29653		45301	27276		48487	32440		41946	11622		146555	1E+05	
H63L	141710	96878	0.88	NA	NA	NA	1E+05	1E+05	0.95	48909	41057	1.06	148817	1E+05	0.91	115297	86819	1	23952	19371	1	1E+05	53006	1.18	105431	64409	0.99	99623	74169	1.04
H63T	144307	86877		NA	NA		81998	77070		48782	43241		59466	40384		138068	1E+05		48438	37132		1E+05	54993		91826	55545		39206	30298	

Table S6 : Whole Genome Sequence Samples

[1]. Values about the coverage were directly extracted from the Complete Genomics "summary-*sample*-ASM-T1.tsv" file, with no filtering.

[2]. The total variation counts were mainly extracted from the Complete Genomics "summary-*sample*-ASM-T1" file, with no filtering. The "number of structural variants within genes" was counted from the Complete Genomics "somaticHighConfidenceJunctionsBeta-PatientId-ASM-T1-N1.tsv" file, filtering the junctions that fall into the genes loci, including the 5000 bases upstream.

[3]. The somatic variation counts were performed after extracting all the variants of high somatic quality as defined by Complete Genomics (tag "SQHIGH"). These variants were directly extracted from the "masterVarBeta-PatientId-ASM-T1-N1.tsv" file. No extra filtering was applied for these counts.

		Coverage[1]								Total variation[2]												Somatic variation[3]										
Sample	Gender	Genome coverage - Fully called genome fraction	Genome coverage - Fully called exome fraction	Genome coverage - Genome fraction where weightSumSequenceCoverage >= 5x	Exome coverage - Genome fraction where weightSumSequenceCoverage >= 5x	Genome coverage - Genome fraction where weightSumSequenceCoverage >= 20x	Exome coverage - Genome fraction where weightSumSequenceCoverage >= 20x	Genome coverage - Genome fraction where weightSumSequenceCoverage >= 40x	Exome coverage - Genome fraction where weightSumSequenceCoverage >= 40x	Genome variations -Small variations total count (high confidence)	Genome variations - SNP total count (high confidence)	Genome variations - SNP novel fraction (high confidence)	Exome variations - SNP total count (high confidence)	Genome variations - INS total count (high confidence)	Exome variations - INS total count (high confidence)	Genome variations - DEL total count (high confidence)	Exome variations - DEL total count (high confidence)	Genome variations - SUB total count (high confidence)	Exome variations - SUB total count (high confidence)	Structural variants - Total junction count (high confidence)	Structural variants - Total junction count within genes (high confidence)	Genome variations -Small variations total count (high confidence)	Genome variations - SNP total count (high confidence)	Exome variations - SNP total count (high confidence)	Genome variations - INS total count (high confidence)	Exome variations - INS total count (high confidence)	Genome variations - DEL total count (high confidence)	Exome variations - DEL total count (high confidence)	Genome variations - SUB total count (high confidence)	Exome variations - SUB total count (high confidence)	Structural variants - Total junction count (high confidence)	Structural variants - Total junction count within genes (high confidence)
H2L	FEMALE	0.974	0.985	0.996	0.998	0.987	0.988	0.954	0.951	16168780	3462025	0.036	21925	272879	319	289597	233	90026	397	1995	750											
H2T	FEMALE	0.976	0.987	0.996	0.998	0.985	0.989	0.948	0.953	15478568	3461775	0.036	21505	267348	299	287317	250	89872	388	1947	724	3192	2461	27	458	0	215	0	58	1	39	12
H7L	MALE	0.975	0.989	0.995	0.998	0.976	0.991	0.911	0.962	15649872	3450005	0.037	21895	242964	332	257481	265	86909	372	1832	669											
H7T	MALE	0.976	0.989	0.995	0.998	0.977	0.991	0.919	0.962	15423067	3453667	0.038	21891	245523	321	259906	264	87527	381	1873	691	3012	2407	31	335	4	211	2	59	0	28	15
H10L	FEMALE	0.973	0.988	0.995	0.998	0.976	0.990	0.918	0.957	18153427	4247323	0.078	26947	293241	353	319293	315	104842	460	2222	831											
H10T	FEMALE	0.972	0.988	0.994	0.998	0.973	0.990	0.908	0.955	18696548	4236738	0.077	26917	284686	344	309604	309	103055	455	2185	803	2715	2229	26	286	6	151	2	49	0	43	15
H11L	FEMALE	0.973	0.989	0.995	0.998	0.976	0.990	0.915	0.957	16928690	3715155	0.057	24004	262372	317	280080	268	93309	465	1962	755											
H11T	FEMALE	0.972	0.989	0.994	0.998	0.973	0.990	0.908	0.954	17318597	3700853	0.056	23913	258573	317	275872	278	92111	428	1954	741	2563	2004	29	338	9	175	2	46	1	38	21
H14L	FEMALE	0.977	0.988	0.996	0.998	0.987	0.990	0.959	0.960	14822190	3478088	0.037	21694	270602	300	291842	244	90743	391	2071	781											
H14T	FEMALE	0.971	0.985	0.996	0.998	0.984	0.988	0.936	0.946	17604110	3462031	0.037	21841	256965	356	268710	254	90385	475	1919	717	4464	3031	67	850	11	257	7	326	12	34	15

Table S7 : List of Small Somatic Variants Identified by Whole Genome Sequencing.

These variants include SNPs, Small eletions, insertions, and substitutions.

[1]. This column specificies the zygosity (heterozygous, haploid and half when one allele is not called), and the variation type (SNP, deletion, insertion, substitution).

[2]. One Polyphen (http://genetics.bwh.harvard.edu/pph2/, version 2.2.2) score is provided for each UniProt Id.

[3]. Sift prediction are provided for each locus (http://sift.jcvi.org/, version 1.0.3)

[4]. The VarScore VAF is provided by Complete Genomics, and reflects the probability that the call is true over the the probability that the call is false, assuming variable allele fractions estimated by a maximum likelihood (expressed in db)

[5]. The somaticScore is provided by Complete Genomics, and reflects the probability that the call is true over the the probability that the call is false, assuming fixed a priori probabilities of somatic mutations (SNP: 1/1Mb, insertion, deletion : 1/10Mb, substitution: 1/20Mb).

[6]. Exact Fisher test the p-values computed from the two alleles readcounts in the tumor and in germline.

[7]. These genomes are germline genomes provided by Complete Genomics.

Gene Symbol	RefSeq	Gene Name	Strand	Chromosome	Begin GRCh37	End GRCh37	Sample	VarClass[1]	Reference Allele	Variant Allele	Impact (Complete Genomics)	UniProt Id[2]	Amino Acid Change[2]	Polyphen Impact	Polyphen P[2]	SiftImpact[3]	SiftScore[3]	Variant Read Count Somatic	total Read Count Somatic	Variant Read Count Germline	total Read Count Germline	Variant VarScoreVAF[4]	Allele2VarScoreVAF[4]	somaticScore[5]	p.FisherTest ReadCounts[6]	Found In Complete Genomics Reference 69 Public Sequences[7]	Validation By Sanger Sequencing
ABCA2	NM_001606 NM_212533	ATP-binding cassette, sub-family A (ABC1), member 2	-	chr 9	139902883	139902884	H10	het-ref-snp	C	T	MISSENSE	Q9BZC7	S2419N	benign	1.71	DAMAGING *Warning! Low confidence.	0	21	51	2	57	285	285	4	2.06E-06	No	No
ALPK3	NM_020778	alpha-kinase 3	+	chr 15	85411474	85411475	H14	het-ref-snp	A	C	MISSENSE	B4DU37 Q96L96	K139Q K1838Q	probablydamaging probablydamaging	2.224 1.981	DAMAGING	0	8	43	1	39	151	151	1	3.10E-02	Yes	No
ANK1	NM_000037 NM_001142446 NM_020475 NM_020476 NM_020477	ankyrin 1, erythrocytic	-	chr 8	41582070	41582071	H7	het-ref-snp	G	A	MISSENSE	P16157-21 P16157-3 P16157-5 P16157 P16157-4	T238M T205M T205M T205M T205M	probablydamaging probablydamaging probablydamaging probablydamaging probablydamaging	3.006 3.006 2.812 2.371 2.86	DAMAGING	0	35	89	0	85	602	602	6	1.21E-12	No	No
ARMC 5	NM_001105247 NM_024742	armadillo repeat containing 5	+	chr 16	31471163	31471165	H14	het-ref-del	TC		FRAMESHIFT							15	27	0	27	259	331	-2	4.02E-06	No	Yes
ARMC 5	NM_001105247 NM_024742	armadillo repeat containing 5	+	chr 16	31471168	31471174	H14	het-ref-del	CCCC GC		DELETE+							14	26	0	38	377	331	-1	2.02E-07	No	Yes
ARMC 5	NM_001105247 NM_024742	armadillo repeat containing 5	+	chr 16	31476092	31476094	H10	het-ref-del	CG		FRAMESHIFT							13	52	0	66	203	203	-2	9.13E-06	No	Yes
ARMC 5	NM_001105247 NM_024742	armadillo repeat containing 5	+	chr 16	31477608	31477609	H7	het-ref-snp	A	C	MISSENSE	Q96C12 F5H156 Q96C12	Y736S Y768S Y736S	possiblydamaging	1.926 1.759 1.759	DAMAGING	0	21	70	0	78	318	340	5	2.32E-08	No	Yes
C14orf 93	NM_001130706 NM_001130708 NM_021944 NM_032876	chromosome 14 open reading frame 93	-	chr 14	23456589	23456589	H10	het-ref-ins		G	FRAMESHIFT							12	80	1	74	154	154	-9	2.54E-03	No	No
C2orf4 7	NM_001039693 NM_024520	chromosome 2 open reading frame 47	+	chr 2	200820742	200820745	H14	het-ref-sub	AGT	CGG	MISSENSE							8	36	0	44	168	168	-4	1.04E-03	No	No
C3	NM_000064	complement component 3	-	chr 19	6697751	6697752	H14	het-ref-snp	C	T	MISSENSE	P01024	D832N	probablydamaging	2.279	DAMAGING	0.01	4	23	0	36	50	50	-10	1.95E-02	No	No
C3orf5 8	NM_001134470 NM_173552	chromosome 3 open reading frame 58	+	chr 3	143708447	143708448	H11	het-ref-snp	G	A	MISSENSE	B7Z1W3 Q8NDZ4	R144H R353H	benign benign	-0.417 2.33	TOLERATED	0.8	35	85	0	62	591	591	5	1.11E-10	No	No

C9orf50	NM_199350	chromosome 9 open reading frame 50	-	chr 9	132377899	132377900	H7	het-ref-snp	C	T	MISSENSE	Q5SZB4	R248K	benign	-0.619	TOLERATED	0.92	35	57	26	67	657	357	-6	1.88E-02	Yes	No
CAPN14	NM_001145122	calpain 14	-	chr 2	31417350	31417351	H14	het-ref-snp	T	A	DISRUPT							12	55	6	69	161	428	0	4.45E-02	No	No
CCDC40	NM_017950	coiled-coil domain containing 40	+	chr 17	78069113	78069114	H14	het-ref-sub	A	CG	FRAMESHIFT					TOLERATED	0.2	9	41	3	53	181	181	-6	2.79E-02	Yes	No
CCR3	NM_001164680 NM_001837 NM_178328 NM_178329	chemokine (C-C motif) receptor 3	+	chr 3	46307270	46307271	H7	het-ref-snp	C	A	MISSENSE	P51677 F5GWL6	L208I L229I	probablydamaging probablydamaging	1.884 1.884	DAMAGING	0	22	68	1	64	377	377	4	1.07E-06	No	No
CDK8	NM_001260	cyclin-dependent kinase 8	+	chr 13	26959382	26959383	H14	het-ref-snp	T	G	MISSENSE	P49336-2 P49336	L184V L184V	probablydamaging probablydamaging	1.741 1.741	TOLERATED	0.3	9	54	0	63	125	125	-2	6.44E-04	No	No
CEP110	NM_007018	centriolin	+	chr 9	123850633	123850634	H2	het-ref-snp	C	G	MISSENSE	Q7Z7A1	F10L	benign	-0.025	TOLERATED	1	41	118	0	108	736	736	1	8.47E-14	No	No
CEP135	NM_025009	centrosomal protein 135kDa	+	chr 4	56877595	56877596	H14	het-ref-snp	G	A	MISSENSE	Q66GS9	E842K	possiblydamaging	1.72	TOLERATED	0.7	18	74	1	58	281	414	-1	1.21E-04	No	No
CEP164	NM_014956	centrosomal protein 164kDa	+	chr 11	117267903	117267903	H14	het-ref-ins		A	FRAMESHIFT							11	58	1	60	113	539	-5	1.87E-03	No	No
CFTR	NM_000492	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	+	chr 7	117170965	117170970	H14	het-ref-sub	CAGTA	TGGAC	MISSENSE							30	161	2	113	433	433	-9	5.03E-06	No	No
CRNN	NM_016190	cornulin	-	chr 1	152384647	152384648	H2	het-ref-snp	G	T	MISSENSE	Q9UBG3	T21K	possiblydamaging	1.734	TOLERATED	0.83	48	95	1	62	875	845	15	1.68E-12	No	No
CUGBP1	NM_001025596 NM_001172639 NM_001172640 NM_006560 NM_198700	CUGBP, Elav-like family member 1	-	chr 11	47496989	47496989	H11	het-ref-ins		G	FRAMESHIFT							13	54	3	56	227	243	-6	6.51E-03	No	No
DHCR24	NM_014762	24-dehydrocholesterol reductase	-	chr 1	55341710	55341713	H14	het-ref-del	CAC		DELETE+							35	97	4	79	829	829	3	3.50E-07	No	No
DNM2	NM_001005360 NM_001005361 NM_001005362 NM_001190716 NM_004945	dynamin 2	+	chr 19	10912978	10912979	H14	het-ref-snp	G	T	MISSENSE	E9PEQ4 P50570 P50570-2 A8K1B6	D480Y D480Y D480Y D480Y	probablydamaging probablydamaging probablydamaging probablydamaging	2.779 3.055 2.944 2.715	DAMAGING	0	9	51	2	63	127	127	-2	1.15E-02	No	No
EPC1	NM_025209	enhancer of polycomb homolog 1 (Drosophila)	-	chr 10	32575860	32575861	H14	het-ref-snp	T	A	MISSENSE	Q9H2F5 Q9H2F5-2 Q9H2F5-3	Y412F Y412F Y362F	probablydamaging probablydamaging probablydamaging	1.827 1.775 1.538	DAMAGING	0.03	8	49	2	74	95	125	-4	1.40E-02	No	No
EPC1	NM_025209	enhancer of polycomb homolog 1 (Drosophila)	-	chr 10	32575864	32575865	H14	het-ref-snp	G	T	MISSENSE	Q9H2F5-3 Q9H2F5 Q9H2F5-2	Q361K Q411K Q411K	benign benign benign	1.436 0.413 1.388	TOLERATED	0.26	8	48	2	73	71	125	-8	1.38E-02	No	No

EVC	NM_153717	Ellis van Creveld syndrome	+	chr 4	5785463	5785463	H11	het-ref-ins		C	FRAMESHIFT							16	75	7	85	166	197	-6	2.37E-02	No	No
EVC	NM_153717	Ellis van Creveld syndrome	+	chr 4	5785468	5785469	H11	het-ref-snp	A	G	MISSENSE	P57679	E585G	benign	1.601	DAMAGING	0	16	70	7	85	197	197	0	1.29E-02	Yes	No
FAM35 A	NM_019054	family with sequence similarity 35, member A	+	chr 10	88930416	88930417	H7	het-ref-del	A		FRAMESHIFT							9	55	1	62	184	210	0	5.95E-03	Yes	No
GIMAP 4	NM_018326	GTPase, IMAP family member 4	+	chr 7	150269882	150269883	H10	het-ref-snp	A	T	MISSENSE	Q9NUV9 G5E9W9	E242V E256V	benign possiblydamaging	1.781 2.112	TOLERATED	0.1	21	90	0	104	222	222	0	2.41E-08	No	No
GON4L	NM_001037533 NM_032292	gon-4-like (C. elegans)	-	chr 1	155792096	155792100	H14	het-ref-sub	TGAC	CGGA	MISSENSE							12	72	0	66	343	343	-7	3.33E-04	No	No
GPR15 6	NM_001168271 NM_153002	G protein-coupled receptor 156	-	chr 3	119900206	119900206	H14	het-ref-ins		C	FRAMESHIFT							3	55	0	47	146	858	-8	2.47E-01	No	No
HUWE 1	NM_031407	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase	-	chr X	53574909	53574910	H14	het-ref-del	G		FRAMESHIFT							14	140	5	153	266	266	5	3.03E-02	No	No
IL34	NM_001172771 NM_001172772 NM_152456	interleukin 34	+	chr 16	70693622	70693622	H14	het-ref-ins		T	FRAMESHIFT							9	68	0	55	115	115	-10	4.23E-03	No	No
KANK4	NM_181712	KN motif and ankyrin repeat domains 4	-	chr 1	62739343	62739344	H14	het-ref-snp	A	G	MISSENSE	Q5T7N3	S478P	benign	0.692	TOLERATED	0.26	16	79	1	48	347	445	6	2.71E-03	No	No
KIF21B	NM_017596	kinesin family member 21B	-	chr 1	200978559	200978559	H14	het-ref-ins		CAGA GGT	FRAMESHIFT							12	53	2	42	131	135	-7	1.88E-02	Yes	No
KLHL3 6	NM_024731	kelch-like 36 (Drosophila)	+	chr 16	84691114	84691114	H14	het-ref-ins		T	FRAMESHIFT							41	123	8	76	717	840	-8	3.11E-04	Yes	No
LAMA2	NM_000426 NM_001079823	laminin, alpha 2	+	chr 6	129513912	129513914	H14	het-ref-del	AG		FRAMESHIFT							9	46	2	46	145	226	-2	4.99E-02	No	No
LBR	NM_002296 NM_194442	lamin B receptor	-	chr 1	225609780	225609783	H14	het-ref-sub	GAA	TCT	MISSENSE							35	156	3	143	850	850	-5	3.54E-08	Yes	No
LHX1	NM_005568	LIM homeobox 1	+	chr 17	35295511	35295514	H14	het-ref-sub	CTG	TTC	MISSENSE							11	69	0	84	244	244	-9	9.78E-05	Yes	No
LOC10 028771 8	NM_001162435		+	chr 6	46719821	46719822	H10	het-ref-snp	C	G	MISSENSE	B4E2M5	T72S	probablydamaging	1.736			40	109	0	107	569	569	1	2.33E-14	No	No
MAD1L 1	NM_001013836 NM_001013837 NM_003550	MAD1 mitotic arrest deficient-like 1 (yeast)	-	chr 7	2262217	2262218	H11	het-ref-snp	C	A	MISSENSE	Q9Y6D9 B3KR41	A155S R16S	benign benign	0.9 1.248	TOLERATED	0.49	9	38	1	36	141	175	9	1.42E-02	Yes	No

MC3R	NM_019888	melanocortin 3 receptor	+	chr 20	54824207	54824208	H2	het-ref-snp	C	A	MISSENSE	P41968	S140R	benign	1.672	DAMAGING	0	28	73	0	82	480	480	5	2.35E-11	No	No
MLL2	NM_003482	myeloid/lymphoid or mixed-lineage leukemia 2	-	chr 12	49442921	49442937	H10	het-ref-del	AGCC GGGC CCGT CCTC		FRAMESHIFT							30	115	0	134	594	616	2	8.34E-12	No	No
MRGPRG	NM_001164377	MAS-related GPR, member G	-	chr 11	3239633	3239634	H14	het-ref-del	A		FRAMESHIFT							4	12	0	24	85	85	-5	8.40E-03	No	No
MRPL46	NM_022163 NM_022839 NM_176805	mitochondrial ribosomal protein L46	-	chr 15	89008892	89008893	H11	het-ref-snp	T	C	MISSENSE	Q9H2W6	I114V	benign	0.304	TOLERATED	0.95	12	68	0	72	146	685	-1	9.99E-05	No	No
MTRNR2L1	NM_001190452	MT-RNR2-like 1	+	chr 17	22023421	22023422	H14	half-snp	C	T	MISSENSE					Not Predicted		22	24	15	101	120	0	0	1.13E-12	Yes	No
MTRNR2L10	NM_001190708 NM_NA	MT-RNR2-like 10	-	chr X	55208385	55208386	H7	hap-snp	C	A	MISSENSE					Not Predicted		57	61	38	64	216		5	6.27E-06	Yes	No
MTRNR2L10	NM_001190708 NM_NA	MT-RNR2-like 10	-	chr X	55208389	55208390	H7	hap-snp	A	G	MISSENSE					Not Predicted		62	65	38	65	216		5	5.17E-07	Yes	No
MUC5B	NM_002458	mucin 5B, oligomeric mucus/gel-forming	+	chr 11	1272682	1272683	H10	het-ref-snp	T	C	MISSENSE	Q9HC84 E9PBJ0	M4858T M4861T	benign benign	-2.408 -2.408	Not Predicted		17	56	10	71	384	736	0	3.05E-02	No	No
NAPB	NM_022080	N-ethylmaleimide-sensitive factor attachment protein, beta	-	chr 20	23377710	23377711	H2	het-ref-snp	T	C	MISSENSE	Q9H115 Q4G0M0	Q98R K20E	benign benign	0.896 1.353	DAMAGING	0.05	26	68	1	77	400	400	6	2.18E-09	No	No
NDUFB6	NM_005802 NM_002493 NM_182739	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	-	chr 9	32553920	32553921	H14	het-ref-snp	C	G	MISSENSE	O95139 Q5VYT2	G114R G99R	benign benign	1.14 1.163	TOLERATED	0.2	14	80	0	75	165	165	-2	7.15E-05	No	No
NPC1L1	NM_001101648 NM_013389	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	-	chr 7	44575482	44575483	H11	het-ref-snp	T	C	MISSENSE	B7ZLE6 D3DVK9 Q17RV5 Q9UHC9-3	I647V I647V I647V I647V	benign probablydamaging benign probablydamaging	0.248 1.248 0.302 1.009	TOLERATED	0.88	19	154	0	159	230	230	-7	7.71E-07	No	No
OR6P1	NM_001160325	olfactory receptor, family 6, subfamily P, member 1	-	chr 1	158532878	158532879	H11	het-ref-snp	G	T	MISSENSE	Q8NGX9	N172K	benign	1.428	DAMAGING	0	18	110	0	120	224	224	-7	7.79E-07	No	No
OR8K5	NM_001004058	olfactory receptor, family 8, subfamily K, member 5	-	chr 11	55927010	55927011	H2	het-ref-snp	C	A	MISSENSE	Q8NH50	Q261H	probablydamaging	2.797	DAMAGING	0.01	17	40	0	41	280	280	10	6.91E-07	No	No
OR9G1	NM_001005213	olfactory receptor, family 9, subfamily G, member 1	+	chr 11	56468703	56468704	H14	het-ref-snp	T	C	MISSENSE	Q8NH87	F281L	benign	0.491	DAMAGING	0	27	95	16	111	357	573	-10	1.62E-02	Yes	No

OXNAD1	NM_138381	oxidoreductase NAD-binding domain containing 1	+	chr3	16344955	16344956	H2	het-ref-snp	A	G	MISSENSE	Q96HP4 F5H620	K276E K294E	benign benign	0.169 0.12	TOLERATED	1	40	115	0	125	651	651	0	2.29E-15	No	No
PABPC3	NM_030979	poly(A) binding protein, cytoplasmic 3	+	chr13	25671026	25671027	H2	het-ref-snp	A	G	MISSENSE	Q9H361	K231E	probablydamaging	2.112	DAMAGING	0	18	106	6	86	156	156	-10	4.77E-02	Yes	No
PCDHA13	NM_018904 NM_031865 NM_018903 NM_018902 NM_018901 NM_031860 NM_018911 NM_018910 NM_018909 NM_031849 NM_018908 NM_018907 NM_018906 NM_018905 NM_018900 NM_031411 NM_031857		+	chr5	140262034	140262035	H2	het-ref-snp	C	A	MISSENSE	Q9Y5I0-2 C9JA99 Q9Y5I0	P61Q P61Q P61Q	benign benign benign	1.039 0.826 1.168	DAMAGING	0	27	81	1	60	433	433	4	7.44E-07	No	No
PDZD2	NM_178140	PDZ domain containing 2	+	chr5	31799459	31799460	H14	het-ref-snp	C	G	MISSENSE	O15018	C35W	probablydamaging	3.481	DAMAGING	0	16	78	3	73	190	227	2	2.70E-03	No	No
PELP1	NM_014389	proline, glutamate and leucine rich protein 1	-	chr17	4576085	4576086	H14	het-ref-snp	A	G	MISSENSE	E7EV54 Q8IZL8	S587P S734P	benign benign	0.138 0.138	TOLERATED	0.29	6	26	0	19	56	56	-8	3.16E-02	No	No
PELP1	NM_014389	proline, glutamate and leucine rich protein 1	-	chr17	4576085	4576086	H14	het-ref-snp	A	G	MISSENSE					TOLERATED	0.29	6	26	0	19	56	56	-8	3.16E-02	No	No
PHF19	NM_015651	PHD finger protein 19	-	chr9	123624915	123624916	H14	het-ref-snp	A	C	MISSENSE	Q5T6S3	N360K	benign	-1.042	TOLERATED	0.57	9	72	1	79	184	204	3	6.95E-03	No	No
PHF19	NM_015651	PHD finger protein 19	-	chr9	123624920	123624921	H14	het-ref-snp	G	T	MISSENSE	Q5T6S3	P359T	benign	0.212	TOLERATED	0.38	9	65	1	76	204	204	3	5.77E-03	No	No
POLR2J3	NM_001097615	polymerase (RNA) II (DNA directed) polypeptide J3	-	chr7	102210365	102210366	H14	het-ref-snp	G	T	MISSENSE	Q9GZM3	T19N	benign	0.903	TOLERATED	0.3	23	88	8	65	189	189	1	4.24E-02	No	No
PTK6	NM_005975	PTK6 protein tyrosine kinase 6	-	chr20	62168518	62168519	H14	het-ref-snp	A	C	MISSENSE	Q13882 B4DWV1	L50R L50R	benign probablydamaging	1.047 2.377	DAMAGING	0.04	9	33	1	29	57	85	-10	1.45E-02	No	No
SETD1A	NM_014712	SET domain containing 1A	+	chr16	30975610	30975611	H14	het-ref-del	C		FRAMESHIFT							40	128	10	95	170	170	-5	2.95E-04	No	No
SH3PXD2A	NM_014631	SH3 and PX domains 2A	-	chr10	105614971	105614972	H14	het-ref-snp	C	G	MISSENSE	Q5TCZ1-3	R18T	possiblydamaging	1.652	TOLERATED	0.4	10	47	1	38	73	140	-7	1.94E-02	No	No

SHPRH	NM_001042683 NM_173082	SNF2 histone linker PHD RING helicase, E3 ubiquitin protein ligase	-	chr 6	146256126	146256127	H7	het-ref-snp	G	C	MISSENSE	Q149N8 Q149N8-2 Q149N8-4	S969C S858C S969C	probablydamaging probablydamaging probablydamaging	2.95 3.241 2.95	TOLERATED	0.06	5	40	0	36	79	181	-7	5.60E-02	Yes	No
SLC26A3	NM_000111	solute carrier family 26, member 3	-	chr 7	107423459	107423460	H14	het-ref-snp	A	C	MISSENSE	G5E9U3 P40879 Q99726 F5H3B7	S365A S400A S311L S306L	possiblydamaging possiblydamaging possiblydamaging possiblydamaging	1.267 1.305 1.823 1.791	DAMAGING	0	7	48	1	53	70	70	-9	2.56E-02	Yes	No
SLC4A7	NM_003615	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-	chr 3	27424690	27424690	H10	het-ref-ins		A	NONSENSE							5	56	0	38	120	880	-9	7.87E-02	No	No
SLC4A9	NM_031467	solute carrier family 4, sodium bicarbonate cotransporter, member 9	+	chr 5	139740524	139740525	H14	het-ref-snp	A	G	MISSENSE	Q96Q91-2 Q96Q91-3 Q96Q91 E9PDK1	D120G D120G D144G D120G	probablydamaging probablydamaging probablydamaging probablydamaging	1.965 1.965 1.965 1.853	DAMAGING	0	17	92	0	60	187	187	-2	1.20E-04	No	No
TAF1L	NM_153809	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	-	chr 9	32634674	32634676	H14	het-ref-sub	TA	GG	MISSENSE							47	203	6	128	1022	1022	-6	2.67E-06	Yes	No
TAGAP	NM_054114 NM_152133	T-cell activation RhoGTPase activating protein	-	chr 6	159458095	159458096	H11	het-ref-del	T		FRAMESHIFT							5	27	0	30	127	127	-5	1.93E-02	Yes	No
TEKT4	NM_144705	tektin 4	+	chr 2	95542358	95542359	H11	het-ref-snp	G	C	MISSENSE	Q8WW24	E385Q	possiblydamaging	1.178	TOLERATED	0.5	24	93	8	77	168	477	-5	1.10E-02	No	No
TLR2	NM_003264	toll-like receptor 2	+	chr 4	154626191	154626192	H2	het-ref-snp	G	C	MISSENSE	O60603	E711D	possiblydamaging	0.99	DAMAGING	0	10	77	0	73	144	144	-3	1.47E-03	No	No
TRPC6	NM_004621	transient receptor potential cation channel, subfamily C, member 6	-	chr 11	101359735	101359735	H14	het-ref-ins		G	FRAMESHIFT							13	80	2	70	214	232	-3	6.40E-03	Yes	No
TTC37	NM_014639	tetratricopeptide repeat domain 37	-	chr 5	94865912	94865915	H14	het-ref-sub	GCC	ACA	NONSENSE							8	42	0	62	194	194	-10	4.58E-04	No	No
UBAP1	NM_001171201 NM_001171202 NM_001171203 NM_001171204 NM_016525	ubiquitin associated protein 1	+	chr 9	34241596	34241597	H14	het-ref-snp	A	G	MISSENSE	Q9NZ09 Q9NZ09 F5GXE2 F5H0J8	M192V M192V M256V M228V	benign benign benign benign	-0.577 -0.335 -0.335 -0.335	TOLERATED, TOLERATED, TOLERATED, TOLERATED	0.6	12	72	7	105	121	121	-5	4.72E-02	No	No
ULBP3	NM_024518	UL16 binding protein 3	-	chr 6	150387264	150387265	H10	het-ref-snp	A	G	MISSENSE	Q9BZM4	I41T	benign	0.314	TOLERATED	0.31	31	70	0	67	557	557	6	1.57E-11	No	No
YSK4	NM_001018046 NM_025052	mitogen-activated protein kinase kinase kinase 19	-	chr 2	135744571	135744572	H10	het-ref-snp	G	A	NONSENSE							41	80	0	72	758	691	11	5.75E-15	No	No

ZBTB12	NM_006709 NM_025256 NM_181842	zinc finger and BTB domain containing 12	-	chr 6	31867967	31867968	H7	het-ref-snp	C	T	MISSENSE	Q9Y330	S372N	benign	0.542	TOLERATED	0.08	8	35	0	31	68	90	-7	5.47E-03	No	No
ZC3H4	NM_015168	zinc finger CCCH-type containing 4	-	chr 19	47569689	47569690	H14	het-ref-snp	C	T	MISSENSE	Q9UPT8	E1279K	possiblydamaging	1.438	TOLERATED	0.15	6	29	0	30	103	103	6	1.05E-02	No	No
ZNF511	NM_006659 NM_145806	zinc finger protein 511	+	chr 10	135123702	135123703	H14	het-ref-snp	C	G	MISSENSE	Q8NB15 Q8NB15-2	F155L F155L	probablydamaging probablydamaging	1.724 1.744	TOLERATED	0.1	8	43	1	40	76	76	-7	3.03E-02	Yes	No
ZNF831	NM_178457	zinc finger protein 831	+	chr 20	57768718	57768719	H14	het-ref-snp	C	T	MISSENSE	Q5JPB2	S882F	benign	1.013	DAMAGING	0	27	86	6	58	142	142	-6	4.20E-03	No	No

Table S8 : List of Genes Impacted by a Junction, Related to a Somatic Structural Variant.

[1]. for genes with alternative transcripts, several RefSeq are provided

[2]. "Exon Or Intron Number" : describes the exon / intron identity; for genes with several transcripts, the exon / intron identity for each transcript (listed in the RefSeq column) is provided

[3]. "Distance To Exons" : pairs of distances to exons are provided, measuring the distance to the exon before, and to the exon after the junction. For genes with several transcripts, one pair is provided for each transcript listed in the RefSeq column

[4]. For intragenic structural variants, the second side of the junction is also inside the gene. The detailed position is provided. Of note, for structural variants that are not intragenic, the second side of the structural variant outside of the gene is not specificed

[5]. Identities are provided by Complete Genomics for each junction. For GBP4 and GBP7, the junction Id is the same because the two genes are impacted by a common junction.

[6]. Number of mate pairs that are discordant from the reference genome in terms of alignment, and that were used for calling the junction.

[7]. These genomes are germline genomes provided by Complete Genomics. Many junctions identified as somatic in our project could be found in these genomes, which make them prone to be a false positives. Therefore any somatic junction called in these baseline genomes was discarded.

					Position of the junction					Second side of the junction (for intra-genic structural variants)4										
Gene Symbol	RefSeq1	Chromosome	The SV is intragenic	The SV is intra-intronic	Physical Position GRCh37	DNA strand	Localisation	Exon Or Intron Number2	Distance To Exons3	Position of the second side of the junction GRCh37	DNA strand of the second side of the junction	Localisation of the second side of the junction	Exon Or Intron Number of the second side of the junction	Distance To Exons of the second side of the junction	Sample	Type of SV	Junction Id5	SV Id	Discordant Mate Pair Alignments6	Frequency In 69 Complete Genomics Baseline Genome Set7
									26510					24878						
	NM_000719						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129827						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129829						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129830						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129831						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129832						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129833						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129834						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129835						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129836						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129837						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129838						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129839						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129840						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129841						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129842						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129843						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129844						intron	3	302035,26510			intron	3	303667,24878						
	NM_001129846						intron	3	302035,26510			intron	3	303667,24878						
	NM_001167623						intron	3	302035,26510			intron	3	303667,24878						
	NM_001167624						intron	3	302035,26510			intron	3	303667,24878						
	NM_001167625						intron	3	302035,26510			intron	3	303667,24878						
CACNA1C	NM_199460	chr12	Yes	Yes	2531631	+	intron	3	302035	2533263	+	intron	3	303667	H7T	complex	535	40	155	0
COMMD10	NM_016144	chr5	Yes	Yes	115542326	+	intron	5	84887 72451	115543262	+	intron	5	83951 73387	H11T	probable-inversion	8811	1617	10	0
DGKI	NM_004717	chr7	Yes	Yes	137301885	-	intron	26	2684 7530	137303375	-	intron	26	1194 9020	H11T	tandem-duplication	3060	170	68	0
DNAH9	NM_001372	chr17	No	No	11634169	+	intron	28	8027 2930						H2T	complex	3468	132	10	0
FAM182A	NR_026713	chr20	No	No	26041726	+	intron	1	7826 6005						H7T	complex	1903	71	15	0
FSIP1	NM_152597	chr15	No	No	39994638	-	intron	2	11006 84192						H11T	distal-duplication	2825	124	226	0

GBP4	NM_052941	chr1	No	No	89651865	-	intron	1	150 713						H10T	distal-duplication	4014	290	10	0
GBP7	NM_207398	chr1	No	No	89598794	-	intron	1	146 708						H10T	distal-duplication	4014	290	10	0
HFM1	NM_001017975	chr1	No	No	91852782	-	intron	35	6867 1391						H11T	complex	3615	77	13	0
KIAA1432	NM_001135920 NM_001206557 NM_020829	chr9	Yes	Yes	5749779	+	intron intron intron	12 12 12	3420 2274,3420 2274,3420 2274	5751390	+	intron intron intron	12 12 12	1809 3885,1809 3885,1809 3885	H11T	deletion	5898	933	14	0
NRXN1	NM_001135659 NM_004801	chr2	Yes	Yes	51138114	-	intron intron	19.2	11678 279871,11678 279871	51139688	-	intron	19.2	10104 281445,10104 281445	H11T	distal-duplication	3344	207	15	0
RBMS2	NM_002898	chr12	No	No	56989358	+	exon	14							H11T	distal-duplication	2825	124	226	0

Table S9 : Exome Variants Server (EVS) Allelic Frequencies of the *ARMC5* Variants Identified in the ACTH-Independent Macronodular Adrenal Hyperplasia Patients.

The number of variants and the sequencing coverage were obtained from the Exome Variant Server, NHLBI GO Exome Sequencing Project (ESP), Seattle, WA (URL: http://evs.gs.washington.edu/EVS/) [December 2012 accessed].

[1]. Each frequency is the frequency of the variant over the total number of alleles sequenced. The latter correspond to twice the number of controls sequenced.

chromosome	Position (GRCh37)	mutation_cDNA	mutation_protein	AllelicFrequency_EVS[1]	sift_Prediction
chr16	31470936	c.91A>T	p.K31X	0/12020	
chr16	31471071	c.226C>T	p.R76X	0/9980	
chr16	31471101	c.256C>T	p.Q86X	0/8076	
chr16	31471260	c.145T>C	p.C139R	0/12336	TOLERATED
chr16	31473667	c.799C>T	p.R267X	1/12594	
chr16	31473811	c.943C>t	p.R315W	0/12554	DAMAGING
chr16	31473860	c.992T>C	p.L331P	0/12534	DAMAGING
chr16	31473953	c.1085G>t	p.R362L	0/12328	DAMAGING
chr16	31474156	c.1288Q>T	p.E430X	0/12450	
chr16	31475987	c.1643T>C	p.L548P	0/12474	DAMAGING
chr16	31476199	c.1855C>T	p.R619X	0/12600	
chr16	31477275	c.1969T>C	p.C657R	0/12946	DAMAGING
chr16	31477609	c.2207A>C	p.Y736S	0/12572	DAMAGING
chr16	31478094	c.2692C>T	p.R898W	0/12546	DAMAGING

Table S10: List of Genes with a HIGH Expression in *ARMC5*-Mutated Compared with *ARMC5* Wild-Type ACTH-Independent Macronodular Adrenal Hyperplasia

[1.] p-values were generated with Limma, and adjusted for multiple testing using the Benjamini- Hochberg correction

[2]. GO stands for Gene Ontology. The significantly enriched Gene Ontologies (GO.1 to GO.20) within the differentially expressed genes are presented, with their annotations and the p-value of their enrichment (generated by DAVID). Whether any of these GO annotations applies to a gene or not, is mentioned for all the genes ("Yes" or "No").

To access the content of the table, please double-clic on the table

Mean.Mutated	Mean.NonMutated	logFoldChange	P.Value[1]	adj.P.Val[1]	Gene.Symbol	Gene.Title	Chromosomal.Location	Probe.Set.ID	Representative.Public.ID	GO.1[2]	GO.2[2]	GO.3[2]	GO.4[2]	GO.5[2]	GO.6[2]	GO.7[2]	GO.8[2]	GO.9[2]	GO.10[2]	GO.11[2]	GO.12[2]	GO.13[2]	GO.14[2]	GO.15[2]	GO.16[2]	GO.17[2]	GO.18[2]	GO.19[2]	GO.20[2]
										GO:0006396	GO:0008380	GO:0006397	GO:0016071	GO:0000375	GO:0000398	GO:0000377	GO:0003723	GO:0031981	GO:0070013	GO:0031974	GO:0043233	GO:0030529	GO:0003729	GO:0005730	GO:0005654	GO:0005681	GO:0030530	GO:0044451	GO:0016607
										RNA processing	RNA splicing	mRNA processing	mRNA metabolic process	RNA splicing, via transesterification reactions	nuclear mRNA splicing, via spliceosome	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RNA binding	nuclear lumen	intracellular organelle lumen	membrane-enclosed lumen	organelle lumen	ribonucleoprotein complex	mRNA binding	nucleolus	nucleoplasm	spliceosome	heterogeneous nuclear ribonucleoprotein complex	nucleoplasm part	nuclear speck
										Biological process	Biological process	Biological process	Biological process	Biological process	Biological process	Biological process	Molecular function	Cellular component	Cellular component	Cellular component	Cellular component	Cellular component	Molecular function	Cellular component	Cellular component	Cellular component	Cellular component	Cellular component	Cellular component
										P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 6e-04	P.adj 0.0068	P.adj 0.0021	P.adj 0.0024	P.adj 0.0022	P.adj 0.0085	P.adj 0.0144	P.adj 0.027
7.50	4.30	3.20	4.39E-09	2.40E-04	GFPT2	glutamine-fructose-6-phosphate transaminase 2	chr5q34-q35	205100_at	NM_005110	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.81	5.62	3.19	1.70E-08	4.66E-04	NMB	neuromedin B	chr15q22-qter	205204_at	NM_021077	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.75	4.28	3.47	1.70E-07	3.10E-03	NP	nucleoside phosphorylase	chr14q13.1	201695_s_at	NM_000270	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.30	4.55	4.75	6.50E-07	4.51E-03	CSRP2	cysteine and glycine-rich protein 2	chr12q21.1	207030_s_at	NM_001321	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.99	6.06	2.93	8.57E-07	4.51E-03	HSPA2	heat shock 70kDa protein 2	chr14q24.1	211538_s_at	U56725	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.66	4.12	2.54	8.51E-07	4.51E-03	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	chr10p14-p15	202464_s_at	NM_004566	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.71	6.25	2.46	3.94E-07	4.51E-03	NXF1	nuclear RNA export factor 1	chr11q12-q13	208922_s_at	BC004904	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	Yes	No	Yes	No	No	Yes	Yes
5.22	3.02	2.21	9.06E-07	4.51E-03	AQP3	aquaporin 3 (Gill blood group)	chr9p13	39248_at	N74607	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.28	5.11	2.17	5.21E-07	4.51E-03	FAM38A	family with sequence similarity 38, member A	chr16q24.3	202771_at	NM_014745	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.77	3.64	2.13	7.27E-07	4.51E-03	CRTAC1	cartilage acidic protein 1	chr10q22	221204_s_at	NM_018058	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.41	2.64	1.77	8.61E-07	4.51E-03	FAM83D	family with sequence similarity 83, member D	chr20q11.22-q12	225687_at	BC001068	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.72	7.52	2.19	9.99E-07	4.55E-03	---	---	---	228049_x_at	AA523172	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.48	3.09	2.39	1.41E-06	5.91E-03	ZCCHC12	zinc finger, CCHC domain containing 12	chrXq24	228715_at	AV725825	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.24	4.45	2.80	1.54E-06	6.01E-03	ACOX2	acyl-Coenzyme A oxidase 2, branched chain	chr3p14.3	205364_at	NM_003500	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.54	4.27	3.27	1.68E-06	6.13E-03	ASB4	ankyrin repeat and SOCS box-containing 4	chr7q21-q22	237720_at	BE220587	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.40	3.93	3.46	2.68E-06	7.45E-03	PILRB	paired immunoglobin-like type 2 receptor beta	chr7q22.1	225321_s_at	AV762653	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.07	4.42	2.65	2.62E-06	7.45E-03	---	---	---	237800_at	BE217811	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.86	2.13	1.73	3.00E-06	7.45E-03	SHISA2	shisa homolog 2 (Xenopus laevis)	chr13q12.13	230493_at	AW664964	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.20	5.55	1.65	2.77E-06	7.45E-03	LOC731049 /// UBE2S	similar to Ubiquitin-conjugating enzyme E2S (Ubiquitin-conjugating enzyme E2-24 kDa) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2-EPF5) /// ubiquitin-conjugating enzyme E2S	chr19q13.43	202779_s_at	NM_014501	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

6.47	5.00	1.47	2.63E-06	7.45E-03	HES6	hairy and enhancer of split 6 (Drosophila)	chr2q37.3	226446_at	AW249678	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
4.80	3.46	1.34	2.96E-06	7.45E-03	---	---	---	230598_at	BF063821	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.11	4.71	3.40	3.31E-06	7.87E-03	CSRP2	cysteine and glycine-rich protein 2	chr12q21.1	211126_s_at	U46006	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.56	3.50	3.06	3.89E-06	8.17E-03	FAT	FAT tumor suppressor homolog 1 (Drosophila)	chr4q35	201579_at	NM_005245	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.29	5.95	2.34	3.78E-06	8.17E-03	LOC100132540 /// LOC100132620 /// LOC339047 /// LOC642799 /// NPIP	similar to LOC339047 protein /// similar to LOC339047 protein /// hypothetical protein LOC339047 /// hypothetical LOC642799 /// nuclear pore complex interacting protein	chr16p12.3 /// chr16p13-p11 /// chr16p13.11	214870_x_at	AC002045	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.96	5.26	1.69	3.73E-06	8.17E-03	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	chr2q11-q14	201920_at	NM_005415	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.35	3.11	2.24	4.18E-06	8.47E-03	NEFM	neurofilament, medium polypeptide 150kDa	chr8p21	205113_at	NM_005382	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.11	4.57	1.54	5.75E-06	1.12E-02	MFHAS1	malignant fibrous histiocytoma amplified sequence 1	chr8p23.1	225478_at	BE783723	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.89	3.14	3.74	6.37E-06	1.17E-02	CHODL	chondrolectin	chr21q11.2	219867_at	NM_024944	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.07	4.23	1.84	6.40E-06	1.17E-02	SMAD3	SMAD family member 3	chr15q22.33	218284_at	NM_015400	Yes	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
5.13	2.92	2.21	7.45E-06	1.31E-02	LOC653380 /// LOC653498 /// LOC729837 /// TBC1D3 /// TBC1D3B /// TBC1D3C /// TBC1D3E /// TBC1D3F /// TBC1D3G /// TBC1D3H	similar to TBC1 domain family, member 3C /// similar to TBC1 domain family member 3 (Rab GTPase-activating protein PRC17) (Prostate cancer gene 17 protein) (TRE17 alpha protein) /// TBC1 domain family member 3-like protein LOC729837 /// TBC1 domain family, member 3 /// TBC1 domain family, member 3B /// TBC1 domain family, member 3C /// TBC1 domain family, member 3E /// TBC1 domain family, member 3F /// TBC1 domain family, member 3G /// TBC1 domain family, member 3H	chr17q12	209403_at	AL136860	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.52	5.80	1.71	8.22E-06	1.32E-02	ACACB	acetyl-Coenzyme A carboxylase beta	chr12q24.11	49452_at	AI057637	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.20	6.76	1.44	8.10E-06	1.32E-02	BRD2	bromodomain containing 2	chr6p21.3	208686_s_at	D42040	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.81	4.51	2.30	8.72E-06	1.36E-02	KLHDC8A	kelch domain containing 8A	chr1q32.1	219331_s_at	NM_018203	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.83	3.19	2.64	9.86E-06	1.38E-02	DACT2	dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis)	chr6q27	1569648_at	AF318336	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.37	2.33	2.04	9.94E-06	1.38E-02	C8orf57	chromosome 8 open reading frame 57	chr8q21.3	223614_at	AL136588	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.40	6.52	1.88	9.38E-06	1.38E-02	ISG15	ISG15 ubiquitin-like modifier	chr1p36.33	205483_s_at	NM_005101	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.06	3.96	1.11	9.70E-06	1.38E-02	TERF2	telomeric repeat binding factor 2	chr16q22.1	229790_at	AW006832	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
3.44	2.58	0.86	1.01E-05	1.38E-02	---	---	---	231890_at	AK022804	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.61	4.45	1.17	1.03E-05	1.38E-02	PCSK5	proprotein convertase subtilisin/kexin type 5	chr9q21.3	205559_s_at	NM_006200	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No	No
6.52	3.13	3.39	1.27E-05	1.51E-02	FLJ44342	hypothetical LOC645460	chr17q22	226419_s_at	AA046439	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.62	3.90	1.72	1.21E-05	1.51E-02	ELA1	elastase 1, pancreatic	chr12q13	224198_at	AF120493	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.17	6.51	1.66	1.27E-05	1.51E-02	ETV5	Ets variant gene 5 (ets-related molecule)	chr3q28	230102_at	AW206458	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.37	5.74	1.63	1.27E-05	1.51E-02	ACACB	acetyl-Coenzyme A carboxylase beta	chr12q24.11	43427_at	AI970898	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.94	9.89	1.05	1.20E-05	1.51E-02	BTG1	B-cell translocation gene 1, anti-proliferative	chr12q22	200920_s_at	AL535380	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.20	5.78	1.42	1.33E-05	1.55E-02	WDR59	WD repeat domain 59	chr16q23.1	218505_at	NM_024673	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.67	6.31	2.36	1.45E-05	1.62E-02	LOC100132540 /// LOC100132620 /// LOC339047 /// NPIP	similar to LOC339047 protein /// similar to LOC339047 protein /// hypothetical protein LOC339047 /// nuclear pore complex interacting protein	chr16p12.3 /// chr16p13-p11 /// chr16p13.11	221501_x_at	AF229069	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.75	5.73	2.02	1.44E-05	1.62E-02	FAM117A	family with sequence similarity 117, member A	chr17q21.33	221249_s_at	NM_030802	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.24	9.05	1.19	1.61E-05	1.76E-02	POLR1D	polymerase (RNA) I polypeptide D, 16kDa	chr13q12.2	218258_at	NM_015972	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	No	No
8.59	6.30	2.28	1.65E-05	1.77E-02	NPIP	nuclear pore complex interacting protein	chr16p13-p11	204538_x_at	NM_006985	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.00	3.63	1.37	1.77E-05	1.79E-02	---	---	---	1555852_at	AI375915	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.37	7.40	0.96	1.75E-05	1.79E-02	MAGED2	melanoma antigen family D, 2	chrXp11.2	208682_s_at	AF126181	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.91	5.40	1.51	1.96E-05	1.95E-02	NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like	chr1q21.2	227067_x_at	AW024960	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.11	5.75	1.36	2.02E-05	1.98E-02	POLS	polymerase (DNA directed) sigma	chr5p15	202466_at	NM_006999	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.55	3.08	3.47	2.33E-05	2.16E-02	ADORA2B	adenosine A2b receptor	chr17p12-p11.2	205891_at	NM_000676	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.69	5.30	1.39	2.31E-05	2.16E-02	BTN2A2	butyrophilin, subfamily 2, member A2	chr6p22.1	205298_s_at	W58757	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.20	6.95	1.25	2.27E-05	2.16E-02	PRPSAP1	phosphoribosyl pyrophosphate synthetase-associated protein 1	chr17q24-q25	202529_at	NM_002766	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.70	4.82	2.88	2.41E-05	2.17E-02	LOC57228	small trans-membrane and glycosylated protein	chr12q13.13	209679_s_at	BC003379	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.43	5.31	2.11	2.44E-05	2.17E-02	PHLDA1	pleckstrin homology-like domain, family A, member 1	chr12q15	217997_at	AI795908	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
7.44	4.17	3.27	2.65E-05	2.30E-02	RPL10	ribosomal protein L10	chrXq28	221989_at	AW057781	No	No	No	No	No	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No
7.83	5.26	2.57	2.70E-05	2.31E-02	LRRN4CL	LRRN4 C-terminal like	chr11q12.3	1556427_s_at	AL834319	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.27	2.31	2.95	2.84E-05	2.31E-02	PTHLH	parathyroid hormone-like hormone	chr12p12.1-p11.2	211756_at	BC005961	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.05	5.11	1.94	2.88E-05	2.31E-02	SNORD104	small nucleolar RNA, C/D box 104	chr17q23.3	228879_at	BG502554	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.37	7.90	1.47	2.84E-05	2.31E-02	FAM150B	family with sequence similarity 150, member B	chr2p25.3	238018_at	BF449053	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.00	5.88	1.11	2.83E-05	2.31E-02	HNRNPL	heterogeneous nuclear ribonucleoprotein L	chr19q13.2	221860_at	AL044078	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	Yes	No	No
4.52	3.23	1.30	2.94E-05	2.33E-02	UBE4B	Ubiquitination factor E4B (UFD2 homolog, yeast)	chr1p36.3	226746_s_at	N21292	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.65	5.59	2.05	3.27E-05	2.47E-02	MTMR11	myotubularin related protein 11	chr1q12-q21	1556034_s_at	AK097000	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.23	5.37	1.86	3.52E-05	2.47E-02	LOC399491	LOC399491 protein	chr16p13.1	214035_x_at	AA308853	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.57	2.74	1.83	3.49E-05	2.47E-02	HOXD1	homeobox D1	chr2q31.1	205975_s_at	NM_024501	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.23	6.58	1.64	3.51E-05	2.47E-02	LTBP3	latent transforming growth factor beta binding protein 3	chr11q12	219922_s_at	NM_021070	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

8.48	6.98	1.51	3.47E-05	2.47E-02	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF12 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 12 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	201103_x_at	BE299495	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.65	8.29	1.36	3.18E-05	2.47E-02	SNHG8	small nucleolar RNA host gene 8 (non-protein coding)	chr4q26	225220_at	BF340290	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.26	3.99	1.28	3.50E-05	2.47E-02	KLHDC5	kelch domain containing 5	chr12p11.22	225963_at	AW293538	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.31	2.92	1.39	3.61E-05	2.50E-02	HDAC8	histone deacetylase 8	chrXq13	223908_at	AF212246	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
4.48	2.67	1.81	3.70E-05	2.52E-02	IL17RB	interleukin 17 receptor B	chr3p21.1	219255_x_at	NM_018725	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.50	6.99	1.50	3.74E-05	2.52E-02	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF12 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 12 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	213612_x_at	AI800419	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.57	5.18	1.39	3.82E-05	2.55E-02	TTC28	tetratricopeptide repeat domain 28	chr22q12.1	213058_at	AL033538	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.74	7.22	1.52	3.98E-05	2.62E-02	CALB2	calbindin 2	chr16q22.2	205428_s_at	NM_001740	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.65	6.51	1.14	4.13E-05	2.69E-02	STARD3NL	STARD3 N-terminal like	chr7p14-p13	223065_s_at	BC003074	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.97	3.48	2.49	4.28E-05	2.75E-02	CROCCL1	ciliary rootlet coiled-coil, rootletin-like 1	chr1p36.13	211038_s_at	BC006312	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.86	3.54	1.32	4.41E-05	2.80E-02	CCT6AP1 /// LOC649553	chaperonin containing TCP1, subunit 6A (zeta 1) pseudogene 1 /// similar to chaperonin containing TCP1, subunit 6A	chr7q11.21	227301_at	BE644816	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.22	6.54	1.68	4.47E-05	2.81E-02	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	229447_x_at	N32025	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.11	5.70	2.42	4.61E-05	2.83E-02	WNT4	wingless-type MMTV integration site family, member 4	chr1p36.23-p35.1	208606_s_at	NM_030761	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.25	6.40	0.86	4.58E-05	2.83E-02	CSNK1D	casein kinase 1, delta	chr17q25	207945_s_at	NM_001893	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.88	6.70	1.18	4.72E-05	2.86E-02	TGIF1	TGFB-induced factor homeobox 1	chr18p11.3	203313_s_at	NM_003244	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.56	7.39	1.17	4.95E-05	2.97E-02	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	chr20p13	208821_at	J04564	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	No
4.09	2.25	1.84	5.16E-05	3.04E-02	---	---	---	230746_s_at	AW003173	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.26	2.38	0.89	5.15E-05	3.04E-02	---	---	---	228387_at	AI384076	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.29	4.93	1.36	5.24E-05	3.05E-02	FAM160A2	family with sequence similarity 160, member A2	chr11p15.4	223637_s_at	AL136723	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.99	7.31	2.69	5.49E-05	3.10E-02	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	chr10p12.3-p11.2	203304_at	NM_012342	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.43	5.41	1.02	5.49E-05	3.10E-02	CD300A	CD300a molecule	chr17q25.1	209933_s_at	AF020314	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.59	5.68	0.91	5.48E-05	3.10E-02	MPPE1	metallophosphoesterase 1	chr18p11.21	213727_x_at	AI743654	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.17	5.19	0.98	5.56E-05	3.10E-02	BTD	biotinidase	chr3p25	214116_at	AI767414	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
5.44	4.07	1.38	5.70E-05	3.11E-02	PLK3	polo-like kinase 3 (Drosophila)	chr1p34.1	204958_at	NM_004073	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.81	3.80	1.01	5.69E-05	3.11E-02	EPN2	epsin 2	chr17p11.2	203463_s_at	H05668	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.22	5.79	2.43	5.95E-05	3.16E-02	MTMR11	myotubularin related protein 11	chr1q12-q21	205076_s_at	NM_006697	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.80	5.71	2.08	5.90E-05	3.16E-02	DOM3Z	dom-3 homolog Z (C. elegans)	chr6p21.3	215982_s_at	AL049547	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.16	7.05	1.11	5.84E-05	3.16E-02	SFRS2B	splicing factor, arginine/serine-rich 2B	chr11q22	214789_x_at	AA524274	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No
10.20	8.95	1.25	6.15E-05	3.23E-02	BTG1	B-cell translocation gene 1, anti-proliferative	chr12q22	200921_s_at	NM_001731	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.91	3.13	1.79	6.25E-05	3.25E-02	LSDP5	lipid storage droplet protein 5	chr19p13.3	241368_at	AI190693	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.07	3.26	1.81	6.56E-05	3.39E-02	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	chr1p36.2	204429_s_at	BE560461	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.70	5.73	2.98	6.83E-05	3.44E-02	CCNL2	cyclin L2	chr1p36.33	222999_s_at	AF251294	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes
5.49	2.59	2.91	6.92E-05	3.44E-02	HNRNPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	213359_at	W74620	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	Yes	Yes	No	No	No	Yes	No	No
7.08	5.56	1.52	6.73E-05	3.44E-02	CLK2	CDC-like kinase 2	chr1q21	203229_s_at	NM_003993	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.00	6.97	1.02	6.92E-05	3.44E-02	WDR45L	WDR45-like	chr17q25.3	209076_s_at	BC000974	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.48	3.19	2.29	7.12E-05	3.46E-02	IL11RA	interleukin 11 receptor, alpha	chr9p13	204773_at	NM_004512	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.97	3.10	1.87	7.17E-05	3.46E-02	HOXD4	homeobox D4	chr2q31.1	205522_at	NM_014621	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.67	2.17	1.50	7.18E-05	3.46E-02	HAS2	Hyaluronan synthase 2	chr8q24.12	230372_at	AI374739	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.66	6.26	1.40	7.32E-05	3.46E-02	RBM5	RNA binding motif protein 5	chr3p21.3	201395_at	NM_005778	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	No	No

5.96	4.67	1.29	7.31E-05	3.46E-02	LOC284454	hypothetical protein LOC284454	chr19p13.13	1555847_a_at	BU617052	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.16	4.78	1.39	7.79E-05	3.61E-02	FAM130A1	family with sequence similarity 130, member A1	chr12q13.11-q13.12	221260_s_at	NM_030809	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.87	5.09	1.77	7.92E-05	3.64E-02	MSX1	msh homeobox 1	chr4p16.3-p16.1	205932_s_at	NM_002448	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.53	6.28	1.24	8.02E-05	3.65E-02	C14orf94	chromosome 14 open reading frame 94	chr14q11.2	218383_at	NM_017815	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.81	5.70	1.11	8.24E-05	3.69E-02	RCC1 /// SNHG3-RCC1	regulator of chromosome condensation 1 /// SNHG3-RCC1	chr1p36.1	206499_s_at	NM_001269	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.32	7.38	0.94	8.19E-05	3.69E-02	TMEM18	transmembrane protein 18	chr2p25.3	225489_at	AI720705	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.14	5.57	2.57	8.71E-05	3.78E-02	KLHDC8A	kelch domain containing 8A	chr1q32.1	222871_at	BF791631	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.60	6.22	1.38	8.63E-05	3.78E-02	H2AFX	H2A histone family, member X	chr11q23.2-q23.3	205436_s_at	NM_002105	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
8.89	7.74	1.15	8.64E-05	3.78E-02	CHD2	Chromodomain helicase DNA binding protein 2	chr15q26	225951_s_at	AV756026	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.30	6.49	0.81	8.77E-05	3.78E-02	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	chr19p13.2	201727_s_at	NM_001419	No	No	No	Yes	No	No	No	Yes	No	No	No	No	No	Yes	No	No	No	No	No	No
8.37	7.03	1.34	9.15E-05	3.86E-02	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	226740_x_at	BF740216	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.36	6.16	1.20	9.04E-05	3.86E-02	MCM7	minichromosome maintenance complex component 7	chr7q21.3-q22.1	208795_s_at	D55716	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
4.47	3.27	1.20	9.18E-05	3.86E-02	---	---	---	229111_at	AA033699	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.08	2.57	1.51	9.34E-05	3.89E-02	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	228111_s_at	AI004779	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.86	7.00	0.86	9.38E-05	3.89E-02	DCTD	dCMP deaminase	chr4q35.1	201571_s_at	AI656493	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.44	2.62	1.82	9.48E-05	3.90E-02	---	---	---	238623_at	AI633559	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.21	6.26	0.95	9.65E-05	3.94E-02	C20orf11	chromosome 20 open reading frame 11	chr20q13.33	218448_at	NM_017896	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.50	5.21	1.29	9.80E-05	3.96E-02	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	chr11q13-q14	226507_at	AU154408	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.28	5.75	1.54	1.01E-04	4.05E-02	POFUT2	protein O-fucosyltransferase 2	chr21q22.3	209578_s_at	BC000626	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.58	4.71	2.87	1.10E-04	4.13E-02	GCH1	GTP cyclohydrolase 1	chr14q22.1-q22.2	204224_s_at	NM_000161	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.12	2.58	2.54	1.10E-04	4.13E-02	F2RL1	coagulation factor II (thrombin) receptor-like 1	chr5q13	213506_at	BE965369	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.72	2.40	2.32	1.10E-04	4.13E-02	TOX2	TOX high mobility group box family member 2	chr20q13.12	228737_at	AA211909	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.45	3.96	1.49	1.08E-04	4.13E-02	PLA2G1B	phospholipase A2, group IB (pancreas)	chr12q23-q24.1	206311_s_at	NM_000928	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.04	6.59	1.45	1.07E-04	4.13E-02	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	chr12p11.23	205304_s_at	NM_004982	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.28	2.07	1.20	1.09E-04	4.13E-02	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	chr2q23.3	206026_s_at	NM_007115	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.81	6.67	1.14	1.05E-04	4.13E-02	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	chr19p13.12	201584_s_at	NM_005804	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No	No
5.88	4.78	1.09	1.09E-04	4.13E-02	MCM7	minichromosome maintenance complex component 7	chr7q21.3-q22.1	210983_s_at	AF279900	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
6.19	5.49	0.70	1.10E-04	4.13E-02	ZNF337	zinc finger protein 337	chr20p11.21	214760_at	AL049942	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.23	4.24	3.00	1.16E-04	4.14E-02	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	chr1p34.3	214016_s_at	AL558875	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No
6.50	4.06	2.44	1.13E-04	4.14E-02	SHROOM2	shroom family member 2	chrXp22.3	204967_at	NM_001649	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.17	2.63	1.54	1.15E-04	4.14E-02	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	chr15q11-q12	221974_at	AW770748	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.76	5.30	1.46	1.15E-04	4.14E-02	LTBP1	latent transforming growth factor beta binding protein 1	chr2p22-p21	202729_s_at	NM_000627	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.01	4.65	1.36	1.17E-04	4.14E-02	LPXN	leupaxin	chr11q12.1	216250_s_at	X77598	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.86	4.95	0.91	1.16E-04	4.14E-02	TTC28	tetratricopeptide repeat domain 28	chr22q12.1	215146_s_at	AB028966	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.92	5.93	1.00	1.21E-04	4.27E-02	LPCAT1	lysophosphatidylcholine acyltransferase 1	chr5p15.33	201818_at	NM_024830	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.95	5.14	2.81	1.34E-04	4.32E-02	PHLDA1	pleckstrin homology-like domain, family A, member 1	chr12q15	217996_at	AA576961	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
5.27	2.70	2.58	1.31E-04	4.32E-02	LOC643670 /// LOC728105 /// tcag7.907	similar to hCG1739109 /// similar to hCG1739109 /// hypothetical LOC402483	chr1p36.33 /// chr3q29 /// chr7q32.1	225899_x_at	AL040396	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.57	4.48	2.09	1.33E-04	4.32E-02	NBPF1	neuroblastoma breakpoint family, member 1	chr1p36.13	236273_at	AW269499	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.52	5.51	2.01	1.33E-04	4.32E-02	MBD6	methyl-CpG binding domain protein 6	---	227833_s_at	AW207668	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.47	4.66	1.81	1.29E-04	4.32E-02	CSNK1E	casein kinase 1, epsilon	chr22q13.1	226858_at	T51255	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.55	6.96	1.59	1.33E-04	4.32E-02	---	---	---	227755_at	AA042983	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.89	4.32	1.57	1.34E-04	4.32E-02	---	---	---	227724_at	T86159	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.80	3.27	1.53	1.34E-04	4.32E-02	RABL2A /// RABL2B	RAB, member of RAS oncogene family-like 2A /// RAB, member of RAS oncogene family-like 2B	chr22q13.33 /// chr2q13	219151_s_at	NM_007081	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.19	5.95	1.24	1.25E-04	4.32E-02	CXCL16	chemokine (C-X-C motif) ligand 16	chr17p13	223454_at	AF275260	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.41	6.28	1.12	1.28E-04	4.32E-02	C12orf44	chromosome 12 open reading frame 44	chr12q13.13	218214_at	NM_021934	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.13	6.08	1.05	1.24E-04	4.32E-02	CPSF3L	cleavage and polyadenylation specific factor 3-like	chr1p36.33	217994_x_at	NM_017871	Yes	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
7.88	6.91	0.97	1.35E-04	4.32E-02	MRP63	mitochondrial ribosomal protein 63	chr13q12.11	224535_s_at	AB049957	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No
10.48	9.59	0.89	1.29E-04	4.32E-02	QARS	glutaminyl-tRNA synthetase	chr3p21.3-p21.1	217846_at	NM_005051	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No	No
6.81	5.98	0.83	1.31E-04	4.32E-02	CYTH1	cytohesin 1	chr17q25	202880_s_at	NM_004762	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.33	8.75	0.58	1.28E-04	4.32E-02	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	chr6p25	211474_s_at	BC004948	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.16	3.93	2.22	1.41E-04	4.32E-02	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	chr4q21	204466_s_at	BG260394	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.05	4.33	1.72	1.40E-04	4.32E-02	C7orf40	chromosome 7 open reading frame 40	chr7p13	225699_at	AI937446	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.10	4.72	1.38	1.41E-04	4.32E-02	C1orf52	chromosome 1 open reading frame 52	chr1p22.3	228135_at	AA738437	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.71	3.56	1.15	1.41E-04	4.32E-02	BAIAP2	BAI1-associated protein 2	chr17q25	205293_x_at	AB017120	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.84	7.77	1.07	1.41E-04	4.32E-02	RBM4	RNA binding motif protein 4	chr11q13	200997_at	NM_002896	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	No	Yes	No
7.19	6.35	0.84	1.40E-04	4.32E-02	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	chr8p11.1	218017_s_at	NM_025070	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.44	3.82	0.62	1.37E-04	4.32E-02	ACACB	acetyl-Coenzyme A carboxylase beta	chr12q24.11	214584_x_at	R99037	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

5.69	3.42	2.27	1.45E-04	4.39E-02	NAPSB	napsin B aspartic peptidase pseudogene	chr19q13.33	228055_at	AI763426	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.85	6.89	0.97	1.48E-04	4.44E-02	C16orf80	chromosome 16 open reading frame 80	chr16q21	217957_at	NM_013242	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.22	3.70	1.52	1.50E-04	4.49E-02	PHC1 /// PHC1B	polyhomeotic homolog 1 (Drosophila) /// polyhomeotic homolog 1B (Drosophila)	chr12p13 /// chr12q13.2	218338_at	NM_004426	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
9.07	7.47	1.59	1.51E-04	4.50E-02	MAT2A	methionine adenosyltransferase II, alpha	chr2p11.2	200768_s_at	BC001686	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.36	8.30	2.05	1.53E-04	4.51E-02	DCN	decorin	chr12q21.33	209335_at	AI281593	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.88	7.71	1.17	1.53E-04	4.51E-02	PTBP1	polypyrimidine tract binding protein 1	chr19p13.3	202189_x_at	NM_002819	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	Yes	No	No
7.76	6.70	1.06	1.54E-04	4.51E-02	SLC35C2	solute carrier family 35, member C2	chr20q13.12	225037_at	AL518563	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.97	3.12	1.85	1.58E-04	4.56E-02	NOVA1	neuro-oncological ventral antigen 1	chr14q	205794_s_at	NM_002515	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	No	No	No
4.48	3.54	0.94	1.62E-04	4.56E-02	---	---	---	244803_at	AI335191	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No
9.44	8.52	0.92	1.61E-04	4.56E-02	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	chr20p13	213175_s_at	AL049650	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	No
6.20	5.29	0.91	1.61E-04	4.56E-02	CCDC130	coiled-coil domain containing 130	chr19p13.13	208094_s_at	NM_030818	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.61	6.92	0.69	1.59E-04	4.56E-02	MRPL43	mitochondrial ribosomal protein L43	chr10q24.31	230027_s_at	N74662	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No
5.66	3.69	1.97	1.66E-04	4.66E-02	LARP6	La ribonucleoprotein domain family, member 6	chr15q23	236565_s_at	BF792126	Yes	No	No	No	No	No	No	No	Yes	No	No	No	No	Yes	No	No	No	No	No
6.38	5.30	1.09	1.71E-04	4.76E-02	HERC2	hect domain and RLD 2	chr15q13	217902_s_at	NM_004667	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.17	5.95	1.22	1.73E-04	4.80E-02	TRIM27	tripartite motif-containing 27	chr6p22	210541_s_at	AF230394	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No
7.92	6.61	1.31	1.76E-04	4.85E-02	COL18A1	collagen, type XVIII, alpha 1	chr21q22.3	209081_s_at	NM_030582	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.66	5.64	1.02	1.80E-04	4.91E-02	SFRS2B	splicing factor, arginine/serine-rich 2B	chr11q22	213152_s_at	AI343248	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
6.58	5.42	1.17	1.81E-04	4.91E-02	NUP85	nucleoporin 85kDa	chr17q25.1	218014_at	NM_024844	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.51	3.42	2.08	1.89E-04	5.01E-02	ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide	chr17p13.1	204311_at	NM_001678	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.53	5.47	2.06	1.88E-04	5.01E-02	---	---	---	230395_at	AI536637	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.24	3.08	1.16	1.87E-04	5.01E-02	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	227926_s_at	AI498207	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.66	2.65	1.01	1.88E-04	5.01E-02	MBOAT1	membrane bound O-acyltransferase domain containing 1	chr6p22.3	227379_at	AI734993	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.75	3.89	0.86	1.86E-04	5.01E-02	GNB5	guanine nucleotide binding protein (G protein), beta 5	chr15q21.2	207124_s_at	NM_006578	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.90	7.74	1.16	1.90E-04	5.02E-02	PTBP1	polypyrimidine tract binding protein 1	chr19p13.3	211270_x_at	BC002397	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	Yes	No	No
6.68	5.02	1.66	1.93E-04	5.06E-02	SDHALP2	succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	chr3q29	226693_at	AW172779	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.31	6.25	1.06	1.93E-04	5.06E-02	TP53BP1	tumor protein p53 binding protein 1	chr15q15-q21	203050_at	NM_005657	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No
5.27	3.53	1.74	1.96E-04	5.10E-02	C21orf86	Chromosome 21 open reading frame 86	chr21q22.3	228909_at	AW131553	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.90	6.87	1.03	1.98E-04	5.10E-02	WRNIP1	Werner helicase interacting protein 1	chr6p25.2	222489_s_at	AA621580	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.14	3.13	1.01	1.97E-04	5.10E-02	HOXA1	homeobox A1	chr7p15.3	214639_s_at	S79910	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.00	6.06	1.94	1.99E-04	5.10E-02	DOM3Z	dom-3 homolog Z (C. elegans)	chr6p21.3	38157_at	AF059252	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.06	6.84	1.23	2.03E-04	5.18E-02	PLEKHO1	pleckstrin homology domain containing, family O member 1	chr1q21.2	218223_s_at	NM_016274	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.68	5.40	1.28	2.05E-04	5.19E-02	BTD	biotinidase	chr3p25	214117_s_at	AI767414	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
8.72	7.52	1.19	2.05E-04	5.19E-02	---	---	---	227473_at	N45140	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.88	4.73	1.15	2.06E-04	5.19E-02	AKAP8	A kinase (PRKA) anchor protein 8	chr19p13.1	203847_s_at	AW341501	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
8.68	7.17	1.50	2.08E-04	5.19E-02	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	chr6q23.3	209357_at	AF109161	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.56	7.57	1.00	2.09E-04	5.19E-02	GLB1	galactosidase, beta 1	chr3p21.33	201576_s_at	NM_000404	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.49	5.11	1.38	2.13E-04	5.23E-02	SNED1	sushi, nidogen and EGF-like domains 1	chr2q37.3	213488_at	N73970	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.51	3.26	1.25	2.15E-04	5.23E-02	---	---	---	228930_at	AI679611	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.32	6.40	0.91	2.14E-04	5.23E-02	RPAIN	RPA interacting protein	chr17p13.2	228183_s_at	BF342428	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	Yes	No
3.02	2.40	0.62	2.15E-04	5.23E-02	C20orf199	chromosome 20 open reading frame 199	chr20q13.13	229899_s_at	AI625235	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.61	3.39	2.22	2.24E-04	5.32E-02	---	---	---	228642_at	BF593636	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.47	5.01	1.46	2.21E-04	5.32E-02	AKT2	v-akt murine thymoma viral oncogene homolog 2	chr19q13.1-q13.2	226156_at	BE866854	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.18	4.72	1.46	2.24E-04	5.32E-02	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	chr3q27	209380_s_at	AF146074	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.55	5.36	1.19	2.25E-04	5.32E-02	IL17RC	interleukin 17 receptor C	chr3p25.3|3p25.3-p24.1	221926_s_at	BF196320	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.81	5.81	1.00	2.27E-04	5.32E-02	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	chr1p36.3	210685_s_at	AB028839	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.32	5.34	0.98	2.27E-04	5.32E-02	CTGLF1 /// CTGLF3 /// CTGLF4 /// CTGLF5 /// KIAA1975	centaurin, gamma-like family, member 1 /// centaurin, gamma-like family, member 3 /// centaurin, gamma-like family, member 4 /// centaurin, gamma-like family, member 5 /// KIAA1975 protein similar to MRIP2	chr10q11.21 /// chr10q11.23 /// chr10q23.2	221850_x_at	AI826075	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.30	3.43	0.88	2.31E-04	5.35E-02	LOC90408	hypothetical protein LOC90408	chr15q14	1560081_at	AL702091	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.49	5.62	0.87	2.30E-04	5.35E-02	C18orf22	chromosome 18 open reading frame 22	chr18q23	219419_at	NM_024805	Yes	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.82	2.66	3.17	2.35E-04	5.36E-02	HERC2P2 /// HERC2P3 /// LOC440248	hect domain and RLD 2 pseudogene 2 /// hect domain and RLD 2 pseudogene 3 /// hect domain and RLD 2 pseudogene	chr15q11.2 /// chr15q13.1	217317_s_at	AB002391	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.38	7.14	1.24	2.33E-04	5.36E-02	ARS2	arsenate resistance protein 2	chr7q21	222047_s_at	AI523895	Yes	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No
6.83	5.61	1.22	2.35E-04	5.36E-02	ILF3	interleukin enhancer binding factor 3, 90kDa	chr19p13.2	217805_at	NM_004516	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	No	No	No
5.78	4.86	0.91	2.34E-04	5.36E-02	---	---	---	239277_at	AI559696	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.24	5.49	1.76	2.38E-04	5.38E-02	ATF7IP2	Activating transcription factor 7 interacting protein 2	chr16p13.13	228381_at	AV716964	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.44	5.27	1.17	2.38E-04	5.38E-02	RBM14	RNA binding motif protein 14	chr11q13.1	204178_s_at	NM_006328	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	No	Yes	No
6.07	4.86	1.21	2.40E-04	5.41E-02	BTN2A1	butyrophilin, subfamily 2, member A1	chr6p22.1	211256_x_at	U90142	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.76	7.48	1.28	2.44E-04	5.43E-02	TUSC1	tumor suppressor candidate 1	chr9p21.2	227388_at	AA479016	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

9.51	8.26	1.26	2.42E-04	5.43E-02	ETV5	ets variant gene 5 (ets-related molecule)	chr3q28	203349_s_at	NM_004454	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.89	3.71	1.18	2.44E-04	5.43E-02	SFRS17A	splicing factor, arginine/serine-rich 17A	chrXp22.32; Ypter-p11.2	210269_s_at	M99578	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes	Yes
8.79	6.56	2.23	2.49E-04	5.44E-02	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	210794_s_at	AF119863	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.14	5.89	1.26	2.49E-04	5.44E-02	SERTAD1	SERTA domain containing 1	chr19q13.1-q13.2	223394_at	BC002670	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.17	5.06	1.11	2.51E-04	5.44E-02	BTN2A1	butyrophilin, subfamily 2, member A1	chr6p22.1	215493_x_at	AL121936	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.67	4.60	1.06	2.49E-04	5.44E-02	SFRS14	Splicing factor, arginine/serine-rich 14	chr19p12	212001_at	AV738039	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No
5.79	4.98	0.80	2.48E-04	5.44E-02	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	chr10q22-q23	227872_at	AA527570	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
5.61	4.47	1.14	2.54E-04	5.48E-02	PADI2	peptidyl arginine deiminase, type II	chr1p36.13	209791_at	AL049569	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.31	3.16	3.15	2.55E-04	5.48E-02	CABP7	calcium binding protein 7	chr22q12.2	243173_at	AI989906	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.99	2.36	0.63	2.56E-04	5.49E-02	LOC100128405	Hypothetical protein LOC100128405	chr6q26	235829_at	AW003893	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
6.86	5.95	0.91	2.57E-04	5.49E-02	ING1	inhibitor of growth family, member 1	chr13q34	208415_x_at	NM_005537	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.78	5.88	0.90	2.65E-04	5.62E-02	TXNDC11	thioredoxin domain containing 11	chr16p13.13	223325_at	AF131780	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.42	2.70	0.72	2.66E-04	5.62E-02	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	chr11q13-q14	230100_x_at	AU147145	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.48	5.76	0.72	2.66E-04	5.62E-02	C9orf119	chromosome 9 open reading frame 119	chr9q34.11	226027_at	BG541668	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.10	2.55	2.56	2.72E-04	5.69E-02	GAS5	growth arrest-specific 5 (non-protein coding)	chr1q25.1	227517_s_at	AI056992	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.88	3.38	1.50	2.75E-04	5.73E-02	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	chr1p36.2-p36.1	208438_s_at	NM_005248	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.15	6.55	0.60	2.75E-04	5.73E-02	RPUSD4	RNA pseudouridylate synthase domain containing 4	chr11q24.2	225398_at	AL580514	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No
8.93	7.85	1.08	2.77E-04	5.73E-02	PABPN1	poly(A) binding protein, nuclear 1	chr14q11.2-q13	201544_x_at	BF675004	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	No	No	No
8.46	7.40	1.06	2.79E-04	5.73E-02	C5orf26	chromosome 5 open reading frame 26	chr5q21-q22	225698_at	BF314746	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.29	7.25	1.03	2.81E-04	5.73E-02	PTBP1	polypyrimidine tract binding protein 1	chr19p13.3	212015_x_at	BF690062	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	Yes	No	No
8.55	7.74	0.80	2.80E-04	5.73E-02	GUSB	glucuronidase, beta	chr7q21.11	202605_at	NM_000181	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.34	4.31	1.02	2.83E-04	5.75E-02	CPOX	coproporphyrinogen oxidase	chr3q12	204172_at	NM_000097	No	No	No	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No
7.99	6.69	1.31	2.88E-04	5.80E-02	SNRP70	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	chr19q13.3	201221_s_at	NM_003089	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	Yes	No	No	No	Yes	No	No	No
4.52	3.75	0.77	2.91E-04	5.86E-02	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	chr12q13.13	1554113_a_at	BC025994	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.11	3.63	1.48	2.94E-04	5.88E-02	LOC149478	Hypothetical protein LOC149478	chr1p34.1	1557049_at	BQ183759	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.62	4.32	1.30	2.94E-04	5.88E-02	HSPA14	heat shock 70kDa protein 14	chr10p13	227650_at	AV757332	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.42	4.30	2.12	2.96E-04	5.88E-02	HOXA9	homeobox A9	chr7p15-p14	214651_s_at	U41813	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
5.43	4.40	1.03	2.97E-04	5.89E-02	LOC729887	hypothetical protein LOC729887	chr16q24.1	230591_at	AI792242	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.35	4.13	3.21	3.03E-04	5.91E-02	EDNRA	endothelin receptor type A	chr4q31.23	204464_s_at	NM_001957	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.71	4.46	1.25	3.01E-04	5.91E-02	TMTC4	transmembrane and tetratricopeptide repeat containing 4	chr13q32.3	225666_at	D80480	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.55	2.38	1.17	3.04E-04	5.91E-02	FAM26F	Family with sequence similarity 26, member F	chr6q22.1	229543_at	AV734646	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.45	5.29	1.16	3.05E-04	5.91E-02	---	---	---	222900_at	AJ400877	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.20	4.18	1.02	3.06E-04	5.91E-02	ARIH2	ariadne homolog 2 (Drosophila)	chr3p21.2-p21.3	227932_at	AI340270	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.97	5.16	0.81	3.06E-04	5.91E-02	ASXL1	additional sex combs like 1 (Drosophila)	chr20q11.1	212238_at	AL117518	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.77	4.63	1.14	3.08E-04	5.92E-02	---	---	---	228466_at	AI150690	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.83	5.80	1.03	3.09E-04	5.92E-02	WIPI1	WD repeat domain, phosphoinositide interacting 1	chr17q24.2	203827_at	NM_017983	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.58	3.88	2.70	3.10E-04	5.92E-02	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	chr1p36.2	204430_s_at	NM_003039	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.65	4.23	1.41	3.11E-04	5.93E-02	---	---	---	210230_at	BC003629	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.02	3.17	3.85	3.13E-04	5.94E-02	---	---	---	230333_at	BE326919	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.33	4.20	3.13	3.21E-04	5.96E-02	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	chr9q32-q33.3	215813_s_at	S36219	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.03	5.06	1.97	3.25E-04	5.96E-02	---	---	---	238389_s_at	AI458208	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.56	6.50	1.06	3.24E-04	5.96E-02	BCL6	B-cell CLL/lymphoma 6	chr3q27	203140_at	NM_001706	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.21	8.16	1.05	3.22E-04	5.96E-02	NBPF10	neuroblastoma breakpoint family, member 10	chr1q21.1	212854_x_at	AB051480	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.50	6.49	1.02	3.23E-04	5.96E-02	BRD2	bromodomain containing 2	chr6p21.3	208685_x_at	AA902767	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.93	5.95	0.98	3.20E-04	5.96E-02	SAFB2	scaffold attachment factor B2	chr19p13.3	32099_at	D50928	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No
9.69	8.85	0.84	3.17E-04	5.96E-02	ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	chr22q13.1	200779_at	NM_001675	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
6.45	5.71	0.74	3.18E-04	5.96E-02	MPPE1	metallophosphoesterase 1	chr18p11.21	206764_x_at	NM_023075	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.07	9.49	0.58	3.23E-04	5.96E-02	UXT	ubiquitously-expressed transcript	chrXp11.23-p11.22	218495_at	NM_004182	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.37	2.84	1.53	3.28E-04	5.97E-02	TTLL3	tubulin tyrosine ligase-like family, member 3	chr3p25.3	230872_s_at	AA534291	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.82	6.73	1.09	3.30E-04	6.00E-02	SPRY4	sprouty homolog 4 (Drosophila)	chr5q31.3	221489_s_at	W48843	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.68	7.79	0.89	3.33E-04	6.04E-02	H2AFZ	H2A histone family, member Z	chr4q24	200853_at	NM_002106	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.21	8.15	1.06	3.35E-04	6.05E-02	PTBP1	polypyrimidine tract binding protein 1	chr19p13.3	216306_x_at	X62006	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	Yes	No	No
5.97	4.93	1.05	3.38E-04	6.08E-02	SSH1	Slingshot homolog 1 (Drosophila)	chr12q24.11	221752_at	AL041728	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.99	3.77	3.22	3.41E-04	6.09E-02	FOXL2	forkhead box L2	chr3q23	220102_at	NM_023067	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.61	4.59	2.02	3.46E-04	6.12E-02	LOC375295	hypothetical gene supported by BC013438	chr2q31.1	228564_at	AI569804	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.91	6.49	1.42	3.46E-04	6.12E-02	ARS2	arsenate resistance protein 2	chr7q21	201680_x_at	NM_015908	Yes	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
3.97	2.84	1.13	3.45E-04	6.12E-02	YEATS4	YEATS domain containing 4	chr12q13-q15	218911_at	NM_006530	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
4.50	3.09	1.42	3.47E-04	6.13E-02	GUSBL2 /// LOC728411	glucuronidase, beta-like 2 /// similar to Beta-glucuronidase precursor	chr5p14.3 /// chr6p11.2	226947_at	AW001628	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.65	4.75	1.91	3.53E-04	6.19E-02	MSRB3	methionine sulfoxide reductase B3	chr12q14.3	225782_at	AW027333	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.51	3.63	2.88	3.57E-04	6.23E-02	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	chr15q21.1	203475_at	NM_000103	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.19	5.90	1.29	3.58E-04	6.23E-02	MZF1	myeloid zinc finger 1	chr19q13.2|19q13.2-q13.4	40569_at	M58297	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.92	6.12	1.80	3.66E-04	6.28E-02	NUSAP1	nucleolar and spindle associated protein 1	chr15q15.1	218039_at	NM_016359	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
6.20	4.76	1.43	3.64E-04	6.28E-02	ZBTB48	zinc finger and BTB domain containing 48	chr1p36.3	205025_at	NM_005341	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.29	6.14	1.15	3.66E-04	6.28E-02	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	chr1p36.3	215533_s_at	AF091093	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.26	6.16	1.10	3.66E-04	6.28E-02	THOC4	THO complex 4	chr17q25.3	226319_s_at	AF047002	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes	Yes
8.32	7.33	0.99	3.69E-04	6.30E-02	PTBP1	polypyrimidine tract binding protein 1	chr19p13.3	211271_x_at	BC004383	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	Yes	No	No

5.75	3.94	1.81	3.71E-04	6.32E-02	---	---	230304_at	AW005298	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.91	7.65	1.26	3.73E-04	6.32E-02	KIAA1191	KIAA1191	chr5q35.2	224502_s_at	BC006316	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.43	7.40	1.02	3.73E-04	6.32E-02	SFRS2	splicing factor, arginine/serine-rich 2	chr17q25.2	214882_s_at	BG254869	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes
8.57	6.13	2.45	3.89E-04	6.36E-02	ASB4	ankyrin repeat and SOCS box-containing 4	chr7q21-q22	237721_s_at	BE220587	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.60	4.41	2.19	3.93E-04	6.36E-02	C10orf65	chromosome 10 open reading frame 65	chr10q24.1	239093_at	BG165743	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.94	4.94	2.00	3.93E-04	6.36E-02	CASP9	caspase 9, apoptosis-related cysteine peptidase	chr1p36.3-p36.1	210775_x_at	AB015653	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.08	4.25	1.83	3.92E-04	6.36E-02	LIMS3	LIM and senescent cell antigen-like domains 3	chr2q14-q21	223800_s_at	AF288404	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.76	5.20	1.56	3.94E-04	6.36E-02	KIAA0495	KIAA0495	chr1p36.32	213340_s_at	AI073551	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.06	5.63	1.42	3.87E-04	6.36E-02	LRRC41	leucine rich repeat containing 41	chr1p33	1555831_s_at	BC004948	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.67	8.45	1.21	3.80E-04	6.36E-02	NDRG1	N-myc downstream regulated gene 1	chr8q24.3	200632_s_at	NM_006096	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.46	6.37	1.09	3.89E-04	6.36E-02	KIAA1967	KIAA1967	chr8p22	225187_at	AK022661	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No
6.78	5.76	1.02	3.84E-04	6.36E-02	JMJD6	jumonji domain containing 6	chr17q25	212722_s_at	AK021780	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.69	4.68	1.02	3.79E-04	6.36E-02	UXS1	UDP-glucuronate decarboxylase 1	chr2q12.2	225583_at	AL573637	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.23	5.24	1.00	3.95E-04	6.36E-02	SETD2	SET domain containing 2	chr3p21.31	212493_s_at	AI761110	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.26	7.26	1.00	3.95E-04	6.36E-02	MRPS11	mitochondrial ribosomal protein S11	chr15q25	211595_s_at	AB049944	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No
8.02	7.15	0.87	3.89E-04	6.36E-02	GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	chr2p23.3	204366_s_at	NM_001521	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
3.08	2.30	0.78	3.85E-04	6.36E-02	---	---	---	238733_at	AI422414	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.32	9.61	0.71	3.91E-04	6.36E-02	SNHG6	small nucleolar RNA host gene 6 (non-protein coding)	chr8q13|8q13	225547_at	BG169443	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.79	6.14	0.66	3.84E-04	6.36E-02	RNPS1	RNA binding protein S1, serine-rich domain	chr16p13.3	207939_x_at	NM_006711	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	Yes	No	No	Yes	Yes
5.81	4.49	1.32	3.98E-04	6.37E-02	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	chr14q24.3	221589_s_at	AW612403	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.39	5.53	0.86	4.00E-04	6.40E-02	UBA7	ubiquitin-like modifier activating enzyme 7	chr3p21	203281_s_at	NM_003335	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.55	6.83	0.73	4.02E-04	6.40E-02	FAM50A	family with sequence similarity 50, member A	chrXq28	203262_s_at	NM_004699	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.66	4.22	1.44	4.07E-04	6.42E-02	TTLL3	tubulin tyrosine ligase-like family, member 3	chr3p25.3	210129_s_at	AF078842	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.66	6.73	0.93	4.06E-04	6.42E-02	RBM23	RNA binding motif protein 23	chr14q11.2	219816_s_at	NM_018107	Yes	No	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
6.93	6.05	0.88	4.06E-04	6.42E-02	MPPE1	metallophosphoesterase 1	chr18p11.21	209858_x_at	BC002877	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.45	6.61	0.85	4.07E-04	6.42E-02	---	---	---	225197_at	W58461	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.42	3.03	1.39	4.09E-04	6.42E-02	FAM122B	family with sequence similarity 122B	chrXq26.3	225362_at	AI341165	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.76	6.42	1.34	4.19E-04	6.50E-02	MSL-1	male-specific lethal-1 homolog	chr17q21.1	224765_at	AA001203	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.99	5.85	1.15	4.21E-04	6.50E-02	ADPGK	ADP-dependent glucokinase	chr15q24.1	220980_s_at	NM_031284	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.03	6.93	1.10	4.21E-04	6.50E-02	TRIM27	tripartite motif-containing 27	chr6p22	212116_at	NM_006510	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
5.98	4.96	1.01	4.20E-04	6.50E-02	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	chr1q23.1	212766_s_at	AW294587	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
4.50	2.92	1.59	4.29E-04	6.54E-02	LRRC15	leucine rich repeat containing 15	chr3q29	213909_at	AU147799	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.57	6.19	1.38	4.30E-04	6.54E-02	RGL2	ral guanine nucleotide dissociation stimulator-like 2	chr6p21.3	209110_s_at	AL050259	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.98	5.76	1.22	4.27E-04	6.54E-02	FAM53C	family with sequence similarity 53, member C	chr5q31	218023_s_at	NM_016605	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.84	6.78	1.06	4.33E-04	6.56E-02	RCC2	regulator of chromosome condensation 2	chr1p36.13	224578_at	AB040903	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
11.80	10.05	1.74	4.37E-04	6.59E-02	DCN	decorin	chr12q21.33	211896_s_at	AF138302	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.19	6.27	0.92	4.36E-04	6.59E-02	TFDP1	transcription factor Dp-1	chr13q34	212330_at	R60866	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
6.90	6.17	0.73	4.45E-04	6.68E-02	INO80	INO80 homolog (S. cerevisiae)	chr15q15.1	229356_x_at	AK002176	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.62	6.32	1.30	4.47E-04	6.69E-02	ECM1	extracellular matrix protein 1	chr1q21	209365_s_at	U65932	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.46	5.52	0.94	4.48E-04	6.69E-02	PRR14	proline rich 14	chr16p11.2	218714_at	NM_024031	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.81	5.62	1.19	4.52E-04	6.72E-02	UGDH	UDP-glucose dehydrogenase	chr4p15.1	203343_at	NM_003359	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.96	6.81	1.15	4.53E-04	6.72E-02	ZNF641	zinc finger protein 641	chr12q13.11	226509_at	AV700302	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.59	7.64	0.95	4.57E-04	6.75E-02	SFRS2	splicing factor, arginine/serine-rich 2	chr17q25.2	200754_x_at	NM_003016	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes
6.95	4.71	2.23	4.61E-04	6.77E-02	DIRAS3	DIRAS family, GTP-binding RAS-like 3	chr1p31	215506_s_at	AK021882	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.22	5.52	1.70	4.60E-04	6.77E-02	PABPN1	poly(A) binding protein, nuclear 1	chr14q11.2-q13	201545_s_at	NM_004643	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	No	No	No
4.72	3.50	1.22	4.63E-04	6.78E-02	IDS	iduronate 2-sulfatase	chrXq28	202439_s_at	NM_000202	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.07	7.09	2.98	4.65E-04	6.78E-02	FCGBP /// LOC100133944	Fc fragment of IgG binding protein /// similar to IgGFc-binding protein precursor (FcgammaBP) (Fcgamma-binding protein antigen)	chr19q13.1	203240_at	NM_003890	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.91	5.61	1.30	4.65E-04	6.78E-02	SFRS17A	splicing factor, arginine/serine-rich 17A	chrXp22.32; Ypter-p11.2	203624_at	NM_005088	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes	Yes
6.42	4.52	1.90	4.72E-04	6.79E-02	ADSSL1	adenylosuccinate synthase like 1	chr14q32.33	226325_at	BF593252	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.14	8.43	1.71	4.73E-04	6.79E-02	MARCKSL1	MARCKS-like 1	chr1p35.1	200644_at	NM_023009	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.66	3.97	1.70	4.72E-04	6.79E-02	HOXD8	Homeobox D8	chr2q31.1	231906_at	BF057634	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.70	5.06	1.64	4.78E-04	6.79E-02	ELK1	ELK1, member of ETS oncogene family	chrXp11.2	210376_x_at	M25269	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.09	3.76	1.33	4.79E-04	6.79E-02	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	chr18q11.2	224279_s_at	AF295039	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.65	2.59	1.06	4.69E-04	6.79E-02	CD1D	CD1d molecule	chr1q22-q23	205789_at	NM_001766	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.40	3.57	0.83	4.79E-04	6.79E-02	CARD8	caspase recruitment domain family, member 8	chr19q13.32	204950_at	NM_014959	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.57	5.02	0.55	4.75E-04	6.79E-02	---	---	---	228972_at	AI028602	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.99	3.66	1.33	4.81E-04	6.80E-02	LOC286208	hypothetical protein LOC286208	chr9q34.11	1560089_at	AL833509	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.85	3.28	1.57	4.83E-04	6.81E-02	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	chr3q27	226363_at	BE550362	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.19	6.39	0.81	4.85E-04	6.82E-02	KLC1	kinesin light chain 1	chr14q32.3	213656_s_at	BF593594	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.01	7.23	0.79	4.90E-04	6.86E-02	GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	chr2p23.3	212429_s_at	AW194657	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
4.70	4.07	0.63	4.89E-04	6.86E-02	TXNRD3	thioredoxin reductase 3	chr3q21.3	59631_at	AI247566	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.33	6.16	1.17	4.94E-04	6.87E-02	IRF2BP2	interferon regulatory factor 2 binding protein 2	chr1q42.3	224570_s_at	AA166696	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.03	7.22	0.81	4.95E-04	6.87E-02	INTS3	integrator complex subunit 3	chr1q21.3	202809_s_at	NM_023015	Yes	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
3.90	3.17	0.73	4.93E-04	6.87E-02	ZNF512B	zinc finger protein 512B	chr20q13.33	221869_at	AL118506	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.48	5.72	1.76	5.02E-04	6.89E-02	TOB2	transducer of ERBB2, 2	chr22q13.2-q13.31	222243_s_at	AB051450	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.24	4.50	1.74	5.01E-04	6.89E-02	PTTG1	pituitary tumor-transforming 1	chr5q35.1	203554_x_at	NM_004219	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.18	6.40	0.79	5.00E-04	6.89E-02	QRICH1	glutamine-rich 1	chr3p21.31	209174_s_at	BC000978	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.73	3.30	1.43	5.10E-04	6.97E-02	PM20D2	peptidase M20 domain containing 2	chr6q15	225421_at	AI654133	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.26	2.00	1.27	5.09E-04	6.97E-02	HAS2	hyaluronan synthase 2	chr8q24.12	206432_at	NM_005328	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.22	3.28	2.94	5.29E-04	6.99E-02	CNTN1	Contactin 1	chr12q11-q12	227209_at	AI091445	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

6.12	3.45	2.66	5.24E-04	6.99E-02	---	---	227044_at	AV705507	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.89	3.92	1.97	5.17E-04	6.99E-02	CIRBP	cold inducible RNA binding protein	chr19p13.3	230142_s_at	AW088030	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No
6.72	5.14	1.57	5.17E-04	6.99E-02	LOC728613	programmed cell death 6 pseudogene	chr5p15.33	1569110_x_at	BC020552	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.54	5.34	1.20	5.24E-04	6.99E-02	ARSD	arylsulfatase D	chrXp22.3	225286_at	AI741110	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.57	6.41	1.17	5.15E-04	6.99E-02	LOC728613 /// PDCD6	programmed cell death 6 pseudogene /// programmed cell death 6	chr5p15.33	1568763_s_at	BC020552	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.13	4.10	1.02	5.22E-04	6.99E-02	SCAND1	SCAN domain containing 1	chr20q11.1-q11.23	235206_at	AA845353	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
9.16	8.20	0.96	5.15E-04	6.99E-02	H2AFZ	H2A histone family, member Z	chr4q24	213911_s_at	BF718636	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.41	2.46	0.96	5.29E-04	6.99E-02	AOC2	amine oxidase, copper containing 2 (retina-specific)	chr17q21	207064_s_at	NM_009590	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.43	2.59	0.84	5.18E-04	6.99E-02	FLJ44342	hypothetical LOC645460	chr17q22	229246_at	AI803504	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.84	6.01	0.83	5.23E-04	6.99E-02	CASP2	caspase 2, apoptosis-related cysteine peptidase	chr7q34-q35	226032_at	AU153405	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.66	3.23	1.43	5.32E-04	6.99E-02	USP36	ubiquitin specific peptidase 36	chr17q25.3	224978_s_at	BF430981	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
4.92	3.06	1.86	5.36E-04	7.00E-02	KLHL7	kelch-like 7 (Drosophila)	chr7p15.3	220239_at	NM_018846	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
6.68	4.87	1.81	5.39E-04	7.00E-02	---	---	---	222302_at	BE813017	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
12.35	10.96	1.39	5.37E-04	7.00E-02	DCN	decorin	chr12q21.33	201893_x_at	AF138300	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.32	6.19	1.13	5.39E-04	7.00E-02	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	chr1p36.3	202316_x_at	AW241715	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.77	8.73	1.04	5.44E-04	7.00E-02	KIAA0114	KIAA0114	chr4q12	224870_at	BG255416	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.32	7.33	0.99	5.37E-04	7.00E-02	INPP1	inositol polyphosphate-1-phosphatase	chr2q32	202794_at	NM_002194	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.72	5.80	0.92	5.40E-04	7.00E-02	FLJ27365 /// LOC150381	FLJ27365 protein /// hypothetical protein LOC150381	chr22q13.31	238058_at	AA603041	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.31	6.61	0.70	5.43E-04	7.00E-02	MED19	mediator complex subunit 19	chr11q12.1	226293_at	BE781103	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
5.31	3.21	2.10	5.46E-04	7.01E-02	C1orf79	chromosome 1 open reading frame 79	chr1p35.3	223773_s_at	AF277181	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.40	6.22	1.17	5.55E-04	7.07E-02	B3GALT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	chr1p36.33	1553959_a_at	N95564	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.98	6.79	1.19	5.60E-04	7.09E-02	JOSD1	Josephin domain containing 1	chr22q13.1	201751_at	NM_014876	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.65	5.54	1.11	5.60E-04	7.09E-02	FLJ41352 /// SMPD4	FLJ41352 protein /// sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	chr2q21.1	207856_s_at	NM_017951	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.46	8.79	0.67	5.59E-04	7.09E-02	PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)	chr1p32-p36	201064_s_at	NM_003819	Yes	No	No	No	No	No	No	Yes	No	No	No	No	Yes	Yes	No	No	No	No	No
5.40	4.49	0.91	5.62E-04	7.10E-02	ZFYVE19	zinc finger, FYVE domain containing 19	chr15q15.1	225843_at	AW015263	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.77	4.96	1.81	5.71E-04	7.15E-02	---	---	---	229849_at	AI807950	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.60	5.20	1.40	5.72E-04	7.15E-02	GTF3A	general transcription factor IIIA	chr13q12.3-q13.1	238880_at	AI241331	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
7.40	6.41	0.99	5.76E-04	7.19E-02	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	chr2q11.2	46665_at	AI949392	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.17	4.97	1.20	5.80E-04	7.22E-02	SCD5	stearoyl-CoA desaturase 5	chr4q21.22	224018_s_at	BC004936	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.31	3.27	3.04	5.86E-04	7.26E-02	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	chr17p12-p11.2	219985_at	NM_006042	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.91	2.90	1.01	5.87E-04	7.26E-02	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	chr6p25	209722_s_at	L40378	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.47	4.52	0.94	5.85E-04	7.26E-02	C12orf32	chromosome 12 open reading frame 32	chr12p13.33	225837_at	AL577977	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.91	6.01	2.90	5.96E-04	7.27E-02	DAPL1	death associated protein-like 1	chr2q24.1	229290_at	AI692575	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.54	6.02	1.52	5.90E-04	7.27E-02	NT5DC2	5'-nucleotidase domain containing 2	chr3p21.1	218051_s_at	NM_022908	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.68	2.20	1.49	5.99E-04	7.27E-02	---	---	---	243555_at	AA573452	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.75	6.51	1.24	6.00E-04	7.27E-02	LOC376475 /// WASH2P /// WASH3P /// WASH6P	CXYorf1-related protein /// WAS protein family homolog 2 pseudogene /// WAS protein family homolog 3 pseudogene /// WAS protein family homolog 6 pseudogene	chr15q26.3 /// chr2q14.1 /// chrXq28 /// chrXq28;Yq12	226340_x_at	AI628311	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.32	7.34	0.99	6.01E-04	7.27E-02	GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	chr22q13.31	50277_at	AW001443	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.11	3.27	0.85	5.90E-04	7.27E-02	PL-5283 /// SLC13A4	PL-5283 protein /// solute carrier family 13 (sodium/sulfate symporters), member 4	chr7q33	238273_at	AW007221	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.00	6.25	0.75	5.96E-04	7.27E-02	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	chr3p25	201244_s_at	NM_002880	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.86	4.57	1.28	6.04E-04	7.28E-02	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	202380_s_at	NM_005385	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.82	2.85	0.97	6.12E-04	7.37E-02	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	chr18q11.2	219928_s_at	NM_012189	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.75	6.10	0.66	6.13E-04	7.37E-02	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	chr6p21.1	209317_at	AF008442	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	No
5.14	3.13	2.01	6.15E-04	7.37E-02	HNRPDL	Heterogeneous nuclear ribonucleoprotein D-like	chr4q13-q21	212454_x_at	AI762552	Yes	No	No	No	No	No	No	Yes	No	No	No	No	Yes	Yes	No	No	No	Yes	No
6.74	5.46	1.28	6.17E-04	7.37E-02	SLC25A37	Solute carrier family 25, member 37	chr8p21.2	226928_x_at	BE677761	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.75	5.57	1.18	6.20E-04	7.37E-02	STX16	syntaxin 16	chr20q13.32	221500_s_at	BE782754	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.86	3.05	0.81	6.18E-04	7.37E-02	TXNL4B	thioredoxin-like 4B	chr16q22.3	222748_s_at	AW194729	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	Yes	No	No	No	Yes	No	No
6.60	3.76	2.83	6.26E-04	7.40E-02	---	---	---	228030_at	AI041522	Yes	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
5.80	4.37	1.43	6.24E-04	7.40E-02	FAM122B /// TMEM57	family with sequence similarity 122B /// transmembrane protein 57	chr1p36.11|1p36.11 /// chrXq26.3	222673_x_at	AI582192	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.55	2.95	0.60	6.26E-04	7.40E-02	LOC400960	Hypothetical gene supported by BC040598	chr2p14	1568640_at	BC012788	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.51	4.83	1.68	6.31E-04	7.43E-02	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	chr15q11-q12	213447_at	AI672541	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.15	4.21	1.95	6.46E-04	7.44E-02	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	chr6p25	242814_at	AI986192	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.44	3.60	1.84	6.65E-04	7.44E-02	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	chr16q11	222774_s_at	AI335263	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.53	4.89	1.63	6.51E-04	7.44E-02	RP5-1022P6.2	hypothetical protein KIAA1434	chr20p12.3	224835_at	AL109935	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.35	4.82	1.53	6.63E-04	7.44E-02	---	---	---	225740_x_at	AA961420	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.98	4.49	1.49	6.36E-04	7.44E-02	MIB2	mindbomb homolog 2 (Drosophila)	chr1p36.33	226644_at	BE222279	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.75	6.28	1.47	6.52E-04	7.44E-02	---	---	---	1555967_at	AA362254	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.34	3.94	1.40	6.46E-04	7.44E-02	TTC32	tetratricopeptide repeat domain 32	chr2p24.1	226838_at	BE465877	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.88	4.51	1.37	6.55E-04	7.44E-02	CREB3L4	cAMP responsive element binding protein 3-like 4	chr1q21.3	226455_at	AL563283	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.45	6.21	1.24	6.57E-04	7.44E-02	NAT9	N-acetyltransferase 9	chr17q25.1	204382_at	NM_015654	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.96	3.76	1.20	6.34E-04	7.44E-02	LOC642852	hypothetical LOC642852	chr21q22.3	1559957_a_at	BG396868	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.64	3.65	1.00	6.54E-04	7.44E-02	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	chrXp11.22	219855_at	NM_018159	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.52	6.54	0.98	6.58E-04	7.44E-02	TM9SF1	transmembrane 9 superfamily member 1	chr14q11.2	209149_s_at	BE899402	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.35	7.46	0.89	6.59E-04	7.44E-02	WDR13	WD repeat domain 13	chrXp11.23	222138_s_at	AF158978	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No

4.65	3.88	0.78	6.46E-04	7.44E-02	TRIOBP	TRIO and F-actin binding protein	chr22q13.1	243690_at	AW444985	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.25	8.50	0.75	6.65E-04	7.44E-02	FAM128B	family with sequence similarity 128, member B	chr2q21.1	212995_x_at	BG255188	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.54	8.81	0.73	6.66E-04	7.44E-02	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	chr14q11.2-q12	210027_s_at	M80261	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
4.51	3.79	0.72	6.51E-04	7.44E-02	LOC643517	hypothetical LOC643517	chr2p25.3	229880_at	H28731	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No
5.96	4.51	1.45	6.72E-04	7.47E-02	ANKRD10	ankyrin repeat domain 10	chr13q34	223251_s_at	BC001727	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.14	3.79	1.35	6.78E-04	7.48E-02	SPATA5L1	spermatogenesis associated 5-like 1	chr15q21.1	222163_s_at	BE890973	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.29	5.03	1.26	6.81E-04	7.48E-02	MDC1	mediator of DNA damage checkpoint 1	chr6p21.3	203062_s_at	NM_014641	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
7.89	6.98	0.91	6.82E-04	7.48E-02	CCDC12	coiled-coil domain containing 12	chr3p21.31	226011_at	BG107767	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.54	7.72	0.82	6.75E-04	7.48E-02	LGTN	ligatin	chr1q31-q32	218253_s_at	NM_006893	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
8.30	7.54	0.75	6.77E-04	7.48E-02	CD2BP2	CD2 (cytoplasmic tail) binding protein 2	chr16p11.2	202257_s_at	NM_006110	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No
9.46	8.86	0.60	6.82E-04	7.48E-02	NEDD8	neural precursor cell expressed, developmentally down-regulated 8	chr14q12	201840_at	NM_006156	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.02	4.05	0.97	6.90E-04	7.52E-02	---	---	---	230580_at	AI222805	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.64	7.84	0.80	6.91E-04	7.52E-02	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	chr16p11.2	200959_at	NM_004960	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
4.93	4.21	0.72	6.92E-04	7.52E-02	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	chr3q13.31	219178_at	NM_024638	Yes	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.69	3.70	0.99	6.97E-04	7.53E-02	EHD1	EH-domain containing 1	chr11q13	209037_s_at	AW182860	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.25	7.35	0.90	6.94E-04	7.53E-02	DCTD	dCMP deaminase	chr4q35.1	201572_x_at	NM_001921	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.99	6.45	2.54	7.13E-04	7.54E-02	ALDH1L1	aldehyde dehydrogenase 1 family, member L1	chr3q21.2	205208_at	NM_012190	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.57	3.62	1.95	7.08E-04	7.54E-02	LOC284356	hypothetical LOC284356	chr19q13.33	1555842_at	BM978026	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.74	3.32	1.41	7.10E-04	7.54E-02	ASXL1	additional sex combs like 1 (Drosophila)	chr20q11.1	244519_at	AI829840	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.79	4.47	1.32	7.00E-04	7.54E-02	CABLES1	Cdk5 and Abl enzyme substrate 1	chr18q11.2	225532_at	AI889160	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.92	4.83	1.09	7.07E-04	7.54E-02	PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	chr1q21.1	202251_at	NM_004698	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes	Yes
7.07	6.07	1.00	7.01E-04	7.54E-02	RAB24	RAB24, member RAS oncogene family	chr5q35.3	225251_at	AK021761	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.89	6.97	0.92	7.10E-04	7.54E-02	BRD2	bromodomain containing 2	chr6p21.3	214911_s_at	S78771	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.08	5.05	1.03	7.15E-04	7.55E-02	NRIP3	nuclear receptor interacting protein 3	chr11p15.3	219557_s_at	NM_020645	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.27	5.17	1.11	7.19E-04	7.57E-02	BTN2A1	butyrophilin, subfamily 2, member A1	chr6p22.1	203944_x_at	NM_007049	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.40	5.68	1.73	7.22E-04	7.57E-02	---	---	---	1555968_a_at	AA362254	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.96	2.87	1.09	7.29E-04	7.62E-02	MGC16121	hypothetical protein MGC16121	chrXq26.3	229784_at	AA234096	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.95	2.15	0.80	7.28E-04	7.62E-02	---	---	---	235147_at	R56118	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.54	5.10	4.44	7.49E-04	7.65E-02	TSPAN8	tetraspanin 8	chr12q14.1-q21.1	203824_at	NM_004616	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.43	3.54	1.89	7.54E-04	7.65E-02	JUB	jub, ajuba homolog (Xenopus laevis)	chr14q11.2	225806_at	AI289311	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.41	4.87	1.54	7.47E-04	7.65E-02	DENND4B	DENN/MADD domain containing 4B	chr1q21	202860_at	NM_014856	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.01	2.62	1.40	7.49E-04	7.65E-02	---	---	---	236488_s_at	AI683805	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.82	4.66	1.16	7.52E-04	7.65E-02	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	chr19p13.13	210463_x_at	BC002492	Yes	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No
5.66	4.56	1.09	7.54E-04	7.65E-02	PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	chr14q24.1	225727_at	AB033026	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.29	7.26	1.03	7.42E-04	7.65E-02	ENOSF1	enolase superfamily member 1	chr18p11.32	204142_at	NM_017512	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.41	6.42	0.99	7.52E-04	7.65E-02	TJAP1	tight junction associated protein 1 (peripheral)	chr6p21.1	47608_at	AI697401	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.28	7.37	0.91	7.49E-04	7.65E-02	RCN1	reticulocalbin 1, EF-hand calcium binding domain	chr11p13	201063_at	NM_002901	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No	No
8.69	7.79	0.90	7.43E-04	7.65E-02	DCTD	dCMP deaminase	chr4q35.1	210137_s_at	BC001286	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.53	5.83	0.70	7.51E-04	7.65E-02	RFX5	regulatory factor X, 5 (influences HLA class II expression)	chr1q21	202964_s_at	NM_000449	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.48	6.93	0.55	7.48E-04	7.65E-02	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	chr10q25.3	209045_at	AF195530	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.38	4.39	0.99	7.62E-04	7.70E-02	KIAA0317	KIAA0317	chr14q24.3	202128_at	NM_014821	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.99	3.68	1.31	7.67E-04	7.71E-02	SOX4	SRY (sex determining region Y)-box 4	chr6p22.3	201416_at	BG528420	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.50	5.41	1.09	7.66E-04	7.71E-02	CTGLF1 /// CTGLF2 /// CTGLF6 /// CTGLF7 /// RP11-144G6.7	centaurin, gamma-like family, member 1 /// centaurin, gamma-like family, member 2 /// centaurin, gamma-like family, member 6 /// centaurin, gamma-like family, member 7 /// hypothetical LOC399753	chr10q11.21 /// chr10q11.22 /// chr10q22.2	221971_x_at	BE672818	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.91	7.91	1.00	7.66E-04	7.71E-02	TM7SF3	transmembrane 7 superfamily member 3	chr12q11-q12	222477_s_at	BC005176	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.44	6.54	0.89	7.70E-04	7.73E-02	---	---	---	230313_at	AA524412	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.73	4.02	1.71	7.76E-04	7.77E-02	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	chr19q13.2-q13.3	228131_at	BG111047	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
9.80	8.68	1.12	7.80E-04	7.78E-02	DDIT4	DNA-damage-inducible transcript 4	chr10pter-q26.12	202887_s_at	NM_019058	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.76	3.15	2.62	8.05E-04	7.84E-02	MEGF10	multiple EGF-like-domains 10	chr5q33	232523_at	AU144892	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.91	3.16	1.75	7.98E-04	7.84E-02	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	chr10p15.1	214132_at	BG232034	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No	No
7.67	6.35	1.32	7.97E-04	7.84E-02	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	chr8p22-p21	209295_at	AF016266	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.29	3.99	1.30	8.04E-04	7.84E-02	PILRB	paired immunoglobin-like type 2 receptor beta	chr7q22.1	220954_s_at	NM_013440	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.15	5.87	1.28	7.94E-04	7.84E-02	RBM5	RNA binding motif protein 5	chr3p21.3	201394_s_at	U23946	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	No	No
7.51	6.48	1.03	8.04E-04	7.84E-02	DDA1	DET1 and DDB1 associated 1	chr19p13.11	218260_at	NM_024050	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.57	4.68	0.89	7.99E-04	7.84E-02	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	chr1p34	213804_at	AI039084	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.02	6.16	0.86	7.97E-04	7.84E-02	PRUNE	prune homolog (Drosophila)	chr1q21	209586_s_at	AF123539	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.74	7.91	0.83	8.06E-04	7.84E-02	SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	chr17q21-q23	201483_s_at	BC002802	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
10.28	9.47	0.80	7.93E-04	7.84E-02	PTMA	prothymosin, alpha	chr2q35-q36	211921_x_at	AF348514	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.73	7.14	0.59	8.06E-04	7.84E-02	UBAP2L	ubiquitin associated protein 2-like	chr1q21.3	201378_s_at	NM_014847	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.86	6.31	0.55	8.00E-04	7.84E-02	PPIE	peptidylprolyl isomerase E (cyclophilin E)	chr1p32	210502_s_at	AF042386	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No	Yes	No	No	No	Yes	No	No	No
6.16	3.87	2.29	8.15E-04	7.86E-02	SFRS3	Splicing factor, arginine/serine-rich 3	chr6p21	232392_at	BE927772	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No
9.01	7.70	1.31	8.22E-04	7.86E-02	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3	chr17q25.3	201303_at	NM_014740	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes
7.31	6.32	0.99	8.14E-04	7.86E-02	METTL3	methyltransferase like 3	chr14q11.1	209265_s_at	BC001650	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes
5.15	4.18	0.98	8.21E-04	7.86E-02	LOC345630	similar to hCG1641252	chr5q35.1	244071_at	AA868464	Yes	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	No	No	No	No
4.76	3.79	0.97	8.16E-04	7.86E-02	ING1	inhibitor of growth family, member 1	chr13q34	210350_x_at	AF044076	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.30	6.39	0.92	8.19E-04	7.86E-02	NXT1	NTF2-like export factor 1	chr20p12-p11.2	218708_at	NM_013248	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

6.49	5.64	0.86	8.22E-04	7.86E-02	MCM3AP	minichromosome maintenance complex component 3 associated protein	chr21q22.3	212269_s_at	AJ010089	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.91	3.07	0.85	8.21E-04	7.86E-02	LOC440944	Hypothetical gene supported by AK128398	chr3p25.3	232052_at	AL110136	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.78	4.11	1.68	8.23E-04	7.86E-02	FAM122B	family with sequence similarity 122B	chrXq26.3	225361_x_at	AI348001	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.79	6.00	1.78	8.28E-04	7.89E-02	MYLIP	myosin regulatory light chain interacting protein	chr6p23-p22.3	223130_s_at	AF212221	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.53	4.35	1.17	8.34E-04	7.90E-02	FLJ37453	hypothetical protein LOC729614	chr1p36.21	227593_at	AW964477	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.48	7.62	0.86	8.33E-04	7.90E-02	AHCY	S-adenosylhomocysteine hydrolase	chr20cen-q13.1	200903_s_at	NM_000687	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.61	4.84	0.77	8.35E-04	7.90E-02	MGC2752	hypothetical LOC65996	chr19q13.43	218624_s_at	NM_023939	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.96	3.44	1.53	8.37E-04	7.90E-02	MBD6	methyl-CpG binding domain protein 6	---	226076_s_at	AI174548	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.71	6.67	1.04	8.44E-04	7.91E-02	SLC25A38	solute carrier family 25, member 38	chr3p22.1	217961_at	NM_017875	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.55	6.35	1.20	8.52E-04	7.95E-02	CTSB	cathepsin B	chr8p22	213274_s_at	AA020826	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.07	6.16	0.91	8.52E-04	7.95E-02	CPSF3L	cleavage and polyadenylation specific factor 3-like	chr1p36.33	233625_x_at	AK021939	Yes	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
6.81	6.05	0.76	8.51E-04	7.95E-02	WDR46	WD repeat domain 46	chr6p21.3	209196_at	BC000388	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.80	3.58	1.22	8.57E-04	7.96E-02	BCOR	BCL6 co-repressor	chrXp21.2-p11.4	223566_s_at	AF317391	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.71	5.58	1.13	8.56E-04	7.96E-02	PPOX	protoporphyrinogen oxidase	chr1q22	204788_s_at	NM_000309	No	No	No	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No
4.21	3.27	0.93	8.65E-04	8.00E-02	LOC646762	hypothetical protein LOC646762	chr7p15.1	1568597_at	CA309468	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.32	6.55	0.77	8.64E-04	8.00E-02	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	chr17p11.2	227305_s_at	N25727	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.90	3.35	1.55	8.67E-04	8.00E-02	HPSE	heparanase	chr4q21.3	219403_s_at	NM_006665	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.50	5.48	1.03	8.70E-04	8.00E-02	C20orf194	chromosome 20 open reading frame 194	chr20p13	226607_at	AI498144	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.19	6.30	0.89	8.75E-04	8.00E-02	ZNF263	zinc finger protein 263	chr16p13.3	203707_at	NM_005741	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.47	6.58	0.89	8.73E-04	8.00E-02	C19orf12	chromosome 19 open reading frame 12	chr19q12	223983_s_at	BC004957	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.49	5.94	0.55	8.71E-04	8.00E-02	ALKBH1	alkB, alkylation repair homolog 1 (E. coli)	chr14q24.3	205621_at	NM_006020	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.44	2.54	1.91	8.90E-04	8.00E-02	FAM84A	family with sequence similarity 84, member A	chr2p24.3	225667_s_at	AI601101	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.35	5.61	1.74	8.83E-04	8.00E-02	HES1	hairy and enhancer of split 1, (Drosophila)	chr3q28-q29	203394_s_at	BE973687	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.84	4.40	1.44	8.88E-04	8.00E-02	CLEC7A	C-type lectin domain family 7, member A	chr12p13.2	221698_s_at	AF313468	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.27	6.37	0.90	8.82E-04	8.00E-02	UBAP2L	ubiquitin associated protein 2-like	chr1q21.3	201377_at	NM_014847	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.81	7.02	0.79	8.81E-04	8.00E-02	AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	chr8p11.21	224776_at	BF513102	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.34	2.73	0.61	8.81E-04	8.00E-02	---	---	---	240032_at	BE463930	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.34	6.87	1.47	8.92E-04	8.01E-02	SLC26A11	solute carrier family 26, member 11	chr17q25.3	226679_at	BE964598	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.20	2.59	0.60	8.97E-04	8.03E-02	---	---	---	243092_at	AI140189	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.21	4.44	0.77	8.99E-04	8.03E-02	ACTR3B /// LOC100133409	ARP3 actin-related protein 3 homolog B (yeast) /// similar to actin-related protein 3-beta	chr7q36.1	1555487_a_at	BC015207	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.29	5.04	1.25	9.10E-04	8.11E-02	MSI2	musashi homolog 2 (Drosophila)	chr17q22	243010_at	BE000929	No	No	No	No	No	No	No	Yes	No	No	No	No	Yes	No	No	No	No	No	No	No
7.22	4.81	2.42	9.16E-04	8.13E-02	C21orf86	Chromosome 21 open reading frame 86	chr21q22.3	226995_at	AV705934	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.80	4.90	1.90	9.16E-04	8.13E-02	SNHG1	small nucleolar RNA host gene 1 (non-protein coding)	chr11q12.3	224610_at	AL530869	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.66	7.93	0.73	9.16E-04	8.13E-02	TBCB	tubulin folding cofactor B	chr19q13.11-q13.12	216194_s_at	AD001527	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.68	5.57	1.11	9.23E-04	8.18E-02	UPP1	uridine phosphorylase 1	chr7p12.3	203234_at	NM_003364	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.55	3.85	1.70	9.25E-04	8.19E-02	---	---	---	238624_at	AA688152	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
4.20	2.67	1.52	9.42E-04	8.29E-02	LOC386597	hypothetical protein LOC386597	chr2p25.2	1556798_a_at	AK090737	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.12	2.54	0.58	9.42E-04	8.29E-02	GLI3	GLI-Kruppel family member GLI3	chr7p13	1569342_at	BC032660	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	Yes	No
4.37	3.55	0.81	9.44E-04	8.30E-02	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	chr8p12	226384_at	BE858787	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.87	3.66	1.21	9.49E-04	8.31E-02	RGMB	RGM domain family, member B	chr5q21.1	227339_at	BE206621	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.19	5.24	0.95	9.49E-04	8.31E-02	C17orf58	chromosome 17 open reading frame 58	chr17q24.2	226901_at	AI214996	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.65	6.75	0.90	9.52E-04	8.33E-02	MXD4	MAX dimerization protein 4	chr4p16.3	212347_x_at	AA831438	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.27	7.02	1.25	9.55E-04	8.33E-02	ETV5	ets variant gene 5 (ets-related molecule)	chr3q28	203348_s_at	BF060791	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.95	3.33	0.62	9.56E-04	8.33E-02	AFP	alpha-fetoprotein	chr4q11-q13	204694_at	NM_001134	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.31	5.20	2.11	9.58E-04	8.34E-02	NANOS1	nanos homolog 1 (Drosophila)	chr10q26.11	228523_at	AW970089	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No
6.33	5.29	1.04	9.63E-04	8.36E-02	---	---	---	229689_s_at	AV721789	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.78	6.91	0.87	9.67E-04	8.38E-02	COQ2	coenzyme Q2 homolog, prenyltransferase (yeast)	chr4q21.23	213379_at	AF091086	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.90	4.55	1.36	9.82E-04	8.46E-02	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	chr14q11.2	235500_at	AA889628	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	Yes	Yes	No	No	Yes	No	No	No
5.46	4.71	0.74	9.94E-04	8.51E-02	COX4NB	COX4 neighbor	chr16q24	222504_s_at	BC001472	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.72	4.59	1.13	1.00E-03	8.55E-02	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	chr8p22-p21	210405_x_at	AF153687	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.02	3.19	0.83	1.00E-03	8.55E-02	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	chr9q33-q34	214925_s_at	AK026484	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.95	7.27	0.67	1.01E-03	8.57E-02	CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1	chr10q22.2	226896_at	AI992290	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.66	6.29	1.37	1.01E-03	8.58E-02	MSL-1	male-specific lethal-1 homolog	chr17q21.1	212708_at	AV721987	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.02	2.75	1.26	1.02E-03	8.60E-02	AFG3L1	AFG3 ATPase family gene 3-like 1 (S. cerevisiae)	chr16q24.3	1552287_s_at	NM_001132	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.12	4.99	1.12	1.02E-03	8.60E-02	GLI3	GLI-Kruppel family member GLI3	chr7p13	227376_at	AW021102	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	Yes	No
4.75	3.62	1.12	1.03E-03	8.60E-02	FAM46B	family with sequence similarity 46, member B	chr1p36.11	229518_at	AA531023	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.68	4.74	0.95	1.03E-03	8.60E-02	PCGF3	polycomb group ring finger 3	chr4p16.3	204564_at	NM_006315	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.22	8.35	0.87	1.02E-03	8.60E-02	C2orf79	chromosome 2 open reading frame 79	chr2p23.3	226243_at	BF590958	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.78	5.95	0.83	1.03E-03	8.60E-02	COMMD5	COMM domain containing 5	chr8q24-qter	223819_x_at	BC003055	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.73	3.33	1.40	1.03E-03	8.62E-02	TNRC18	trinucleotide repeat containing 18	chr7p22.1	229257_at	AI625045	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.99	7.89	1.10	1.03E-03	8.62E-02	TUBB3	tubulin, beta 3	chr16q24.3	213476_x_at	AL565749	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.83	5.76	1.07	1.04E-03	8.62E-02	WDR54	WD repeat domain 54	chr2p13.1	225898_at	AK023015	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.59	6.93	0.66	1.03E-03	8.62E-02	RNF7	ring finger protein 7	chr3q22-q24	218286_s_at	NM_014245	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.52	4.49	1.03	1.04E-03	8.63E-02	TTLL4	tubulin tyrosine ligase-like family, member 4	chr2p24.3-p24.1	203702_s_at	AL043927	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.32	5.34	0.98	1.04E-03	8.67E-02	FBXL12	F-box and leucine-rich repeat protein 12	chr19p13.2	220127_s_at	NM_017703	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.58	6.89	1.69	1.05E-03	8.71E-02	CASP9	caspase 9, apoptosis-related cysteine peptidase	chr1p36.3-p36.1	203984_s_at	U60521	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.03	7.38	0.65	1.06E-03	8.75E-02	LSM1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr8p11.2	203534_at	NM_014462	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No	Yes	No	No	No	No	No	No	No
7.34	6.46	0.89	1.06E-03	8.77E-02	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	chr7q36.3	224698_at	AB033054	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.47	3.22	2.26	1.08E-03	8.80E-02	IFRD1	interferon-related developmental regulator 1	chr7q22-q31	202146_at	AA747426	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

6.80	4.60	2.21	1.08E-03	8.80E-02	CCNL2	cyclin L2	chr1p36.33	221427_s_at	NM_030937	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes
4.83	3.15	1.68	1.08E-03	8.80E-02	PLAC8	placenta-specific 8	chr4q21.22	219014_at	NM_016619	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.09	6.53	1.56	1.07E-03	8.80E-02	LEF1	lymphoid enhancer-binding factor 1	chr4q23-q25	221558_s_at	AF288571	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	Yes	No
7.24	6.43	0.81	1.08E-03	8.80E-02	DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	chr7p13	217754_at	NM_019082	Yes	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
6.50	5.86	0.63	1.07E-03	8.80E-02	FECH	ferrochelatase (protoporphyria)	chr18q21.3	203116_s_at	NM_000140	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No	No
5.77	2.45	3.32	1.08E-03	8.81E-02	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	chr15q11.2	208798_x_at	AF204231	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.18	7.18	0.99	1.09E-03	8.83E-02	MEPCE	methylphosphate capping enzyme	chr7q22.1	219798_s_at	NM_019606	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.91	7.97	0.94	1.09E-03	8.83E-02	PHC2	polyhomeotic homolog 2 (Drosophila)	chr1p34.3	200919_at	NM_004427	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.23	5.32	0.92	1.09E-03	8.83E-02	LOC100134560	similar to hCG1821214	---	241353_s_at	AW471181	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.06	8.28	0.79	1.09E-03	8.83E-02	FAM128A	family with sequence similarity 128, member A	chr2q21.1	213166_x_at	BG332462	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.93	8.29	0.64	1.09E-03	8.83E-02	RNF7	ring finger protein 7	chr3q22-q24	224439_x_at	BC005966	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.48	4.64	1.84	1.10E-03	8.87E-02	BOK	BCL2-related ovarian killer	chr2q37.3	223349_s_at	BE614255	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.75	4.26	1.49	1.10E-03	8.87E-02	ERP27	endoplasmic reticulum protein 27 kDa	chr12p12.3	227450_at	AI051248	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No	No
5.53	4.48	1.04	1.11E-03	8.87E-02	ZNF513	zinc finger protein 513	chr2p23.3	225753_at	AW003280	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.35	5.40	0.95	1.10E-03	8.87E-02	ARIH2	ariadne homolog 2 (Drosophila)	chr3p21.2-p21.3	201230_s_at	NM_006321	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.82	4.89	0.93	1.11E-03	8.87E-02	L3MBTL2	l(3)mbt-like 2 (Drosophila)	chr22q13.31-q13.33	1555815_a_at	AL136564	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.82	5.98	0.84	1.11E-03	8.87E-02	FAM21A /// FAM21B /// FAM21C /// FAM21D	family with sequence similarity 21, member A /// family with sequence similarity 21, member B /// family with sequence similarity 21, member C /// family with sequence similarity 21, member D	chr10q11.1 /// chr10q11.22 /// chr10q11.23	212929_s_at	W68158	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.88	2.31	0.57	1.11E-03	8.87E-02	---	---	---	1557667_at	N64762	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.75	5.18	1.57	1.12E-03	8.87E-02	SLC44A4	solute carrier family 44, member 4	chr6p21.3	205597_at	NM_025257	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.52	3.72	0.79	1.11E-03	8.87E-02	C6orf81	chromosome 6 open reading frame 81	chr6p21.31	231263_at	AA778643	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.61	3.51	2.10	1.13E-03	8.93E-02	C21orf86	Chromosome 21 open reading frame 86	chr21q22.3	228908_s_at	AW131553	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.14	6.31	1.83	1.13E-03	8.94E-02	ARGLU1	arginine and glutamate rich 1	chr13q33.3	218067_s_at	NM_018011	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.97	5.94	1.03	1.13E-03	8.95E-02	C12orf41	chromosome 12 open reading frame 41	chr12q13.11	221821_s_at	AK022732	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.87	4.02	0.85	1.13E-03	8.95E-02	C22orf29	chromosome 22 open reading frame 29	chr22q11.21	226204_at	AI832193	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.33	6.57	0.76	1.14E-03	8.95E-02	THOC4	THO complex 4	chr17q25.3	226320_at	AF047002	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes	Yes
7.68	6.26	1.42	1.15E-03	8.99E-02	SOX4	SRY (sex determining region Y)-box 4	chr6p22.3	201417_at	AL136179	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.11	6.07	1.04	1.14E-03	8.99E-02	DSP	desmoplakin	chr6p24	200606_at	NM_004415	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.06	4.42	0.64	1.15E-03	8.99E-02	WDR91	WD repeat domain 91	chr7q33	218971_s_at	NM_014149	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.16	2.84	2.31	1.16E-03	9.00E-02	HNRNPA1 /// LOC728844	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC728844	chr12q13.1 /// chr12q13.13	222040_at	AI144007	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	No	No
8.22	6.80	1.42	1.16E-03	9.00E-02	PYCR2	pyrroline-5-carboxylate reductase family, member 2	chr1q42.12	231715_s_at	NM_013328	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.58	4.19	1.40	1.16E-03	9.00E-02	PHLDB3	pleckstrin homology-like domain, family B, member 3	chr19q13.31	1557948_at	BC007947	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.77	2.80	0.96	1.15E-03	9.00E-02	ARC	activity-regulated cytoskeleton-associated protein	chr8q24.3	210090_at	AF193421	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.66	5.75	0.90	1.16E-03	9.00E-02	PSPC1	paraspeckle component 1	chr13q12.11	226574_at	AI872384	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	Yes	No
7.94	7.04	0.90	1.16E-03	9.00E-02	KLHL21	kelch-like 21 (Drosophila)	chr1p36.31	203068_at	NM_014851	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.59	4.96	0.63	1.16E-03	9.00E-02	SFRS8	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	chr12q24.33	202774_s_at	AI871457	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No
8.27	7.42	0.85	1.16E-03	9.01E-02	MRPL46	mitochondrial ribosomal protein L46	chr15q24-q25	219244_s_at	NM_022163	No	No	No	No	No	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No
11.00	10.12	0.88	1.18E-03	9.07E-02	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	chr14q13	201502_s_at	AI078167	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.15	5.94	1.21	1.18E-03	9.08E-02	SC65	synaptonemal complex protein SC65	chr17q21.2	204078_at	NM_006455	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
7.00	5.92	1.09	1.18E-03	9.08E-02	IHPK2	inositol hexaphosphate kinase 2	chr3p21.31	218192_at	NM_016291	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.67	3.01	1.66	1.18E-03	9.09E-02	JUB	jub, ajuba homolog (Xenopus laevis)	chr14q11.2	1553764_a_at	NM_032876	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.97	6.40	0.57	1.19E-03	9.09E-02	---	---	---	226116_at	BF064224	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.90	3.37	1.53	1.20E-03	9.11E-02	LOC283922	hypothetical protein LOC283922	chr16q22.3	228688_at	AA843726	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.52	2.58	0.94	1.20E-03	9.11E-02	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	chr6q22-q23	229088_at	BF591996	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.30	4.49	0.81	1.19E-03	9.11E-02	PDLIM3	PDZ and LIM domain 3	chr4q35	209621_s_at	AF002280	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
8.30	7.56	0.74	1.20E-03	9.11E-02	NT5C3L	5'-nucleotidase, cytosolic III-like	chr17q21.2	225044_at	AL526783	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.51	3.94	0.58	1.20E-03	9.11E-02	PPA2	pyrophosphatase (inorganic) 2	chr4q25	228366_at	BF446912	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.43	6.30	1.13	1.20E-03	9.11E-02	SRRM2	serine/arginine repetitive matrix 2	chr16p13.3	207435_s_at	NM_016333	Yes	Yes	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes	Yes
5.37	4.30	1.07	1.21E-03	9.15E-02	ZNF626	zinc finger protein 626	chr19p12	1552643_at	NM_145297	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.66	4.84	1.81	1.21E-03	9.16E-02	FNBP4	formin binding protein 4	chr11p11.2	212232_at	AB023231	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.89	6.08	0.81	1.22E-03	9.16E-02	CIRBP	cold inducible RNA binding protein	chr19p13.3	228519_x_at	AW027567	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
7.66	6.73	0.93	1.22E-03	9.20E-02	RFX5	regulatory factor X, 5 (influences HLA class II expression)	chr1q21	202963_at	AW027312	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.75	3.43	2.32	1.24E-03	9.23E-02	DACH1	dachshund homolog 1 (Drosophila)	chr13q22	228915_at	AI650353	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
5.10	3.43	1.67	1.23E-03	9.23E-02	SLC25A37	solute carrier family 25, member 37	chr8p21.2	242335_at	AA382004	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.76	4.32	1.44	1.24E-03	9.26E-02	SHB	Src homology 2 domain containing adaptor protein B	chr9p13.2-p13.1	1557458_s_at	BU685917	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.67	6.54	1.13	1.24E-03	9.26E-02	JMJD6	jumonji domain containing 6	chr17q25	212723_at	AK021780	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.82	3.54	2.28	1.26E-03	9.29E-02	CREBZF	CREB/ATF bZIP transcription factor	chr11q14	225594_at	AL038866	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.56	2.63	1.93	1.25E-03	9.29E-02	ARG2	arginase, type II	chr14q24.1-q24.3	203946_s_at	U75667	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.46	4.12	1.34	1.26E-03	9.29E-02	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	chr16q22.1	203580_s_at	NM_003983	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.96	6.98	0.98	1.25E-03	9.29E-02	EWSR1	Ewing sarcoma breakpoint region 1	chr22q12.2	209214_s_at	BC004817	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No
8.76	8.08	0.68	1.26E-03	9.29E-02	UROD	uroporphyrinogen decarboxylase	chr1p34	208971_at	M14016	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.14	3.14	1.00	1.27E-03	9.32E-02	RFX2	regulatory factor X, 2 (influences HLA class II expression)	chr19p13.3-p13.2	226872_at	AK024288	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.10	4.00	2.10	1.29E-03	9.34E-02	RBMX	RNA binding motif protein, X-linked	chrXq26.3	225310_at	AI928344	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	Yes	No	No	No	Yes	Yes	No	No
6.71	4.88	1.82	1.30E-03	9.34E-02	C1orf63	chromosome 1 open reading frame 63	chr1p36.13-p35.1	209007_s_at	AF267856	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.87	7.29	1.58	1.29E-03	9.34E-02	NGEF	neuronal guanine nucleotide exchange factor	chr2q37	227240_at	AV703769	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.82	5.64	1.18	1.29E-03	9.34E-02	TBPL1	TBP-like 1	chr6q22.1-q22.3	208398_s_at	NM_004865	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No

7.09	6.02	1.07	1.29E-03	9.34E-02	CSGLCA-T	chondroitin sulfate glucuronyltransferase	chr7q36.1	55093_at	AA534198	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.69	3.73	0.96	1.28E-03	9.34E-02	ZNF202	zinc finger protein 202	chr11q23.3	204327_s_at	N91520	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.50	4.59	0.92	1.28E-03	9.34E-02	AP4S1	Adaptor-related protein complex 4, sigma 1 subunit	chr14q12	235647_at	AI298279	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.70	5.91	0.79	1.28E-03	9.34E-02	NOL1	nucleolar protein 1, 120kDa	chr12p13	214427_at	NM_006170	Yes	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
7.88	7.24	0.64	1.28E-03	9.34E-02	PTMAP7	prothymosin, alpha pseudogene 7	chr14q32	208549_x_at	NM_016171	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.45	8.96	0.49	1.29E-03	9.34E-02	LOC643287 /// PTMA	similar to prothymosin alpha /// prothymosin, alpha	chr12p13.2 /// chr2q35-q36	216515_x_at	AL121585	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.99	10.50	0.48	1.29E-03	9.34E-02	PTMA	prothymosin, alpha	chr2q35-q36	200773_x_at	NM_002823	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.49	4.70	1.79	1.30E-03	9.35E-02	GADD45G	growth arrest and DNA-damage-inducible, gamma	chr9q22.1-q22.2	204121_at	NM_006705	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.48	2.35	1.13	1.31E-03	9.36E-02	EPPK1	epiplakin 1	chr8q24.3	232164_s_at	AL137725	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.74	3.00	0.75	1.31E-03	9.36E-02	---	---	---	227306_at	AK024898	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.72	3.98	1.74	1.31E-03	9.36E-02	ZNF512B	zinc finger protein 512B	chr20q13.33	55872_at	AI493119	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.71	7.93	0.78	1.32E-03	9.36E-02	IMP3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	chr15q24	221688_s_at	AL136913	Yes	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	No	No	No
8.24	6.92	1.32	1.32E-03	9.41E-02	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	chr6q23.3	207980_s_at	NM_006079	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.07	6.97	1.11	1.33E-03	9.41E-02	ENOSF1	enolase superfamily member 1	chr18p11.32	204143_s_at	NM_017512	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.39	4.30	1.09	1.33E-03	9.41E-02	BAIAP2	BAI1-associated protein 2	chr17q25	209502_s_at	BC002495	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.44	4.60	0.84	1.33E-03	9.44E-02	WHDC1	WAS protein homology region 2 domain containing 1	chr15q25.2	228953_at	AI023634	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.25	3.94	1.31	1.34E-03	9.47E-02	GAS5	growth arrest-specific 5 (non-protein coding)	chr1q25.1	228238_at	AW105301	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.67	5.80	0.87	1.35E-03	9.49E-02	ASMTL	acetylserotonin O-methyltransferase-like	chrXp22.3; Yp11.3	36554_at	Y15521	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.55	5.94	0.61	1.35E-03	9.51E-02	UBA7	ubiquitin-like modifier activating enzyme 7	chr3p21	1294_at	L13852	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.55	3.92	2.63	1.36E-03	9.57E-02	C20orf103	chromosome 20 open reading frame 103	chr20p12	219463_at	NM_012261	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.70	4.72	2.98	1.38E-03	9.61E-02	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	chr22q13.1	36711_at	AL021977	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.40	4.08	1.33	1.38E-03	9.61E-02	NPAS2	neuronal PAS domain protein 2	chr2q11.2	213462_at	AW000928	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
4.19	3.20	0.99	1.38E-03	9.61E-02	CDK3	cyclin-dependent kinase 3	chr17q22-qter	229468_at	AI885421	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.08	6.31	0.77	1.38E-03	9.61E-02	ASXL1	additional sex combs like 1 (Drosophila)	chr20q11.1	212237_at	N64780	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.61	4.88	0.74	1.38E-03	9.61E-02	TRIO	triple functional domain (PTPRF interacting)	chr5p15.2	209011_at	BF223718	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.29	2.09	1.21	1.38E-03	9.62E-02	---	---	---	1556773_at	M31157	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.29	5.02	1.27	1.38E-03	9.62E-02	PRR6	proline rich 6	chr17p11.2	226610_at	AA722878	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.12	5.09	1.03	1.38E-03	9.62E-02	TRRAP	transformation/transcription domain-associated protein	chr7q21.2-q22.1	202642_s_at	NM_003496	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
7.58	6.56	1.02	1.40E-03	9.68E-02	NARF	nuclear prelamin A recognition factor	chr17q25.3	219862_s_at	NM_012336	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No
9.15	6.46	2.69	1.40E-03	9.71E-02	MCOLN3	mucolipin 3	chr1p22.3	229797_at	AI636080	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.43	7.79	1.64	1.41E-03	9.71E-02	NDRG4	NDRG family member 4	chr16q21-q22.1	209159_s_at	AV724216	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.29	5.77	0.53	1.41E-03	9.71E-02	PATL1	protein associated with topoisomerase II homolog 1 (yeast)	chr11q12.1	225466_at	BG291961	No	No	No	No	No	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No	No
8.31	7.08	1.23	1.41E-03	9.74E-02	BEX4	BEX family member 4	chrXq22.1-q22.3	215440_s_at	AL523320	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.85	7.14	0.71	1.42E-03	9.74E-02	EIF2B4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	chr2p23.3	209429_x_at	AF112207	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.72	7.12	0.60	1.42E-03	9.74E-02	SF3B3	splicing factor 3b, subunit 3, 130kDa	chr16q22.1	200687_s_at	NM_012426	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	Yes	No	No	No	Yes	No	No	No
4.34	2.93	1.40	1.43E-03	9.76E-02	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	chrXq23	205583_s_at	NM_024810	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.99	4.69	1.30	1.43E-03	9.76E-02	HOXD9	homeobox D9	chr2q31.1	205604_at	AI432470	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.47	5.52	0.95	1.43E-03	9.76E-02	RUVBL1	RuvB-like 1 (E. coli)	chr3q21	201614_s_at	NM_003707	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	No
7.13	6.37	0.76	1.43E-03	9.76E-02	SF4	splicing factor 4	chr19p13.11	209547_s_at	BC001043	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	No	Yes	No	No	No
5.32	4.75	0.57	1.43E-03	9.76E-02	MGC27345	hypothetical protein MGC27345	chr7q32.1	231844_at	AW072547	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.47	4.31	1.16	1.44E-03	9.77E-02	KIF5C	kinesin family member 5C	chr2q23.1	1557089_at	CA449408	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.57	2.57	1.00	1.45E-03	9.77E-02	PGM2L1	phosphoglucomutase 2-like 1	chr11q13.4	229256_at	AV724329	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.97	2.14	0.83	1.44E-03	9.77E-02	FLJ44342	hypothetical LOC645460	chr17q22	239384_at	R18746	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.43	4.64	0.79	1.44E-03	9.77E-02	CHRNB1	cholinergic receptor, nicotinic, beta 1 (muscle)	chr17p13.1	206703_at	NM_000747	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.11	2.68	0.43	1.44E-03	9.77E-02	ZAN	zonadhesin	chr7q22	224265_s_at	AF332980	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.09	5.29	0.79	1.45E-03	9.77E-02	HSPC111	hypothetical protein HSPC111	chr5q35.2	203023_at	NM_016391	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
4.67	3.17	1.50	1.46E-03	9.81E-02	DLL1	delta-like 1 (Drosophila)	chr6q27	224215_s_at	AF196571	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.40	5.02	1.37	1.46E-03	9.81E-02	PAN2	PAN2 polyA specific ribonuclease subunit homolog (S. cerevisiae)	chr12q13.2-q13.3	203117_s_at	NM_014871	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.93	6.85	1.08	1.46E-03	9.81E-02	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF12 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 12 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	201104_x_at	NM_015383	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.51	6.48	1.02	1.46E-03	9.81E-02	NEFH	neurofilament, heavy polypeptide 200kDa	chr22q12.2	33767_at	X15306	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
9.81	9.17	0.64	1.46E-03	9.81E-02	C6orf48	chromosome 6 open reading frame 48	chr6p21.3	220755_s_at	NM_016947	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.14	5.54	0.60	1.46E-03	9.81E-02	SPEN	spen homolog, transcriptional regulator (Drosophila)	chr1p36.33-p36.11	201997_s_at	NM_015001	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
7.32	6.55	0.77	1.47E-03	9.82E-02	LUZP1	leucine zipper protein 1	chr1p36	225831_at	AW016830	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.53	6.69	0.84	1.48E-03	9.87E-02	NUBP1	nucleotide binding protein 1 (MinD homolog, E. coli)	chr16p13.13	203978_at	NM_002484	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.93	5.70	1.23	1.48E-03	9.87E-02	SFRS14	splicing factor, arginine/serine-rich 14	chr19p12	214092_x_at	AI928127	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No	No	No	No	No	No	No	No	No

7.39	6.61	0.77	1.48E-03	9.87E-02	COX4NB	COX4 neighbor	chr16q24	218057_x_at	NM_006067	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.67	6.64	1.03	1.49E-03	9.88E-02	TSPYL2	TSPY-like 2	chrXp11.2	218012_at	NM_022117	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
5.36	4.39	0.97	1.49E-03	9.89E-02	COX4I1	cytochrome c oxidase subunit IV isoform 1	chr16q22-qter	213758_at	AW337510	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.57	3.25	1.32	1.52E-03	9.93E-02	CNNM2	cyclin M2	chr10q24.32	1554522_at	BC021222	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.79	3.71	1.08	1.50E-03	9.93E-02	ZC3H12A	zinc finger CCCH-type containing 12A	chr1p34.3	218810_at	NM_025079	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.17	4.10	1.07	1.53E-03	9.93E-02	C14orf149	chromosome 14 open reading frame 149	chr14q23.1	227699_at	BF511003	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.40	5.35	1.04	1.52E-03	9.93E-02	KPNA2 /// LOC728860	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) /// karyopherin alpha-2 subunit like	chr17q24.2	201088_at	NM_002266	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	No	No
7.06	6.08	0.98	1.52E-03	9.93E-02	SLC35E3	solute carrier family 35, member E3	chr12q15	218988_at	NM_018656	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.31	6.45	0.86	1.52E-03	9.93E-02	CSGLCA-T	chondroitin sulfate glucuronyltransferase	chr7q36.1	221799_at	AB037823	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.28	6.46	0.82	1.51E-03	9.93E-02	PRMT5	protein arginine methyltransferase 5	chr14q11.2-q21	217786_at	NM_006109	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No
6.32	5.62	0.70	1.52E-03	9.93E-02	UBP1	upstream binding protein 1 (LBP-1a)	chr3p22.3	218082_s_at	NM_014517	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.43	3.76	0.67	1.52E-03	9.93E-02	AQP3	aquaporin 3 (Gill blood group)	chr9p13	39249_at	AB001325	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.19	3.62	0.57	1.51E-03	9.93E-02	LOC100127955 /// LOC100128374	hypothetical LOC100127955 /// hypothetical LOC100128374	chr7p22.3	1563709_at	AK095485	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.99	5.45	0.54	1.52E-03	9.93E-02	TBP	TATA box binding protein	chr6q27	203135_at	NM_003194	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	Yes	No
5.93	5.07	0.86	1.53E-03	9.93E-02	MAML3	mastermind-like 3 (Drosophila)	chr4q28	242794_at	AI569476	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes
6.10	4.52	1.58	1.54E-03	9.94E-02	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene	chr15q11.2	213737_x_at	AI620911	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.86	4.49	1.37	1.55E-03	9.94E-02	NGEF	neuronal guanine nucleotide exchange factor	chr2q37	243556_at	R89026	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.30	5.06	1.25	1.55E-03	9.94E-02	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	chr7q22.1	212666_at	AB046845	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.14	5.26	0.89	1.54E-03	9.94E-02	LOC729570	Similar to hCG1793303	chr2q33.3	227837_at	BF057711	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.34	7.52	0.82	1.54E-03	9.94E-02	UBE2Z	ubiquitin-conjugating enzyme E2Z	chr17q21.32	217750_s_at	NM_023079	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
8.80	7.99	0.80	1.54E-03	9.94E-02	TBCB	tubulin folding cofactor B	chr19q13.11-q13.12	211759_x_at	BC005969	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.95	2.42	0.53	1.54E-03	9.94E-02	CXorf52 /// LOC100132967	chromosome X open reading frame 52 /// similar to hCG2042244	chrXq28	1552607_at	NM_173168	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.35	5.40	0.95	1.55E-03	9.96E-02	TPST1	tyrosylprotein sulfotransferase 1	chr7q11.21	204140_at	NM_003596	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.49	2.67	0.82	1.55E-03	9.96E-02	MBD1	methyl-CpG binding domain protein 1	chr18q21	241813_at	BG252318	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes	Yes
9.66	7.78	1.88	1.56E-03	1.00E-01	TIMP3	TIMP metallopeptidase inhibitor 3	chr22q12.1-q13.2|22q12.3	201147_s_at	BF347089	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.24	4.77	1.46	1.57E-03	1.00E-01	HHEX	hematopoietically expressed homeobox	chr10q23.33	204689_at	NM_001529	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.63	5.36	1.27	1.57E-03	1.00E-01	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	chr16q24.3	202104_s_at	NM_003119	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.00	5.17	0.83	1.57E-03	1.00E-01	PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	chr1q23-q25	216593_s_at	AB000359	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.03	7.26	0.77	1.57E-03	1.00E-01	TRIP6	thyroid hormone receptor interactor 6	chr7q22	209129_at	AF000974	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.17	6.43	0.74	1.57E-03	1.00E-01	NOL9	nucleolar protein 9	chr1p36.31	218754_at	NM_024654	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
8.37	7.45	0.91	1.58E-03	1.00E-01	TUBB3	tubulin, beta 3	chr16q24.3	202154_x_at	NM_006086																			
5.43	4.43	0.99	1.58E-03	1.00E-01	NLRC5	NLR family, CARD domain containing 5	chr16q13	226474_at	NM_032206																			
12.39	10.90	1.49	1.58E-03	1.01E-01	DCN	decorin	chr12q21.33	211813_x_at	NM_001920 /// NM_133503 /// NM_133504 /// NM_133505 /// NM_133506 /// NM_133507																			
6.75	5.78	0.97	1.59E-03	1.01E-01	WDR73	WD repeat domain 73	chr15q25.2	213031_s_at	NM_032856																			
7.53	6.59	0.94	1.59E-03	1.01E-01	CDK5RAP3	CDK5 regulatory subunit associated protein 3	chr17q21.32	218740_s_at	NM_176096																			
6.82	5.93	0.89	1.59E-03	1.01E-01	PHF23	PHD finger protein 23	chr17p13.1	1555789_s_at	NM_024297																			
5.14	3.89	1.25	1.59E-03	1.01E-01	---	---	---	231952_at	---																			
3.94	3.12	0.82	1.60E-03	1.01E-01	---	---	---	227505_at	---																			
6.58	6.10	0.48	1.61E-03	1.01E-01	NFYC	nuclear transcription factor Y, gamma	chr1p32|1p32	202216_x_at	NM_014223																			
9.09	8.44	0.65	1.62E-03	1.01E-01	CAMTA1	calmodulin binding transcription activator 1	chr1p36.31-p36.23	225693_s_at	NM_015215																			
7.36	6.32	1.04	1.62E-03	1.01E-01	NSUN5	NOL1/NOP2/Sun domain family, member 5	chr7q11.23	213773_x_at	NM_018044 /// NM_148956																			
10.11	9.11	1.01	1.62E-03	1.01E-01	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	chr22q13.1	208718_at	NM_001098504 /// NM_001098505 /// NM_006386 /// NM_030881																			
6.67	5.81	0.86	1.62E-03	1.01E-01	ACD	adrenocortical dysplasia homolog (mouse)	chr16q22.1	204617_s_at	NM_001082486 /// NM_001082487 /// NM_022914																			
6.73	5.84	0.89	1.64E-03	1.02E-01	PCGF5	polycomb group ring finger 5	chr10q23.32	227935_s_at	NM_032373																			

6.75	6.17	0.58	1.64E-03	1.02E-01	PMS2L3	postmeiotic segregation increased 2-like 3	chr7q11.23	216525_x_at	NM_001003686 /// NM_005395 /// XM_001716315																				
2.97	2.32	0.65	1.64E-03	1.02E-01	SPIN4	spindlin family, member 4	chrXq11.1	228654_at	NM_001012968																				
5.53	4.56	0.98	1.65E-03	1.02E-01	AKAP8L	A kinase (PRKA) anchor protein 8-like	chr19p13.12	218064_s_at	NM_014371																				
5.71	3.47	2.24	1.65E-03	1.03E-01	RGS7	regulator of G-protein signaling 7	chr1q43|1q23.1	206290_s_at	NM_002924																				
3.87	3.17	0.70	1.66E-03	1.03E-01	LASS6	LAG1 homolog, ceramide synthase 6	chr2q24.3	235463_s_at	NM_203463																				
6.46	5.35	1.11	1.66E-03	1.03E-01	ETV5	ets variant gene 5 (ets-related molecule)	chr3q28	216375_s_at	NM_004454																				
6.18	3.39	2.79	1.66E-03	1.03E-01	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	chr2p23.2	1568768_s_at	NM_004899 /// NM_199191 /// NM_199192 /// NM_199193 /// NM_199194																				
5.94	4.52	1.41	1.67E-03	1.03E-01	NSUN5B	NOL1/NOP2/Sun domain family, member 5B	chr7q11.23	213670_x_at	NM_001039575 /// NM_001039576 /// NM_145645																				
7.32	6.67	0.65	1.68E-03	1.03E-01	EHD1	EH-domain containing 1	chr11q13	209039_x_at	NM_006795																				
6.47	5.36	1.11	1.68E-03	1.03E-01	LMBR1L	limb region 1 homolog (mouse)-like	chr12q13.12	220036_s_at	NM_018113																				
5.26	4.50	0.76	1.69E-03	1.04E-01	FNTB	farnesyltransferase, CAAX box, beta	chr14q23-q24	1773_at	NM_002028																				
5.61	4.53	1.08	1.70E-03	1.04E-01	MIZF	MBD2-interacting zinc finger	chr11q23.3	206495_s_at	NM_015517 /// NM_198971																				
6.50	5.02	1.47	1.71E-03	1.05E-01	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	chr13q14	218352_at	NM_018191																				
7.30	6.36	0.94	1.72E-03	1.05E-01	GRAMD1A	GRAM domain containing 1A	chr19q13.11	224807_at	NM_020895																				
3.22	1.97	1.25	1.72E-03	1.05E-01	PTHLH	parathyroid hormone-like hormone	chr12p12.1-p11.2	210355_at	NM_002820 /// NM_198964 /// NM_198965 /// NM_198966																				
7.34	6.08	1.26	1.72E-03	1.05E-01	CYBRD1	cytochrome b reductase 1	chr2q31.1	217889_s_at	NM_001127383 /// NM_024843																				
3.92	2.41	1.51	1.72E-03	1.05E-01	LOC100130837	Hypothetical protein LOC100130837	chr10p15.3	242255_at	XM_001717688 /// XM_001720700 /// XM_001724535																				
8.31	7.63	0.68	1.74E-03	1.05E-01	IRF2BP2	interferon regulatory factor 2 binding protein 2	chr1q42.3	224572_s_at	NM_001077397 /// NM_182972																				
10.08	9.32	0.76	1.74E-03	1.05E-01	PTMA	prothymosin, alpha	chr2q35-q36	200772_x_at	NM_001099285 /// NM_002823																				
8.02	7.05	0.97	1.74E-03	1.05E-01	WDR45	WD repeat domain 45	chrXp11.23	209217_s_at	NM_001029896 /// NM_007075																				
6.72	5.08	1.64	1.75E-03	1.06E-01	HES1	hairy and enhancer of split 1, (Drosophila)	chr3q28-q29	203395_s_at	NM_005524																				
4.36	3.54	0.82	1.76E-03	1.06E-01	NRF1	nuclear respiratory factor 1	chr7q32	204651_at	NM_001040110 /// NM_005011																				
7.58	7.03	0.55	1.76E-03	1.06E-01	TMEM183A /// TMEM183B	transmembrane protein 183A /// transmembrane protein 183B	chr1q32.1 /// chr3q25.1	212165_at	NM_001079809 /// NM_138391																				
9.10	6.98	2.11	1.76E-03	1.06E-01	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	chr2q33-q34	202718_at	NM_000597																				
6.35	4.19	2.16	1.76E-03	1.06E-01	tcag7.907	hypothetical LOC402483	chr7q32.1	227129_x_at	XR_040932 /// XR_040933 /// XR_040934 /// XR_040935																				
4.66	3.76	0.90	1.78E-03	1.06E-01	PER2	period homolog 2 (Drosophila)	chr2q37.3	205251_at	NM_022817																				

6.93	5.97	0.97	1.78E-03	1.06E-01	FAM127B	family with sequence similarity 127, member B	chrXq26.3	217948_at	NM_001078172 /// NM_001134321																				
7.35	5.77	1.58	1.78E-03	1.06E-01	HHEX	hematopoietically expressed homeobox	chr10q23.33	215933_s_at	NM_002729																				
7.27	6.61	0.66	1.78E-03	1.06E-01	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	213772_s_at	NM_015044																				
6.00	4.61	1.40	1.79E-03	1.06E-01	---	---	---	227356_at	---																				
5.17	2.74	2.43	1.79E-03	1.06E-01	GOLGA8A /// GOLGA8B	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B	chr15q11.2 /// chr15q14	210425_x_at	NM_001023567 /// NM_181077 /// XM_001714558																				
5.96	4.32	1.65	1.79E-03	1.06E-01	C1orf85	chromosome 1 open reading frame 85	chr1q22	1558692_at	NM_144580																				
8.12	7.45	0.67	1.80E-03	1.06E-01	NAGK	N-acetylglucosamine kinase	chr2p13.3	218231_at	NM_017567																				
7.20	6.03	1.18	1.80E-03	1.06E-01	ILF3	interleukin enhancer binding factor 3, 90kDa	chr19p13.2	211375_s_at	NM_004516 /// NM_012218 /// NM_153464																				
7.79	7.15	0.64	1.80E-03	1.06E-01	CDC37	cell division cycle 37 homolog (S. cerevisiae)	chr19p13.2	209953_s_at	NM_007065																				
9.38	7.97	1.41	1.80E-03	1.06E-01	TIMP3	TIMP metallopeptidase inhibitor 3	chr22q12.1-q13.2|22q12.3	201148_s_at	NM_000362																				
4.97	3.37	1.60	1.80E-03	1.06E-01	SMG1	PI-3-kinase-related kinase SMG-1	chr16p12.3	224842_at	NM_015092																				
5.25	3.81	1.45	1.82E-03	1.07E-01	LOC400027	hypothetical gene supported by BC047417	chr12q12	226413_at	XM_001718517 /// XM_931434 /// XM_943193																				
6.65	5.66	1.00	1.83E-03	1.07E-01	SMC1A	structural maintenance of chromosomes 1A	chrXp11.22-p11.21	201589_at	NM_006306																				
8.60	7.67	0.92	1.83E-03	1.07E-01	GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	chr22q13.31	45572_s_at	NM_001001560 /// NM_001001561 /// NM_013365																				
5.46	4.86	0.60	1.83E-03	1.07E-01	ZNF133	zinc finger protein 133	chr20p11.23-p11.22	216960_s_at	NM_001083330 /// NM_003434																				
8.84	8.24	0.60	1.83E-03	1.07E-01	HBXIP	hepatitis B virus x interacting protein	chr1p13.3	202300_at	NM_006402																				
7.26	6.27	0.99	1.84E-03	1.08E-01	NAB2	NGFI-A binding protein 2 (EGR1 binding protein 2)	chr12q13.3-q14.1	212803_at	NM_005967																				
9.65	8.56	1.10	1.84E-03	1.08E-01	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	chr1q21	214853_s_at	NM_001130040 /// NM_001130041 /// NM_003029 /// NM_183001																				
5.34	4.59	0.75	1.85E-03	1.08E-01	SOX13	SRY (sex determining region Y)-box 13	chr1q32	38918_at	NM_005686																				
6.00	5.15	0.85	1.85E-03	1.08E-01	---	---	---	225499_at	---																				
5.64	5.01	0.63	1.86E-03	1.08E-01	TTC9C	tetratricopeptide repeat domain 9C	chr11q12.3	226175_at	NM_173810																				
6.65	5.92	0.73	1.87E-03	1.08E-01	NADSYN1	NAD synthetase 1	chr11q13.4	232946_s_at	NM_018161																				
4.42	3.23	1.19	1.87E-03	1.08E-01	WDR4	WD repeat domain 4	chr21q22.3	241937_s_at	NM_018669 /// NM_033661																				
7.66	7.04	0.62	1.87E-03	1.08E-01	PQBP1	polyglutamine binding protein 1	chrXp11.23	214527_s_at	NM_001032381 /// NM_001032382 /// NM_001032383 /// NM_001032384 /// NM_005710																				
6.67	5.90	0.77	1.87E-03	1.08E-01	CERK	ceramide kinase	chr22q13.31	218421_at	NM_022766																				
8.14	7.16	0.98	1.88E-03	1.08E-01	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	chr16q24.3	214494_s_at	NM_003119 /// NM_199367																				
5.22	4.29	0.92	1.88E-03	1.08E-01	CLTCL1	clathrin, heavy chain-like 1	chr22q11.2|22q11.21	205944_s_at	NM_007098																				
5.77	4.38	1.39	1.89E-03	1.08E-01	SLC25A37	Solute carrier family 25, member 37	chr8p21.2	228527_s_at	NM_016612																				
6.36	4.99	1.37	1.90E-03	1.09E-01	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	chr7p15.3	204681_s_at	NM_012294																				
8.95	8.10	0.84	1.90E-03	1.09E-01	RNASET2	ribonuclease T2	chr6q27	217983_s_at	NM_003730																				
6.78	6.05	0.73	1.90E-03	1.09E-01	ERLIN1	ER lipid raft associated 1	chr10q21-q22	202441_at	NM_001100626 /// NM_006459																				

10.08	9.24	0.84	1.91E-03	1.09E-01	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	chr17q22	208161_s_at	NM_003786																					
6.80	6.04	0.76	1.92E-03	1.09E-01	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	chr20q13.13	219108_x_at	NM_017895																					
4.11	3.29	0.82	1.92E-03	1.09E-01	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B	chr12q23.1	227439_at	NM_020140 /// NM_152788 /// NM_181670																					
7.96	6.42	1.54	1.92E-03	1.09E-01	CXorf40A	chromosome X open reading frame 40A	chrXq28	213315_x_at	NM_178124																					
4.75	4.05	0.70	1.93E-03	1.09E-01	ACACB	acetyl-Coenzyme A carboxylase beta	chr12q24.11	1552616_a_at	NM_001093																					
7.44	5.50	1.94	1.93E-03	1.09E-01	CCDC84	coiled-coil domain containing 84	chr11q23.3	227208_at	NM_198489																					
9.21	8.43	0.78	1.93E-03	1.09E-01	DUT	deoxyuridine triphosphatase	chr15q15-q21.1	208956_x_at	NM_001025248 /// NM_001025249 /// NM_001948																					
7.94	7.27	0.68	1.93E-03	1.09E-01	LOC100130633 /// ZMYM6	similar to ZMYM6 protein /// zinc finger, MYM-type 6	chr1p34.2 /// chr1p34.3	213698_at	NM_007167 /// XM_001723998 /// XM_001724926 /// XM_001725169																					
5.93	3.58	2.35	1.94E-03	1.09E-01	EDNRA	endothelin receptor type A	chr4q31.23	204463_s_at	NM_001957																					
6.55	5.75	0.80	1.94E-03	1.09E-01	RPS28	ribosomal protein S28	chr19p13.2	208903_at	NM_001031																					
5.82	4.57	1.26	1.94E-03	1.09E-01	---	---	---	240991_at	---																					
4.50	2.45	2.06	1.94E-03	1.09E-01	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	chr2p15	226665_at	NM_152392																					
11.87	11.42	0.45	1.94E-03	1.09E-01	RPL15	ribosomal protein L15	chr3p24.2	221475_s_at	NM_002948																					
8.99	7.10	1.89	1.95E-03	1.09E-01	---	---	---	227826_s_at	---																					
6.31	5.10	1.21	1.95E-03	1.09E-01	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	chr9q21.32	203222_s_at	NM_005077																					
7.95	6.43	1.51	1.95E-03	1.09E-01	CXorf40A /// CXorf40B	chromosome X open reading frame 40A /// chromosome X open reading frame 40B	chrXq28	214112_s_at	NM_001013845 /// NM_178124																					
7.82	7.09	0.73	1.96E-03	1.09E-01	YY1AP1	YY1 associated protein 1	chr1q22	217836_s_at	NM_139118 /// NM_139119																					
6.83	6.08	0.75	1.96E-03	1.09E-01	EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	chr3q27.1	212351_at	NM_003907																					
7.09	5.65	1.44	1.96E-03	1.09E-01	PVT1	Pvt1 oncogene (non-protein coding)	chr8q24	1558290_a_at	NR_003367																					
6.22	5.28	0.94	1.96E-03	1.09E-01	GPN2	GPN-loop GTPase 2	chr1p36.11	218799_at	NM_018066																					
8.58	7.69	0.89	1.96E-03	1.09E-01	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	chr17q22	209641_s_at	NM_003786																					
5.06	3.93	1.13	1.96E-03	1.09E-01	LOC100131731	hypothetical protein LOC100131731	chr14q11.2	1557263_s_at	XM_001714984 /// XM_001716923 /// XM_001717178																					
7.55	6.65	0.90	1.97E-03	1.09E-01	TMCO3	transmembrane and coiled-coil domains 3	chr13q34	226050_at	NM_017905																					
7.82	6.94	0.88	1.98E-03	1.10E-01	TENC1	tensin like C1 domain containing phosphatase (tensin 2)	chr12q13.13	212494_at	NM_015319 /// NM_170754 /// NM_198316																					
5.32	4.46	0.86	1.98E-03	1.10E-01	TMCO3	transmembrane and coiled-coil domains 3	chr13q34	220240_s_at	NM_017905																					
5.09	3.19	1.90	1.98E-03	1.10E-01	FAM46A	family with sequence similarity 46, member A	chr6q14	224973_at	NM_017633																					
3.83	2.88	0.95	1.99E-03	1.10E-01	---	---	---	1561367_a_at	---																					
7.16	6.07	1.09	1.99E-03	1.10E-01	RPUSD3	RNA pseudouridylate synthase domain containing 3	chr3p25.3	225743_at	NM_173659																					
7.24	6.26	0.98	1.99E-03	1.10E-01	ACACB	acetyl-Coenzyme A carboxylase beta	chr12q24.11	221928_at	NM_001093																					
5.49	4.58	0.92	2.00E-03	1.10E-01	SETD6	SET domain containing 6	chr16q21	1554555_a_at	NM_024860																					
7.05	6.38	0.67	2.00E-03	1.10E-01	EHD1	EH-domain containing 1	chr11q13	222221_x_at	NM_006795																					
6.31	5.20	1.11	2.01E-03	1.10E-01	GALE	UDP-galactose-4-epimerase	chr1p36-p35	202528_at	NM_000403 /// NM_001008216 /// NM_001127621																					
6.47	5.72	0.75	2.01E-03	1.10E-01	CPSF3L	cleavage and polyadenylation specific factor 3-like	chr1p36.33	233563_s_at	NM_017871																					
7.19	6.38	0.81	2.02E-03	1.10E-01	CDC2L2	cell division cycle 2-like 2 (PITSLRE proteins)	chr1p36.33	212401_s_at	NM_024011 /// NM_033529																					

3.14	2.47	0.67	2.02E-03	1.10E-01	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B	chr12q23.1	227441_s_at	NM_020140 /// NM_152788 /// NM_181670																				
3.47	2.59	0.88	2.03E-03	1.10E-01	---	---	---	240343_at	---																				
7.50	6.78	0.72	2.03E-03	1.10E-01	PDIA4	protein disulfide isomerase family A, member 4	chr7q35	211048_s_at	NM_004911																				
6.51	5.40	1.11	2.03E-03	1.10E-01	FAM131A	family with sequence similarity 131, member A	chr3q27.1	221904_at	NM_144635																				
6.42	4.41	2.01	2.04E-03	1.11E-01	KIAA0907	KIAA0907	chr1q22	202220_at	NM_014949																				
2.94	2.24	0.70	2.05E-03	1.11E-01	SNHG3	small nucleolar RNA host gene 3 (non-protein coding)	chr1p36.1	215011_at	NR_002909																				
3.69	2.45	1.24	2.06E-03	1.11E-01	EPPK1	epiplakin 1	chr8q24.3	232165_at	NM_031308																				
6.66	5.98	0.68	2.06E-03	1.11E-01	SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	chr2pter-p25.1	201837_s_at	NM_014860																				
5.84	4.52	1.33	2.06E-03	1.11E-01	PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	chr16q22.1	228171_s_at	NM_001129727 /// NM_001129728 /// NM_001129729 /// NM_001129731 /// NM_015432																				
9.08	7.12	1.96	2.06E-03	1.11E-01	LOC572558	hypothetical locus LOC572558	chr9q13	230595_at	XR_017794 /// XR_041305																				
5.71	4.84	0.87	2.06E-03	1.11E-01	NFRKB	nuclear factor related to kappaB binding protein	chr11q24-q25	213028_at	NM_006165																				
6.05	4.83	1.22	2.07E-03	1.11E-01	KCTD5	potassium channel tetramerisation domain containing 5	chr16p13.3	218474_s_at	NM_018992																				
7.55	6.56	1.00	2.07E-03	1.11E-01	PPP1R10	protein phosphatase 1, regulatory (inhibitor) subunit 10	chr6p21.3	201703_s_at	NM_002714																				
8.24	7.69	0.55	2.08E-03	1.11E-01	MRPS18B	mitochondrial ribosomal protein S18B	chr6p21.3	208907_s_at	NM_014046																				
4.98	4.15	0.84	2.08E-03	1.11E-01	HP1BP3	Heterochromatin protein 1, binding protein 3	chr1p36.12	229204_at	NM_016287																				
6.67	6.15	0.52	2.09E-03	1.12E-01	POLR2J2 /// POLR2J3 /// POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J2 /// polymerase (RNA) II (DNA directed) polypeptide J3 /// polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13 /// chr7q22.1	216242_x_at	NM_001097615 /// NM_032959 /// NR_003655 /// XR_042143 /// XR_042182																				
6.66	5.40	1.26	2.09E-03	1.12E-01	PCF11	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	chr11q13	227622_at	NM_015885																				
7.66	6.91	0.75	2.09E-03	1.12E-01	C16orf61	chromosome 16 open reading frame 61	chr16q23.2	218447_at	NM_020188																				
7.42	6.36	1.06	2.11E-03	1.12E-01	SGSM2	small G protein signaling modulator 2	chr17p13.3	36129_at	NM_001098509 /// NM_014853																				
6.17	4.91	1.26	2.11E-03	1.12E-01	LOC100128259 /// LOC346887	hypothetical protein LOC100128259 /// similar to solute carrier family 16 (monocarboxylic acid transporters), member 14	chr8q23.1	235205_at	XM_001717648 /// XM_001717651 /// XM_001717743 /// XM_294450 /// XM_943533																				
5.02	3.58	1.44	2.11E-03	1.12E-01	GPRC5A	G protein-coupled receptor, family C, group 5, member A	chr12p13-p12.3	203108_at	NM_003979																				
6.84	6.17	0.66	2.12E-03	1.13E-01	FAM58A	family with sequence similarity 58, member A	chrXq28	226466_s_at	NM_001130997 /// NM_152274																				
5.42	4.70	0.72	2.12E-03	1.13E-01	USP54	ubiquitin specific peptidase 54	chr10q22.2	227334_at	NM_152586																				
5.84	4.52	1.33	2.12E-03	1.13E-01	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	chr15q26.3	206055_s_at	NM_003090																				
4.20	2.72	1.48	2.13E-03	1.13E-01	---	---	---	235092_at	---																				
6.52	5.68	0.84	2.14E-03	1.13E-01	RCL1	RNA terminal phosphate cyclase-like 1	chr9p24.1-p23	222666_s_at	NM_005772																				
5.94	4.50	1.44	2.14E-03	1.13E-01	PMEPA1	prostate transmembrane protein, androgen induced 1	chr20q13.31|20q13.31-q13.33	222449_at	NM_020182 /// NM_199169 /// NM_199170 /// NM_199171																				
7.16	5.94	1.21	2.14E-03	1.13E-01	LOC389023	hypothetical gene supported by BC032913; BC048425	chr2q14.1	236351_at	XM_001716001 /// XM_001716702																				
8.22	7.35	0.87	2.16E-03	1.14E-01	STAT2	signal transducer and activator of transcription 2, 113kDa	chr12q13.2	225636_at	NM_005419																				
4.40	3.44	0.97	2.17E-03	1.14E-01	---	---	---	1556103_at	---																				
5.72	5.20	0.52	2.17E-03	1.14E-01	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	chr6p25.2	226551_at	NM_003804																				

7.60	6.91	0.70	2.18E-03	1.14E-01	C21orf33	chromosome 21 open reading frame 33	chr21q22.3	210667_s_at	NM_004649 /// NM_198155
7.56	4.93	2.63	2.18E-03	1.14E-01	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	chr9q32-q33.3	205128_x_at	NM_000962 /// NM_080591
2.84	2.34	0.50	2.18E-03	1.14E-01	CCHCR1	coiled-coil alpha-helical rod protein 1	chr6p21.3	42361_g_at	NM_001105563 /// NM_001105564 /// NM_019052
5.67	4.48	1.19	2.18E-03	1.14E-01	SATB2	SATB homeobox 2	chr2q33	213435_at	NM_015265
6.03	5.09	0.93	2.19E-03	1.14E-01	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	chr11p15.5	221562_s_at	NM_001017524 /// NM_012239
4.56	2.71	1.85	2.20E-03	1.14E-01	IL17RB	interleukin 17 receptor B	chr3p21.1	224156_x_at	NM_018725
5.40	4.20	1.20	2.20E-03	1.14E-01	CREB3L2	cAMP responsive element binding protein 3-like 2	chr7q34	228759_at	NM_194071
5.69	3.65	2.05	2.20E-03	1.14E-01	MREG	melanoregulin	chr2q35	219648_at	NM_018000
9.17	8.47	0.70	2.20E-03	1.14E-01	TUBB2C	tubulin, beta 2C	chr9q34	208977_x_at	NM_006088
3.79	2.23	1.56	2.20E-03	1.14E-01	FLJ40113 /// LOC440295 /// LOC728636	golgi autoantigen, golgin subfamily a-like pseudogene /// hypothetical protein LOC440295 /// similar to golgi autoantigen, golgin subfamily a-like	chr15q25.2	213212_x_at	NM_198079 /// NM_198181 /// NR_003246 /// XM_001714387
7.03	6.37	0.66	2.21E-03	1.14E-01	MRPL9	mitochondrial ribosomal protein L9	chr1q21	211594_s_at	NM_031420
9.21	7.84	1.37	2.21E-03	1.14E-01	HIST2H2AA3 /// HIST2H2AA4	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	chr1q21.2	214290_s_at	NM_001040874 /// NM_003516
6.83	6.05	0.78	2.21E-03	1.14E-01	IDS	iduronate 2-sulfatase	chrXq28	212221_x_at	NM_000202 /// NM_006123
7.37	6.25	1.12	2.21E-03	1.14E-01	KIAA0913	KIAA0913	chr10q22.2	212359_s_at	NM_015037
4.50	3.91	0.58	2.21E-03	1.14E-01	NFRKB	nuclear factor related to kappaB binding protein	chr11q24-q25	206968_s_at	NM_006165
4.46	3.70	0.76	2.22E-03	1.14E-01	CDRT4	CMT1A duplicated region transcript 4	chr17p12	228482_at	NM_173622
8.69	7.58	1.11	2.22E-03	1.14E-01	WDR6	WD repeat domain 6	chr3p21.31	217734_s_at	NM_018031
7.36	6.54	0.81	2.23E-03	1.14E-01	---	---	---	227762_at	---
5.52	4.87	0.65	2.23E-03	1.14E-01	C6orf64	chromosome 6 open reading frame 64	chr6p21.2	222741_s_at	NM_018322
5.88	5.21	0.67	2.23E-03	1.14E-01	FAM130A1	family with sequence similarity 130, member A1	chr12q13.11-q13.12	225042_s_at	NM_030809
8.08	6.52	1.56	2.23E-03	1.14E-01	MYLIP	myosin regulatory light chain interacting protein	chr6p23-p22.3	228098_s_at	NM_013262
3.46	2.85	0.61	2.23E-03	1.14E-01	---	---	---	233728_at	---
5.35	4.44	0.91	2.24E-03	1.14E-01	PHC1	polyhomeotic homolog 1 (Drosophila)	chr12p13	225958_at	NM_004426
8.15	7.17	0.98	2.24E-03	1.14E-01	ABHD14A	abhydrolase domain containing 14A	chr3p21.1	210006_at	NM_015407
6.76	6.18	0.58	2.24E-03	1.14E-01	ZBTB5	zinc finger and BTB domain containing 5	chr9p13.2	203026_at	NM_014872
7.77	6.70	1.07	2.24E-03	1.14E-01	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	chr9q21.32	203221_at	NM_005077
6.32	4.92	1.40	2.26E-03	1.15E-01	INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	chr9q34.3	204706_at	NM_019892
8.09	6.69	1.40	2.27E-03	1.15E-01	MGC3207	hypothetical protein MGC3207	chr19p13.13	228077_at	NM_001031727 /// NM_032285
6.00	5.29	0.71	2.27E-03	1.15E-01	SKP2	S-phase kinase-associated protein 2 (p45)	chr5p13	203625_x_at	NM_005983 /// NM_032637
6.31	5.52	0.78	2.27E-03	1.15E-01	MTMR1	myotubularin related protein 1	chrXq28	213511_s_at	NM_003828
6.92	6.15	0.77	2.27E-03	1.15E-01	ZNF593	zinc finger protein 593	chr1p36.11	204175_at	NM_015871
6.11	4.88	1.23	2.29E-03	1.15E-01	FLJ10404	hypothetical protein FLJ10404	chr5q35.3	218920_at	NM_019057 /// NR_024019
8.50	7.70	0.80	2.29E-03	1.16E-01	PELO	pelota homolog (Drosophila)	chr5q11.2	218472_s_at	NM_015946
6.58	5.04	1.53	2.31E-03	1.16E-01	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	chr9q21.32	228284_at	NM_005077
5.86	4.27	1.59	2.32E-03	1.16E-01	FAM83H	family with sequence similarity 83, member H	chr8q24.3	226129_at	NM_198488
6.85	6.33	0.52	2.32E-03	1.16E-01	U1SNRNPBP	U11/U12 snRNP 35K	chr12q24.31	205300_s_at	NM_022717 /// NM_180699 /// NM_180703
8.44	7.64	0.80	2.33E-03	1.17E-01	POP5	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	chr12q24.31	204839_at	NM_015918 /// NM_198202
6.97	6.28	0.69	2.33E-03	1.17E-01	C1orf149	chromosome 1 open reading frame 149	chr1p35.3-p33	218165_at	NM_022756
5.13	4.26	0.86	2.33E-03	1.17E-01	TXNL4B	thioredoxin-like 4B	chr16q22.3	218794_s_at	NM_017853
6.05	5.58	0.47	2.33E-03	1.17E-01	WDR68	WD repeat domain 68	chr17q23.3	209592_s_at	NM_005828
8.50	7.49	1.01	2.34E-03	1.17E-01	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	chr16q24.1	221541_at	NM_031476

8.34	7.49	0.85	2.35E-03	1.17E-01	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	chr1p36.3	202317_s_at	NM_001105562 /// NM_006048
6.40	4.18	2.22	2.35E-03	1.17E-01	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	chr2p15	226334_s_at	NM_152392
5.74	4.90	0.84	2.36E-03	1.17E-01	FKBP4	FK506 binding protein 4, 59kDa	chr12p13.33	200894_s_at	NM_002014
6.65	5.51	1.14	2.36E-03	1.17E-01	GIPC2	GIPC PDZ domain containing family, member 2	chr1p31.1	219970_at	NM_017655
5.69	4.95	0.73	2.36E-03	1.17E-01	LOC285074	hypothetical protein LOC285074	chr2p11.2	230588_s_at	XR_040022
5.75	4.44	1.30	2.37E-03	1.17E-01	STK36	serine/threonine kinase 36, fused homolog (Drosophila)	chr2q35	231806_s_at	NM_015690
6.69	5.65	1.04	2.37E-03	1.17E-01	LOC649851 /// MYL5	similar to Superfast myosin regulatory light chain 2 (MyLC-2) (MYLC2) (Myosin regulatory light chain 5) /// myosin, light chain 5, regulatory	chr4p16.3	205145_s_at	NM_002477 /// XR_038355
2.96	2.23	0.73	2.38E-03	1.18E-01	UROD	uroporphyrinogen decarboxylase	chr1p34	222074_at	NM_000374
8.37	7.41	0.97	2.39E-03	1.18E-01	TMEM98	transmembrane protein 98	chr17q11.2	223170_at	NM_001033504 /// NM_015544
4.46	3.57	0.89	2.39E-03	1.18E-01	SLC45A4	solute carrier family 45, member 4	chr8q24.3	225597_at	NM_001080431
4.80	2.88	1.92	2.39E-03	1.18E-01	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	chr1p34.3	221768_at	NM_005066
3.41	2.81	0.60	2.39E-03	1.18E-01	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	chr13q34	217596_at	NM_023011 /// NM_080687
6.37	5.69	0.68	2.39E-03	1.18E-01	WBSCR16	Williams-Beuren syndrome chromosome region 16	chr7q11.23	1554410_a_at	NM_030798
7.83	6.46	1.37	2.40E-03	1.18E-01	MYLIP	myosin regulatory light chain interacting protein	chr6p23-p22.3	220319_s_at	NM_013262
5.74	2.84	2.90	2.40E-03	1.18E-01	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	chr7p15	225107_at	NM_002137 /// NM_031243
6.45	5.73	0.72	2.42E-03	1.19E-01	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	chr7q22.1	216843_x_at	NR_003613
8.34	7.82	0.52	2.43E-03	1.19E-01	GORASP2	golgi reassembly stacking protein 2, 55kDa	chr2q31.1-q31.2	208842_s_at	NM_015530
4.66	2.89	1.76	2.43E-03	1.19E-01	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	chr2p13	201448_at	NM_022037 /// NM_022173
9.59	9.14	0.45	2.43E-03	1.19E-01	ERP29	endoplasmic reticulum protein 29	chr12q24.13	201216_at	NM_001034025 /// NM_006817
8.11	7.59	0.52	2.44E-03	1.19E-01	COX7C	cytochrome c oxidase subunit VIIc	chr5q14	213846_at	NM_001867
4.31	2.99	1.32	2.44E-03	1.19E-01	SFXN3	Sideroflexin 3	chr10q24.31	1559993_at	NM_030971
4.96	3.19	1.78	2.47E-03	1.19E-01	CA2	carbonic anhydrase II	chr8q22	209301_at	NM_000067
3.33	2.67	0.66	2.47E-03	1.19E-01	SIX1	SIX homeobox 1	chr14q23.1	228347_at	NM_005982
7.72	6.84	0.88	2.47E-03	1.19E-01	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	chr12q24.2	213812_s_at	NM_006549 /// NM_153499 /// NM_153500 /// NM_172214 /// NM_172215 /// NM_172216 /// NM_172226
9.72	9.04	0.68	2.48E-03	1.20E-01	SFRS9	splicing factor, arginine/serine-rich 9	chr12q24.31	201698_s_at	NM_003769
9.05	8.05	1.00	2.48E-03	1.20E-01	SFRS5	splicing factor, arginine/serine-rich 5	chr14q24	203380_x_at	NM_001039465 /// NM_006925
8.27	7.38	0.90	2.48E-03	1.20E-01	LETMD1	LETM1 domain containing 1	chr12q13.13	207170_s_at	NM_001024668 /// NM_015416
5.55	4.89	0.66	2.49E-03	1.20E-01	---	---	---	229423_at	---
8.24	7.71	0.53	2.50E-03	1.20E-01	TH1L	TH1-like (Drosophila)	chr20q13	220607_x_at	NM_198976
4.29	2.66	1.63	2.50E-03	1.20E-01	ZNF738	zinc finger protein 738	chr19p12	229700_at	XR_040185 /// XR_040186 /// XR_040187
6.76	5.79	0.97	2.51E-03	1.20E-01	C7orf23	chromosome 7 open reading frame 23	chr7q21.1-q21.2	204215_at	NM_024315
4.10	2.78	1.31	2.51E-03	1.20E-01	UQCC	ubiquinol-cytochrome c reductase complex chaperone	chr20q11.22	229672_at	NM_018244 /// NM_199487
6.67	5.49	1.18	2.52E-03	1.20E-01	FAM36A	family with sequence similarity 36, member A	chr1q44	224824_at	NM_198076
7.74	7.16	0.58	2.52E-03	1.20E-01	ARF6	ADP-ribosylation factor 6	chr14q21.3	203311_s_at	NM_001663
6.25	5.56	0.69	2.52E-03	1.20E-01	KRT10	keratin 10	chr17q21	207023_x_at	NM_000421

5.66	4.88	0.78	2.52E-03	1.20E-01	SLC35C2	solute carrier family 35, member C2	chr20q13.12	219447_s_at	NM_015945 /// NM_173073 /// NM_173179 /// XM_001722057 /// XM_001722102 /// XM_001722502																				
8.41	6.76	1.66	2.53E-03	1.20E-01	CAMK1	calcium/calmodulin-dependent protein kinase I	chr3p25.3	204392_at	NM_003656																				
5.93	5.19	0.74	2.53E-03	1.20E-01	GPATCH8	G patch domain containing 8	chr17q21.31	212485_at	NM_001002909																				
9.34	8.27	1.07	2.53E-03	1.20E-01	TSC22D1	TSC22 domain family, member 1	chr13q14	215111_s_at	NM_006022 /// NM_183422																				
8.55	7.69	0.86	2.53E-03	1.20E-01	USP22	ubiquitin specific peptidase 22	chr17p11.2	200083_at	NM_015276																				
6.82	5.83	0.99	2.54E-03	1.20E-01	TMEM69	transmembrane protein 69	chr1p34.1	223335_at	NM_016486																				
7.12	5.29	1.83	2.54E-03	1.20E-01	ARGLU1	arginine and glutamate rich 1	chr13q33.3	228477_at	NM_018011																				
5.87	5.09	0.79	2.55E-03	1.21E-01	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	chr16q24.3	230884_s_at	NM_003119 /// NM_199367																				
6.40	5.57	0.83	2.57E-03	1.21E-01	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	chr8p11.2	209341_s_at	NM_001556																				
3.74	2.58	1.16	2.58E-03	1.22E-01	LOC440895	LIM and senescent cell antigen-like domains 3-like	chr2q13	229095_s_at	XM_001726941 /// XM_496582																				
7.43	6.78	0.64	2.59E-03	1.22E-01	COX4NB	COX4 neighbor	chr16q24	227363_s_at	NM_006067																				
5.32	4.75	0.57	2.60E-03	1.22E-01	RNF216	ring finger protein 216	chr7p22.1	227065_at	NM_207111 /// NM_207116																				
7.51	6.86	0.65	2.60E-03	1.22E-01	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	chr8p22-p21.3	213902_at	NM_001127505 /// NM_004315 /// NM_177924																				
7.23	6.24	0.99	2.60E-03	1.22E-01	TMED3	transmembrane emp24 protein transport domain containing 3	chr15q24-q25	208837_at	NM_007364																				
4.06	2.59	1.47	2.61E-03	1.22E-01	HPSE	heparanase	chr4q21.3	222881_at	NM_001098540 /// NM_006665																				
7.86	6.94	0.92	2.61E-03	1.22E-01	HEXIM1	hexamethylene bis-acetamide inducible 1	chr17q21.31	202814_s_at	NM_006460																				
8.50	7.78	0.72	2.62E-03	1.22E-01	STOML2	stomatin (EPB72)-like 2	chr9p13.1	215416_s_at	NM_013442																				
7.44	6.64	0.80	2.63E-03	1.23E-01	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	chr3p21.31	212674_s_at	NM_014966 /// NM_138615																				
7.28	6.11	1.17	2.64E-03	1.23E-01	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	chr12q24.1	201834_at	NM_006253																				
4.77	4.12	0.65	2.64E-03	1.23E-01	ANGPTL4	angiopoietin-like 4	chr19p13.3	223333_s_at	NM_001039667 /// NM_139314																				

3.10	2.30	0.80	2.65E-03	1.23E-01	FLJ14186 /// LOC100128460 /// LOC100133177 /// LOC349114 /// LOC399744 /// LOC441124 /// LOC729021 /// LOC729660 /// LOC730235 /// tcag7.907	hypothetical gene supported by AK024248; AL137733 /// similar to hCG1793472 /// hypothetical LOC100133177 /// hypothetical LOC349114 /// hypothetical LOC399744 /// hypothetical gene supported by AK093729; BX647918 /// hypothetical protein LOC729021 /// hypothetical LOC729660 /// hypothetical LOC730235 /// hypothetical LOC402483	chr10p11.21 /// chr1q42.11 /// chr1q43 /// chr4q26 /// chr7p12.1 /// chr7p13 /// chr7p14.1 /// chr7q32.1	231821_x_at	XM_001714118 /// XM_001717656 /// XM_001725538 /// XM_001732867 /// XM_379273 /// XM_499022 /// XR_015615 /// XR_015834 /// XR_036901 /// XR_036907 /// XR_037016 /// XR_037641 /// XR_037866 /// XR_038205 /// XR_039044 /// XR_040227 /// XR_040228 /// XR_040229 /// XR_040230 /// XR_040932 /// XR_040933 /// XR_040934 /// XR_040935 /// XR_041048 /// XR_041049 /// XR_041050 /// XR_042026																				
7.36	6.29	1.08	2.66E-03	1.23E-01	TRIM27	tripartite motif-containing 27	chr6p22	212118_at	NM_006510																				
5.49	5.02	0.47	2.67E-03	1.23E-01	TRIM39	tripartite motif-containing 39	chr6p21.3	222732_at	NM_021253 /// NM_172016																				
7.42	6.33	1.09	2.67E-03	1.23E-01	RPL22L1	ribosomal protein L22-like 1	chr3q26.2	225541_at	NM_001099645																				
6.67	6.11	0.56	2.68E-03	1.24E-01	PITPNA	phosphatidylinositol transfer protein, alpha	chr17p13.3	201192_s_at	NM_006224																				
4.90	3.31	1.60	2.68E-03	1.24E-01	LENG8	leukocyte receptor cluster (LRC) member 8	chr19q13.42	224673_at	NM_052925																				
5.93	4.64	1.29	2.70E-03	1.24E-01	IFFO	intermediate filament family orphan	chr12p13.3	36030_at	NM_001039670 /// NM_080730 /// NM_080731																				
4.33	3.68	0.65	2.70E-03	1.24E-01	LOC255374	similar to hypothetical protein MGC49416	chr7q22.1	1554170_a_at	NM_203397																				
7.50	6.24	1.27	2.71E-03	1.24E-01	IHPK2	inositol hexaphosphate kinase 2	chr3p21.31	223165_s_at	NM_001005909 /// NM_001005910 /// NM_001005911 /// NM_016291																				
6.08	4.75	1.33	2.71E-03	1.24E-01	FAM26F	family with sequence similarity 26, member F	chr6q22.1	229390_at	NM_001010919																				
6.55	5.84	0.70	2.71E-03	1.24E-01	MTMR1	myotubularin related protein 1	chrXq28	216095_x_at	NM_003828																				

4.49	2.49	2.00	2.71E-03	1.24E-01	NACA /// NACA2 /// NACAP1	nascent polypeptide-associated complex alpha subunit /// nascent polypeptide-associated complex alpha subunit 2 /// nascent-polypeptide-associated complex alpha polypeptide pseudogene 1	chr12q23-q24.1 /// chr17q23.2 /// chr8q22.3	222018_at	NM_001113201 /// NM_001113202 /// NM_001113203 /// NM_005594 /// NM_199290 /// NR_002182																				
7.43	6.72	0.71	2.72E-03	1.24E-01	UNC50	unc-50 homolog (C. elegans)	chr2q11.2	203583_at	NM_014044																				
6.88	5.81	1.07	2.72E-03	1.24E-01	BYSL	bystin-like	chr6p21.1	203612_at	NM_004053																				
6.83	6.07	0.76	2.72E-03	1.25E-01	FAM111A	family with sequence similarity 111, member A	chr11q12.1	218248_at	NM_022074 /// NM_198847																				
7.74	6.75	0.98	2.73E-03	1.25E-01	LOC376475 /// WASH1 /// WASH2P /// WASH3P /// WASH4P /// WASH6P	CXYorf1-related protein /// WAS protein family homolog 1 /// WAS protein family homolog 2 pseudogene /// WAS protein family homolog 3 pseudogene /// WAS protein family homolog 4 pseudogene /// WAS protein family homolog 6 pseudogene	chr15q26.3 /// chr16p13.3 /// chr2q14.1 /// chr9p24.3 /// chrXq28 /// chrXq28;Yq12	233929_x_at	NM_182905 /// NM_199163 /// NR_003659 /// NR_024077 /// XM_377073 /// XR_040204																				
8.33	7.57	0.75	2.73E-03	1.25E-01	RING1	ring finger protein 1	chr6p21.3	35685_at	NM_002931																				
7.38	6.36	1.03	2.73E-03	1.25E-01	RANGRF	RAN guanine nucleotide release factor	chr17p13	218526_s_at	NM_016492																				
7.08	6.26	0.82	2.74E-03	1.25E-01	C1QTNF1	C1q and tumor necrosis factor related protein 1	chr17q25.3	220975_s_at	NM_030968 /// NM_198593 /// NM_198594																				
6.46	5.78	0.69	2.75E-03	1.25E-01	HYI	hydroxypyruvate isomerase homolog (E. coli)	chr1p34.2	223622_s_at	NM_031207																				
6.34	5.52	0.82	2.76E-03	1.25E-01	SYNE2	spectrin repeat containing, nuclear envelope 2	chr14q23.2	202761_s_at	NM_015180 /// NM_182910 /// NM_182913 /// NM_182914																				
8.56	7.87	0.69	2.76E-03	1.25E-01	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	chr5q12-q13	209623_at	NM_022132																				
6.10	5.18	0.92	2.76E-03	1.25E-01	UBQLN4	ubiquilin 4	chr1q21	224513_s_at	NM_020131																				
6.47	5.68	0.80	2.77E-03	1.25E-01	DCPS	decapping enzyme, scavenger	chr11q24.2	218774_at	NM_014026																				
6.59	5.90	0.69	2.77E-03	1.25E-01	C11orf83	chromosome 11 open reading frame 83	chr11q12.3	229099_at	NM_001085372																				
6.71	6.13	0.58	2.78E-03	1.25E-01	RBM22	RNA binding motif protein 22	chr5q33.1	218134_s_at	NM_018047																				
3.11	2.59	0.52	2.79E-03	1.25E-01	ZSCAN12	zinc finger and SCAN domain containing 12	chr6p22.2-p21.3	206507_at	XR_041200 /// XR_041201 /// XR_041202																				
7.27	6.04	1.23	2.79E-03	1.25E-01	GMPR	guanosine monophosphate reductase	chr6p23	204187_at	NM_006877																				
7.57	6.67	0.90	2.79E-03	1.25E-01	C12orf10	chromosome 12 open reading frame 10	chr12q13	218220_at	NM_021640																				
8.66	8.16	0.50	2.80E-03	1.25E-01	MGST2	microsomal glutathione S-transferase 2	chr4q28.3	204168_at	NM_002413																				
9.89	9.25	0.64	2.80E-03	1.25E-01	JTB	jumping translocation breakpoint	chr1q21	210434_x_at	NM_006694																				

5.79	4.03	1.76	2.80E-03	1.25E-01	FLJ43663	hypothetical LOC378805	chr7q32.3	228702_at	XM_380146 /// XM_930545 /// XM_935361 /// XM_935362 /// XM_935363 /// XM_935364 /// XM_935365 /// XM_935366 /// XM_935367 /// XM_935688 /// XM_935957 /// XM_935958 /// XM_935959 /// XM_935960 /// XM_935961 /// XM_935962 /// XM_935963 /// XM_935964 /// XM_940526 /// XM_944629 /// XM_944633 /// XM_944638 /// XM_944640 /// XM_944641 /// XM_944643 /// XM_944645 /// XM_944647																				
9.07	8.29	0.78	2.81E-03	1.25E-01	CDK2AP1	CDK2-associated protein 1	chr12q24.31	201938_at	NM_004642																				
7.12	6.30	0.82	2.81E-03	1.25E-01	ASMTL	acetylserotonin O-methyltransferase-like	chrXp22.3; Yp11.3	209394_at	NM_004192 /// XM_001713702																				
4.29	3.71	0.59	2.82E-03	1.25E-01	MFN2	mitofusin 2	chr1p36.22	216205_s_at	NM_001127660 /// NM_014874																				
7.50	6.79	0.71	2.82E-03	1.25E-01	RPS21	ribosomal protein S21	chr20q13.3	214097_at	NM_001024																				
7.82	6.65	1.17	2.82E-03	1.25E-01	PYCR2	pyrroline-5-carboxylate reductase family, member 2	chr1q42.12	224855_at	NM_013328																				
3.79	2.84	0.96	2.82E-03	1.25E-01	PTK2	PTK2 protein tyrosine kinase 2	chr8q24-qter	241453_at	NM_005607 /// NM_153831																				
5.78	4.64	1.13	2.82E-03	1.25E-01	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	chr16p11.2	212809_at	NM_032815																				
5.73	4.84	0.90	2.82E-03	1.25E-01	UBIAD1	UbiA prenyltransferase domain containing 1	chr1p36-p34.1	219131_at	NM_013319																				
5.78	4.80	0.98	2.83E-03	1.25E-01	FBXL10	F-box and leucine-rich repeat protein 10	chr12q24.31	226215_s_at	NM_001005366 /// NM_032590																				
5.79	4.80	0.99	2.83E-03	1.25E-01	COQ4	coenzyme Q4 homolog (S. cerevisiae)	chr9q34.11	228931_at	NM_016035																				
7.78	5.89	1.88	2.83E-03	1.25E-01	KIAA1024	KIAA1024	chr15q25.1	215081_at	NM_015206																				
7.88	6.38	1.50	2.84E-03	1.25E-01	CXorf40A /// CXorf40B	chromosome X open reading frame 40A /// chromosome X open reading frame 40B	chrXq28	212961_x_at	NM_001013845 /// NM_178124																				
5.38	4.85	0.53	2.84E-03	1.25E-01	TUBB2A /// TUBB2B	tubulin, beta 2A /// tubulin, beta 2B	chr6p25	209372_x_at	NM_001069 /// NM_178012																				

7.60	5.81	1.79	2.84E-03	1.25E-01	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	chr7p22.3	226206_at	NM_002360
6.16	3.74	2.42	2.84E-03	1.25E-01	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	chr12p	213326_at	NM_014231 /// NM_016830 /// NM_199245
7.76	6.80	0.96	2.84E-03	1.25E-01	SYNGR1	synaptogyrin 1	chr22q13.1	210613_s_at	NM_004711 /// NM_145731 /// NM_145738
3.30	2.54	0.76	2.84E-03	1.25E-01	EIF2C2	Eukaryotic translation initiation factor 2C, 2	chr8q24	213310_at	NM_012154
7.09	6.00	1.08	2.85E-03	1.25E-01	ECHDC2	enoyl Coenzyme A hydratase domain containing 2	chr1p32.3	235305_s_at	NM_018281
7.77	6.82	0.95	2.85E-03	1.26E-01	SLC25A28	solute carrier family 25, member 28	chr10q23-q24	221432_s_at	NM_031212
9.21	8.36	0.85	2.86E-03	1.26E-01	SAT1	spermidine/spermine N1-acetyltransferase 1	chrXp22.1	203455_s_at	NM_002970
5.99	5.08	0.91	2.86E-03	1.26E-01	ATF7	activating transcription factor 7	chr12q13	228829_at	NM_001130059 /// NM_001130060 /// NM_006856
8.42	7.60	0.82	2.87E-03	1.26E-01	LIX1L	Lix1 homolog (mouse)-like	chr1q21.1	225793_at	NM_153713
4.37	3.61	0.76	2.87E-03	1.26E-01	PCSK5	proprotein convertase subtilisin/kexin type 5	chr9q21.3	205560_at	NM_006200
4.22	2.98	1.24	2.87E-03	1.26E-01	TRIM45	tripartite motif-containing 45	chr1p13.1	242056_at	NM_025188
6.52	5.90	0.62	2.88E-03	1.26E-01	RPL28	ribosomal protein L28	chr19q13.4	213223_at	NM_000991
6.95	6.41	0.54	2.88E-03	1.26E-01	SNUPN	snurportin 1	chr15q24.2	207438_s_at	NM_001042581 /// NM_001042588 /// NM_005701
6.65	6.06	0.59	2.88E-03	1.26E-01	CDC2L1 /// CDC2L2	cell division cycle 2-like 1 (PITSLRE proteins) /// cell division cycle 2-like 2 (PITSLRE proteins)	chr1p36.33	207428_x_at	NM_024011 /// NM_033486 /// NM_033487 /// NM_033488 /// NM_033489 /// NM_033492 /// NM_033493 /// NM_033529 /// XM_001713735 /// XM_001713748 /// XM_001715985 /// XM_001716018 /// XM_001716037 /// XM_001716055
3.71	2.85	0.85	2.89E-03	1.26E-01	RPS20	ribosomal protein S20	chr8q12	216247_at	NM_001023
7.14	5.89	1.24	2.89E-03	1.26E-01	UBTF	upstream binding transcription factor, RNA polymerase I	chr17q21.3	225982_at	NM_001076683 /// NM_001076684 /// NM_014233
8.48	6.78	1.71	2.90E-03	1.26E-01	RNF144A	ring finger protein 144A	chr2p25.2-p25.1	204040_at	NM_014746
7.93	5.85	2.07	2.90E-03	1.26E-01	NRK	Nik related kinase	chrXq22.3	227971_at	NM_198465
7.67	5.72	1.95	2.90E-03	1.26E-01	---	---	---	235434_at	---
6.31	5.33	0.97	2.90E-03	1.26E-01	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	chr7q22.1	218378_s_at	NM_024653
3.24	2.27	0.97	2.91E-03	1.26E-01	C7orf30	Chromosome 7 open reading frame 30	chr7p15.3	230516_at	NM_138446
5.14	4.30	0.84	2.92E-03	1.26E-01	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	chr17p13	215113_s_at	NM_015670
8.98	8.37	0.61	2.93E-03	1.26E-01	RNF7	ring finger protein 7	chr3q22-q24	224395_s_at	NM_014245 /// NM_183237
6.82	5.97	0.85	2.93E-03	1.26E-01	MZF1	myeloid zinc finger 1	chr19q13.2|19q13.2-q13.4	210336_x_at	NM_003422 /// NM_198055

6.84	6.09	0.75	2.93E-03	1.26E-01	EXOSC5	exosome component 5	chr19q13.1	218481_at	NM_020158																			
7.19	6.50	0.69	2.94E-03	1.27E-01	NECAP2	NECAP endocytosis associated 2	chr1p36.13	220731_s_at	NM_018090																			
4.85	3.88	0.97	2.95E-03	1.27E-01	ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	---	1553956_at	NM_001044385 /// NM_152388																			
4.96	4.44	0.52	2.95E-03	1.27E-01	IFT172	intraflagellar transport 172 homolog (Chlamydomonas)	chr2p23.3	226324_s_at	NM_015662																			
5.10	4.24	0.86	2.96E-03	1.27E-01	IRF1	interferon regulatory factor 1	chr5q31.1	238725_at	NM_002198																			
5.08	4.08	1.00	2.96E-03	1.27E-01	MSTO1 /// MSTO2P	misato homolog 1 (Drosophila) /// misato homolog 2 pseudogene	chr1q22	224233_s_at	NM_018116 /// NR_024117 /// XM_001713716 /// XR_039074 /// XR_039412																			
7.35	6.17	1.17	2.96E-03	1.27E-01	LOC376475 /// WASH1 /// WASH2P /// WASH3P /// WASH4P /// WASH6P	CXYorf1-related protein /// WAS protein family homolog 1 /// WAS protein family homolog 2 pseudogene /// WAS protein family homolog 3 pseudogene /// WAS protein family homolog 4 pseudogene /// WAS protein family homolog 6 pseudogene	chr15q26.3 /// chr16p13.3 /// chr2q14.1 /// chr9p24.3 /// chrXq28 /// chrXq28;Yq12	225035_x_at	NM_182905 /// NM_199163 /// NR_003659 /// NR_024077 /// XM_377073 /// XR_040204																			
3.80	2.88	0.92	2.97E-03	1.27E-01	PANK2	Pantothenate kinase 2	chr20p13	235130_at	NM_024960 /// NM_153638 /// NM_153640																			
8.48	7.83	0.65	2.98E-03	1.27E-01	ARL6IP4 /// OGFOD2	ADP-ribosylation-like factor 6 interacting protein 4 /// 2-oxoglutarate and iron-dependent oxygenase domain containing 2	chr12q24.31	220597_s_at	NM_001002251 /// NM_001002252 /// NM_016638 /// NM_018694 /// NM_024623																			
9.57	9.09	0.49	2.98E-03	1.27E-01	HINT1	histidine triad nucleotide binding protein 1	chr5q31.2	200093_s_at	NM_005340																			
7.22	6.71	0.51	2.98E-03	1.27E-01	SART3	squamous cell carcinoma antigen recognized by T cells 3	chr12q24.1	209128_s_at	NM_014706																			
7.22	6.47	0.75	2.98E-03	1.27E-01	FASTK	Fas-activated serine/threonine kinase	chr7q35	210975_x_at	NM_006712 /// NM_033015																			
3.42	2.55	0.87	2.99E-03	1.27E-01	IL15	interleukin 15	chr4q31	205992_s_at	NM_000585 /// NM_172174																			
3.81	3.16	0.64	2.99E-03	1.27E-01	---	---	---	239081_at	---																			
6.63	5.89	0.75	2.99E-03	1.27E-01	COMMD5	COMM domain containing 5	chr8q24-qter	223198_x_at	NM_001081003 /// NM_001081004 /// NM_014066																			
3.88	2.27	1.62	3.00E-03	1.27E-01	TRPV1	transient receptor potential cation channel, subfamily V, member 1	chr17p13.3	219632_s_at	NM_018727 /// NM_080704 /// NM_080705 /// NM_080706																			
4.39	3.76	0.63	3.01E-03	1.27E-01	POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	chr19q13.3	203422_at	NM_002691																			
5.23	3.83	1.40	3.01E-03	1.27E-01	NUP98	nucleoporin 98kDa	chr11p15.5	210793_s_at	NM_005387 /// NM_016320 /// NM_139131 /// NM_139132																			
7.96	7.10	0.85	3.01E-03	1.27E-01	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	chr20p	209171_at	NM_033453 /// NM_181493																			
3.82	3.01	0.80	3.02E-03	1.28E-01	C1orf109	chromosome 1 open reading frame 109	chr1p34.3	218712_at	NM_017850																			

8.13	7.54	0.59	3.03E-03	1.28E-01	TCEAL1	transcription elongation factor A (SII)-like 1	chrXq22.1	204045_at	NM_001006639 /// NM_001006640 /// NM_004780																				
4.45	3.51	0.95	3.03E-03	1.28E-01	ARL9	ADP-ribosylation factor-like 9	chr4q12	229062_at	NM_206919																				
4.09	2.23	1.86	3.04E-03	1.28E-01	DHRS2	dehydrogenase/reductase (SDR family) member 2	chr14q11.2	214079_at	NM_005794 /// NM_182908																				
6.40	4.73	1.67	3.05E-03	1.28E-01	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	chr7q21.3-q22	202627_s_at	NM_000602																				
7.90	6.83	1.06	3.05E-03	1.28E-01	SEC24C	SEC24 related gene family, member C (S. cerevisiae)	chr10q22.2	202361_at	NM_004922 /// NM_198597																				
5.46	4.40	1.06	3.06E-03	1.28E-01	C12orf51	chromosome 12 open reading frame 51	chr12q24.13	211034_s_at	NM_001109662																				
6.10	5.20	0.90	3.06E-03	1.28E-01	ProSAPiP1	ProSAPiP1 protein	chr20p13	204447_at	NM_014731																				
5.82	3.72	2.10	3.06E-03	1.28E-01	ANKRD37	ankyrin repeat domain 37	chr4q35.1	227337_at	NM_181726																				
3.75	3.20	0.55	3.09E-03	1.29E-01	NPEPL1	Aminopeptidase-like 1	chr20q13.32	235033_at	NM_024663																				
6.15	5.31	0.84	3.09E-03	1.29E-01	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	chr1p34-p33	210093_s_at	NM_002370																				
7.90	6.97	0.93	3.09E-03	1.29E-01	PDIA5	protein disulfide isomerase family A, member 5	chr3q21.1	203857_s_at	NM_006810																				
3.88	2.91	0.97	3.09E-03	1.29E-01	SGSM1	small G protein signaling modulator 1	chr22q11.23	230287_at	NM_001039948 /// NM_001098497 /// NM_001098498 /// NM_133454																				
7.80	6.94	0.86	3.10E-03	1.29E-01	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	chr1p36	226160_at	NM_004285																				
5.18	3.85	1.33	3.10E-03	1.29E-01	PHLDA1	pleckstrin homology-like domain, family A, member 1	chr12q15	217999_s_at	NM_007350																				
5.13	4.60	0.53	3.10E-03	1.29E-01	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	chr8q24.22	208322_s_at	NM_003033 /// NM_173344																				
8.69	8.12	0.58	3.11E-03	1.29E-01	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	chr1p36.1	208674_x_at	NM_005216																				
5.55	4.70	0.85	3.11E-03	1.29E-01	DFNA5	deafness, autosomal dominant 5	chr7p15	203695_s_at	NM_001127453 /// NM_001127454 /// NM_004403																				
3.01	2.49	0.51	3.11E-03	1.29E-01	ING5 /// LOC727773	inhibitor of growth family, member 5 /// similar to p28 ING5	chr2q37.3	229197_at	NM_032329 /// XM_001126273																				
4.29	3.59	0.70	3.12E-03	1.29E-01	CENTG2	centaurin, gamma 2	chr2q37	204066_s_at	NM_001037131 /// NM_014914																				
7.28	6.68	0.60	3.13E-03	1.30E-01	PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	chr1q23-q25	202846_s_at	NM_002642 /// NM_153747																				
3.34	2.52	0.81	3.13E-03	1.30E-01	AVIL	advillin	chr12q14.1	205539_at	NM_006576																				
8.40	7.59	0.81	3.13E-03	1.30E-01	SFT2D1	SFT2 domain containing 1	chr6q27	225849_s_at	NM_145169																				
7.05	6.36	0.68	3.15E-03	1.30E-01	TMEM127	transmembrane protein 127	chr2q11.2	219460_s_at	NM_017849																				
6.01	5.27	0.74	3.15E-03	1.30E-01	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	chr16q22.1	202577_s_at	NM_018332																				
5.97	5.37	0.60	3.15E-03	1.30E-01	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	chr21q22.3	1557053_s_at	NM_003343 /// NM_182688																				
8.46	7.76	0.70	3.16E-03	1.30E-01	EIF6	eukaryotic translation initiation factor 6	chr20q12	210213_s_at	NM_002212 /// NM_181466 /// NM_181468																				
7.99	7.35	0.64	3.17E-03	1.31E-01	SFT2D1	SFT2 domain containing 1	chr6q27	225850_at	NM_145169																				
5.50	4.52	0.98	3.17E-03	1.31E-01	MAP3K4	mitogen-activated protein kinase kinase kinase 4	chr6q26	204089_x_at	NM_005922 /// NM_006724																				
8.49	7.25	1.24	3.18E-03	1.31E-01	HIST2H2AA3 /// HIST2H2AA4	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	chr1q21.2	218280_x_at	NM_001040874 /// NM_003516																				
6.02	4.63	1.39	3.18E-03	1.31E-01	STK36	serine/threonine kinase 36, fused homolog (Drosophila)	chr2q35	226166_x_at	NM_015690																				
6.29	4.67	1.62	3.18E-03	1.31E-01	LUC7L	LUC7-like (S. cerevisiae)	chr16p13.3	223295_s_at	NM_018032 /// NM_201412																				
6.53	5.45	1.08	3.19E-03	1.31E-01	GBA2	glucosidase, beta (bile acid) 2	chr9p13.3	224627_at	NM_020944																				

6.22	5.05	1.17	3.19E-03	1.31E-01	ALKBH6 /// C19orf46	alkB, alkylation repair homolog 6 (E. coli) /// chromosome 19 open reading frame 46	chr19q13.12	225969_at	NM_001039876 /// NM_032878 /// NM_198867																				
5.79	4.46	1.32	3.19E-03	1.31E-01	TTMA	Two transmembrane domain family member A	chr18p11.31	229523_at	NM_001080209																				
5.67	4.48	1.18	3.20E-03	1.31E-01	DISP1	Dispatched homolog 1 (Drosophila)	chr1q41	235466_s_at	NM_032890																				
7.51	6.35	1.16	3.20E-03	1.31E-01	---	---	---	236798_at	---																				
5.64	3.96	1.68	3.21E-03	1.31E-01	TAGAP	T-cell activation RhoGTPase activating protein	chr6q25.3	229723_at	NM_054114 /// NM_138810 /// NM_152133																				
5.18	4.36	0.82	3.22E-03	1.31E-01	ZC3HAV1	zinc finger CCCH-type, antiviral 1	chr7q34	220104_at	NM_020119 /// NM_024625																				
6.12	5.34	0.78	3.22E-03	1.31E-01	KIAA0226	KIAA0226	chr3q29	212733_at	NM_014687																				
6.33	5.04	1.29	3.24E-03	1.32E-01	---	---	---	227603_at	---																				
3.37	2.85	0.52	3.25E-03	1.32E-01	SAMD4A	sterile alpha motif domain containing 4A	chr14q22.2	215495_s_at	NM_015589																				
7.93	6.99	0.94	3.26E-03	1.32E-01	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10q25.3	212761_at	NM_030756																				
6.25	5.61	0.64	3.26E-03	1.32E-01	USP40	ubiquitin specific peptidase 40	chr2q37.1	225085_at	NM_018218																				
2.84	2.10	0.74	3.27E-03	1.33E-01	SEC24A	SEC24 related gene family, member A (S. cerevisiae)	chr5q31.1	244841_at	NM_021982																				
4.52	3.98	0.54	3.27E-03	1.33E-01	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	chr8p11.1	1557064_s_at	NM_152419																				
9.54	8.97	0.57	3.28E-03	1.33E-01	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	chr1p36.1	208675_s_at	NM_005216																				
7.52	6.63	0.89	3.29E-03	1.33E-01	C7orf55	chromosome 7 open reading frame 55	chr7q34	226781_at	NM_197964																				
7.74	6.94	0.80	3.29E-03	1.33E-01	NME3	non-metastatic cells 3, protein expressed in	chr16q13	204862_s_at	NM_002513																				
4.93	4.07	0.86	3.29E-03	1.33E-01	SNORA78	small nucleolar RNA, H/ACA box 78	chr16p13.3	1558954_at	NR_003020																				
3.46	2.40	1.06	3.29E-03	1.33E-01	FZD10	frizzled homolog 10 (Drosophila)	chr12q24.33	219764_at	NM_007197																				
5.16	2.34	2.82	3.31E-03	1.33E-01	---	---	---	228528_at	---																				
7.51	6.89	0.62	3.32E-03	1.33E-01	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1	chr20q13.12	224825_at	NM_052951																				
10.33	9.49	0.84	3.33E-03	1.33E-01	C17orf45	chromosome 17 open reading frame 45	chr17p11.2	225065_x_at	NM_152350																				
7.92	7.16	0.76	3.33E-03	1.33E-01	---	---	---	224644_at	---																				
3.41	2.05	1.36	3.33E-03	1.33E-01	CNTN1	Contactin 1	chr12q11-q12	227202_at	NM_001843 /// NM_175038																				
6.85	6.18	0.66	3.33E-03	1.33E-01	PPIC	peptidylprolyl isomerase C (cyclophilin C)	chr5q23.2	204518_s_at	NM_000943																				
7.12	5.97	1.15	3.34E-03	1.33E-01	LOC441150	similar to RIKEN cDNA 2310039H08	chr6p21.1	228458_at	NM_001008739																				
7.01	6.16	0.85	3.34E-03	1.33E-01	SERTAD3	SERTA domain containing 3	chr19q13.2	219382_at	NM_013368 /// NM_203344																				
7.36	4.86	2.50	3.34E-03	1.33E-01	ERN1	endoplasmic reticulum to nucleus signaling 1	chr17q24.2	235745_at	NM_001433																				
6.42	5.60	0.82	3.35E-03	1.33E-01	NCOA6	nuclear receptor coactivator 6	chr20q11	208979_at	NM_014071																				
5.41	4.76	0.65	3.35E-03	1.33E-01	PMS2L3	postmeiotic segregation increased 2-like 3	chr7q11.23	214473_x_at	NM_001003686 /// NM_005395 /// XM_001716315																				
6.25	5.52	0.73	3.36E-03	1.34E-01	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	chr2q37.3	221548_s_at	NM_030768																				
3.45	2.65	0.80	3.37E-03	1.34E-01	GABRE	gamma-aminobutyric acid (GABA) A receptor, epsilon	chrXq28	204537_s_at	NM_004961 /// NM_021984 /// NM_021987 /// NM_021990																				
7.64	7.06	0.58	3.38E-03	1.34E-01	NEFH	neurofilament, heavy polypeptide 200kDa	chr22q12.2	204412_s_at	NM_021076																				
8.35	7.36	0.98	3.39E-03	1.34E-01	PNMA1	paraneoplastic antigen MA1	chr14q24.3	218224_at	NM_006029																				
5.34	4.50	0.84	3.39E-03	1.34E-01	WIBG	within bgcn homolog (Drosophila)	chr12q13.2	242304_at	NM_032345																				
7.52	6.81	0.71	3.39E-03	1.34E-01	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	chr5q11-q14	217106_x_at	NM_014473																				
7.72	7.20	0.52	3.39E-03	1.34E-01	SUMF1	sulfatase modifying factor 1	chr3p26.2	226850_at	NM_182760																				
8.99	8.30	0.68	3.39E-03	1.34E-01	MRPL17	mitochondrial ribosomal protein L17	chr11p15.5-p15.4	222216_s_at	NM_022061																				
7.14	5.30	1.85	3.40E-03	1.34E-01	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	chr6p25	209723_at	NM_004155																				
6.71	5.97	0.74	3.40E-03	1.34E-01	CPSF3L	cleavage and polyadenylation specific factor 3-like	chr1p36.33	224312_x_at	NM_017871																				
8.25	7.66	0.59	3.41E-03	1.34E-01	C7orf30	chromosome 7 open reading frame 30	chr7p15.3	226386_at	NM_138446																				
7.00	6.30	0.70	3.41E-03	1.34E-01	NFS1	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	chr20q11.22	218455_at	NM_021100																				

6.35	5.60	0.75	3.42E-03	1.35E-01	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	chr12q24.2	212252_at	NM_006549 /// NM_153499 /// NM_153500 /// NM_172214 /// NM_172215 /// NM_172216 /// NM_172226																				
8.11	7.34	0.77	3.42E-03	1.35E-01	MPG	N-methylpurine-DNA glycosylase	chr16p13.3	203686_at	NM_001015052 /// NM_001015054 /// NM_002434																				
5.99	3.82	2.17	3.45E-03	1.35E-01	CIRBP	cold inducible RNA binding protein	chr19p13.3	225191_at	NM_001280 /// NR_023312 /// NR_023313																				
6.81	4.08	2.74	3.47E-03	1.36E-01	PTPN7	protein tyrosine phosphatase, non-receptor type 7	chr1q32.1	204852_s_at	NM_002832 /// NM_080588																				
3.78	2.87	0.91	3.48E-03	1.36E-01	---	---	---	238069_at	---																				
7.90	7.02	0.89	3.48E-03	1.36E-01	LRRC41	leucine rich repeat containing 41	chr1p33	201932_at	NM_006369																				
7.43	6.71	0.72	3.49E-03	1.36E-01	EIF2B4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	chr2p23.3	215482_s_at	NM_001034116 /// NM_015636 /// NM_172195																				
2.86	2.45	0.41	3.49E-03	1.36E-01	---	---	---	229185_at	---																				
6.35	5.47	0.88	3.51E-03	1.36E-01	LUC7L	LUC7-like (S. cerevisiae)	chr16p13.3	220143_x_at	NM_018032 /// NM_201412																				
5.58	4.41	1.17	3.51E-03	1.36E-01	LOC386597	hypothetical protein LOC386597	chr2p25.2	1556797_at	---																				
4.62	3.18	1.44	3.52E-03	1.36E-01	LOC439911	hypothetical gene supported by NM_194304	chr10q11.21	1558345_a_at	---																				
7.77	7.05	0.72	3.53E-03	1.37E-01	NDUFAF2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	chr5q12.1	228355_s_at	NM_174889																				
5.74	4.87	0.87	3.54E-03	1.37E-01	PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2	chr6q21	1555886_at	NM_020381																				
7.28	6.57	0.70	3.54E-03	1.37E-01	RAE1	RAE1 RNA export 1 homolog (S. pombe)	chr20q13.31	201558_at	NM_001015885 /// NM_003610																				
4.45	3.47	0.99	3.56E-03	1.37E-01	TUBGCP6	tubulin, gamma complex associated protein 6	chr22q13.31-q13.33	225758_s_at	NM_020461																				
7.68	7.07	0.61	3.56E-03	1.38E-01	PFDN2	prefoldin subunit 2	chr1q23.3	218336_at	NM_012394																				
8.09	6.20	1.89	3.57E-03	1.38E-01	BCAT1	branched chain aminotransferase 1, cytosolic	chr12p12.1	225285_at	NM_005504																				
3.52	2.86	0.66	3.58E-03	1.38E-01	TAL1	T-cell acute lymphocytic leukemia 1	chr1p32	206283_s_at	NM_003189																				
6.35	5.51	0.84	3.59E-03	1.38E-01	FAM113A	family with sequence similarity 113, member A	chr20p13	225505_s_at	NM_022760																				
4.39	3.86	0.53	3.60E-03	1.38E-01	TAOK2	TAO kinase 2	chr16p11.2	204877_s_at	NM_004783 /// NM_016151																				
7.49	6.65	0.83	3.62E-03	1.38E-01	VARS2	valyl-tRNA synthetase 2, mitochondrial (putative)	---	226200_at	NM_020442																				
7.55	7.01	0.55	3.63E-03	1.39E-01	MFF	mitochondrial fission factor	chr2q36.3	223091_x_at	NM_020194																				
6.33	5.54	0.79	3.63E-03	1.39E-01	FAM85A	family with sequence similarity 85, member A	chr8p23.1	227917_at	---																				
7.89	6.68	1.20	3.65E-03	1.39E-01	IRS1	insulin receptor substrate 1	chr2q36	204686_at	NM_005544																				
3.55	2.96	0.58	3.65E-03	1.39E-01	PHC2	polyhomeotic homolog 2 (Drosophila)	chr1p34.3	238131_at	NM_004427 /// NM_198040																				
6.73	5.88	0.85	3.66E-03	1.39E-01	EP400	E1A binding protein p400	chr12q24.33	212375_at	NM_015409																				
8.67	8.07	0.60	3.66E-03	1.39E-01	LAMB2	laminin, beta 2 (laminin S)	chr3p21	216264_s_at	NM_002292																				
8.18	7.63	0.56	3.66E-03	1.39E-01	GMPR2	guanosine monophosphate reductase 2	chr14q12	217990_at	NM_001002000 /// NM_001002001 /// NM_001002002 /// NM_016576																				
10.52	9.84	0.68	3.67E-03	1.39E-01	HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B	chr5q35.3	201277_s_at	NM_004499 /// NM_031266																				
5.58	4.55	1.03	3.68E-03	1.39E-01	C19orf42	chromosome 19 open reading frame 42	chr19p13.11	221988_at	NM_024104																				
5.97	5.11	0.86	3.68E-03	1.39E-01	C16orf45	chromosome 16 open reading frame 45	chr16p13.11	212736_at	NM_033201																				
6.32	5.58	0.74	3.69E-03	1.39E-01	BRD1	bromodomain containing 1	chr22q13.33	204520_x_at	NM_014577																				

8.58	7.13	1.45	3.70E-03	1.39E-01	TIMP3	TIMP metallopeptidase inhibitor 3	chr22q12.1-q13.2|22q12.3	201149_s_at	NM_000362																				
5.94	5.18	0.76	3.70E-03	1.39E-01	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	chr1q21	201469_s_at	NM_001130040 /// NM_001130041 /// NM_003029 /// NM_183001																				
7.00	6.23	0.77	3.70E-03	1.39E-01	RFXANK	regulatory factor X-associated ankyrin-containing protein	chr19p12	202758_s_at	NM_003721 /// NM_134440																				
6.54	5.38	1.16	3.70E-03	1.39E-01	C1orf77	chromosome 1 open reading frame 77	chr1q21.3	202560_s_at	NM_015607																				
8.37	7.93	0.44	3.71E-03	1.39E-01	PRICKLE4 /// TOMM6	prickle homolog 4 (Drosophila) /// translocase of outer mitochondrial membrane 6 homolog (yeast)	chr6p21.31	223516_s_at	NM_001134493 /// NM_013397																				
7.75	6.82	0.94	3.71E-03	1.39E-01	COQ10A	coenzyme Q10 homolog A (S. cerevisiae)	chr12q13.2	225747_at	NM_001099337 /// NM_144576																				
6.04	4.81	1.23	3.71E-03	1.39E-01	LOC728903 /// MGC21881	hypothetical LOC728903 /// hypothetical locus MGC21881	chr9p11.2 /// chr9q21.11	1555872_a_at	NR_015363 /// XM_001128866 /// XM_001718591 /// XR_041522 /// XR_041523																				
6.69	5.08	1.61	3.72E-03	1.39E-01	ATP10A	ATPase, class V, type 10A	chr15q11.2	214255_at	NM_024490																				
6.77	5.84	0.93	3.72E-03	1.39E-01	INPPL1	inositol polyphosphate phosphatase-like 1	chr11q23	201598_s_at	NM_001567																				
3.39	2.23	1.16	3.73E-03	1.39E-01	ZNF141	zinc finger protein 141	chr4p16.3	235580_at	NM_003441																				
6.54	5.33	1.21	3.73E-03	1.39E-01	MED24	mediator complex subunit 24	chr17q21.1	213043_s_at	NM_001079518 /// NM_014815																				
7.74	6.73	1.01	3.73E-03	1.39E-01	ARF6	ADP-ribosylation factor 6	chr14q21.3	203312_x_at	NM_001663																				
6.28	4.77	1.51	3.74E-03	1.39E-01	CDO1	cysteine dioxygenase, type I	chr5q22-q23	204154_at	NM_001801																				
4.58	3.96	0.62	3.74E-03	1.39E-01	GALE	UDP-galactose-4-epimerase	chr1p36-p35	1557651_x_at	NM_000403 /// NM_001008216 /// NM_001127621																				
8.03	6.78	1.25	3.75E-03	1.39E-01	MYLIP	myosin regulatory light chain interacting protein	chr6p23-p22.3	223129_x_at	NM_013262																				
5.84	5.13	0.72	3.76E-03	1.39E-01	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	chr16q22.1	202578_s_at	NM_018332																				
5.62	4.91	0.71	3.76E-03	1.39E-01	KLF3	Kruppel-like factor 3 (basic)	chr4p14	219657_s_at	NM_016531																				
7.96	7.14	0.82	3.77E-03	1.40E-01	UBE2E3	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	chr2q32.1	210024_s_at	NM_006357 /// NM_182678																				
7.06	6.03	1.03	3.78E-03	1.40E-01	---	---	---	228710_at	---																				
8.09	7.09	1.00	3.80E-03	1.40E-01	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	chr3q28	209302_at	NM_006232																				
6.49	5.53	0.96	3.80E-03	1.40E-01	MORN4	MORN repeat containing 4	chr10q24.1	236813_at	NM_001098831 /// NM_178832																				
7.16	6.60	0.56	3.81E-03	1.40E-01	CSNK2A1	casein kinase 2, alpha 1 polypeptide	chr20p13	212072_s_at	NM_001895 /// NM_177559 /// NM_177560																				
6.14	5.34	0.80	3.81E-03	1.40E-01	KIAA0892	KIAA0892	chr19p13.11	212505_s_at	NM_015329																				
7.36	6.49	0.87	3.82E-03	1.40E-01	GALT	galactose-1-phosphate uridylyltransferase	chr9p13	203179_at	NM_000155																				
6.90	6.20	0.70	3.83E-03	1.40E-01	QTRT1	queuine tRNA-ribosyltransferase 1	chr19p13.3	221270_s_at	NM_031209																				
6.55	5.89	0.66	3.83E-03	1.40E-01	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	chr12q13-q14	201321_s_at	NM_001130420 /// NM_003075 /// NM_139067																				
4.86	3.99	0.87	3.83E-03	1.40E-01	BCL2L11	BCL2-like 11 (apoptosis facilitator)	chr2q13	1553096_s_at	NM_006538 /// NM_138621 /// NM_207002																				
7.34	5.17	2.17	3.84E-03	1.41E-01	GSTT2	glutathione S-transferase theta 2	chr22q11.2|22q11.23	205439_at	NM_000854																				
9.83	9.40	0.42	3.84E-03	1.41E-01	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	chr22q13.2-q13.31	201077_s_at	NM_001003796 /// NM_005008																				

2.87	2.06	0.81	3.86E-03	1.41E-01	CRISP3	cysteine-rich secretory protein 3	chr6p12.3	207802_at	NM_006061																			
6.58	5.33	1.25	3.86E-03	1.41E-01	C19orf66	chromosome 19 open reading frame 66	chr19p13.2	53720_at	NM_018381																			
5.54	4.82	0.72	3.87E-03	1.41E-01	DGKD	diacylglycerol kinase, delta 130kDa	chr2q37.1	208072_s_at	NM_003648 /// NM_152879																			
4.34	2.81	1.52	3.87E-03	1.41E-01	C4BPA	complement component 4 binding protein, alpha	chr1q32	205654_at	NM_000715																			
6.13	4.84	1.29	3.87E-03	1.41E-01	NSUN5	NOL1/NOP2/Sun domain family, member 5	chr7q11.23	203802_x_at	NM_018044 /// NM_148956																			
7.12	6.00	1.12	3.88E-03	1.41E-01	TMEM39A	transmembrane protein 39A	chr3q13.33	222690_s_at	NM_018266																			
7.44	6.66	0.77	3.88E-03	1.41E-01	CDK2AP2	CDK2-associated protein 2	chr11q13	203252_at	NM_005851																			
6.93	6.04	0.89	3.89E-03	1.41E-01	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	chr11p12-p11.12	218744_s_at	NM_016223																			
8.01	6.79	1.22	3.89E-03	1.41E-01	LOC731602 /// METT11D1	similar to methyltransferase 11 domain containing 1 isoform 2 /// methyltransferase 11 domain containing 1	chr14q11.2	218366_x_at	NM_001029991 /// NM_022734 /// XR_037376																			
3.77	3.14	0.63	3.90E-03	1.41E-01	C2orf60	chromosome 2 open reading frame 60	chr2q33.1	241825_at	NM_001039693 /// NR_004862																			
7.21	6.71	0.50	3.90E-03	1.41E-01	MARS	methionyl-tRNA synthetase	chr12q13.2	213671_s_at	NM_004990																			
6.70	5.72	0.98	3.91E-03	1.41E-01	MTMR3	myotubularin related protein 3	chr22q12.2	202197_at	NM_021090 /// NM_153050 /// NM_153051																			
5.85	4.96	0.89	3.91E-03	1.41E-01	ARSD	arylsulfatase D	chrXp22.3	223696_at	NM_001669 /// NM_009589																			
7.22	6.27	0.96	3.91E-03	1.41E-01	WSB1	WD repeat and SOCS box-containing 1	chr17q11.1	201296_s_at	NM_015626 /// NM_134265																			
3.52	2.70	0.82	3.92E-03	1.41E-01	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	chr2p22.1	225385_s_at	NM_138394																			
7.66	6.96	0.70	3.92E-03	1.41E-01	LOC152217	hypothetical LOC152217	chr3q29	225657_at	XR_017713 /// XR_017724 /// XR_040188																			
6.33	5.05	1.29	3.92E-03	1.41E-01	NSUN5C	NOL1/NOP2/Sun domain family, member 5C	chr7q11.23	213460_x_at	NM_001039487 /// NM_032158 /// NM_148936																			
4.06	3.30	0.76	3.93E-03	1.42E-01	LOC100131914	hypothetical protein LOC100131914	chr6p24.3	240382_at	XM_001714686 /// XM_001718356 /// XM_001718462																			
4.93	3.86	1.06	3.95E-03	1.42E-01	---	---	---	229480_at	---																			
6.86	5.85	1.01	3.95E-03	1.42E-01	SMNDC1	survival motor neuron domain containing 1	chr10q23	200071_at	NM_005871																			
8.74	8.12	0.62	3.96E-03	1.42E-01	RNPS1	RNA binding protein S1, serine-rich domain	chr16p13.3	200060_s_at	NM_006711 /// NM_080594																			
8.26	7.12	1.14	3.97E-03	1.42E-01	SULT1A2	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	chr16p12.1	211385_x_at	NM_001054 /// NM_177528																			
7.08	6.24	0.85	3.98E-03	1.43E-01	NUDCD2	NudC domain containing 2	chr5q34	226642_s_at	NM_145266																			
7.43	5.94	1.50	3.99E-03	1.43E-01	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	chr2p22.1	213649_at	NM_001031684																			
3.24	2.55	0.69	3.99E-03	1.43E-01	NPAS2	neuronal PAS domain protein 2	chr2q11.2	39548_at	NM_002518																			

12.08	11.62	0.45	3.99E-03	1.43E-01	LOC388524 /// LOC653162 /// RP11-556K13.1 /// RPSA	ribosomal protein SA pseudogene /// similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag) /// 40S ribosomal protein SA pseudogene /// ribosomal protein SA	chr19p12 /// chr1p21.1 /// chr3p22.2 /// chr9q21.13	213801_x_at	NM_001005472 /// NM_001012321 /// NM_002295 /// NR_003662 /// XM_001134241 /// XM_001719602 /// XM_001724845 /// XM_001724847 /// XM_001724848 /// XM_944171 /// XR_038181 /// XR_038418 /// XR_038820
3.66	3.11	0.55	3.99E-03	1.43E-01	ORAOV1	oral cancer overexpressed 1	chr11q13.2	243531_at	NM_153451
4.20	2.82	1.38	4.01E-03	1.43E-01	---	---	---	1561195_at	---
6.17	5.37	0.79	4.01E-03	1.43E-01	PPRC1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	chr10q24.32	203737_s_at	NM_015062
7.59	7.04	0.55	4.01E-03	1.43E-01	UBR4	ubiquitin protein ligase E3 component n-recognin 4	chr1p36.13	211950_at	NM_020765
7.02	6.28	0.74	4.02E-03	1.43E-01	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	chr12p13.32	212954_at	NM_003845
9.12	8.41	0.72	4.03E-03	1.43E-01	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	chr16q22.1	201634_s_at	NM_030579
8.95	7.44	1.51	4.03E-03	1.43E-01	CKS2	CDC28 protein kinase regulatory subunit 2	chr9q22	204170_s_at	NM_001827
6.93	6.36	0.57	4.04E-03	1.44E-01	CCND2	cyclin D2	chr12p13	200951_s_at	NM_001759
3.74	3.17	0.57	4.05E-03	1.44E-01	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	chr1p34	213643_s_at	NM_005540
3.19	2.70	0.49	4.06E-03	1.44E-01	---	---	---	238704_at	---
8.11	7.46	0.65	4.07E-03	1.44E-01	PSENEN	presenilin enhancer 2 homolog (C. elegans)	chr19q13.12	218302_at	NM_172341
5.49	4.46	1.03	4.09E-03	1.44E-01	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	chr8p22-p21	209294_x_at	NM_003842 /// NM_147187
8.29	7.09	1.20	4.09E-03	1.44E-01	ECHDC2	enoyl Coenzyme A hydratase domain containing 2	chr1p32.3	218552_at	NM_018281
6.45	5.86	0.59	4.10E-03	1.44E-01	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	208915_s_at	NM_015044
6.99	6.30	0.69	4.10E-03	1.44E-01	DDEF1	development and differentiation enhancing factor 1	chr8q24.1-q24.2	224791_at	NM_018482
4.23	3.51	0.71	4.10E-03	1.44E-01	BMS1P5 /// CTGLF1 /// CTGLF6 /// CTGLF7	BMS1 pseudogene 5 /// centaurin, gamma-like family, member 1 /// centaurin, gamma-like family, member 6 /// centaurin, gamma-like family, member 7	chr10q11.21 /// chr10q11.22	243937_x_at	NM_133446 /// NR_003611 /// XM_001714786 /// XM_001716810
4.11	3.17	0.94	4.11E-03	1.44E-01	C7orf44	chromosome 7 open reading frame 44	chr7p13	209446_s_at	NM_018224
6.56	5.96	0.60	4.12E-03	1.45E-01	ANKRD40	ankyrin repeat domain 40	chr17q21.33	227064_at	NM_052855
8.38	7.68	0.70	4.13E-03	1.45E-01	SF1	splicing factor 1	chr11q13	208313_s_at	NM_004630 /// NM_201995 /// NM_201997 /// NM_201998
4.66	3.93	0.73	4.14E-03	1.45E-01	PRDM15	PR domain containing 15	chr21q22.3	230777_s_at	NM_001040424 /// NM_022115
5.71	4.96	0.75	4.17E-03	1.46E-01	KIAA0355	KIAA0355	chr19q13.11	203288_at	NM_014686
6.33	4.54	1.79	4.17E-03	1.46E-01	VCAN	versican	chr5q14.3	204619_s_at	NM_001126336 /// NM_004385
5.28	3.48	1.80	4.18E-03	1.46E-01	---	---	---	1557051_s_at	---

7.04	6.28	0.76	4.18E-03	1.46E-01	UBE2J2	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	chr1p36.33	225209_s_at	NM_058167 /// NM_194315 /// NM_194457 /// NM_194458																			
7.72	7.13	0.59	4.19E-03	1.46E-01	SFRS4	splicing factor, arginine/serine-rich 4	chr1p35.3	201696_at	NM_005626																			
10.95	10.27	0.69	4.22E-03	1.46E-01	SSR4	signal sequence receptor, delta (translocon-associated protein delta)	chrXq28	201004_at	NM_006280																			
5.65	4.91	0.74	4.22E-03	1.46E-01	EP400	E1A binding protein p400	chr12q24.33	212376_s_at	NM_015409																			
4.62	3.46	1.17	4.22E-03	1.46E-01	C20orf112	chromosome 20 open reading frame 112	chr20q11.1-q11.23	230954_at	NM_080616																			
7.01	6.00	1.01	4.23E-03	1.46E-01	ZNF581	zinc finger protein 581	chr19q13.42	223389_s_at	NM_016535																			
7.85	7.29	0.56	4.23E-03	1.47E-01	NOSIP	nitric oxide synthase interacting protein	chr19q13.33	217950_at	NM_015953																			
3.64	2.76	0.87	4.23E-03	1.47E-01	---	---	---	225742_at	---																			
6.69	5.31	1.38	4.24E-03	1.47E-01	YAP1	Yes-associated protein 1, 65kDa	chr11q13	213342_at	NM_001130145 /// NM_006106																			
7.95	7.36	0.59	4.24E-03	1.47E-01	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	chr12q24.31-q24.32	207805_s_at	NM_002813																			
7.57	6.72	0.85	4.25E-03	1.47E-01	CYHR1	cysteine/histidine-rich 1	chr8q24.3	223421_at	NM_001129888 /// NM_032687 /// NM_138496																			
8.27	7.57	0.69	4.26E-03	1.47E-01	AMPD3	adenosine monophosphate deaminase (isoform E)	chr11p15	207992_s_at	NM_000480 /// NM_001025389 /// NM_001025390																			
4.05	3.23	0.82	4.27E-03	1.47E-01	---	---	---	235814_at	---																			
2.66	2.19	0.48	4.27E-03	1.47E-01	---	---	---	1559509_at	---																			
8.05	7.40	0.65	4.27E-03	1.47E-01	ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	chr2q11.1-q11.2	202135_s_at	NM_005735																			
4.01	2.91	1.10	4.28E-03	1.47E-01	LOC286367	FP944	chr9q31.1	229015_at	NR_024011																			
5.90	4.75	1.15	4.28E-03	1.47E-01	GLS	glutaminase	chr2q32-q34	221510_s_at	NM_014905																			
7.15	5.01	2.14	4.29E-03	1.47E-01	---	---	---	241824_at	---																			
6.12	5.09	1.03	4.29E-03	1.47E-01	LOC202781	hypothetical protein LOC202781	chr7q36.2	235587_at	XM_001714395 /// XM_001715403 /// XM_001719263																			
6.64	6.12	0.52	4.30E-03	1.47E-01	DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11	chr1p36.31	1555360_a_at	NM_018198																			
7.69	6.74	0.95	4.30E-03	1.47E-01	MED19	mediator complex subunit 19	chr11q12.1	226300_at	NM_153450																			
7.13	6.28	0.84	4.30E-03	1.47E-01	COL18A1	collagen, type XVIII, alpha 1	chr21q22.3	209082_s_at	NM_030582 /// NM_130445																			
8.22	7.46	0.76	4.31E-03	1.47E-01	ARPC4 /// TTLL3	actin related protein 2/3 complex, subunit 4, 20kDa /// tubulin tyrosine ligase-like family, member 3	chr3p25.3	211672_s_at	NM_001024959 /// NM_001024960 /// NM_001025930 /// NM_005718 /// NM_015644																			
6.06	5.38	0.67	4.31E-03	1.47E-01	FLJ10038	hypothetical protein FLJ10038	chr15q15.3	205510_s_at	---																			
8.70	8.04	0.66	4.32E-03	1.47E-01	TBCB	tubulin folding cofactor B	chr19q13.11-q13.12	201804_x_at	NM_001281																			
3.59	2.94	0.65	4.32E-03	1.47E-01	---	---	---	239474_at	---																			
5.18	1.98	3.20	4.32E-03	1.47E-01	RPS24	Ribosomal protein S24	chr10q22-q23	1555878_at	NM_001026 /// NM_033022																			
6.75	6.14	0.60	4.32E-03	1.47E-01	CCR1	chemokine (C-C motif) receptor 1	chr3p21	205098_at	NM_001295																			
7.39	6.51	0.87	4.33E-03	1.47E-01	MFSD5	major facilitator superfamily domain containing 5	chr12q13.13	212861_at	NM_032889																			
9.45	8.87	0.58	4.35E-03	1.48E-01	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	chr2q12-q21	202428_x_at	NM_001079862 /// NM_001079863 /// NM_020548																			

6.38	5.29	1.09	4.37E-03	1.48E-01	BOLA2 /// LOC440354 /// LOC595101	bolA homolog 2 (E. coli) /// PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1 pseudogene	chr16p11.2	210396_s_at	NM_001031827 /// NR_002453 /// NR_002473 /// XR_042165
3.90	3.08	0.82	4.37E-03	1.48E-01	RHBDL3	rhomboid, veinlet-like 3 (Drosophila)	chr17q11.2	1553268_at	NM_138328
7.47	6.87	0.60	4.38E-03	1.48E-01	GLOD4	glyoxalase domain containing 4	chr17p13.3	209092_s_at	NM_016080
2.84	2.26	0.58	4.38E-03	1.48E-01	---	---	---	244559_at	---
6.98	6.28	0.71	4.38E-03	1.48E-01	KRT10	keratin 10	chr17q21	210633_x_at	NM_000421
7.90	7.19	0.71	4.40E-03	1.48E-01	RING1	ring finger protein 1	chr6p21.3	208371_s_at	NM_002931
4.79	3.76	1.03	4.40E-03	1.48E-01	ZNF764	zinc finger protein 764	chr16p11.2	57516_at	NM_033410
5.12	3.17	1.94	4.41E-03	1.48E-01	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	chr1q25	207426_s_at	NM_003326
6.87	6.38	0.50	4.41E-03	1.48E-01	FTSJ3	FtsJ homolog 3 (E. coli)	chr17q23.3	218103_at	NM_017647
11.90	11.43	0.47	4.41E-03	1.48E-01	RPL13A	ribosomal protein L13a	chr19q13.3	200715_x_at	NM_012423
5.18	4.20	0.98	4.42E-03	1.48E-01	---	---	---	239866_at	---
5.85	5.15	0.70	4.42E-03	1.48E-01	---	---	---	242139_s_at	---
5.02	4.25	0.77	4.42E-03	1.48E-01	---	---	---	225396_at	---
8.67	7.85	0.82	4.43E-03	1.48E-01	ITGB5	integrin, beta 5	chr3q21.2	201125_s_at	NM_002213
5.01	4.22	0.79	4.43E-03	1.48E-01	CRAMP1L /// HN1L	Crm, cramped-like (Drosophila) /// hematological and neurological expressed 1-like	chr16p13.3	225172_at	NM_020825 /// NM_144570
6.45	5.20	1.25	4.44E-03	1.48E-01	---	---	---	239069_s_at	---
5.63	3.83	1.79	4.44E-03	1.48E-01	SCARB1	scavenger receptor class B, member 1	chr12q24.31	232421_at	NM_001082959 /// NM_005505
4.35	3.25	1.10	4.44E-03	1.48E-01	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	chr6p25.2	202127_at	NM_003913
8.26	7.42	0.84	4.44E-03	1.48E-01	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	chr16p13.3	46256_at	NM_080861
2.83	2.20	0.63	4.45E-03	1.48E-01	CAPN3	calpain 3, (p94)	chr15q15.1-q21.1	214475_x_at	NM_000070 /// NM_024344 /// NM_173087 /// NM_173088 /// NM_173089 /// NM_173090 /// NM_212464 /// NM_212465 /// NM_212467
4.24	3.60	0.64	4.47E-03	1.48E-01	HPS1	Hermansky-Pudlak syndrome 1	chr10q23.1-q23.3	210112_at	NM_000195 /// NM_182639
7.25	6.26	0.99	4.47E-03	1.48E-01	RAB2B	RAB2B, member RAS oncogene family	chr14q11.2	225074_at	NM_032846
5.02	3.38	1.64	4.47E-03	1.48E-01	WISP1	WNT1 inducible signaling pathway protein 1	chr8q24.1-q24.3	206796_at	NM_003882 /// NM_080838
4.01	3.52	0.49	4.48E-03	1.48E-01	KIAA1609	KIAA1609	chr16q24.1	221843_s_at	NM_020947
3.45	2.59	0.86	4.48E-03	1.48E-01	---	---	---	1556775_at	---
4.65	3.60	1.05	4.49E-03	1.49E-01	MGC16121	hypothetical protein MGC16121	chrXq26.3	228235_at	XM_001128419 /// XM_001715787 /// XM_001715872
5.94	5.24	0.70	4.50E-03	1.49E-01	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	chr8p23	216620_s_at	NM_014629
3.68	2.91	0.77	4.51E-03	1.49E-01	FAM76B	family with sequence similarity 76, member B	chr11q21	226753_at	NM_144664
6.96	4.94	2.02	4.52E-03	1.49E-01	ATF3	activating transcription factor 3	chr1q32.3	202672_s_at	NM_001030287 /// NM_001040619 /// NM_001674 /// NM_004024
9.38	8.62	0.76	4.52E-03	1.49E-01	C11orf31	chromosome 11 open reading frame 31	chr11q12.1	231045_x_at	NM_170746
3.92	2.26	1.66	4.53E-03	1.49E-01	FLRT2	Fibronectin leucine rich transmembrane protein 2	chr14q24-q32	240259_at	NM_013231
5.44	4.76	0.68	4.53E-03	1.49E-01	---	---	---	235109_at	---
8.12	7.51	0.61	4.55E-03	1.49E-01	OAZ2	ornithine decarboxylase antizyme 2	chr15q22.31	201364_s_at	NM_002537
6.06	5.60	0.46	4.56E-03	1.50E-01	HIRIP3	HIRA interacting protein 3	chr16p11.2	204504_s_at	NM_003609

7.80	6.37	1.43	4.56E-03	1.50E-01	FAM156A /// FAM156B	family with sequence similarity 156, member A /// family with sequence similarity 156, member B	chrXp11.22	223203_at	NM_001099684 /// NM_014138
6.27	5.20	1.07	4.57E-03	1.50E-01	NKX3-1	NK3 homeobox 1	chr8p21	209706_at	NM_006167
7.90	7.25	0.65	4.58E-03	1.50E-01	ARID1A	AT rich interactive domain 1A (SWI-like)	chr1p35.3	218917_s_at	NM_006015 /// NM_139135
7.20	4.59	2.61	4.59E-03	1.50E-01	MCOLN3	mucolipin 3	chr1p22.3	1557292_a_at	NM_018298
8.53	6.61	1.92	4.59E-03	1.50E-01	GADD45B	growth arrest and DNA-damage-inducible, beta	chr19p13.3	207574_s_at	NM_015675
4.36	3.48	0.89	4.59E-03	1.50E-01	NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	chr8p23.1-p21.3	214440_at	NM_000662
8.41	7.82	0.58	4.59E-03	1.50E-01	LOC100131801	similar to hCG2036585	chr19p13.2	226006_at	XM_001723846 /// XM_001726504 /// XM_001726553
8.50	7.52	0.98	4.60E-03	1.50E-01	TADA3L	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	chr3p25.3	215273_s_at	NM_006354 /// NM_133480
4.58	3.56	1.02	4.60E-03	1.50E-01	TMEM68	transmembrane protein 68	chr8q12.1	227936_at	NM_152417
4.72	2.67	2.05	4.61E-03	1.50E-01	7A5	putative binding protein 7a5	chr7p15.3	1566766_a_at	NM_182762
3.10	2.66	0.44	4.62E-03	1.50E-01	PCGF5	Polycomb group ring finger 5	chr10q23.32	229996_s_at	NM_032373
7.27	6.25	1.02	4.62E-03	1.50E-01	YAP1	Yes-associated protein 1, 65kDa	chr11q13	224894_at	NM_001130145 /// NM_006106
6.50	5.96	0.55	4.63E-03	1.50E-01	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10q25.3	216035_x_at	NM_030756
6.55	5.89	0.65	4.63E-03	1.50E-01	RAB11FIP5	RAB11 family interacting protein 5 (class I)	chr2p13-p12	210879_s_at	NM_015470
7.54	6.79	0.74	4.63E-03	1.50E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	208794_s_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072
10.40	9.04	1.35	4.66E-03	1.51E-01	TIMP3	TIMP metallopeptidase inhibitor 3	chr22q12.1-q13.2|22q12.3	201150_s_at	NM_000362
3.74	3.13	0.62	4.68E-03	1.51E-01	C1orf43	chromosome 1 open reading frame 43	chr1q21.2	1555225_at	NM_001098616 /// NM_015449 /// NM_138740
4.55	3.30	1.25	4.69E-03	1.51E-01	DIDO1	death inducer-obliterator 1	chr20q13.33	213213_at	NM_022105 /// NM_033081 /// NM_080796 /// NM_080797
8.28	7.64	0.64	4.71E-03	1.52E-01	GORASP2	golgi reassembly stacking protein 2, 55kDa	chr2q31.1-q31.2	208843_s_at	NM_015530
4.71	3.33	1.37	4.71E-03	1.52E-01	KCNK1	potassium channel, subfamily K, member 1	chr1q42-q43	204678_s_at	NM_002245
5.90	4.66	1.23	4.71E-03	1.52E-01	DUSP28	dual specificity phosphatase 28	chr2q37.3	229211_at	NM_001033575
4.16	3.46	0.69	4.71E-03	1.52E-01	FLJ45244	hypothetical locus FLJ45244	chr14q32.13	229227_at	NM_207443
6.29	5.17	1.12	4.73E-03	1.52E-01	SERF1A /// SERF1B	small EDRK-rich factor 1A (telomeric) /// small EDRK-rich factor 1B (centromeric)	chr5q12.2-q13.3 /// chr5q13.2	223538_at	NM_021967 /// NM_022968 /// NM_022978 /// XM_001713905 /// XM_001720851 /// XM_001720856
7.02	6.53	0.49	4.73E-03	1.52E-01	C6orf153	chromosome 6 open reading frame 153	chr6p21.1	225788_at	NM_033112
3.66	2.29	1.37	4.74E-03	1.52E-01	C1orf173	chromosome 1 open reading frame 173	chr1p31.1	229973_at	NM_001002912
4.51	3.58	0.93	4.75E-03	1.52E-01	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	chr7q22.2	218984_at	NM_019042
5.71	4.96	0.75	4.75E-03	1.52E-01	OBSL1	obscurin-like 1	chr2q35	227573_s_at	NM_015311

6.33	5.30	1.03	4.77E-03	1.52E-01	USP21	ubiquitin specific peptidase 21	chr1q22	218367_x_at	NM_001014443 /// NM_012475
5.19	4.27	0.91	4.77E-03	1.52E-01	CHEK2	CHK2 checkpoint homolog (S. pombe)	chr22q11|22q12.1	210416_s_at	NM_001005735 /// NM_007194 /// NM_145862
7.80	5.27	2.53	4.77E-03	1.52E-01	MCOLN3	Mucolipin 3	chr1p22.3	242308_at	NM_018298
6.20	4.72	1.48	4.77E-03	1.52E-01	PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	chr14q24.1	225726_s_at	NM_020715
6.80	5.95	0.85	4.79E-03	1.53E-01	ANKRD10	ankyrin repeat domain 10	chr13q34	218093_s_at	NM_017664
7.58	6.73	0.85	4.79E-03	1.53E-01	EID2	EP300 interacting inhibitor of differentiation 2	chr19q13.2	225936_at	NM_153232
6.67	6.27	0.40	4.80E-03	1.53E-01	CDK3 /// LOC100134934	cyclin-dependent kinase 3 /// hypothetical protein LOC100134934	chr17q22-qter	226396_at	NM_001113324 /// NM_001258
9.22	8.04	1.18	4.80E-03	1.53E-01	EIF1B	eukaryotic translation initiation factor 1B	chr3p22.1	201738_at	NM_005875
5.78	5.03	0.75	4.81E-03	1.53E-01	GATAD1	GATA zinc finger domain containing 1	chr7q21-q22	213018_at	NM_021167
5.46	4.55	0.90	4.81E-03	1.53E-01	C16orf48	chromosome 16 open reading frame 48	chr16q22.1	223407_at	NM_032140
7.38	6.82	0.56	4.81E-03	1.53E-01	NOL5A	nucleolar protein 5A (56kDa with KKE/D repeat)	chr20p13	200875_s_at	NM_006392
6.08	5.20	0.88	4.82E-03	1.53E-01	ST7L	suppression of tumorigenicity 7 like	chr1p13.2	230079_at	NM_017744 /// NM_138727 /// NM_138728 /// NM_138729
6.10	5.32	0.78	4.83E-03	1.53E-01	FZD1	frizzled homolog 1 (Drosophila)	chr7q21	204451_at	NM_003505
7.66	6.91	0.75	4.83E-03	1.53E-01	HSPC111	hypothetical protein HSPC111	chr5q35.2	214011_s_at	NM_016391
5.96	5.05	0.91	4.83E-03	1.53E-01	MZF1	myeloid zinc finger 1	chr19q13.2|19q13.2-q13.4	204139_x_at	NM_003422 /// NM_198055
6.78	6.13	0.65	4.83E-03	1.53E-01	WDR74	WD repeat domain 74	chr11q12.3	221712_s_at	NM_018093
7.47	6.98	0.49	4.83E-03	1.53E-01	EXT2	exostoses (multiple) 2	chr11p12-p11	202012_s_at	NM_000401 /// NM_207122
6.94	6.22	0.72	4.83E-03	1.53E-01	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	210658_s_at	NM_015044
5.32	4.35	0.96	4.84E-03	1.53E-01	ADHFE1	alcohol dehydrogenase, iron containing, 1	chr8q13.1	227113_at	NM_144650
4.00	2.79	1.21	4.84E-03	1.53E-01	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	chr11p13	229665_at	NM_001033505 /// NM_001033506 /// NM_001326
8.31	7.06	1.25	4.85E-03	1.53E-01	LEPREL1	leprecan-like 1	chr3q28	218717_s_at	NM_001134418 /// NM_018192
5.95	4.98	0.97	4.87E-03	1.53E-01	MST150	MSTP150	chr5q33.1	223276_at	NM_032947
9.41	8.72	0.69	4.87E-03	1.53E-01	RNF181	ring finger protein 181	chr2p11.2	223064_at	NM_016494
7.13	6.29	0.84	4.88E-03	1.53E-01	ADO	2-aminoethanethiol (cysteamine) dioxygenase	chr10q21.2	212502_at	NM_032804
3.69	3.06	0.63	4.89E-03	1.53E-01	---	---	---	240355_at	---
6.66	6.02	0.64	4.89E-03	1.53E-01	PRPF38A	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	chr1p33-p32.1	1553709_a_at	NM_032864
4.68	2.29	2.39	4.91E-03	1.53E-01	PABPC1L	poly(A) binding protein, cytoplasmic 1-like	---	226670_s_at	NM_001124756 /// XM_001130728 /// XM_001131956 /// XM_001722078
7.29	6.65	0.65	4.91E-03	1.53E-01	SIVA1	SIVA1, apoptosis-inducing factor	chr14q32.33	210792_x_at	NM_006427 /// NM_021709
4.82	4.26	0.57	4.91E-03	1.54E-01	TRRAP	transformation/transcription domain-associated protein	chr7q21.2-q22.1	214908_s_at	NM_003496
5.57	4.84	0.73	4.92E-03	1.54E-01	LOC100132532	hypothetical protein LOC100132532	chr14q32.31	214083_at	XM_001725096 /// XM_001726536
9.07	8.46	0.61	4.92E-03	1.54E-01	LOC728453	similar to 40S ribosomal protein S28	chr7q11.22	216380_x_at	XM_001126850 /// XM_001127303 /// XM_001721304
6.88	6.31	0.57	4.92E-03	1.54E-01	TATDN2	TatD DNase domain containing 2	chr3p25.3	203648_at	NM_014760
4.42	3.88	0.54	4.93E-03	1.54E-01	FAM120C	family with sequence similarity 120C	chrXp11.22	220685_at	NM_017848

6.09	5.33	0.76	4.95E-03	1.54E-01	GNB5	guanine nucleotide binding protein (G protein), beta 5	chr15q21.2	204000_at	NM_006578 /// NM_016194																				
5.00	4.53	0.46	4.96E-03	1.54E-01	SPATA5L1	spermatogenesis associated 5-like 1	chr15q21.1	218933_at	NM_024063																				
9.30	8.77	0.53	4.96E-03	1.54E-01	SRPR	signal recognition particle receptor ('docking protein')	chr11q24.3	200918_s_at	NM_003139																				
6.71	6.11	0.60	4.97E-03	1.54E-01	YLPM1	YLP motif containing 1	chr14q24.3	212787_at	NM_019589																				
7.93	7.23	0.71	4.98E-03	1.54E-01	C17orf95	chromosome 17 open reading frame 95	chr17q25.2	225808_at	NM_001080510																				
5.74	4.40	1.34	4.99E-03	1.55E-01	TUFT1	tuftelin 1	chr1q21	205807_s_at	NM_001126337 /// NM_020127																				
6.54	5.87	0.67	5.02E-03	1.55E-01	LYK5	protein kinase LYK5	chr17q23.3	221554_at	NM_001003786 /// NM_001003787 /// NM_001003788 /// NM_153335																				
7.13	6.37	0.76	5.02E-03	1.55E-01	BET1	blocked early in transport 1 homolog (S. cerevisiae)	chr7q21.1-q22	202710_at	NM_005868																				
5.97	5.47	0.50	5.02E-03	1.55E-01	---	---	---	225653_at	---																				
6.46	5.67	0.79	5.03E-03	1.55E-01	ZNF335	zinc finger protein 335	chr20q11.21-q13.12	221890_at	NM_022095																				
3.67	3.13	0.55	5.04E-03	1.56E-01	NLE1	notchless homolog 1 (Drosophila)	chr17q12	203866_at	NM_001014445 /// NM_018096																				
8.63	7.93	0.71	5.06E-03	1.56E-01	MRPL16	mitochondrial ribosomal protein L16	chr11q12-q13.1	217980_s_at	NM_017840																				
7.51	6.35	1.15	5.08E-03	1.56E-01	FTSJ1	FtsJ homolog 1 (E. coli)	chrXp11.23	205324_s_at	NM_012280 /// NM_177434 /// NM_177439																				
5.60	4.78	0.82	5.08E-03	1.56E-01	C7orf38	Chromosome 7 open reading frame 38	chr7q22.1	229762_at	NM_145111																				
8.53	8.08	0.45	5.08E-03	1.56E-01	RDBP	RD RNA binding protein	chr6p21.3	209219_at	NM_002904																				
8.16	7.45	0.71	5.09E-03	1.57E-01	MRPS18B	mitochondrial ribosomal protein S18B	chr6p21.3	217408_at	NM_014046																				
7.90	7.44	0.47	5.10E-03	1.57E-01	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	chr20p13	210014_x_at	NM_006899 /// NM_174855 /// NM_174856																				
7.09	6.24	0.85	5.10E-03	1.57E-01	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	chr16p12.1	218016_s_at	NM_018119																				
6.20	5.13	1.07	5.11E-03	1.57E-01	USP36	Ubiquitin specific peptidase 36	chr17q25.3	227093_at	NM_025090																				
3.74	3.03	0.71	5.11E-03	1.57E-01	IDUA	iduronidase, alpha-L-	chr4p16.3	205057_s_at	NM_000203																				
2.87	2.34	0.54	5.12E-03	1.57E-01	DKK1	dickkopf homolog 1 (Xenopus laevis)	chr10q11.2	204602_at	NM_012242																				
8.17	7.07	1.11	5.12E-03	1.57E-01	GOLSYN	Golgi-localized protein	chr8q23.2	218692_at	NM_001099743 /// NM_001099744 /// NM_001099745 /// NM_001099746 /// NM_001099747 /// NM_001099748 /// NM_001099749 /// NM_001099750 /// NM_001099751 /// NM_001099752 /// NM_001099753 /// NM_001099754 /// NM_001099755 /// NM_001099756 /// NM_017786																		
12.02	11.61	0.40	5.14E-03	1.57E-01	RPS9	ribosomal protein S9	chr19q13.4	217747_s_at	NM_001013																				
5.69	4.72	0.97	5.14E-03	1.57E-01	GTPBP5	GTP binding protein 5 (putative)	chr20q13.33	226606_s_at	NM_015666																				
6.04	5.47	0.56	5.15E-03	1.57E-01	PDCD11	programmed cell death 11	chr10q24.33	212422_at	NM_014976																				

3.43	2.46	0.97	5.15E-03	1.57E-01	---	---	---	230491_at	---
5.37	4.01	1.36	5.15E-03	1.57E-01	---	---	---	237062_at	---
3.09	2.68	0.42	5.16E-03	1.57E-01	ZAN	zonadhesin	chr7q22	224267_x_at	NM_003386 /// NM_173059
5.41	4.88	0.53	5.16E-03	1.57E-01	GON4L	gon-4-like (C. elegans)	chr1q22	218873_at	NM_001037533 /// NM_032292
5.53	4.83	0.70	5.17E-03	1.57E-01	EPN2	epsin 2	chr17p11.2	203464_s_at	NM_001102664 /// NM_014964 /// NM_148921
3.96	3.24	0.72	5.18E-03	1.57E-01	---	---	---	214148_at	---
4.05	3.50	0.55	5.18E-03	1.57E-01	---	---	---	239841_at	---
8.82	8.17	0.64	5.18E-03	1.57E-01	SCAND1	SCAN domain containing 1	chr20q11.1-q11.23	218206_x_at	NM_016558 /// NM_033630
4.69	3.78	0.91	5.18E-03	1.57E-01	RPL23	ribosomal protein L23	chr17q	214744_s_at	NM_000978
7.60	7.00	0.60	5.19E-03	1.57E-01	ECOP	EGFR-coamplified and overexpressed protein	chr7p11.2	208091_s_at	NM_030796
6.88	4.61	2.27	5.19E-03	1.57E-01	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	chr6q22	222938_x_at	NM_005021
4.66	3.87	0.79	5.20E-03	1.57E-01	TTC7B	tetratricopeptide repeat domain 7B	chr14q32.11	226152_at	NM_001010854
3.79	2.36	1.43	5.21E-03	1.58E-01	CHD2	chromodomain helicase DNA binding protein 2	chr15q26	228999_at	NM_001042572 /// NM_001271
3.02	2.21	0.81	5.22E-03	1.58E-01	LOC440350	similar to nuclear pore complex interacting protein	chr16p11.2	215921_at	NM_001018122 /// XM_001713614
6.04	5.21	0.83	5.25E-03	1.58E-01	C10orf72	chromosome 10 open reading frame 72	chr10q11.22	244058_at	NM_001031746 /// NM_144984
4.43	3.85	0.58	5.25E-03	1.58E-01	RIG	regulated in glioma	chr11p15.1	221127_s_at	XM_932493 /// XM_944753
8.23	7.47	0.76	5.25E-03	1.58E-01	TM2D3	TM2 domain containing 3	chr15q26.3	221702_s_at	NM_025141 /// NM_078474
7.90	7.03	0.87	5.27E-03	1.58E-01	EPB41L2	erythrocyte membrane protein band 4.1-like 2	chr6q23	201719_s_at	NM_001431
7.20	6.34	0.86	5.27E-03	1.58E-01	ZHX2	zinc fingers and homeoboxes 2	chr8q24.13	203556_at	NM_014943
4.38	3.44	0.94	5.28E-03	1.58E-01	CAPN3	calpain 3, (p94)	chr15q15.1-q21.1	210944_s_at	NM_000070 /// NM_024344 /// NM_173087 /// NM_173088 /// NM_173089 /// NM_173090 /// NM_212464 /// NM_212465 /// NM_212467
8.30	7.32	0.98	5.28E-03	1.58E-01	MIDN	midnolin	chr19p13.3	225954_s_at	NM_177401
9.24	8.73	0.51	5.28E-03	1.58E-01	LOC388789	hypothetical LOC388789	chr20p11.23	226236_at	XM_001718252 /// XM_373908 /// XM_939954
4.93	4.33	0.61	5.28E-03	1.58E-01	GMEB1	glucocorticoid modulatory element binding protein 1	chr1p35.3	235232_at	NM_006582 /// NM_024482
3.03	2.08	0.94	5.28E-03	1.58E-01	MKX	mohawk homeobox	chr10p12.1	239468_at	NM_173576
5.89	4.28	1.61	5.29E-03	1.58E-01	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	chr22q13.1	205193_at	NM_012323 /// NM_152878
6.76	5.27	1.49	5.29E-03	1.58E-01	MARCO	macrophage receptor with collagenous structure	chr2q12-q13	205819_at	NM_006770
5.36	4.99	0.37	5.30E-03	1.59E-01	YARS2	tyrosyl-tRNA synthetase 2, mitochondrial	chr12p11.21	218470_at	NM_001040436

7.43	5.42	2.01	5.30E-03	1.59E-01	LOC728473	hypothetical LOC728473	chr18q11.2	236118_at	XM_001126087 /// XM_001129466 /// XM_001723431																			
7.92	6.64	1.28	5.32E-03	1.59E-01	C17orf91	chromosome 17 open reading frame 91	chr17p13.3	214696_at	NM_001001870 /// NM_032895																			
4.76	3.40	1.36	5.32E-03	1.59E-01	---	---	---	241991_at	---																			
7.84	6.60	1.24	5.33E-03	1.59E-01	PER1	period homolog 1 (Drosophila)	chr17p13.1-p12	202861_at	NM_002616																			
4.45	3.15	1.29	5.34E-03	1.59E-01	CCDC45	coiled-coil domain containing 45	chr17q24.1	225705_at	NM_138363																			
6.28	5.03	1.25	5.35E-03	1.59E-01	SGSM2	small G protein signaling modulator 2	chr17p13.3	212319_at	NM_001098509 /// NM_014853																			
4.90	4.17	0.73	5.36E-03	1.59E-01	EPHA2	EPH receptor A2	chr1p36	203499_at	NM_004431																			
6.35	5.39	0.96	5.38E-03	1.60E-01	UNC84A	unc-84 homolog A (C. elegans)	chr7p22.3	212074_at	NM_001130965 /// NM_025154																			
10.24	9.84	0.39	5.38E-03	1.60E-01	ADI1	acireductone dioxygenase 1	chr2p25.3	222400_s_at	NM_018269																			
3.52	2.88	0.64	5.38E-03	1.60E-01	USP36	ubiquitin specific peptidase 36	chr17q25.3	220370_s_at	NM_025090																			
3.99	3.22	0.77	5.39E-03	1.60E-01	TMTC4	transmembrane and tetratricopeptide repeat containing 4	chr13q32.3	1554102_a_at	NM_001079669 /// NM_032813																			
3.46	2.95	0.51	5.39E-03	1.60E-01	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	chr19p13.3	231297_at	NM_032482																			
7.05	6.38	0.68	5.41E-03	1.60E-01	NOL12 /// TRIOBP	nucleolar protein 12 /// TRIO and F-actin binding protein	chr22q13.1	219324_at	NM_001039141 /// NM_007032 /// NM_024313 /// NM_138632																			
3.01	2.39	0.62	5.41E-03	1.60E-01	---	---	---	244484_at	---																			
6.62	6.04	0.58	5.42E-03	1.60E-01	IL17RC	interleukin 17 receptor C	chr3p25.3|3p25.3-p24.1	64440_at	NM_032732 /// NM_153460 /// NM_153461																			
3.27	2.43	0.84	5.42E-03	1.60E-01	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	chr2q23.3	225711_at	NM_152522																			
8.43	7.85	0.59	5.43E-03	1.60E-01	DERL1	Der1-like domain family, member 1	chr8q24.13	219402_s_at	NM_001134671 /// NM_024295																			
7.38	6.77	0.61	5.43E-03	1.60E-01	C16orf13	chromosome 16 open reading frame 13	chr16p13.3	1554466_a_at	NM_001040160 /// NM_001040161 /// NM_001040162 /// NM_001040165 /// NM_032366																			
5.78	5.08	0.70	5.44E-03	1.60E-01	SAP30L	SAP30-like	chr5q33.2	219129_s_at	NM_001131062 /// NM_001131063 /// NM_024632 /// NR_024084																			
5.54	4.69	0.85	5.45E-03	1.60E-01	BID	BH3 interacting domain death agonist	chr22q11.1	211725_s_at	NM_001196 /// NM_197966 /// NM_197967																			
9.08	8.04	1.04	5.45E-03	1.60E-01	SFRS5	splicing factor, arginine/serine-rich 5	chr14q24	212266_s_at	NM_001039465 /// NM_006925																			
10.79	9.06	1.73	5.46E-03	1.60E-01	CPB1	carboxypeptidase B1 (tissue)	chr3q24	205509_at	NM_001871																			
6.25	5.58	0.67	5.46E-03	1.60E-01	ARSD	arylsulfatase D	chrXp22.3	225280_x_at	NM_001669 /// NM_009589																			
6.78	5.75	1.04	5.46E-03	1.60E-01	TBRG1	transforming growth factor beta regulator 1	chr11q24.2	225819_at	NM_032811 /// NR_016021																			
6.28	5.49	0.80	5.46E-03	1.60E-01	EXOSC6	exosome component 6	chr16q22.1	1553947_at	NM_058219																			
7.98	7.13	0.85	5.47E-03	1.60E-01	ARFIP2	ADP-ribosylation factor interacting protein 2	chr11p15	202109_at	NM_012402																			
5.16	4.54	0.62	5.47E-03	1.60E-01	PHF8	PHD finger protein 8	chrXp11.22	212916_at	NM_015107																			

7.17	6.57	0.60	5.48E-03	1.60E-01	TM9SF4	transmembrane 9 superfamily protein member 4	chr20q11.21	212194_s_at	NM_014742
7.05	5.81	1.24	5.48E-03	1.60E-01	C19orf54	chromosome 19 open reading frame 54	chr19q13.2	222052_at	NM_198476
4.18	3.27	0.91	5.48E-03	1.60E-01	CADM4	cell adhesion molecule 4	chr19q13.31	215259_s_at	NM_145296
5.91	5.16	0.75	5.48E-03	1.60E-01	ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	chr17p13.2	212601_at	NM_015113 /// XM_001127649 /// XM_001719617 /// XM_001723898
5.68	4.93	0.75	5.48E-03	1.60E-01	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	chr10q22	203916_at	NM_003635
9.20	8.62	0.58	5.48E-03	1.60E-01	PRMT1	protein arginine methyltransferase 1	chr19q13.3	206445_s_at	NM_001536 /// NM_198318 /// NM_198319
3.57	2.38	1.19	5.48E-03	1.60E-01	ZNF207	zinc finger protein 207	chr17q11.2	228157_at	NM_001032293 /// NM_001098507 /// NM_003457
8.45	7.97	0.48	5.50E-03	1.60E-01	KIAA0174	KIAA0174	chr16q22.3	200851_s_at	NM_014761
2.43	1.91	0.51	5.50E-03	1.60E-01	HMCN1	hemicentin 1	chr1q25.3-q31.1	235944_at	NM_031935
8.46	7.89	0.58	5.52E-03	1.61E-01	POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	chr19q12	212955_s_at	NM_006233
6.04	3.95	2.09	5.54E-03	1.61E-01	GRTP1	growth hormone regulated TBC protein 1	chr13q34	229377_at	NM_024719
5.33	4.80	0.53	5.56E-03	1.62E-01	---	---	---	236794_at	---
8.30	7.37	0.92	5.58E-03	1.62E-01	SFXN4	sideroflexin 4	chr10q26.11	225143_at	NM_213649
5.89	5.10	0.79	5.58E-03	1.62E-01	EP300	E1A binding protein p300	chr22q13.2	202221_s_at	NM_001429
6.05	5.00	1.05	5.59E-03	1.62E-01	OR7E37P	olfactory receptor, family 7, subfamily E, member 37 pseudogene	chr13q14.11	217499_x_at	NR_002163 /// XR_042149
3.24	2.76	0.48	5.59E-03	1.62E-01	GPR107	G protein-coupled receptor 107	chr9q34.11	220264_s_at	NM_020960
5.17	4.53	0.64	5.59E-03	1.62E-01	PARP6	poly (ADP-ribose) polymerase family, member 6	chr15q23	234710_s_at	NM_020214
5.57	4.66	0.90	5.60E-03	1.62E-01	WDR8	WD repeat domain 8	chr1p36.3	219322_s_at	NM_017818
7.17	6.72	0.45	5.60E-03	1.62E-01	SRRM1	serine/arginine repetitive matrix 1	chr1p36.11	201224_s_at	NM_005839
6.44	5.15	1.30	5.62E-03	1.62E-01	PRR6	proline rich 6	chr17p11.2	226611_s_at	NM_181716
4.64	3.44	1.20	5.62E-03	1.62E-01	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	chr1p36.11	244261_at	NM_170743 /// NM_173064 /// NM_173065
5.53	4.55	0.98	5.63E-03	1.62E-01	LOC25845	hypothetical LOC25845	chr5p15.33	225458_at	XR_017708 /// XR_017745 /// XR_040817
3.40	2.70	0.70	5.63E-03	1.62E-01	EIF4E2	eukaryotic translation initiation factor 4E family member 2	chr2q37.1	213570_at	NM_004846
6.21	5.29	0.92	5.64E-03	1.62E-01	AKAP8	A kinase (PRKA) anchor protein 8	chr19p13.1	203848_at	NM_005858
4.43	3.74	0.69	5.64E-03	1.62E-01	PHF15	PHD finger protein 15	chr5q31.1	232279_at	NM_015288
5.74	4.93	0.81	5.64E-03	1.62E-01	TMPO	thymopoietin	chr12q22	203432_at	NM_001032283 /// NM_001032284 /// NM_003276
7.01	6.00	1.01	5.65E-03	1.63E-01	HTRA2	HtrA serine peptidase 2	chr2p12	203089_s_at	NM_013247 /// NM_145074
8.24	7.56	0.68	5.66E-03	1.63E-01	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	chr15q23-q25	202862_at	NM_000137
6.44	5.66	0.78	5.68E-03	1.63E-01	HOXA10	homeobox A10	chr7p15-p14	213147_at	NM_018951 /// NM_153715
8.30	7.28	1.02	5.69E-03	1.63E-01	RNF5	ring finger protein 5	chr6p21.3	209111_at	NM_006913
3.40	2.56	0.84	5.69E-03	1.63E-01	ULBP2	UL16 binding protein 2	chr6q25	238542_at	NM_025217
2.96	2.55	0.41	5.70E-03	1.63E-01	LOC643201	hypothetical protein LOC643201	chr5q35.2	1570445_a_at	XM_001716444 /// XM_001717933 /// XM_932161
4.57	3.51	1.06	5.71E-03	1.63E-01	CNPY3	canopy 3 homolog (zebrafish)	chr6pter-p12.1	1556389_at	NM_006586
3.25	2.30	0.95	5.72E-03	1.63E-01	---	---	---	244832_at	---
7.72	7.02	0.69	5.72E-03	1.63E-01	SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	chr17q21-q23	201484_at	NM_003168
8.22	7.34	0.87	5.72E-03	1.63E-01	SRRM1	serine/arginine repetitive matrix 1	chr1p36.11	201225_s_at	NM_005839
4.77	4.20	0.57	5.72E-03	1.63E-01	ANKRD40	ankyrin repeat domain 40	chr17q21.33	211717_at	NM_052855
5.39	4.85	0.54	5.73E-03	1.63E-01	RPL35A	ribosomal protein L35a	chr3q29-qter	238026_at	NM_000996

5.14	4.18	0.95	5.75E-03	1.64E-01	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	chr5q33.1	1554010_at	NM_001543
7.18	6.61	0.56	5.76E-03	1.64E-01	ZMYM6	zinc finger, MYM-type 6	chr1p34.2	219924_s_at	NM_007167
5.87	5.14	0.73	5.76E-03	1.64E-01	DNMT1	DNA (cytosine-5-)-methyltransferase 1	chr19p13.2	201697_s_at	NM_001130823 /// NM_001379
7.96	6.60	1.36	5.77E-03	1.64E-01	FOSL2	FOS-like antigen 2	chr2p23.3	218880_at	NM_005253
6.89	6.34	0.55	5.78E-03	1.64E-01	GPKOW	G patch domain and KOW motifs	chrXp11.23	203776_at	NM_015698
3.80	2.91	0.89	5.79E-03	1.64E-01	EIF3B	eukaryotic translation initiation factor 3, subunit B	chr7p22.2	242550_at	NM_001037283 /// NM_003751
4.58	3.44	1.14	5.79E-03	1.64E-01	---	---	---	239834_at	---
7.10	5.80	1.30	5.81E-03	1.65E-01	LOC731602 /// METT11D1	similar to methyltransferase 11 domain containing 1 isoform 2 /// methyltransferase 11 domain containing 1	chr14q11.2	223528_s_at	NM_001029991 /// NM_022734 /// XR_037376
6.35	5.21	1.14	5.82E-03	1.65E-01	RC3H1	ring finger and CCCH-type zinc finger domains 1	chr1q25.1	225893_at	NM_172071
7.81	7.10	0.72	5.82E-03	1.65E-01	CRELD2	cysteine-rich with EGF-like domains 2	chr22q13.33	218358_at	NM_024324
7.25	6.29	0.97	5.83E-03	1.65E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	213811_x_at	NM_003200
5.29	4.18	1.11	5.84E-03	1.65E-01	ZNF747	zinc finger protein 747	chr16p11.2	238606_at	NM_023931
4.54	3.49	1.05	5.84E-03	1.65E-01	AMY2B	amylase, alpha 2B (pancreatic)	chr1p21	228023_x_at	NM_020978
9.16	8.59	0.57	5.84E-03	1.65E-01	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	chr2q12-q21	211070_x_at	NM_001079862 /// NM_001079863 /// NM_020548
7.67	7.15	0.52	5.85E-03	1.65E-01	KIAA1310	KIAA1310	chr2p12-p11.2	224318_s_at	NM_001115016 /// NM_017991
8.18	7.73	0.45	5.86E-03	1.65E-01	SF3B2	splicing factor 3b, subunit 2, 145kDa	chr11q13.1	200619_at	NM_006842
7.63	7.01	0.62	5.86E-03	1.65E-01	NMRAL1	NmrA-like family domain containing 1	chr16p13.3	223206_s_at	NM_020677
5.95	5.09	0.86	5.86E-03	1.65E-01	PANK4	pantothenate kinase 4	chr1p36.32	218771_at	NM_018216
6.25	5.63	0.62	5.89E-03	1.65E-01	AMMECR1L	AMME chromosomal region gene 1-like	chr2q21	223297_at	NM_031445
5.56	5.02	0.53	5.89E-03	1.65E-01	UBE3C	ubiquitin protein ligase E3C	chr7q36.3	201817_at	NM_014671
3.79	2.61	1.18	5.89E-03	1.65E-01	CREBZF	CREB/ATF bZIP transcription factor	chr11q14	202979_s_at	NM_001039618
6.97	5.45	1.52	5.89E-03	1.65E-01	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	chr5q23.3	225835_at	NM_001046
6.77	6.03	0.73	5.89E-03	1.65E-01	LOC439994 /// LOC642361	hypothetical gene supported by AF064843; AK025716 /// hypothetical LOC642361	chr10q22.3 /// chr10q23.2	228839_s_at	XR_041355 /// XR_041356 /// XR_041627 /// XR_041628
3.08	2.64	0.44	5.89E-03	1.65E-01	SPIN3	spindlin family, member 3	chrXp11.1	1554099_a_at	NM_001010862
6.81	6.07	0.75	5.90E-03	1.65E-01	ATG4B	ATG4 autophagy related 4 homolog B (S. cerevisiae)	chr2q37.3	204903_x_at	NM_013325 /// NM_178326
6.59	5.95	0.63	5.90E-03	1.65E-01	C14orf179	chromosome 14 open reading frame 179	chr14q24.3	226196_s_at	NM_001102564 /// NM_052873
7.90	6.83	1.08	5.91E-03	1.65E-01	SULT1A3 /// SULT1A4	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	chr16p11.2	209607_x_at	NM_001017387 /// NM_001017389 /// NM_001017390 /// NM_001017391 /// NM_003166 /// NM_177552
5.14	4.57	0.57	5.91E-03	1.65E-01	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	chr7q22	37796_at	NM_002319
8.76	8.22	0.54	5.91E-03	1.65E-01	RNASET2	ribonuclease T2	chr6q27	217984_at	NM_003730
8.38	7.75	0.64	5.91E-03	1.65E-01	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	chr5q31.2	201345_s_at	NM_003339 /// NM_181838
5.46	4.58	0.89	5.94E-03	1.66E-01	TMEM63A	transmembrane protein 63A	chr1q42.12	202699_s_at	NM_014698
9.01	8.53	0.48	5.94E-03	1.66E-01	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5	chr14q11.2	208799_at	NM_001130725 /// NM_002797

7.97	6.88	1.09	5.95E-03	1.66E-01	LOC731602 /// METT11D1	similar to methyltransferase 11 domain containing 1 isoform 2 /// methyltransferase 11 domain containing 1	chr14q11.2	223988_x_at	NM_001029991 /// NM_022734 /// XR_037376
4.09	3.13	0.95	5.96E-03	1.66E-01	REV1	REV1 homolog (S. cerevisiae)	chr2q11.1-q11.2	222629_at	NM_001037872 /// NM_016316
5.85	4.30	1.54	5.98E-03	1.66E-01	---	---	---	229802_at	---
8.27	7.36	0.91	5.99E-03	1.66E-01	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	chr5q35	224598_at	NM_014275 /// NM_054013
7.91	7.18	0.74	5.99E-03	1.66E-01	UNG	uracil-DNA glycosylase	chr12q23-q24.1	202330_s_at	NM_003362 /// NM_080911
4.45	3.50	0.95	6.00E-03	1.66E-01	C17orf56	chromosome 17 open reading frame 56	chr17q25.3	227668_at	NM_144679
4.95	4.30	0.65	6.00E-03	1.66E-01	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	chr16p11.2	217526_at	NM_032815
3.30	2.61	0.69	6.01E-03	1.66E-01	NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	chr3q13.33	228940_at	NM_004547
4.34	3.42	0.92	6.05E-03	1.67E-01	---	---	---	229879_at	---
6.27	3.71	2.56	6.06E-03	1.67E-01	CDH12	cadherin 12, type 2 (N-cadherin 2)	chr5p14-p13	207149_at	NM_004061
4.43	3.72	0.72	6.08E-03	1.67E-01	MAGEE1	melanoma antigen family E, 1	chrXq13.3	1556047_s_at	NM_020932
9.76	9.17	0.59	6.08E-03	1.67E-01	JTB	jumping translocation breakpoint	chr1q21	210927_x_at	NM_006694
2.95	2.06	0.89	6.09E-03	1.67E-01	---	---	---	227921_at	---
8.16	7.43	0.73	6.09E-03	1.67E-01	ASMTL	acetylserotonin O-methyltransferase-like	chrXp22.3; Yp11.3	36553_at	NM_004192 /// XM_001713702
3.36	2.94	0.42	6.10E-03	1.67E-01	---	---	---	1570071_at	---
4.26	3.59	0.67	6.10E-03	1.67E-01	RUNDC1	RUN domain containing 1	chr17q21.31	235040_at	NM_173079
7.80	7.18	0.62	6.11E-03	1.67E-01	VGLL4	vestigial like 4 (Drosophila)	chr3p25.2	212399_s_at	NM_001128219 /// NM_001128220 /// NM_001128221 /// NM_014667
5.93	4.91	1.02	6.12E-03	1.67E-01	EIF4A1	Eukaryotic translation initiation factor 4A, isoform 1	chr17p13	214805_at	NM_001416
4.57	3.90	0.67	6.12E-03	1.67E-01	TMEM18	transmembrane protein 18	chr2p25.3	225487_at	NM_152834
4.34	3.67	0.67	6.12E-03	1.67E-01	ENDOGL1	endonuclease G-like 1	chr3p21.3	205521_at	NM_005107
10.09	9.40	0.69	6.12E-03	1.67E-01	SAT1	spermidine/spermine N1-acetyltransferase 1	chrXp22.1	210592_s_at	NM_002970
4.71	3.51	1.20	6.13E-03	1.67E-01	SNX5	sorting nexin 5	chr20p11	223666_at	NM_014426 /// NM_152227
8.21	7.32	0.90	6.15E-03	1.68E-01	BEX2	brain expressed X-linked 2	chrXq22	224367_at	NM_032621
4.09	3.63	0.46	6.16E-03	1.68E-01	ZNF333	zinc finger protein 333	chr19p13	1569250_at	NM_032433
5.80	4.79	1.01	6.16E-03	1.68E-01	KIAA0323	KIAA0323	chr14q12	212356_at	NM_015299
3.80	2.80	1.01	6.18E-03	1.68E-01	UNK	unkempt homolog (Drosophila)	chr17q25.1	228357_at	NM_001080419
5.14	4.60	0.53	6.18E-03	1.68E-01	SETD8	SET domain containing (lysine methyltransferase) 8	chr12q24.31	225094_at	NM_020382
4.08	3.45	0.63	6.20E-03	1.68E-01	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	chr12p	207101_at	NM_014231 /// NM_016830 /// NM_199245
7.34	6.54	0.79	6.20E-03	1.68E-01	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	chr17q22	239217_x_at	NM_003786
3.62	3.13	0.49	6.20E-03	1.68E-01	TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	chr6p21.1	1556176_at	NM_138572
4.75	4.11	0.64	6.20E-03	1.68E-01	KCNA4	potassium voltage-gated channel, shaker-related subfamily, member 4	chr11p14	207248_at	NM_002233
7.38	6.94	0.44	6.21E-03	1.68E-01	TOR1A	torsin family 1, member A (torsin A)	chr9q34	202348_s_at	NM_000113
5.49	5.11	0.38	6.21E-03	1.68E-01	BUD13	BUD13 homolog (S. cerevisiae)	chr11q23.3	224504_s_at	NM_032725
7.23	6.63	0.60	6.22E-03	1.68E-01	EHD1	EH-domain containing 1	chr11q13	208112_x_at	NM_006795
7.10	6.57	0.54	6.22E-03	1.68E-01	MRPS36	mitochondrial ribosomal protein S36	chr5q13.2	224302_s_at	NM_033281
4.27	3.00	1.27	6.23E-03	1.68E-01	ZNF767	zinc finger family member 767	chr7q36.1	219627_at	NM_024910
6.76	6.18	0.57	6.23E-03	1.68E-01	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	chr20q13.13	215693_x_at	NM_017895
2.75	2.39	0.36	6.25E-03	1.68E-01	LOC554207	hypothetical LOC554207	chr14q11.2	1555244_at	XR_040104 /// XR_040105 /// XR_040106

7.37	6.60	0.77	6.26E-03	1.68E-01	CKLF	chemokine-like factor	chr16q21	221058_s_at	NM_001040138 /// NM_016326 /// NM_016951 /// NM_181640 /// NM_181641
5.05	4.00	1.05	6.27E-03	1.69E-01	GCS1	glucosidase I	chr2p13-p12	210627_s_at	NM_006302
8.70	7.87	0.83	6.28E-03	1.69E-01	FNDC4	fibronectin type III domain containing 4	chr2p23.3	218843_at	NM_022823
6.23	3.53	2.69	6.28E-03	1.69E-01	LEFTY2	left-right determination factor 2	chr1q42.1	206012_at	NM_003240
2.39	2.01	0.37	6.30E-03	1.69E-01	RUFY2	RUN and FYVE domain containing 2	chr10q21.3	233191_at	NM_001042417 /// NM_017987
8.41	7.48	0.92	6.30E-03	1.69E-01	ELK1	ELK1, member of ETS oncogene family	chrXp11.2	203617_x_at	NM_001114123 /// NM_005229
6.41	5.44	0.98	6.33E-03	1.69E-01	TMEM107	transmembrane protein 107	chr17p13.1	239824_s_at	NM_032354 /// NM_183065
6.39	5.80	0.59	6.34E-03	1.69E-01	WDR74	WD repeat domain 74	chr11q12.3	218278_at	NM_018093
5.34	4.35	0.99	6.35E-03	1.69E-01	SHB	Src homology 2 domain containing adaptor protein B	chr9p13.2-p13.1	204656_at	NM_003028
6.90	5.27	1.63	6.35E-03	1.69E-01	FAM171A1	family with sequence similarity 171, member A1	chr10p13	212771_at	NM_001010924
8.16	7.51	0.65	6.35E-03	1.69E-01	HNRNPM	heterogeneous nuclear ribonucleoprotein M	chr19p13.3-p13.2	1555844_s_at	NM_005968 /// NM_031203
4.86	4.32	0.54	6.36E-03	1.69E-01	SYNPO	synaptopodin	chr5q33.1	235914_at	NM_001109974 /// NM_007286
7.02	6.35	0.67	6.36E-03	1.69E-01	ANKRD11	ankyrin repeat domain 11	chr16q24.3	238538_at	NM_013275
6.32	5.65	0.67	6.36E-03	1.69E-01	HTRA2	HtrA serine peptidase 2	chr2p12	211152_s_at	NM_013247 /// NM_145074
8.09	7.42	0.67	6.38E-03	1.69E-01	HMGN4	high mobility group nucleosomal binding domain 4	chr6p21.3	202579_x_at	NM_006353
4.98	4.33	0.64	6.38E-03	1.69E-01	JARID2	jumonji, AT rich interactive domain 2	chr6p24-p23	203298_s_at	NM_004973
7.56	6.86	0.70	6.39E-03	1.70E-01	POGZ	pogo transposable element with ZNF domain	chr1q21.3	212153_at	NM_015100 /// NM_145796 /// NM_207171
2.78	2.05	0.73	6.40E-03	1.70E-01	VIM	vimentin	chr10p13	1555938_x_at	NM_003380
3.99	2.90	1.09	6.41E-03	1.70E-01	IL17RB	interleukin 17 receptor B	chr3p21.1	224361_s_at	NM_018725
7.58	7.06	0.52	6.42E-03	1.70E-01	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	chr11q22.3	223151_at	NM_032299
5.39	4.11	1.27	6.44E-03	1.70E-01	RP3-402G11.5	selenoprotein O	chr22q13.33	233167_at	NM_031454
6.21	5.12	1.08	6.45E-03	1.70E-01	GGCX	gamma-glutamyl carboxylase	chr2p12	214005_at	NM_000821
8.33	7.25	1.08	6.47E-03	1.71E-01	---	---	---	230466_s_at	---
7.51	6.45	1.07	6.47E-03	1.71E-01	TOMM34	translocase of outer mitochondrial membrane 34	---	201870_at	NM_006809
7.05	6.29	0.77	6.47E-03	1.71E-01	SPRY2	sprouty homolog 2 (Drosophila)	chr13q31.1	204011_at	NM_005842
7.50	6.54	0.96	6.48E-03	1.71E-01	C15orf61	chromosome 15 open reading frame 61	chr15q23	229742_at	XM_001718659 /// XM_096885 /// XM_940644
7.54	7.08	0.46	6.48E-03	1.71E-01	MRPS16	mitochondrial ribosomal protein S16	chr10q22.1	218046_s_at	NM_016065
3.36	2.74	0.62	6.49E-03	1.71E-01	---	---	---	235848_x_at	---
8.46	7.46	1.00	6.49E-03	1.71E-01	C5orf13	chromosome 5 open reading frame 13	chr5q22.1	201310_s_at	NM_004772
2.98	2.46	0.51	6.51E-03	1.71E-01	HINT3	histidine triad nucleotide binding protein 3	chr6q22.32	226537_at	NM_138571
7.53	6.53	0.99	6.51E-03	1.71E-01	SFRS2	splicing factor, arginine/serine-rich 2	chr17q25.2	200753_x_at	NM_003016
4.77	4.15	0.62	6.52E-03	1.71E-01	LLGL2	lethal giant larvae homolog 2 (Drosophila)	chr17q24-q25	203713_s_at	NM_001015002 /// NM_001031803 /// NM_004524
6.16	5.40	0.76	6.52E-03	1.71E-01	INO80C	INO80 complex subunit C	chr18q12.2	229582_at	NM_001098817 /// NM_194281
7.97	7.16	0.82	6.53E-03	1.71E-01	ADPRHL2	ADP-ribosylhydrolase like 2	chr1p34.3	223097_at	NM_017825
7.20	6.54	0.66	6.53E-03	1.71E-01	PTPN6	protein tyrosine phosphatase, non-receptor type 6	chr12p13	206687_s_at	NM_002831 /// NM_080548 /// NM_080549

2.61	2.16	0.45	6.55E-03	1.71E-01	C2orf30	Chromosome 2 open reading frame 30	chr2p16.2	244452_at	NM_001127397 /// NM_001127398 /// NM_015701																				
7.06	5.78	1.28	6.56E-03	1.71E-01	NSUN5B	NOL1/NOP2/Sun domain family, member 5B	chr7q11.23	214100_x_at	NM_001039575 /// NM_001039576 /// NM_145645																				
8.39	6.78	1.61	6.56E-03	1.71E-01	CIT	citron (rho-interacting, serine/threonine kinase 21)	chr12q24	212801_at	NM_007174																				
4.49	3.76	0.72	6.56E-03	1.71E-01	NCAPD3	non-SMC condensin II complex, subunit D3	chr11q25	212789_at	NM_015261																				
5.51	4.53	0.98	6.57E-03	1.71E-01	ZNF143	zinc finger protein 143	chr11p15.4	221873_at	NM_003442																				
8.90	8.01	0.88	6.57E-03	1.71E-01	REPIN1	replication initiator 1	chr7q36.1	219041_s_at	NM_001099695 /// NM_001099696 /// NM_013400 /// NM_014374																				
6.35	5.64	0.72	6.59E-03	1.71E-01	RAE1	RAE1 RNA export 1 homolog (S. pombe)	chr20q13.31	211318_s_at	NM_001015885 /// NM_003610																				
5.56	5.03	0.54	6.60E-03	1.71E-01	MID2	midline 2	chrXq22	208384_s_at	NM_012216 /// NM_052817																				
5.20	4.45	0.75	6.61E-03	1.71E-01	PRUNE	prune homolog (Drosophila)	chr1q21	210988_s_at	NM_021222																				
3.47	2.91	0.55	6.61E-03	1.71E-01	---	---	---	227805_at	---																				
3.67	2.12	1.56	6.63E-03	1.72E-01	PTHLH	parathyroid hormone-like hormone	chr12p12.1-p11.2	206300_s_at	NM_002820 /// NM_198964 /// NM_198965 /// NM_198966																				
3.13	2.57	0.56	6.64E-03	1.72E-01	C1orf58	Chromosome 1 open reading frame 58	chr1q41	241908_at	NM_144695																				
3.73	3.16	0.57	6.68E-03	1.73E-01	POPDC2	popeye domain containing 2	chr3q13.33	219647_at	NM_022135																				
3.36	2.46	0.90	6.71E-03	1.73E-01	SCIN	scinderin	chr7p21.3	1552365_at	NM_001112706 /// NM_033128																				
3.05	2.58	0.48	6.71E-03	1.73E-01	EPC1	Enhancer of polycomb homolog 1 (Drosophila)	chr10p11	238633_at	NM_025209																				
7.54	6.69	0.85	6.71E-03	1.73E-01	TCEA2	transcription elongation factor A (SII), 2	chr20q13.33	203919_at	NM_003195 /// NM_198723																				
6.91	6.24	0.67	6.72E-03	1.73E-01	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	chr19q13.42	202408_s_at	NM_015629																				
5.75	4.94	0.82	6.72E-03	1.73E-01	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	chr18p11.2	203126_at	NM_014214																				
8.30	7.64	0.66	6.73E-03	1.73E-01	AXL	AXL receptor tyrosine kinase	chr19q13.1	202686_s_at	NM_001699 /// NM_021913																				
3.31	2.58	0.73	6.75E-03	1.73E-01	METTL3	methyltransferase like 3	chr14q11.1	213653_at	NM_019852																				
9.02	8.20	0.82	6.75E-03	1.73E-01	DLG5	discs, large homolog 5 (Drosophila)	chr10q23	201681_s_at	NM_004747																				
6.40	5.47	0.93	6.77E-03	1.73E-01	ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	chr11q25	221669_s_at	NM_014384																				
7.29	6.00	1.29	6.77E-03	1.73E-01	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	chr12p11.23	205303_at	NM_004982																				
5.67	5.02	0.65	6.78E-03	1.73E-01	LOC100131998	hypothetical protein LOC100131998	chr16p12.1	238412_at	XM_001725049																				
3.86	3.25	0.61	6.78E-03	1.73E-01	RNF24	ring finger protein 24	chr20p13-p12.1	204669_s_at	NM_001134337 /// NM_001134338 /// NM_007219																				
7.79	7.05	0.74	6.78E-03	1.73E-01	PRKAR2A	Protein kinase, cAMP-dependent, regulatory, type II, alpha	chr3p21.3-p21.2	225011_at	NM_004157																				

3.32	2.83	0.49	6.79E-03	1.73E-01	CAPN3	calpain 3, (p94)	chr15q15.1-q21.1	211890_x_at	NM_000070 /// NM_024344 /// NM_173087 /// NM_173088 /// NM_173089 /// NM_173090 /// NM_212464 /// NM_212465 /// NM_212467																				
2.89	2.18	0.71	6.80E-03	1.74E-01	---	---	---	244663_at	---																				
7.85	7.37	0.48	6.80E-03	1.74E-01	WIPI2	WD repeat domain, phosphoinositide interacting 2	chr7p22.1	202031_s_at	NM_001033518 /// NM_001033519 /// NM_001033520 /// NM_015610 /// NM_016003																				
3.00	2.68	0.32	6.82E-03	1.74E-01	ID2B	inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)	chr3p14.2	210911_at	---																				
5.71	5.03	0.68	6.82E-03	1.74E-01	SART3	squamous cell carcinoma antigen recognized by T cells 3	chr12q24.1	200069_at	NM_014706																				
6.48	5.95	0.53	6.83E-03	1.74E-01	CNIH4	cornichon homolog 4 (Drosophila)	chr1q42.11	218728_s_at	NM_014184																				
6.08	5.49	0.58	6.84E-03	1.74E-01	PHF17	PHD finger protein 17	chr4q26-q27	235024_at	NM_024900 /// NM_199320																				
6.14	5.42	0.72	6.84E-03	1.74E-01	LAMB3	laminin, beta 3	chr1q32	209270_at	NM_000228 /// NM_001017402 /// NM_001127641																				
7.14	6.72	0.42	6.85E-03	1.74E-01	RANBP3	RAN binding protein 3	chr19p13.3	202639_s_at	NM_003624 /// NM_007320 /// NM_007322																				
7.97	7.35	0.62	6.85E-03	1.74E-01	MRPS12	mitochondrial ribosomal protein S12	chr19q13.1-q13.2	204331_s_at	NM_021107 /// NM_033362 /// NM_033363																				
6.57	5.65	0.91	6.86E-03	1.74E-01	DVL2	dishevelled, dsh homolog 2 (Drosophila)	chr17p13.2	57532_at	NM_004422																				
6.72	5.84	0.88	6.88E-03	1.74E-01	FOSL2	FOS-like antigen 2	chr2p23.3	205409_at	NM_005253																				
3.27	2.60	0.67	6.88E-03	1.74E-01	PM20D2	peptidase M20 domain containing 2	chr6q15	225431_x_at	NM_001010853																				
6.06	5.27	0.80	6.89E-03	1.74E-01	C12orf24	chromosome 12 open reading frame 24	chr12q24.11	204521_at	NM_013300																				
6.27	5.43	0.84	6.89E-03	1.74E-01	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	chr2p23	222640_at	NM_022552 /// NM_153759 /// NM_175629 /// NM_175630																				
3.64	3.07	0.57	6.90E-03	1.74E-01	LEF1	lymphoid enhancer-binding factor 1	chr4q23-q25	210948_s_at	NM_001130713 /// NM_001130714 /// NM_016269																				
5.16	4.45	0.70	6.90E-03	1.74E-01	IQCB1	IQ motif containing B1	chr3q13.33|3q21.1	205995_x_at	NM_001023570 /// NM_001023571																				
6.98	6.09	0.89	6.90E-03	1.74E-01	UCKL1	uridine-cytidine kinase 1-like 1	chr20q13.33	218533_s_at	NM_017859																				
3.68	3.03	0.65	6.91E-03	1.74E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	232005_at	NM_015512																				
5.67	4.44	1.24	6.91E-03	1.74E-01	DGKQ	diacylglycerol kinase, theta 110kDa	chr4p16.3	226605_at	NM_001347																				
7.50	6.62	0.89	6.92E-03	1.74E-01	DHRS1	dehydrogenase/reductase (SDR family) member 1	chr14q12	213279_at	NM_138452																				
6.92	6.24	0.68	6.94E-03	1.74E-01	WDR37	WD repeat domain 37	chr10p15.3	211383_s_at	NM_014023																				

9.51	8.91	0.60	6.94E-03	1.74E-01	SERP1	stress-associated endoplasmic reticulum protein 1	chr3q25.1	200971_s_at	NM_014445																			
8.66	7.96	0.70	6.95E-03	1.74E-01	C1QBP	complement component 1, q subcomponent binding protein	chr17p13.3	208910_s_at	NM_001212																			
3.94	2.96	0.98	6.95E-03	1.74E-01	TMEM219	transmembrane protein 219	chr16p11.2	228513_at	NM_001083613 /// NM_194280																			
8.24	7.51	0.73	6.97E-03	1.74E-01	FKBP9	FK506 binding protein 9, 63 kDa	chr7p11.1	212169_at	NM_007270																			
5.96	5.31	0.64	6.97E-03	1.75E-01	PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	chr22q11.21	207081_s_at	NM_002650 /// NM_058004 /// XM_001721947																			
3.25	2.35	0.90	6.99E-03	1.75E-01	BDNF	brain-derived neurotrophic factor	chr11p13	206382_s_at	NM_001709 /// NM_170731 /// NM_170732 /// NM_170733 /// NM_170734 /// NM_170735																			
3.96	2.09	1.87	7.00E-03	1.75E-01	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	chr15q21.1	1554296_at	NM_000103 /// NM_031226																			
9.47	8.87	0.60	7.01E-03	1.75E-01	C19orf53	chromosome 19 open reading frame 53	chr19p13.13	217926_at	NM_014047																			
3.06	2.63	0.44	7.01E-03	1.75E-01	LOC554175	hypothetical LOC554175	chr15q23	1570057_x_at	XR_016015 /// XR_040089 /// XR_040090																			
5.33	4.81	0.52	7.02E-03	1.75E-01	E2F6	E2F transcription factor 6	chr2p25.1	203957_at	NM_198256 /// NR_003092 /// NR_003093 /// NR_003094 /// NR_003095																			
6.45	5.73	0.72	7.03E-03	1.75E-01	PGPEP1	pyroglutamyl-peptidase I	chr19p13.11	219891_at	NM_017712																			
3.26	2.92	0.34	7.04E-03	1.75E-01	---	---	---	238730_at	---																			
4.37	3.57	0.80	7.05E-03	1.75E-01	SHROOM3	shroom family member 3	chr4q21.1	228400_at	NM_020859																			
3.87	3.28	0.60	7.05E-03	1.75E-01	HAP1	huntingtin-associated protein 1	chr17q21.2-q21.3	238275_at	NM_001079870 /// NM_001079871 /// NM_003949 /// NM_177977																			
2.73	2.32	0.41	7.05E-03	1.75E-01	GARNL3	GTPase activating Rap/RanGAP domain-like 3	chr9q33.3	216165_at	NM_032293																			
5.84	4.95	0.89	7.06E-03	1.75E-01	C1orf38	chromosome 1 open reading frame 38	chr1p35.3	207571_x_at	NM_001039477 /// NM_001105556 /// NM_004848																			
6.83	6.01	0.81	7.06E-03	1.75E-01	TBC1D20	TBC1 domain family, member 20	chr20p13	226409_at	NM_144628																			
6.82	5.51	1.31	7.07E-03	1.75E-01	LOC100133585 /// RABEP2	similar to RABEP2 protein /// rabaptin, RAB GTPase binding effector protein 2	chr16p11.2	74694_s_at	NM_024816 /// XM_001717918																			
6.83	6.43	0.40	7.07E-03	1.75E-01	ATXN1L	ataxin 1-like	chr16q22.3	226095_s_at	XM_001724473 /// XM_001724532 /// XM_928464																			
6.77	6.17	0.59	7.08E-03	1.75E-01	OSBPL2	oxysterol binding protein-like 2	chr20q13.3	209222_s_at	NM_014835 /// NM_144498																			
3.07	2.63	0.44	7.09E-03	1.76E-01	---	---	---	228529_at	---																			
8.54	7.87	0.67	7.11E-03	1.76E-01	LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr19p13.3	204559_s_at	NM_016199																			

5.50	4.44	1.06	7.12E-03	1.76E-01	IDS	iduronate 2-sulfatase	chrXq28	206342_x_at	NM_000202 /// NM_006123																				
7.76	7.16	0.60	7.12E-03	1.76E-01	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	chr5q11-q14	204405_x_at	NM_014473																				
6.60	6.03	0.56	7.13E-03	1.76E-01	EXOSC1	exosome component 1	chr10q24	222609_s_at	NM_016046																				
6.38	5.62	0.75	7.13E-03	1.76E-01	FNBP1	formin binding protein 1	chr9q34	212288_at	NM_015033																				
5.68	4.17	1.51	7.14E-03	1.76E-01	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	chr6q22-q23	205066_s_at	NM_006208																				
4.16	3.54	0.62	7.14E-03	1.76E-01	CA5BL	carbonic anhydrase VB-like	chrXp22.2	213363_at	XM_001715245 /// XM_001716189 /// XM_001719208 /// XM_001719213																				
5.86	5.27	0.60	7.15E-03	1.76E-01	NFYC	nuclear transcription factor Y, gamma	chr1p32|1p32	211797_s_at	NM_014223																				
4.90	3.89	1.01	7.15E-03	1.76E-01	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	chr11q23.2-q24.2	212560_at	NM_003105																				
7.66	6.73	0.93	7.15E-03	1.76E-01	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	chr17q22-q23	201207_at	NM_021137																				
2.93	2.18	0.75	7.16E-03	1.76E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	1560981_a_at	NM_001001928 /// NM_005036																				
11.35	10.98	0.36	7.18E-03	1.76E-01	RPS8	ribosomal protein S8	chr1p34.1-p32	200858_s_at	NM_001012																				
6.23	5.60	0.63	7.19E-03	1.76E-01	C11orf79	chromosome 11 open reading frame 79	chr11q12.2	223048_at	NM_017841																				
4.76	3.81	0.96	7.20E-03	1.76E-01	ZNF7	zinc finger protein 7	chr8q24	205089_at	NM_003416																				
3.57	2.36	1.22	7.21E-03	1.77E-01	HNRNPA1 /// LOC728844	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical	chr12q13.1 /// chr12q13.13	221919_at	NM_002136 /// NM_031157 /// XM_001133051 /// XM_001133058 /// XM_001721844																				
6.57	5.90	0.67	7.22E-03	1.77E-01	FBXW4	F-box and WD repeat domain containing 4	chr10q24	221519_at	NM_022039																				
4.74	4.03	0.72	7.23E-03	1.77E-01	TMEM33	transmembrane protein 33	chr4p13	235907_at	NM_018126																				
8.92	8.19	0.73	7.24E-03	1.77E-01	VKORC1	vitamin K epoxide reductase complex, subunit 1	chr16p11.2	217949_s_at	NM_024006 /// NM_206824																				
5.09	4.24	0.85	7.25E-03	1.77E-01	MREG	melanoregulin	chr2q35	232682_at	NM_018000																				
3.63	2.32	1.31	7.26E-03	1.77E-01	DSEL	dermatan sulfate epimerase-like	chr18q22.1	232235_at	NM_032160																				
7.27	6.52	0.74	7.27E-03	1.77E-01	PEX5	peroxisomal biogenesis factor 5	chr12p13.31	203244_at	NM_000319 /// NM_001131023 /// NM_001131024 /// NM_001131025 /// NM_001131026																				
4.06	3.35	0.70	7.27E-03	1.77E-01	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	chr10q22	1559701_s_at	NM_003635																				
7.14	5.81	1.34	7.27E-03	1.77E-01	FRMD8	FERM domain containing 8	chr11q13	227964_at	NM_031904																				
3.34	2.57	0.77	7.27E-03	1.77E-01	RPL27A	ribosomal protein L27a	chr11p15	223707_at	NM_000990																				
6.83	6.04	0.80	7.27E-03	1.77E-01	ABT1	activator of basal transcription 1	chr6p22.1	218405_at	NM_013375																				
4.82	4.21	0.60	7.28E-03	1.77E-01	SPEN	spen homolog, transcriptional regulator (Drosophila)	chr1p36.33-p36.11	1556059_s_at	NM_015001																				
6.70	5.89	0.81	7.28E-03	1.77E-01	FHOD1	formin homology 2 domain containing 1	chr16q22	218530_at	NM_013241																				
5.31	4.28	1.03	7.28E-03	1.77E-01	PCSK5	Proprotein convertase subtilisin/kexin type 5	chr9q21.3	213652_at	NM_006200																				
6.54	5.44	1.11	7.29E-03	1.77E-01	RNF43	ring finger protein 43	chr17q22	218704_at	NM_017763																				
4.83	4.19	0.64	7.29E-03	1.77E-01	JMJD7 /// LOC100137047-PLA2G4B /// PLA2G4B	jumonji domain containing 7 /// hypothetical protein LOC8681 /// phospholipase A2, group IVB (cytosolic)	chr15q11.2-q21.3 /// chr15q15.1	60528_at	NM_001114632 /// NM_001114633 /// NM_005090 /// NR_015346 /// XM_001720570 /// XM_001723659 /// XM_001725545																				

5.58	4.74	0.84	7.31E-03	1.77E-01	VISA	virus-induced signaling adapter	chr20p13	220305_at	NM_020746																			
7.71	6.94	0.77	7.31E-03	1.77E-01	FASTK	Fas-activated serine/threonine kinase	chr7q35	214114_x_at	NM_006712 /// NM_033015																			
7.19	6.15	1.04	7.33E-03	1.77E-01	CNPY2	canopy 2 homolog (zebrafish)	chr12q15	209797_at	NM_014255																			
7.36	6.52	0.84	7.34E-03	1.77E-01	TRIM8	tripartite motif-containing 8	chr10q24.3	221012_s_at	NM_030912																			
3.02	2.47	0.56	7.34E-03	1.77E-01	---	---	---	228441_s_at	---																			
6.05	5.35	0.70	7.36E-03	1.78E-01	ELMO2	engulfment and cell motility 2	chr20q13	221528_s_at	NM_133171 /// NM_182764																			
4.80	3.74	1.06	7.37E-03	1.78E-01	---	---	---	229926_at	---																			
7.16	6.64	0.52	7.37E-03	1.78E-01	CNPY4	canopy 4 homolog (zebrafish)	chr7q22.1	227313_at	NM_152755																			
10.06	9.37	0.69	7.41E-03	1.78E-01	JTB	jumping translocation breakpoint	chr1q21	200048_s_at	NM_006694																			
5.74	5.08	0.67	7.42E-03	1.78E-01	ZNF193	zinc finger protein 193	chr6p21.3	205181_at	NM_006299																			
4.39	3.66	0.73	7.43E-03	1.78E-01	TTLL3	tubulin tyrosine ligase-like family, member 3	chr3p25.3	230873_at	NM_001025930 /// NM_015644																			
4.46	3.49	0.97	7.43E-03	1.78E-01	---	---	---	214867_at	---																			
2.93	2.22	0.71	7.44E-03	1.79E-01	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	chr12q13	210047_at	NM_000617																			
10.40	9.79	0.61	7.44E-03	1.79E-01	MRP63	mitochondrial ribosomal protein 63	chr13q12.11	204386_s_at	NM_024026																			
7.21	6.58	0.63	7.44E-03	1.79E-01	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	chr2q35	213179_at	NM_005444																			
7.23	6.60	0.63	7.46E-03	1.79E-01	LSM8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr7q31.1-q31.3	219119_at	NM_016200																			
3.97	3.22	0.75	7.46E-03	1.79E-01	C15orf37	chromosome 15 open reading frame 37	chr15q25.1	1556588_at	NM_175898																			
6.05	4.71	1.33	7.48E-03	1.79E-01	HOXA9	homeobox A9	chr7p15-p14	209905_at	NM_152739																			
10.94	10.57	0.38	7.49E-03	1.79E-01	RPS9	ribosomal protein S9	chr19q13.4	214317_x_at	NM_001013																			
3.41	2.70	0.71	7.50E-03	1.79E-01	HOXA3	homeobox A3	chr7p15-p14	235521_at	NM_030661 /// NM_153631 /// NM_153632																			
8.19	7.44	0.74	7.51E-03	1.79E-01	CBY1	chibby homolog 1 (Drosophila)	chr22q12	203450_at	NM_001002880 /// NM_015373																			

9.11	8.67	0.43	7.52E-03	1.79E-01	SNRPN /// SNURF	small nuclear ribonucleoprotein polypeptide N /// SNRPN upstream reading frame	chr15q11.2 /// chr15q12	206042_x_at	NM_003097 /// NM_005678 /// NM_022804 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 ///																				
7.06	6.32	0.75	7.53E-03	1.79E-01	KIAA0892	KIAA0892	chr19p13.11	227465_at	NM_015329																			
6.69	5.86	0.84	7.55E-03	1.80E-01	PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	chr13q12.2	225563_at	NM_175854																			
7.18	6.41	0.77	7.55E-03	1.80E-01	PEX11B	peroxisomal biogenesis factor 11 beta	chr1q21.1	202658_at	NM_003846																			
5.59	4.73	0.86	7.55E-03	1.80E-01	tcag7.1196	similar to GLI-Kruppel family member HKR1	chr7q36.1	225909_at	XR_041712 /// XR_041713 /// XR_041714																			
7.35	6.68	0.66	7.57E-03	1.80E-01	CCDC115	coiled-coil domain containing 115	chr2q21.1	224946_s_at	NM_032357																			
6.02	5.33	0.69	7.57E-03	1.80E-01	LOC644617	hypothetical LOC644617	chr2q12.1	221235_s_at	XM_927735																			
5.41	4.39	1.03	7.57E-03	1.80E-01	IGSF5	immunoglobulin superfamily, member 5	chr21q22.2	243027_at	NM_001080444																			
7.08	6.43	0.65	7.58E-03	1.80E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	215714_s_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072																			

5.23	4.57	0.66	7.60E-03	1.80E-01	ZXDC	ZXD family zinc finger C	chr3q21.2	218639_s_at	NM_001040653 /// NM_025112																				
7.84	7.16	0.68	7.61E-03	1.80E-01	CNPY2	canopy 2 homolog (zebrafish)	chr12q15	209796_s_at	NM_014255																				
3.37	2.98	0.39	7.62E-03	1.80E-01	TSEN2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	chr3p25.1	244391_at	NM_025265																				
7.97	7.43	0.54	7.64E-03	1.80E-01	C7orf59	chromosome 7 open reading frame 59	chr7q22.1	224890_s_at	NM_001008395																				
8.11	7.57	0.53	7.65E-03	1.81E-01	C1orf128	chromosome 1 open reading frame 128	chr1p36.11	223124_s_at	NM_020362																				
6.16	5.58	0.58	7.66E-03	1.81E-01	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	chr15q22	218306_s_at	NM_003922																				
4.92	4.24	0.67	7.66E-03	1.81E-01	SNIP1	Smad nuclear interacting protein 1	chr1p34.3	219409_at	NM_024700																				
4.04	2.78	1.26	7.71E-03	1.81E-01	SYN2	synapsin II	chr3p25	229039_at	NM_003178 /// NM_133625																				
8.72	7.70	1.02	7.71E-03	1.81E-01	SULT1A2	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	chr16p12.1	207122_x_at	NM_001054 /// NM_177528																				
6.24	5.30	0.94	7.71E-03	1.81E-01	AP1G2	adaptor-related protein complex 1, gamma 2 subunit	chr14q11.2	201613_s_at	NM_003917 /// NM_080545																				
7.26	6.35	0.91	7.72E-03	1.81E-01	TP53I3	tumor protein p53 inducible protein 3	chr2p23.3	210609_s_at	NM_004881 /// NM_147184																				
4.62	3.92	0.70	7.72E-03	1.81E-01	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	chr19p13.12	218115_at	NM_018154																				
5.24	4.31	0.93	7.73E-03	1.81E-01	TMEM50B	transmembrane protein 50B	chr21q22.11	228001_at	NM_006134																				
6.65	6.01	0.64	7.73E-03	1.81E-01	PTPN1	protein tyrosine phosphatase, non-receptor type 1	chr20q13.1-q13.2	202716_at	NM_002827																				
2.66	2.12	0.55	7.75E-03	1.82E-01	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	chr2p16.1	1568627_at	NM_001122964 /// NM_020463																				
8.09	7.61	0.49	7.75E-03	1.82E-01	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	chr20p13	210418_s_at	NM_006899 /// NM_174855 /// NM_174856																				
6.96	6.51	0.45	7.76E-03	1.82E-01	PAF1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	chr19q13.1	202093_s_at	NM_019088																				
7.86	6.94	0.92	7.77E-03	1.82E-01	GPR177	G protein-coupled receptor 177	chr1p31.3	228949_at	NM_001002292 /// NM_024911																				
4.45	4.02	0.43	7.77E-03	1.82E-01	LOC642533	hypothetical LOC642533	chr16q24.3	1556129_at	XR_016325 /// XR_041225 /// XR_041226																				
6.12	5.45	0.67	7.79E-03	1.82E-01	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	chr16p11.2	217527_s_at	NM_032815																				
8.44	6.92	1.52	7.81E-03	1.82E-01	CACHD1	cache domain containing 1	chr1p31.3	225627_s_at	NM_020925																				
11.61	11.24	0.37	7.82E-03	1.82E-01	RPS16	ribosomal protein S16	chr19q13.1	201258_at	NM_001020																				
5.33	4.43	0.90	7.82E-03	1.82E-01	SFRS8	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	chr12q24.33	202775_s_at	NM_004592																				
6.39	5.23	1.16	7.83E-03	1.82E-01	KIAA0323	KIAA0323	chr14q12	212355_at	NM_015299																				
6.04	4.81	1.23	7.83E-03	1.82E-01	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	chr16q11	218888_s_at	NM_018092																				
5.87	4.39	1.48	7.83E-03	1.82E-01	RAGE	renal tumor antigen	chr14q32	205130_at	NM_014226																				
6.42	5.92	0.50	7.86E-03	1.82E-01	PMF1	polyamine-modulated factor 1	chr1q12	202337_at	NM_007221																				
3.95	3.43	0.52	7.86E-03	1.82E-01	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	chr17q11-q21	205829_at	NM_000413																				
8.26	7.72	0.54	7.88E-03	1.83E-01	PITPNA	phosphatidylinositol transfer protein, alpha	chr17p13.3	201190_s_at	NM_006224																				
4.28	3.46	0.82	7.89E-03	1.83E-01	---	---	---	1558613_at	---																				
5.50	4.93	0.57	7.91E-03	1.83E-01	GOLGA3	golgi autoantigen, golgin subfamily a, 3	chr12q24.33	226949_at	NM_005895																				
6.50	5.96	0.53	7.91E-03	1.83E-01	PMS2L11	postmeiotic segregation increased 2-like 11 pseudogene	chr7q11.23	210707_x_at	NR_023383 /// XM_001715908 /// XM_001717503																				
6.37	5.85	0.52	7.95E-03	1.84E-01	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	chr6p21.1	207515_s_at	NM_004875 /// NM_203290																				
3.26	2.30	0.96	7.96E-03	1.84E-01	---	---	---	226316_at	---																				
6.11	5.22	0.88	7.97E-03	1.84E-01	CHKA	choline kinase alpha	chr11q13.2	204266_s_at	NM_001277 /// NM_212469																				

3.79	3.26	0.53	7.98E-03	1.84E-01	MICAL3	Microtubule associated monoxygenase, calponin and LIM domain containing 3	chr22q11.21	229474_at	NM_001122731 /// NM_015241 /// XM_001721205 /// XM_001725408 /// XM_001726352																			
4.54	3.96	0.58	7.98E-03	1.84E-01	C18orf18	chromosome 18 open reading frame 18	chr18p11.31	229829_at	XM_001719942 /// XM_001720671 /// XM_001722386																			
5.44	4.30	1.14	7.99E-03	1.84E-01	PGS1	phosphatidylglycerophosphate synthase 1	chr17q25.3	219394_at	NM_024419																			
5.21	4.27	0.95	8.00E-03	1.84E-01	WDR55	WD repeat domain 55	chr5q31.3	219809_at	NM_017706																			
8.86	8.06	0.80	8.01E-03	1.84E-01	SRGN	serglycin	chr10q22.1	201859_at	NM_002727																			
5.90	4.98	0.93	8.02E-03	1.84E-01	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	chr19p13.13	203701_s_at	NM_017722																			
4.89	4.10	0.79	8.02E-03	1.84E-01	SPHK2	sphingosine kinase 2	chr19q13.2	40273_at	NM_020126																			
4.19	3.25	0.94	8.02E-03	1.84E-01	---	---	---	229756_at	---																			
6.59	5.58	1.01	8.02E-03	1.84E-01	PRKCZ	protein kinase C, zeta	chr1p36.33-p36.2	202178_at	NM_001033581 /// NM_001033582 /// NM_002744																			
5.54	4.39	1.15	8.04E-03	1.84E-01	PRPF40B	PRP40 pre-mRNA processing factor 40 homolog B (S. cerevisiae)	chr12q	226966_at	NM_001031698 /// NM_012272																			
5.79	4.76	1.03	8.06E-03	1.84E-01	IRF1	interferon regulatory factor 1	chr5q31.1	202531_at	NM_002198																			
9.12	8.33	0.78	8.08E-03	1.84E-01	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	chr12q13.1	214280_x_at	NM_002136 /// NM_031157																			
2.91	2.36	0.55	8.09E-03	1.85E-01	NSD1	nuclear receptor binding SET domain protein 1	chr5q35.2-q35.3	235760_at	NM_022455 /// NM_172349																			
2.27	1.91	0.36	8.09E-03	1.85E-01	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	chr2q33.2	1552489_s_at	NM_033066																			
7.10	6.21	0.89	8.10E-03	1.85E-01	DDIT3	DNA-damage-inducible transcript 3	chr12q13.1-q13.2	209383_at	NM_004083																			
2.96	2.47	0.49	8.11E-03	1.85E-01	KISS1R	KISS1 receptor	chr19p13.3	242517_at	NM_032551																			
5.66	4.86	0.80	8.12E-03	1.85E-01	PUS1	pseudouridylate synthase 1	chr12q24.33	218670_at	NM_001002019 /// NM_001002020 /// NM_025215																			
9.03	8.63	0.39	8.13E-03	1.85E-01	FBL	fibrillarin	chr19q13.1	211623_s_at	NM_001436																			
10.07	8.39	1.69	8.15E-03	1.85E-01	LOC387763	hypothetical LOC387763	chr11p11.2	227099_s_at	XM_001716706 /// XM_373497 /// XM_941665																			
6.91	6.33	0.58	8.16E-03	1.85E-01	COX18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr4q13.3	227442_at	NM_173827																			
2.59	2.22	0.37	8.16E-03	1.85E-01	C21orf58	chromosome 21 open reading frame 58	chr21q22.3	1553789_a_at	NM_058180																			
7.28	6.58	0.70	8.17E-03	1.85E-01	DAZAP1	DAZ associated protein 1	chr19p13.3	229813_x_at	NM_018959 /// NM_170711																			
7.39	6.38	1.02	8.18E-03	1.85E-01	IER5	immediate early response 5	chr1q25.3	218611_at	NM_016545																			
8.37	7.97	0.40	8.18E-03	1.85E-01	MRPL18	mitochondrial ribosomal protein L18	chr6q25.3	217907_at	NM_014161																			
8.05	7.19	0.86	8.19E-03	1.86E-01	CCNG2	cyclin G2	chr4q21.1	202769_at	NM_004354																			
9.20	8.69	0.51	8.21E-03	1.86E-01	GLRX	glutaredoxin (thioltransferase)	chr5q14	206662_at	NM_001118890 /// NM_002064																			
6.71	4.94	1.77	8.21E-03	1.86E-01	EGR3	early growth response 3	chr8p23-p21	206115_at	NM_004430																			

10.48	10.03	0.45	8.23E-03	1.86E-01	LOC100131713 /// LOC283412 /// LOC284064 /// LOC391019 /// LOC643531 /// LOC647285 /// LOC728820 /// RPL29 /// RPL29P4	similar to ribosomal protein L29 /// hypothetical LOC283412 /// similar to ribosomal protein L29 /// similar to ribosomal protein L29 /// similar to ribosomal protein L29 /// similar to ribosomal protein L29 /// similar to ribosomal protein L29 /// ribosomal protein L29 /// ribosomal protein L29 pseudogene 4	chr12q22 /// chr17q21.31 /// chr1p36.12 /// chr3p21.3-p21.2 /// chr3p22.2 /// chr3q27.3 /// chr5p12 /// chr5q14.1 /// chr6q22.2	216570_x_at	NM_000992 /// XM_001721013 /// XM_001722116 /// XM_001723470 /// XM_001723471 /// XM_001724270 /// XM_001724272 /// XM_001725513 /// XM_001725514 /// XM_210334 /// XM_497352 /// XM_937685 /// XM_938790 /// XR_015551 /// XR_015758 /// XR_016725 /// XR_017506 /// XR_017676 /// XR_019563 /// XR_019567 /// XR_019605 /// XR_038223 /// XR_038516 /// XR_038580 /// XR_039495																				
4.55	3.95	0.60	8.23E-03	1.86E-01	C17orf85	chromosome 17 open reading frame 85	chr17p13.2	218896_s_at	NM_001114118 /// NM_018553																				
6.01	4.20	1.81	8.24E-03	1.86E-01	ABAT	4-aminobutyrate aminotransferase	chr16p13.2	209459_s_at	NM_000663 /// NM_001127448 /// NM_020686																				
7.79	7.26	0.54	8.24E-03	1.86E-01	NMT1	N-myristoyltransferase 1	chr17q21.31	201157_s_at	NM_021079																				
5.81	5.21	0.60	8.25E-03	1.86E-01	FAM125B	family with sequence similarity 125, member B	chr9q33.3	52975_at	NM_001011703 /// NM_033446																				
7.16	6.18	0.98	8.25E-03	1.86E-01	CKLF	chemokine-like factor	chr16q21	219161_s_at	NM_001040138 /// NM_016326 /// NM_016951 /// NM_181640 /// NM_181641																				
4.10	2.58	1.51	8.25E-03	1.86E-01	COL27A1	collagen, type XXVII, alpha 1	chr9q32	225288_at	NM_032888																				
8.96	7.17	1.79	8.25E-03	1.86E-01	---	---	---	227827_at	---																				
7.09	6.50	0.59	8.26E-03	1.86E-01	RHOT2	ras homolog gene family, member T2	chr16p13.3	221789_x_at	NM_138769																				

6.02	4.92	1.10	8.27E-03	1.86E-01	NR1H3	nuclear receptor subfamily 1, group H, member 3	chr11p11.2	203920_at	NM_001130101 /// NM_001130102 /// NM_005693																				
6.29	5.78	0.52	8.28E-03	1.86E-01	FARSA	phenylalanyl-tRNA synthetase, alpha subunit	chr19p13.2	202159_at	NM_004461																				
4.36	3.64	0.72	8.28E-03	1.86E-01	TEP1	telomerase-associated protein 1	chr14q11.2	228670_at	NM_007110																				
6.85	5.70	1.15	8.28E-03	1.86E-01	PHF10	PHD finger protein 10	chr6q27	225048_at	NM_018288 /// NM_133325																				
7.89	6.66	1.23	8.29E-03	1.86E-01	PTP4A1	protein tyrosine phosphatase type IVA, member 1	chr6q12	200733_s_at	NM_003463																				
6.63	5.88	0.75	8.29E-03	1.86E-01	ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	chr2q21	202176_at	NM_000122																				
6.61	5.24	1.36	8.29E-03	1.86E-01	---	---	---	220494_s_at	---																				
3.97	2.72	1.25	8.30E-03	1.86E-01	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	chr1p36.2	219423_x_at	NM_001039664 /// NM_003790 /// NM_148965 /// NM_148966 /// NM_148967 /// NM_148970																				
5.91	5.06	0.84	8.32E-03	1.86E-01	FBXO46	F-box protein 46	chr19q13.3	205310_at	NM_001080469																				
3.60	3.03	0.57	8.33E-03	1.86E-01	---	---	---	217019_at	---																				
9.70	8.60	1.10	8.34E-03	1.86E-01	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H1 (H)	chr5q35.3	213619_at	NM_005520																				
6.28	5.59	0.69	8.34E-03	1.86E-01	TMEM136	transmembrane protein 136	chr11q23.3	1554076_s_at	NM_174926																				
3.10	2.48	0.62	8.34E-03	1.86E-01	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	chr16q24.3	230885_at	NM_003119 /// NM_199367																				
6.07	5.49	0.57	8.34E-03	1.86E-01	PHKA2	phosphorylase kinase, alpha 2 (liver)	chrXp22.2-p22.1	209439_s_at	NM_000292																				
2.81	2.31	0.50	8.35E-03	1.86E-01	ELK1	ELK1, member of ETS oncogene family	chrXp11.2	210850_s_at	NM_001114123 /// NM_005229																				
6.12	5.17	0.96	8.35E-03	1.86E-01	SLC30A1	solute carrier family 30 (zinc transporter), member 1	chr1q32-q41	228181_at	NM_021194																				
7.00	6.39	0.61	8.36E-03	1.86E-01	SH3BP4	SH3-domain binding protein 4	chr2q37.1-q37.2	222258_s_at	NM_014521																				
4.15	3.06	1.09	8.37E-03	1.86E-01	REN	renin	chr1q32	206367_at	NM_000537																				
3.30	2.77	0.54	8.38E-03	1.86E-01	TBX3	T-box 3	chr12q24.1	243234_at	NM_005996 /// NM_016569																				
3.55	3.15	0.40	8.38E-03	1.86E-01	TTLL1	tubulin tyrosine ligase-like family, member 1	chr22q13.1	1570085_at	NM_001008572 /// NM_012263																				
10.22	9.78	0.44	8.39E-03	1.86E-01	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	chr12q13.13	208764_s_at	NM_001002031 /// NM_005176																				
3.01	2.15	0.86	8.40E-03	1.87E-01	PDCD5	Programmed cell death 5	chr19q12-q13.1	227751_at	NM_004708																				
7.07	6.65	0.42	8.41E-03	1.87E-01	LOC100133946 /// MTCP1	similar to mature T-cell proliferations 1 /// mature T-cell proliferation 1	chrXq28	216862_s_at	NM_001018024 /// NM_001018025 /// NM_014221 /// XM_001719446																				
5.68	4.68	1.00	8.42E-03	1.87E-01	ZNF862	zinc finger protein 862	chr7q36.1	213444_at	NM_001099220																				
7.37	6.47	0.90	8.42E-03	1.87E-01	RSAD1	radical S-adenosyl methionine domain containing 1	chr17q21.33	218307_at	NM_018346																				
7.14	6.26	0.87	8.45E-03	1.87E-01	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	chr12q24.1	201835_s_at	NM_006253																				
7.76	7.29	0.47	8.45E-03	1.87E-01	RNF4	ring finger protein 4	chr4p16.3	212696_s_at	NM_002938																				
4.95	4.43	0.52	8.45E-03	1.87E-01	PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	chr9p13.3	214991_s_at	NM_032634 /// NM_152850																				
7.42	6.88	0.55	8.47E-03	1.87E-01	PTBP1	polypyrimidine tract binding protein 1	chr19p13.3	212016_s_at	NM_002819 /// NM_031990 /// NM_031991 /// NM_175847																				
7.40	6.56	0.84	8.47E-03	1.87E-01	PCGF2	polycomb group ring finger 2	chr17q12	214239_x_at	NM_007144																				
3.24	2.71	0.53	8.50E-03	1.87E-01	---	---	---	241982_at	---																				

7.62	6.87	0.75	8.51E-03	1.87E-01	MINK1	misshapen-like kinase 1 (zebrafish)	chr17p13.2	214246_x_at	NM_001024937 /// NM_015716 /// NM_153827 /// NM_170663
5.83	5.10	0.72	8.51E-03	1.87E-01	DTNBP1	dystrobrevin binding protein 1	chr6p22.3	223445_at	NM_032122 /// NM_183040 /// NM_183041
6.30	5.74	0.55	8.51E-03	1.87E-01	UXS1	UDP-glucuronate decarboxylase 1	chr2q12.2	219675_s_at	NM_025076
5.64	4.78	0.87	8.51E-03	1.87E-01	GARNL3	GTPase activating Rap/RanGAP domain-like 3	chr9q33.3	223604_at	NM_032293
2.90	2.42	0.48	8.52E-03	1.87E-01	GPR173	G protein-coupled receptor 173	chrXp11	1556039_s_at	NM_018969
6.89	6.30	0.59	8.52E-03	1.87E-01	RBM10	RNA binding motif protein 10	chrXp11.23	208984_x_at	NM_005676 /// NM_152856
8.32	7.58	0.74	8.53E-03	1.87E-01	HP1BP3	heterochromatin protein 1, binding protein 3	chr1p36.12	224591_at	NM_016287
8.20	7.56	0.64	8.56E-03	1.88E-01	CTTN	cortactin	chr11q13	201059_at	NM_005231 /// NM_138565
7.39	6.59	0.80	8.57E-03	1.88E-01	HMGN4	high mobility group nucleosomal binding domain 4	chr6p21.3	209787_s_at	NM_006353
5.99	5.18	0.82	8.59E-03	1.88E-01	SUOX	sulfite oxidase	chr12q13.2	1553030_a_at	NM_000456 /// NM_001032386 /// NM_001032387
8.03	7.52	0.52	8.59E-03	1.88E-01	POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	chr22q13.1	209511_at	NM_021974
5.12	4.53	0.58	8.59E-03	1.88E-01	ZNF318	zinc finger protein 318	chr6pter-p12.1	203521_s_at	NM_014345
7.25	6.75	0.50	8.60E-03	1.88E-01	ZNHIT3	zinc finger, HIT type 3	chr17q12	212544_at	NM_004773
4.16	3.69	0.47	8.61E-03	1.88E-01	SH3RF1	SH3 domain containing ring finger 1	chr4q32.3-q33	225589_at	NM_020870
8.44	7.94	0.50	8.64E-03	1.88E-01	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	chr11q13	212680_x_at	NM_138689
4.16	3.61	0.56	8.64E-03	1.88E-01	LOC388780	hypothetical LOC388780	chr20p13	236674_at	XM_001717821 /// XM_373904 /// XM_943910
6.40	5.75	0.65	8.65E-03	1.88E-01	LOC730324	similar to postmeiotic segregation increased 2-like 2	---	215667_x_at	XM_001722095
7.83	5.37	2.46	8.67E-03	1.88E-01	MCOLN3	mucolipin 3	chr1p22.3	220484_at	NM_018298
5.23	4.25	0.97	8.67E-03	1.88E-01	ARPC5L	actin related protein 2/3 complex, subunit 5-like	chr9q33.3	226914_at	NM_030978
7.21	6.40	0.81	8.67E-03	1.88E-01	ZMIZ2	zinc finger, MIZ-type containing 2	chr7p13	54970_at	NM_031449 /// NM_174929
5.49	4.29	1.20	8.67E-03	1.88E-01	C10orf97	chromosome 10 open reading frame 97	chr10p13	1554509_a_at	NM_024948
6.26	5.54	0.72	8.68E-03	1.89E-01	C1orf174	chromosome 1 open reading frame 174	chr1p36.32	222000_at	NM_207356
8.25	7.87	0.37	8.70E-03	1.89E-01	COPG	coatomer protein complex, subunit gamma	chr3q21.3	217749_at	NM_016128
7.78	6.44	1.34	8.70E-03	1.89E-01	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	chr12q13.11	204254_s_at	NM_000376 /// NM_001017535
7.54	6.85	0.69	8.70E-03	1.89E-01	POLG	polymerase (DNA directed), gamma	chr15q25	203366_at	NM_001126131 /// NM_002693
6.54	5.62	0.93	8.70E-03	1.89E-01	BRD1	bromodomain containing 1	chr22q13.33	215460_x_at	NM_014577
6.89	6.38	0.51	8.71E-03	1.89E-01	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	chr10q24.3	217791_s_at	NM_001017423 /// NM_002860
6.40	5.80	0.60	8.74E-03	1.89E-01	SAP30BP	SAP30 binding protein	chr17q25.1	217965_s_at	NM_013260
8.16	7.46	0.70	8.74E-03	1.89E-01	C5orf15	chromosome 5 open reading frame 15	chr5q31.1	203024_s_at	NM_020199
7.70	6.94	0.76	8.75E-03	1.89E-01	DPH1 /// OVCA2	DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor in ovarian cancer 2	chr17p13.3	202632_at	NM_001383 /// NM_080822
4.87	3.93	0.93	8.75E-03	1.89E-01	LUC7L	LUC7-like (S. cerevisiae)	chr16p13.3	1557067_s_at	NM_018032 /// NM_201412
7.07	6.30	0.78	8.76E-03	1.89E-01	CECR5	cat eye syndrome chromosome region, candidate 5	---	218592_s_at	NM_017829 /// NM_033070
8.15	7.37	0.78	8.77E-03	1.89E-01	RP11-345P4.4 /// SLC35E2	similar to solute carrier family 35, member E2 /// solute carrier family 35, member E2	chr1p36.33	217122_s_at	NM_001110781 /// NM_182838 /// XM_001717735

6.29	5.66	0.64	8.77E-03	1.89E-01	LOC93622	hypothetical LOC93622	chr4p16.1	225391_at	XR_017848 /// XR_017952 /// XR_041372
5.57	4.87	0.69	8.78E-03	1.89E-01	C8orf38	chromosome 8 open reading frame 38	chr8q22.1	235509_at	NM_152416
7.78	6.85	0.93	8.78E-03	1.89E-01	PER1	period homolog 1 (Drosophila)	chr17p13.1-p12	36829_at	NM_002616
5.90	4.59	1.31	8.80E-03	1.89E-01	ZNF692	zinc finger protein 692	chr1q44	220661_s_at	NM_017865
5.28	4.47	0.81	8.81E-03	1.89E-01	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	chr2q24	203339_at	NM_003705
6.08	5.55	0.53	8.81E-03	1.89E-01	LOC145842	hypothetical protein LOC145842	chr15q22.2	226358_at	---
6.13	4.63	1.50	8.81E-03	1.89E-01	RUFY3	RUN and FYVE domain containing 3	chr4q13.3	229334_at	NM_001037442 /// NM_001130709 /// NM_014961
2.87	2.26	0.61	8.81E-03	1.89E-01	FAM133A	family with sequence similarity 133, member A	chrXq21.32	231131_at	NM_173698
7.25	6.60	0.65	8.82E-03	1.89E-01	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	chr17q25	210428_s_at	NM_004712
8.73	8.17	0.56	8.84E-03	1.90E-01	NONO	non-POU domain containing, octamer-binding	chrXq13.1	210470_x_at	NM_007363
6.27	5.81	0.46	8.86E-03	1.90E-01	LOC100133946 /// MTCP1	similar to mature T-cell proliferations 1 /// mature T-cell proliferation 1	chrXq28	210212_x_at	NM_001018024 /// NM_001018025 /// NM_014221 /// XM_001719446
6.10	5.24	0.86	8.86E-03	1.90E-01	RHBDF2	rhomboid 5 homolog 2 (Drosophila)	chr17q25.1	219202_at	NM_001005498 /// NM_024599
8.95	8.30	0.64	8.87E-03	1.90E-01	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	chrXq28	207809_s_at	NM_001183
3.93	3.03	0.91	8.88E-03	1.90E-01	ING5 /// LOC727773	inhibitor of growth family, member 5 /// similar to p28 ING5	chr2q37.3	228287_at	NM_032329 /// XM_001126273
2.27	1.92	0.35	8.92E-03	1.90E-01	PCDHB4	protocadherin beta 4	chr5q31	231750_at	NM_018938
3.66	2.86	0.80	8.93E-03	1.90E-01	OGFRL1	opioid growth factor receptor-like 1	chr6q13	219582_at	NM_024576
5.87	5.31	0.55	8.93E-03	1.90E-01	GSR	glutathione reductase	chr8p21.1	225609_at	NM_000637
4.28	3.44	0.84	8.94E-03	1.90E-01	CIB4	calcium and integrin binding family member 4	chr2p23.3	236378_at	NM_001029881
3.97	3.10	0.87	8.95E-03	1.91E-01	TMEM63A	transmembrane protein 63A	chr1q42.12	214833_at	NM_014698
5.74	4.86	0.88	8.96E-03	1.91E-01	ATP11A	ATPase, class VI, type 11A	chr13q34	230875_s_at	NM_015205 /// NM_032189
2.61	2.10	0.51	8.98E-03	1.91E-01	RPL23 /// SNORA21	ribosomal protein L23 /// small nucleolar RNA, H/ACA box 21	chr17q /// chr17q12	215224_at	NM_000978 /// NR_002576
4.47	3.67	0.80	9.00E-03	1.91E-01	ZNF33A	zinc finger protein 33A	chr10p11.2	232873_at	NM_006954 /// NM_006974
6.16	5.54	0.62	9.01E-03	1.91E-01	DHTKD1	dehydrogenase E1 and transketolase domain containing 1	chr10p14	227094_at	NM_018706
6.38	5.61	0.77	9.02E-03	1.91E-01	POLR2J2	polymerase (RNA) II (DNA directed) polypeptide J2	chr7q22.1	1552621_at	NM_032959
6.01	4.87	1.14	9.03E-03	1.91E-01	ZC3HAV1L	zinc finger CCCH-type, antiviral 1-like	chr7q34	228280_at	NM_080660
6.88	6.00	0.88	9.04E-03	1.91E-01	JDP2	Jun dimerization protein 2	chr14q24.3	226267_at	NM_130469
6.03	5.50	0.53	9.04E-03	1.91E-01	SCMH1	sex comb on midleg homolog 1 (Drosophila)	chr1p34	221216_s_at	NM_001031694 /// NM_012236
7.37	6.23	1.14	9.04E-03	1.91E-01	NSUN5C	NOL1/NOP2/Sun domain family, member 5C	chr7q11.23	213842_x_at	NM_001039487 /// NM_032158 /// NM_148936
5.16	4.37	0.79	9.08E-03	1.92E-01	BCL6	B-cell CLL/lymphoma 6	chr3q27	215990_s_at	NM_001130845 /// NM_001134738 /// NM_001706 /// NM_138931
4.82	3.92	0.89	9.08E-03	1.92E-01	---	---	---	242358_at	---
5.45	4.75	0.70	9.09E-03	1.92E-01	LOC400960	hypothetical gene supported by BC040598	chr2p14	235482_at	XM_934552 /// XM_945536
5.83	5.06	0.78	9.10E-03	1.92E-01	MYO1F	myosin IF	chr19p13.3-p13.2	213733_at	NM_012335
2.98	2.59	0.39	9.10E-03	1.92E-01	---	---	---	228913_at	---

8.02	7.35	0.67	9.10E-03	1.92E-01	LDOC1L	leucine zipper, down-regulated in cancer 1-like	chr22q13.31	223228_at	NM_032287
3.89	2.37	1.52	9.12E-03	1.92E-01	---	---	---	226444_at	---
4.96	4.01	0.95	9.12E-03	1.92E-01	IQCB1	IQ motif containing B1	chr3q13.33|3q21.1	211707_s_at	NM_001023570 /// NM_001023571
6.91	5.99	0.92	9.13E-03	1.92E-01	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	chr11cen-q22.3	204663_at	NM_001014811 /// NM_006680
7.02	6.55	0.48	9.14E-03	1.92E-01	SAR1A	SAR1 gene homolog A (S. cerevisiae)	chr10q22.1	201543_s_at	NM_020150
8.04	7.34	0.70	9.14E-03	1.92E-01	DAZAP1	DAZ associated protein 1	chr19p13.3	226620_x_at	NM_018959 /// NM_170711
7.45	6.72	0.73	9.15E-03	1.92E-01	SLC25A39	solute carrier family 25, member 39	chr17q12	223649_s_at	NM_016016
7.11	6.00	1.12	9.17E-03	1.92E-01	DBNDD2 /// SYS1-DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing 2 /// SYS1-DBNDD2	chr20q13.12	218094_s_at	NM_001048221 /// NM_001048222 /// NM_001048223 /// NM_001048224 /// NM_001048225 /// NM_001048226 /// NR_003189
8.15	6.84	1.32	9.19E-03	1.92E-01	SLC25A37	solute carrier family 25, member 37	chr8p21.2	226179_at	NM_016612
4.83	4.02	0.81	9.20E-03	1.92E-01	CNPY3	canopy 3 homolog (zebrafish)	chr6pter-p12.1	228369_at	NM_006586
6.83	5.89	0.93	9.20E-03	1.92E-01	DVL3	dishevelled, dsh homolog 3 (Drosophila)	chr3q27	201908_at	NM_004423
8.27	7.21	1.06	9.22E-03	1.92E-01	ZFP36L1	zinc finger protein 36, C3H type-like 1	chr14q22-q24	211962_s_at	NM_004926
5.78	4.74	1.04	9.22E-03	1.92E-01	C20orf20	chromosome 20 open reading frame 20	chr20q13.33	218586_at	NM_018270
4.23	2.93	1.30	9.22E-03	1.92E-01	LOC284576	hypothetical protein LOC284576	chr1q32.1	1561280_at	---
2.98	2.63	0.36	9.23E-03	1.92E-01	OR1J4	olfactory receptor, family 1, subfamily J, member 4	chr9q34.11	1567282_at	NM_001004452
3.10	2.75	0.36	9.23E-03	1.92E-01	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	chr16q22.1	1554677_s_at	NM_178818 /// NM_181521
8.28	6.74	1.55	9.23E-03	1.92E-01	FGF11	fibroblast growth factor 11	chr17p13.1	227271_at	NM_004112
4.07	3.05	1.01	9.24E-03	1.92E-01	---	---	---	234104_at	---
8.63	7.64	0.99	9.24E-03	1.92E-01	TMEM14A	transmembrane protein 14A	chr6p12.1	218477_at	NM_014051
4.75	4.08	0.67	9.26E-03	1.92E-01	BCL2L12	BCL2-like 12 (proline rich)	chr19q13.3	233110_s_at	NM_001040668 /// NM_138639
2.44	1.94	0.50	9.27E-03	1.93E-01	---	---	---	235607_at	---
5.02	3.86	1.16	9.27E-03	1.93E-01	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	chr18q11.2	235020_at	NM_005640
8.08	6.73	1.35	9.28E-03	1.93E-01	PS1TP4	HBV preS1-transactivated protein 4	---	226381_at	---
4.45	3.73	0.72	9.31E-03	1.93E-01	FAM165B	family with sequence similarity 165, member B	chr21q22.12	228239_at	NM_058182
5.86	5.18	0.68	9.32E-03	1.93E-01	RP9P	retinitis pigmentosa 9 pseudogene	chr7p14.3	223945_x_at	NR_003500
6.85	5.85	1.00	9.33E-03	1.93E-01	CDC42SE1	CDC42 small effector 1	chr1q21.2	222537_s_at	NM_001038707 /// NM_020239
2.66	2.33	0.34	9.33E-03	1.93E-01	---	---	---	236423_at	---
3.50	2.98	0.52	9.34E-03	1.93E-01	NFKBIL2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	chr8q24.3	1558330_x_at	NM_013432
6.17	5.40	0.77	9.34E-03	1.93E-01	RAB40B	RAB40B, member RAS oncogene family	chr17q25.3	204547_at	NM_006822
7.02	5.83	1.19	9.34E-03	1.93E-01	CA11	carbonic anhydrase XI	chr19q13.3	209726_at	NM_001217
8.80	8.07	0.72	9.36E-03	1.93E-01	ADI1	acireductone dioxygenase 1	chr2p25.3	217761_at	NM_018269
6.12	5.30	0.82	9.37E-03	1.93E-01	TMEM150	transmembrane protein 150	chr2p11.2	226239_at	NM_001031738 /// NM_153342
4.03	2.97	1.07	9.37E-03	1.93E-01	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	chr20q11.2	206004_at	NM_003245
7.13	6.23	0.90	9.37E-03	1.93E-01	MESDC1	mesoderm development candidate 1	chr15q13	223264_at	NM_022566
7.18	6.54	0.63	9.38E-03	1.93E-01	UBQLN2	ubiquilin 2	chrXp11.23-p11.1	215884_s_at	NM_013444
4.97	3.93	1.03	9.38E-03	1.93E-01	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	chr11p15.2	227109_at	NM_024514
9.11	8.48	0.63	9.40E-03	1.94E-01	C22orf32	chromosome 22 open reading frame 32	chr22q13.2	225795_at	NM_033318
7.34	6.82	0.52	9.40E-03	1.94E-01	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	chr20p13	201509_at	NM_006899 /// NM_174855 /// NM_174856
8.00	7.51	0.49	9.44E-03	1.94E-01	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	chr4p16.3	201186_at	NM_002337
6.12	5.47	0.65	9.46E-03	1.94E-01	RP9 /// RP9P	retinitis pigmentosa 9 (autosomal dominant) /// retinitis pigmentosa 9 pseudogene	chr7p14.3	227640_s_at	NM_203288 /// NR_003500

5.71	4.93	0.78	9.46E-03	1.94E-01	FAM40A	family with sequence similarity 40, member A	chr1p13.3	225226_at	NM_033088
8.91	8.10	0.81	9.47E-03	1.94E-01	IRF2BP2	interferon regulatory factor 2 binding protein 2	chr1q42.3	224569_s_at	NM_001077397 /// NM_182972
4.95	4.35	0.60	9.48E-03	1.94E-01	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	chr12q13	203125_x_at	NM_000617
3.55	2.93	0.62	9.49E-03	1.94E-01	FBXL17 /// LOC100130089	F-box and leucine-rich repeat protein 17 /// similar to FBXL17 protein	chr5q21.3	244360_at	NM_022824 /// XM_001714289 /// XM_001714815 /// XM_001717204
5.00	4.10	0.90	9.49E-03	1.94E-01	PAXIP1	PAX interacting (with transcription-activation domain) protein 1	chr7q36	212825_at	NM_007349
4.28	3.18	1.10	9.49E-03	1.94E-01	PPP1R3E	protein phosphatase 1, regulatory (inhibitor) subunit 3E	chr14q11.2	227412_at	XR_040048 /// XR_040049 /// XR_040050
6.64	5.28	1.36	9.50E-03	1.94E-01	EPN3	epsin 3	chr17q21.33	223895_s_at	NM_017957
7.82	6.88	0.94	9.50E-03	1.94E-01	SULT1A3 /// SULT1A4	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	chr16p11.2	210580_x_at	NM_001017387 /// NM_001017389 /// NM_001017390 /// NM_001017391 /// NM_003166 /// NM_177552
4.52	3.50	1.02	9.53E-03	1.95E-01	DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	chrXq26.3	227485_at	NM_182540
6.62	5.88	0.74	9.54E-03	1.95E-01	IRF3	interferon regulatory factor 3	chr19q13.3-q13.4	202621_at	NM_001571
4.29	3.47	0.82	9.55E-03	1.95E-01	SOLH	small optic lobes homolog (Drosophila)	chr16p13.3	204275_at	NM_005632
6.72	6.05	0.67	9.56E-03	1.95E-01	PCTK1	PCTAIRE protein kinase 1	chrXp11.3-p11.23	208823_s_at	NM_006201 /// NM_033018
6.69	5.32	1.37	9.57E-03	1.95E-01	FGFR1OP2	FGFR1 oncogene partner 2	chr12p11.23	1556283_s_at	NM_015633
8.90	8.39	0.52	9.60E-03	1.95E-01	RBMX	RNA binding motif protein, X-linked	chrXq26.3	213762_x_at	NM_002139
5.72	5.08	0.64	9.60E-03	1.95E-01	SETDB1	SET domain, bifurcated 1	chr1q21	203155_at	NM_012432
5.39	4.47	0.92	9.60E-03	1.95E-01	ARHGAP9	Rho GTPase activating protein 9	chr12q14	232543_x_at	NM_001080156 /// NM_001080157 /// NM_032496
6.27	5.15	1.12	9.61E-03	1.95E-01	DUSP4	dual specificity phosphatase 4	chr8p12-p11	204015_s_at	NM_001394 /// NM_057158
9.19	8.57	0.62	9.63E-03	1.96E-01	TUBB2C	tubulin, beta 2C	chr9q34	213726_x_at	NM_006088
10.54	9.79	0.75	9.64E-03	1.96E-01	IRS2	insulin receptor substrate 2	chr13q34	209185_s_at	NM_003749
5.88	5.17	0.70	9.66E-03	1.96E-01	TMEM129	transmembrane protein 129	chr4p16.3	225588_s_at	NM_001127266 /// NM_138385
4.45	3.94	0.51	9.66E-03	1.96E-01	HEATR3	HEAT repeat containing 3	chr16q12.1	219289_at	NM_182922
7.43	6.52	0.91	9.66E-03	1.96E-01	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	chr21q22.3	202671_s_at	NM_003681
5.33	4.36	0.97	9.68E-03	1.96E-01	ARSD	arylsulfatase D	chrXp22.3	223695_s_at	NM_001669 /// NM_009589
6.79	5.85	0.94	9.69E-03	1.96E-01	KLHDC9	kelch domain containing 9	chr1q23.3	227582_at	NM_001007255 /// NM_001007256 /// NM_152366
6.37	5.38	0.99	9.70E-03	1.96E-01	LOC401504	Hypothetical gene supported by AK091718	chr9p13.2	226635_at	---
6.33	5.46	0.86	9.71E-03	1.96E-01	SH2B1	SH2B adaptor protein 1	chr16p11.2	40149_at	NM_015503
6.45	5.53	0.92	9.72E-03	1.96E-01	LUC7L	LUC7-like (S. cerevisiae)	chr16p13.3	223546_x_at	NM_018032 /// NM_201412
8.02	7.17	0.85	9.73E-03	1.96E-01	C17orf61	chromosome 17 open reading frame 61	chr17p13.1	227063_at	NM_152766
4.97	3.96	1.00	9.73E-03	1.96E-01	C8orf58	chromosome 8 open reading frame 58	chr8p21	227263_at	NM_001013842

6.14	5.23	0.92	9.74E-03	1.96E-01	LOC91316	similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific)	chr22q11.23	213502_x_at	XR_038140 /// XR_040205 /// XR_040206																			
11.86	11.46	0.40	9.76E-03	1.96E-01	LOC390354 /// RPL18A	ribosomal protein L18a pseudogene /// ribosomal protein L18a	chr12q23.3 /// chr19p13	200869_at	NM_000980 /// NR_001593 /// XR_042140 /// XR_042141																			
3.28	2.62	0.66	9.78E-03	1.97E-01	C6orf26 /// MSH5	chromosome 6 open reading frame 26 /// mutS homolog 5 (E. coli)	chr6p21.3 /// chr6p21.33	210410_s_at	NM_001039651 /// NM_002441 /// NM_025259 /// NM_172165 /// NM_172166																			
7.54	6.92	0.62	9.79E-03	1.97E-01	ACYP2	acylphosphatase 2, muscle type	chr2p16.2	206833_s_at	NM_138448																			
4.34	3.36	0.98	9.79E-03	1.97E-01	MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	chr22q11.21	212715_s_at	NM_001122731 /// NM_015241 /// XM_001721205 /// XM_001725408 /// XM_001726352																			
6.11	5.47	0.64	9.80E-03	1.97E-01	C5orf45	chromosome 5 open reading frame 45	chr5q35.3	220341_s_at	NM_001017987 /// NM_016175																			
8.63	8.26	0.37	9.81E-03	1.97E-01	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	chr1q21.2	210460_s_at	NM_002810																			
6.73	5.15	1.57	9.81E-03	1.97E-01	DMD	dystrophin	chrXp21.2	203881_s_at	NM_000109 /// NM_004006 /// NM_004007 /// NM_004009 /// NM_004010 /// NM_004011 /// NM_004012 /// NM_004013 /// NM_004014 /// NM_004015 /// NM_004016 /// NM_004017 /// NM_004018 /// NM_004019 /// NM_004020 /// NM_004021 /// NM_004022 /// NM_004023																			
5.78	5.31	0.48	9.83E-03	1.97E-01	THADA	thyroid adenoma associated	chr2p21	220212_s_at	NM_001083953 /// NM_022065																			
7.92	7.28	0.65	9.85E-03	1.97E-01	RNF149	ring finger protein 149	chr2q11.2	225414_at	NM_173647																			

6.32	5.76	0.56	9.85E-03	1.97E-01	MRPS30	mitochondrial ribosomal protein S30	chr5q11	218398_at	NM_016640
2.76	2.38	0.39	9.85E-03	1.97E-01	CCKBR	Cholecystokinin B receptor	chr11p15.4	234475_x_at	NM_176875
3.80	3.35	0.45	9.86E-03	1.97E-01	MT4	metallothionein 4	chr16q13	217395_at	NM_032935
6.73	5.92	0.81	9.86E-03	1.97E-01	---	---	---	226773_at	---
5.84	5.50	0.34	9.88E-03	1.97E-01	C3orf19	chromosome 3 open reading frame 19	chr3p25.1	225559_at	NM_016474
7.71	7.20	0.51	9.89E-03	1.97E-01	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	chr22q12-q13	217960_s_at	NM_020243
6.93	6.07	0.86	9.91E-03	1.98E-01	LOC729776	hypothetical LOC729776	chr6p21.31	229444_at	XM_001133820 /// XM_001721490 /// XM_001721562
7.17	6.61	0.55	9.92E-03	1.98E-01	SLC35B1	solute carrier family 35, member B1	chr17q21.33	202433_at	NM_005827
6.09	5.40	0.69	9.93E-03	1.98E-01	GEMIN7	gem (nuclear organelle) associated protein 7	chr19q13.32	1555751_a_at	NM_001007269 /// NM_001007270 /// NM_024707
7.30	6.78	0.52	9.94E-03	1.98E-01	C1orf77	chromosome 1 open reading frame 77	chr1q21.3	202559_x_at	NM_015607
6.56	5.37	1.19	9.94E-03	1.98E-01	HRBL	HIV-1 Rev binding protein-like	chr7q22.1	222126_at	NM_006076
6.02	4.66	1.36	9.98E-03	1.98E-01	OBSL1	obscurin-like 1	chr2q35	227574_at	NM_015311
12.41	11.99	0.42	9.98E-03	1.98E-01	RPS29	ribosomal protein S29	chr14q	201094_at	NM_001030001 /// NM_001032
4.21	2.91	1.31	9.99E-03	1.98E-01	EXOC3L /// LOC100130525 /// LOC100134333 /// LOC653319	exocyst complex component 3-like /// hypothetical protein LOC100130525 /// hypothetical protein LOC100134333 /// hypothetical protein LOC653319	chr16q22.1	1558041_a_at	NM_001040715 /// NM_178516 /// XM_001713762 /// XM_001713763
6.71	5.99	0.72	1.00E-02	1.98E-01	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1	chr20q13.12	234942_s_at	NM_052951
6.00	5.23	0.77	1.00E-02	1.98E-01	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	chr5q33.2	207357_s_at	NM_017540 /// NM_198321
6.16	5.36	0.80	1.00E-02	1.99E-01	ZCCHC8	zinc finger, CCHC domain containing 8	chr12q24.31	218478_s_at	NM_017612
5.28	4.71	0.57	1.00E-02	1.99E-01	NUP98	nucleoporin 98kDa	chr11p15.5	203194_s_at	NM_005387 /// NM_016320 /// NM_139131 /// NM_139132
5.55	4.64	0.91	1.01E-02	1.99E-01	---	---	---	222968_at	---
3.29	2.54	0.75	1.01E-02	1.99E-01	TGFB2	transforming growth factor, beta 2	chr1q41	220407_s_at	NM_003238
8.49	7.80	0.69	1.01E-02	1.99E-01	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced	chr12q13	201331_s_at	NM_003153
3.82	3.29	0.53	1.01E-02	1.99E-01	HIBADH	3-hydroxyisobutyrate dehydrogenase	chr7p15.2	234452_at	NM_152740
4.91	3.98	0.93	1.01E-02	1.99E-01	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	chr15q22	228340_at	NM_001105192 /// NM_005078 /// NM_020908
9.29	8.75	0.54	1.01E-02	1.99E-01	DUT	deoxyuridine triphosphatase	chr15q15-q21.1	209932_s_at	NM_001025248 /// NM_001025249 /// NM_001948
6.07	5.61	0.45	1.01E-02	1.99E-01	NUP214	nucleoporin 214kDa	chr9q34.1	202155_s_at	NM_005085
9.51	8.79	0.72	1.01E-02	1.99E-01	ZNF503	zinc finger protein 503	chr10q22.2	227195_at	NM_032772
3.60	2.99	0.61	1.01E-02	1.99E-01	---	---	---	229205_at	---
5.73	5.01	0.72	1.01E-02	1.99E-01	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	chr12q13.2	1554451_s_at	NM_032364
4.71	3.80	0.90	1.01E-02	1.99E-01	SHROOM3	shroom family member 3	chr4q21.1	225548_at	NM_020859
3.18	2.12	1.06	1.01E-02	1.99E-01	FLJ22639	hypothetical protein FLJ22639	chr1p36.33	220399_at	XR_017693 /// XR_040152
7.09	6.09	0.99	1.01E-02	1.99E-01	LOC100130624	hypothetical LOC100130624	chr22q12.1	217266_at	XR_038453 /// XR_039025 /// XR_039678
7.46	6.66	0.80	1.01E-02	1.99E-01	C1orf162	chromosome 1 open reading frame 162	chr1p13.2	228532_at	NM_174896
6.24	5.11	1.14	1.01E-02	1.99E-01	OGFRL1	opioid growth factor receptor-like 1	chr6q13	226810_at	NM_024576
6.49	5.70	0.79	1.01E-02	1.99E-01	DGCR14	DiGeorge syndrome critical region gene 14	chr22q11.21|22q11.2	32032_at	NM_022719

3.74	3.01	0.72	1.01E-02	1.99E-01	---	---	---	230991_at	---
7.13	6.32	0.81	1.01E-02	1.99E-01	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	chrXp22.2-p22.1	226335_at	NM_004586
7.22	6.83	0.39	1.02E-02	1.99E-01	NIP30	NEFA-interacting nuclear protein NIP30	chr16q13	223406_x_at	NM_024946
6.01	4.78	1.22	1.02E-02	1.99E-01	SFRS18	splicing factor, arginine/serine-rich 18	chr6q16.3	212176_at	NM_015491 /// NM_032870
5.98	4.95	1.03	1.02E-02	1.99E-01	FBXL11	F-box and leucine-rich repeat protein 11	chr11q13.1	208988_at	NM_012308
6.44	5.66	0.79	1.02E-02	1.99E-01	SAP30	Sin3A-associated protein, 30kDa	chr4q34.1	204900_x_at	NM_003864
8.14	6.64	1.50	1.02E-02	1.99E-01	TRIB1	tribbles homolog 1 (Drosophila)	chr8q24.13	202241_at	NM_025195
6.68	6.03	0.65	1.02E-02	1.99E-01	PRMT5	protein arginine methyltransferase 5	chr14q11.2-q21	1564521_x_at	NM_001039619 /// NM_006109
3.08	2.43	0.64	1.02E-02	2.00E-01	LOC100129455	hypothetical LOC100129455	chr2q31.1	1560475_at	XM_001722087 /// XM_001722106 /// XM_001725873
13.00	12.70	0.30	1.02E-02	2.00E-01	RPL13A	ribosomal protein L13a	chr19q13.3	212790_x_at	NM_012423
8.03	7.48	0.55	1.03E-02	2.00E-01	C19orf10	chromosome 19 open reading frame 10	chr19p13.3	216483_s_at	NM_019107
8.66	8.11	0.54	1.03E-02	2.00E-01	UBXN1	UBX domain protein 1	chr11q12.3	201871_s_at	NM_015853
8.88	8.19	0.69	1.03E-02	2.00E-01	YY1	YY1 transcription factor	chr14q	200047_s_at	NM_003403
5.91	5.30	0.60	1.03E-02	2.00E-01	WIPF1	WAS/WASL interacting protein family, member 1	chr2q31.1	202664_at	NM_001077269 /// NM_003387
7.67	6.96	0.72	1.03E-02	2.00E-01	FAM134A	family with sequence similarity 134, member A	chr2q35	221984_s_at	NM_024293
5.75	5.01	0.74	1.03E-02	2.00E-01	DNMBP	dynamin binding protein	chr10q24.2	212838_at	NM_015221
8.13	7.50	0.63	1.04E-02	2.01E-01	NUMA1	nuclear mitotic apparatus protein 1	chr11q13	200747_s_at	NM_006185
8.18	7.43	0.75	1.04E-02	2.01E-01	EXT1	exostoses (multiple) 1	chr8q24.11-q24.13	201995_at	NM_000127
7.51	5.83	1.68	1.04E-02	2.02E-01	BHLHB3	basic helix-loop-helix domain containing, class B, 3	chr12p11.23-p12.1	221530_s_at	NM_030762
2.89	2.39	0.50	1.04E-02	2.02E-01	WDR33	WD repeat domain 33	chr2q14.3	229141_at	NM_001006622 /// NM_001006623 /// NM_018383
5.20	4.45	0.74	1.04E-02	2.02E-01	SMAD3	SMAD family member 3	chr15q22.33	205398_s_at	NM_005902
6.73	6.04	0.69	1.05E-02	2.02E-01	POM121 /// POM121C	POM121 membrane glycoprotein (rat) /// POM121 membrane glycoprotein C	chr7q11.2 /// chr7q11.23	212178_s_at	NM_001099415 /// NM_172020
5.64	5.00	0.64	1.05E-02	2.02E-01	LOC92249	hypothetical LOC92249	chrXq11.2	212957_s_at	NR_015353
4.09	3.22	0.87	1.05E-02	2.02E-01	MSRB3	methionine sulfoxide reductase B3	chr12q14.3	1554127_s_at	NM_001031679 /// NM_198080
5.27	4.54	0.72	1.05E-02	2.02E-01	COMMD5	COMM domain containing 5	chr8q24-qter	224387_at	NM_001081003 /// NM_001081004 /// NM_014066
5.52	4.83	0.69	1.05E-02	2.02E-01	PHLDA1	pleckstrin homology-like domain, family A, member 1	chr12q15	218000_s_at	NM_007350
8.58	8.09	0.49	1.05E-02	2.03E-01	LOC643287	similar to prothymosin alpha	chr12p13.2	216384_x_at	XM_001723401 /// XM_928075 /// XM_945078
6.27	4.23	2.04	1.06E-02	2.03E-01	PABPN1	poly(A) binding protein, nuclear 1	chr14q11.2-q13	213046_at	NM_004643
3.27	2.73	0.54	1.06E-02	2.03E-01	MUC20	mucin 20, cell surface associated	chr3q29	226622_at	NM_001098516 /// NM_152673 /// XM_001726694

7.31	6.32	0.99	1.06E-02	2.03E-01	DKFZp547E087 /// LOC100132247 /// LOC23117 /// LOC348162 /// LOC440345	hypothetical gene LOC283846 /// similar to Uncharacterized protein KIAA0220 /// KIAA0220-like protein /// hypothetical protein 348162 /// hypothetical protein LOC440345	chr16p11.2 /// chr16p12.1 /// chr16p12.2 /// chr18p11.21	211996_s_at	NM_130464 /// XM_001724791 /// XM_496136 /// XM_931802 /// XM_931808 /// XM_931814 /// XM_931818 /// XM_931827 /// XM_931837 /// XM_931840 /// XR_015786																				
4.68	3.96	0.72	1.06E-02	2.03E-01	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	chr7q22.1	215458_s_at	NM_020429 /// NM_181349																				
2.96	2.22	0.74	1.06E-02	2.03E-01	MMP16	matrix metallopeptidase 16 (membrane-inserted)	chr8q21	207012_at	NM_005941 /// NM_022564																				
6.98	5.80	1.18	1.06E-02	2.03E-01	YPEL2	yippee-like 2 (Drosophila)	chr17q22	227020_at	NM_001005404																				
4.77	4.29	0.48	1.06E-02	2.03E-01	ZBTB2	zinc finger and BTB domain containing 2	chr6q25.1	226284_at	NM_020861																				
2.92	2.41	0.51	1.06E-02	2.03E-01	KLHL9	kelch-like 9 (Drosophila)	chr9p22	233197_at	NM_018847																				
8.45	7.81	0.64	1.06E-02	2.03E-01	SLC39A14	solute carrier family 39 (zinc transporter), member 14	chr8p21.3	212110_at	NM_001128431 /// NM_015359																				
8.36	7.95	0.41	1.06E-02	2.03E-01	C7orf42	chromosome 7 open reading frame 42	chr7q11.21	218008_at	NM_017994																				
4.71	3.83	0.88	1.06E-02	2.03E-01	SPIN3	spindlin family, member 3	chrXp11.1	1555883_s_at	NM_001010862																				
7.17	5.83	1.35	1.06E-02	2.03E-01	MT3	metallothionein 3	chr16q13	205970_at	NM_005954																				
7.37	6.43	0.94	1.06E-02	2.03E-01	SFXN4	sideroflexin 4	chr10q26.11	229236_s_at	NM_213649																				
8.24	7.69	0.55	1.07E-02	2.03E-01	FAM62A	family with sequence similarity 62 (C2 domain containing), member A	chr12q13.2	208858_s_at	NM_015292																				
3.97	2.80	1.17	1.07E-02	2.03E-01	---	---	---	235902_at	---																				
11.27	10.91	0.36	1.07E-02	2.03E-01	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	chr17p13	201530_x_at	NM_001416																				
7.54	6.95	0.59	1.07E-02	2.03E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	214728_x_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072																				
4.46	3.67	0.79	1.07E-02	2.03E-01	PPAT	Phosphoribosyl pyrophosphate amidotransferase	chr4q12	235833_at	NM_002703																				
9.12	8.61	0.51	1.07E-02	2.03E-01	SFRS9	splicing factor, arginine/serine-rich 9	chr12q24.31	200044_at	NM_003769																				
7.75	6.85	0.90	1.07E-02	2.03E-01	TP53INP2	tumor protein p53 inducible nuclear protein 2	chr20q11.22	224836_at	NM_021202																				
3.72	2.55	1.18	1.07E-02	2.03E-01	LOC120376	hypothetical protein LOC120376	chr11q23.1	228338_at	XM_001718669 /// XM_071712 /// XM_943506																				
7.01	6.42	0.59	1.07E-02	2.03E-01	TMEM189 /// UBE2V1	transmembrane protein 189 /// ubiquitin-conjugating enzyme E2 variant 1	chr20q13.2	223186_at	NM_001032288 /// NM_021988 /// NM_022442 /// NM_199129 /// NM_199144																				
5.11	4.66	0.45	1.07E-02	2.03E-01	ZNF516	zinc finger protein 516	chr18q23	203604_at	NM_014643																				
6.63	5.68	0.95	1.08E-02	2.03E-01	WFS1	Wolfram syndrome 1 (wolframin)	chr4p16	202908_at	NM_006005																				
3.76	2.99	0.77	1.08E-02	2.03E-01	KLHDC4	kelch domain containing 4	chr16q24.3	232171_x_at	NM_017566																				

4.23	3.00	1.23	1.08E-02	2.03E-01	---	---	---	226125_at	---
4.78	3.86	0.92	1.08E-02	2.03E-01	---	---	---	226478_at	---
7.59	6.47	1.12	1.08E-02	2.03E-01	RAB38	RAB38, member RAS oncogene family	chr11q14	219412_at	NM_022337
5.31	4.70	0.61	1.08E-02	2.04E-01	PTK7	PTK7 protein tyrosine kinase 7	chr6p21.1-p12.2	207011_s_at	NM_002821 /// NM_152880 /// NM_152881 /// NM_152882
3.16	2.81	0.35	1.08E-02	2.04E-01	---	---	---	244177_at	---
6.56	6.02	0.54	1.08E-02	2.04E-01	IL17RC	interleukin 17 receptor C	chr3p25.3|3p25.3-p24.1	224514_x_at	NM_032732 /// NM_153460 /// NM_153461
8.47	7.65	0.82	1.08E-02	2.04E-01	HCLS1	hematopoietic cell-specific Lyn substrate 1	chr3q13	202957_at	NM_005335
4.75	4.42	0.33	1.08E-02	2.04E-01	GTF3C4	General transcription factor IIIC, polypeptide 4, 90kDa	chr9q34.13	243228_at	NM_012204
3.03	2.66	0.38	1.08E-02	2.04E-01	RPS14	Ribosomal protein S14	chr5q31-q33	241241_at	NM_001025070 /// NM_001025071 /// NM_005617
7.99	7.46	0.53	1.08E-02	2.04E-01	MRPS6	mitochondrial ribosomal protein S6	chr21q21.3-q22.1	224919_at	NM_032476
5.26	4.13	1.14	1.08E-02	2.04E-01	GNB2L1	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	chr5q35.3	222034_at	NM_006098
8.19	7.47	0.72	1.09E-02	2.04E-01	TMED4	transmembrane emp24 protein transport domain containing 4	chr7p13	224676_at	NM_182547
5.94	5.17	0.77	1.09E-02	2.04E-01	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	chr2q23.3	225707_at	NM_152522
7.63	6.87	0.76	1.09E-02	2.04E-01	MAGEH1	melanoma antigen family H, 1	chrXp11.21	218573_at	NM_014061
5.73	4.89	0.84	1.09E-02	2.04E-01	PRR3	proline rich 3	chr6p21.33	204795_at	NM_001077497 /// NM_025263
3.67	3.00	0.67	1.09E-02	2.04E-01	LOC731884	Similar to programmed cell death 6 interacting protein	---	217520_x_at	XR_015639
7.69	6.91	0.78	1.09E-02	2.05E-01	TSEN34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	chr19q13.4	218132_s_at	NM_001077446 /// NM_024075
6.76	5.71	1.05	1.09E-02	2.05E-01	ABHD12	abhydrolase domain containing 12	chr20p11.21	228124_at	NM_001042472 /// NM_015600
7.46	5.52	1.94	1.10E-02	2.05E-01	GADD45B	growth arrest and DNA-damage-inducible, beta	chr19p13.3	209305_s_at	NM_015675
6.89	6.25	0.63	1.10E-02	2.05E-01	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10q25.3	216037_x_at	NM_030756
8.39	7.74	0.65	1.10E-02	2.06E-01	PH-4	hypoxia-inducible factor prolyl 4-hydroxylase	chr3p21.31	222125_s_at	NM_177938 /// NM_177939
6.02	5.45	0.57	1.10E-02	2.06E-01	SF3A1	splicing factor 3a, subunit 1, 120kDa	chr22q12.2	227516_at	NM_001005409 /// NM_005877
6.25	4.23	2.02	1.10E-02	2.06E-01	CTHRC1	collagen triple helix repeat containing 1	chr8q22.3	225681_at	NM_138455
4.61	4.02	0.59	1.10E-02	2.06E-01	STAT2	signal transducer and activator of transcription 2, 113kDa	chr12q13.2	205170_at	NM_005419
11.42	11.06	0.36	1.11E-02	2.06E-01	RPLP0 /// RPLP0-like	ribosomal protein, large, P0 /// ribosomal protein P0-like	chr12q24.2 /// chr2p22.1	214167_s_at	NM_001002 /// NM_053275 /// XR_015741 /// XR_017813 /// XR_041288
5.31	4.17	1.15	1.11E-02	2.06E-01	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	chr2p13	201447_at	NM_022037 /// NM_022173
6.10	5.37	0.73	1.11E-02	2.06E-01	PIGG	phosphatidylinositol glycan anchor biosynthesis, class G	chr4p16.3	218652_s_at	NM_001127178 /// NM_017733
5.55	4.26	1.29	1.11E-02	2.06E-01	LOC388796	hypothetical LOC388796	chr20q11.23	65588_at	NR_015366 /// XM_001720823 /// XM_001720894 /// XM_001721371
6.05	5.24	0.81	1.11E-02	2.06E-01	NSUN4	NOL1/NOP2/Sun domain family, member 4	chr1p34	226351_at	NM_199044
5.94	4.97	0.97	1.11E-02	2.06E-01	NRBP2	nuclear receptor binding protein 2	chr8q24.3	225949_at	NM_178564
7.88	6.82	1.07	1.11E-02	2.06E-01	DDB2	damage-specific DNA binding protein 2, 48kDa	chr11p12-p11	203409_at	NM_000107

3.33	2.75	0.58	1.11E-02	2.06E-01	C17orf44	chromosome 17 open reading frame 44	chr17p13.1	230012_at	XR_040149 /// XR_040150 /// XR_040151																				
9.88	9.17	0.71	1.11E-02	2.06E-01	LGALS3	lectin, galactoside-binding, soluble, 3	chr14q21-q22	208949_s_at	NM_002306 /// NR_003225																				
7.67	6.70	0.97	1.11E-02	2.06E-01	ABR	active BCR-related gene	chr17p13.3	212895_s_at	NM_001092 /// NM_021962																				
3.77	3.11	0.66	1.11E-02	2.07E-01	KIFC3	kinesin family member C3	chr16q13-q21	1559759_at	NM_001130099 /// NM_001130100 /// NM_005550																				
3.27	2.60	0.67	1.12E-02	2.07E-01	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	chr15q22	206472_s_at	NM_001105192 /// NM_005078 /// NM_020908																				
6.11	5.56	0.55	1.12E-02	2.07E-01	RPRD1B	regulation of nuclear pre-mRNA domain containing 1B	chr20q11.21-q12	225024_at	NM_021215																				
7.41	5.02	2.39	1.12E-02	2.07E-01	NXPH1	neurexophilin 1	chr7p22	232377_at	NM_152745																				
2.54	2.20	0.34	1.12E-02	2.08E-01	MTHFD1L	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	chr6q25.1	1561125_at	NM_015440																				
6.61	5.30	1.31	1.13E-02	2.08E-01	FGFR1OP2	FGFR1 oncogene partner 2	chr12p11.23	233898_s_at	NM_015633																				
6.05	5.15	0.90	1.13E-02	2.08E-01	SLC4A11	solute carrier family 4, sodium borate transporter, member 11	chr20p12	223748_at	NM_032034																				
2.62	2.07	0.55	1.13E-02	2.08E-01	RBM15	RNA binding motif protein 15	chr1p13	228455_at	NM_022768																				
5.62	4.94	0.68	1.13E-02	2.08E-01	---	---	---	213700_s_at	---																				
8.01	7.43	0.58	1.13E-02	2.08E-01	FAM96A	family with sequence similarity 96, member A	chr15q22.31	224779_s_at	NM_001014812 /// NM_032231																				
8.23	7.88	0.34	1.13E-02	2.08E-01	NAT5	N-acetyltransferase 5	chr20p11.23	223040_at	NM_016100 /// NM_181527 /// NM_181528																				
7.25	6.59	0.66	1.13E-02	2.08E-01	TCTN1	tectonic family member 1	chr12q24.11	218584_at	NM_001082537 /// NM_001082538 /// NM_024549																				
7.28	6.63	0.65	1.13E-02	2.08E-01	PPIC	peptidylprolyl isomerase C (cyclophilin C)	chr5q23.2	204517_at	NM_000943																				
6.49	5.80	0.69	1.13E-02	2.08E-01	PARP6	poly (ADP-ribose) polymerase family, member 6	chr15q23	232683_s_at	NM_020214																				
6.79	6.24	0.55	1.14E-02	2.09E-01	MKRN1	makorin ring finger protein 1	chr7q34	209845_at	NM_013446																				
3.12	2.62	0.51	1.14E-02	2.09E-01	ATP7B	ATPase, Cu++ transporting, beta polypeptide	chr13q14.3	204624_at	NM_000053 /// NM_001005918																				
5.44	4.78	0.67	1.14E-02	2.09E-01	HOXA4	homeobox A4	chr7p15-p14	206289_at	NM_002141																				
5.96	4.80	1.16	1.14E-02	2.09E-01	LOC100133130	PRO1102	chr10q11.21	229428_at	XM_001724485																				
5.84	5.17	0.67	1.14E-02	2.09E-01	LOC388795	similar to hCG2019498	chr20q11.21	227547_at	XM_001720320 /// XM_371397 /// XM_936526																				
8.20	7.64	0.56	1.14E-02	2.09E-01	DLST /// DLSTP	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) /// dihydrolipoamide S-succinyltransferase pseudogene (E2 component of 2-oxo-glutarate complex)	chr14q24.3 /// chr1p31	215210_s_at	NM_001933																				
7.04	6.46	0.58	1.14E-02	2.09E-01	chromosome 18 open reading frame 50	Transcribed locus	---	238480_at	---																				
2.97	2.17	0.79	1.14E-02	2.09E-01	SKIL	SKI-like oncogene	chr3q26	206675_s_at	NM_005414																				
5.35	4.72	0.63	1.15E-02	2.09E-01	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	chr2q35	1553510_s_at	NM_005444																				
6.89	6.39	0.50	1.15E-02	2.09E-01	SAE1	SUMO1 activating enzyme subunit 1	chr19q13.32	217946_s_at	NM_005500																				
3.43	2.45	0.98	1.15E-02	2.10E-01	RBM8A	RNA binding motif protein 8A	chr1q12	1554602_at	NM_005105																				
7.11	5.95	1.16	1.15E-02	2.10E-01	TMEM22	transmembrane protein 22	chr3q22.3	219569_s_at	NM_001097599 /// NM_001097600 /// NM_025246																				
6.36	5.84	0.51	1.15E-02	2.10E-01	COG7	component of oligomeric golgi complex 7	chr16p12.1	213190_at	NM_153603																				

7.99	7.49	0.50	1.15E-02	2.10E-01	ZDHHC7	zinc finger, DHHC-type containing 7	chr16q24.1	218606_at	NM_017740																				
3.89	3.28	0.60	1.15E-02	2.10E-01	---	---	---	230483_at	---																				
3.31	2.81	0.50	1.15E-02	2.10E-01	HKR1	GLI-Kruppel family member HKR1	chr19q13.12	1569979_at	NM_181786																				
8.42	7.94	0.48	1.15E-02	2.10E-01	DDT	D-dopachrome tautomerase	chr22q11.23	202929_s_at	NM_001084392 /// NM_001355																				
6.63	5.66	0.97	1.16E-02	2.10E-01	PCGF3	polycomb group ring finger 3	chr4p16.3	212753_at	NM_006315																				
7.94	7.12	0.82	1.16E-02	2.10E-01	RHEB	Ras homolog enriched in brain	chr7q36	213404_s_at	NM_005614																				
3.64	2.64	0.99	1.16E-02	2.10E-01	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	chr10q23.2-q23.33	214241_at	NM_005004																				
7.29	6.77	0.52	1.16E-02	2.10E-01	ACOT9	acyl-CoA thioesterase 9	chrXp22.11	221641_s_at	NM_001033583 /// NM_001037171																				
3.57	3.04	0.54	1.16E-02	2.10E-01	PIGW	phosphatidylinositol glycan anchor biosynthesis, class W	chr17q12	1558292_s_at	NM_178517																				
2.93	2.04	0.89	1.16E-02	2.10E-01	---	---	---	238456_at	---																				
6.07	5.38	0.70	1.17E-02	2.11E-01	STX4	syntaxin 4	chr16p11.2	229395_at	NM_004604																				
13.14	12.86	0.28	1.17E-02	2.11E-01	RPL13A	ribosomal protein L13a	chr19q13.3	210646_x_at	NM_012423																				
3.38	3.07	0.32	1.17E-02	2.11E-01	RPS9	ribosomal protein S9	chr19q13.4	1557981_at	NM_001013																				
5.51	4.88	0.64	1.17E-02	2.11E-01	TUBGCP4	Tubulin, gamma complex associated protein 4	chr15q15	213266_at	NM_014444																				
4.56	3.51	1.05	1.17E-02	2.11E-01	LOC441124	hypothetical gene supported by AK093729; BX647918	chr1q42.11	227922_x_at	XM_499022																				
4.47	3.71	0.76	1.17E-02	2.11E-01	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	chr16p12.1	222490_at	NM_018119																				
7.26	6.89	0.38	1.17E-02	2.11E-01	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	chrXq24-q25	201899_s_at	NM_003336 /// NM_181762 /// NM_181777																				
6.29	5.62	0.68	1.17E-02	2.11E-01	SPRED2	sprouty-related, EVH1 domain containing 2	chr2p14	212458_at	NM_001128210 /// NM_181784																				
7.76	7.06	0.70	1.18E-02	2.12E-01	LYSMD2	LysM, putative peptidoglycan-binding, domain containing 2	chr15q21.2	226748_at	NM_153374																				
9.68	8.62	1.06	1.18E-02	2.12E-01	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	chr8p11.2-p11.1	203973_s_at	NM_005195																				
6.60	5.89	0.71	1.18E-02	2.12E-01	KIAA0141	KIAA0141	chr5q31.3	201977_s_at	NM_014773																				
7.68	6.75	0.93	1.18E-02	2.12E-01	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	chr6p21.3	211654_x_at	NM_002123 /// XM_001722253 /// XM_001723447																				
7.03	5.44	1.58	1.19E-02	2.13E-01	TncRNA	trophoblast-derived noncoding RNA	chr11q13.1	224566_at	NR_002802																				
6.87	6.10	0.77	1.19E-02	2.13E-01	SFRS14	splicing factor, arginine/serine-rich 14	chr19p12	213505_s_at	NM_001017392 /// NM_014884																				
7.01	6.16	0.85	1.19E-02	2.13E-01	SH3PXD2A	SH3 and PX domains 2A	chr10q24.33	224817_at	NM_014631																				
8.44	7.54	0.90	1.19E-02	2.13E-01	PHF1	PHD finger protein 1	chr6p21.3	40446_at	NM_002636 /// NM_024165																				
6.19	5.50	0.68	1.19E-02	2.13E-01	C4orf8	chromosome 4 open reading frame 8	chr4p16.3	203600_s_at	NM_003704																				
7.07	5.88	1.19	1.19E-02	2.13E-01	CHERP	calcium homeostasis endoplasmic reticulum protein	chr19p13.1	202230_s_at	NM_006387																				
4.81	4.13	0.68	1.19E-02	2.13E-01	C19orf29	chromosome 19 open reading frame 29	chr19p13.3	215954_s_at	NM_001080543 /// NM_021231																				
8.96	8.35	0.62	1.20E-02	2.13E-01	RPL10	ribosomal protein L10	chrXq28	217379_at	NM_006013																				
5.01	4.04	0.98	1.20E-02	2.13E-01	MSTP9	macrophage stimulating, pseudogene 9	chr1p36.13	213380_x_at	NR_002729																				
6.55	6.03	0.52	1.20E-02	2.13E-01	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	chr7q31.1-q31.33	218219_s_at	NM_018697																				
6.94	5.71	1.23	1.20E-02	2.13E-01	LOC400043	hypothetical gene supported by BC009385	chr12q13.13	226582_at	---																				
8.71	7.97	0.74	1.20E-02	2.13E-01	LRRC47	leucine rich repeat containing 47	chr1p36.32	212904_at	NM_020710																				
6.51	5.44	1.07	1.20E-02	2.13E-01	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	chr1q42-q43	202834_at	NM_000029																				
5.36	4.71	0.65	1.20E-02	2.13E-01	AKIRIN1	akirin 1	chr1p34.3	222459_at	NM_024595																				
4.73	2.52	2.21	1.20E-02	2.14E-01	RBBP6	retinoblastoma binding protein 6	chr16p12.2	1552329_at	NM_006910 /// NM_018703 /// NM_032626																				
8.45	7.09	1.36	1.20E-02	2.14E-01	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	chr19q13.1	227006_at	NM_033256																				
10.68	10.36	0.32	1.21E-02	2.14E-01	HINT1	histidine triad nucleotide binding protein 1	chr5q31.2	1555961_a_at	NM_005340																				
5.67	5.06	0.61	1.21E-02	2.14E-01	ZNF585A	zinc finger protein 585A	chr19q13.12	227674_at	NM_152655 /// NM_199126																				

9.66	9.23	0.43	1.21E-02	2.14E-01	CIRBP	cold inducible RNA binding protein	chr19p13.3	200811_at	NM_001280 /// NR_023312 /// NR_023313																				
8.23	7.60	0.63	1.21E-02	2.14E-01	MRPS26	mitochondrial ribosomal protein S26	chr20p13	225196_s_at	NM_030811																				
2.56	2.24	0.32	1.21E-02	2.14E-01	SRCAP	Snf2-related CREBBP activator protein	chr16p11.2	215053_at	NM_006662																				
3.79	3.15	0.64	1.21E-02	2.14E-01	ST7OT1	ST7 overlapping transcript 1 (antisense non-coding RNA)	chr7q31.1-q31.2	1555912_at	NR_002330																				
6.26	5.78	0.48	1.21E-02	2.14E-01	GMPPA	GDP-mannose pyrophosphorylase A	chr2q35	218070_s_at	NM_013335 /// NM_205847																				
5.59	4.42	1.16	1.21E-02	2.14E-01	CHFR	checkpoint with forkhead and ring finger domains	chr12q24.33	218803_at	NM_018223																				
7.44	6.81	0.64	1.21E-02	2.14E-01	ABHD12	abhydrolase domain containing 12	chr20p11.21	228123_s_at	NM_001042472 /// NM_015600																				
5.63	5.00	0.63	1.21E-02	2.14E-01	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	chr11q23.3	225231_at	NM_005188																				
5.06	3.72	1.35	1.21E-02	2.14E-01	---	---	---	1563357_at	---																				
4.04	3.57	0.47	1.22E-02	2.15E-01	VTI1A	Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	chr10q25.2	242356_at	NM_145206																				
7.36	6.76	0.59	1.22E-02	2.15E-01	COG1	component of oligomeric golgi complex 1	chr17q25.1	227784_s_at	NM_018714																				
9.44	9.02	0.42	1.23E-02	2.16E-01	PGM1	phosphoglucomutase 1	chr1p31	201968_s_at	NM_002633																				
6.21	5.39	0.81	1.23E-02	2.16E-01	LZTS2	leucine zipper, putative tumor suppressor 2	chr10q24	232129_s_at	NM_032429																				
6.24	5.38	0.87	1.23E-02	2.16E-01	UBR1	ubiquitin protein ligase E3 component n-recognin 1	chr15q13	226921_at	NM_174916																				
7.52	5.92	1.60	1.23E-02	2.16E-01	---	---	---	238697_at	---																				
3.88	2.47	1.42	1.23E-02	2.16E-01	CSAD	cysteine sulfinic acid decarboxylase	chr12q13.11-q14.3	221139_s_at	NM_015989																				
5.49	4.59	0.90	1.23E-02	2.16E-01	---	---	---	226886_at	---																				
4.30	3.80	0.51	1.23E-02	2.16E-01	DNM2	dynamin 2	chr19p13.2	1555895_at	NM_001005360 /// NM_001005361 /// NM_001005362 /// NM_004945																				
8.87	8.40	0.47	1.23E-02	2.16E-01	C14orf156	chromosome 14 open reading frame 156	chr14q24.3	221434_s_at	NM_031210																				
5.46	3.66	1.80	1.23E-02	2.16E-01	EDNRA	endothelin receptor type A	chr4q31.23	216235_s_at	NM_001957																				
4.75	3.65	1.11	1.24E-02	2.16E-01	---	---	---	240075_at	---																				
4.39	3.71	0.68	1.24E-02	2.16E-01	FLJ20433	hypothetical protein FLJ20433	chr9q34.3	241363_at	NM_017820																				
6.30	5.73	0.57	1.24E-02	2.16E-01	ANKLE2	ankyrin repeat and LEM domain containing 2	chr12q24.33	212201_at	NM_015114																				
6.17	5.54	0.63	1.24E-02	2.16E-01	EDEM1	ER degradation enhancer, mannosidase alpha-like 1	chr3p26.2	203279_at	NM_014674																				
6.98	6.56	0.42	1.24E-02	2.16E-01	POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	chr16p13.3	218866_s_at	NM_016310																				
3.84	3.02	0.81	1.24E-02	2.16E-01	MGC11082	hypothetical LOC84777	chr18p11.31	223974_at	---																				
8.59	8.25	0.34	1.24E-02	2.16E-01	ANAPC5	anaphase promoting complex subunit 5	chr12q24.31	211036_x_at	NM_016237																				
9.38	8.74	0.63	1.24E-02	2.16E-01	SF3B5	splicing factor 3b, subunit 5, 10kDa	chr6q24.2	221263_s_at	NM_031287																				
6.72	5.90	0.82	1.24E-02	2.16E-01	CREBBP	CREB binding protein	chr16p13.3	202160_at	NM_001079846 /// NM_004380																				
5.74	5.17	0.57	1.24E-02	2.16E-01	POLR3D	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	chr8q21	208361_s_at	NM_001722																				
5.01	4.50	0.50	1.24E-02	2.16E-01	C22orf9	chromosome 22 open reading frame 9	chr22q13.31	227144_at	NM_001009880 /// NM_015264																				
5.26	4.61	0.65	1.24E-02	2.16E-01	GBA2	glucosidase, beta (bile acid) 2	chr9p13.3	223921_s_at	NM_020944																				
6.24	5.75	0.49	1.24E-02	2.16E-01	SAPS2	SAPS domain family, member 2	chr22q13.33	202791_s_at	NM_014678																				
5.75	4.16	1.59	1.25E-02	2.17E-01	KCNK1	potassium channel, subfamily K, member 1	chr1q42-q43	204679_at	NM_002245																				
3.69	2.82	0.87	1.25E-02	2.17E-01	---	---	---	236668_at	---																				
7.19	5.89	1.30	1.25E-02	2.17E-01	VSNL1	visinin-like 1	chr2p24.3	203797_at	NM_003385																				
6.16	5.15	1.01	1.25E-02	2.17E-01	CROP	cisplatin resistance-associated overexpressed protein	chr17q21.33	203804_s_at	NM_006107 /// NM_016424																				
8.65	8.26	0.39	1.25E-02	2.17E-01	ANAPC5	anaphase promoting complex subunit 5	chr12q24.31	200098_s_at	NM_016237																				
3.95	3.17	0.77	1.25E-02	2.17E-01	RBM33	RNA binding motif protein 33	chr7q36.3	225839_at	NM_001008408 /// NM_053043																				
3.22	2.12	1.10	1.25E-02	2.17E-01	RPL37A	ribosomal protein L37a	chr2q35	213459_at	NM_000998																				
6.67	5.63	1.04	1.26E-02	2.18E-01	FAM26F	family with sequence similarity 26, member F	chr6q22.1	229391_s_at	NM_001010919																				
5.58	4.74	0.84	1.26E-02	2.18E-01	MSTO1	misato homolog 1 (Drosophila)	chr1q22	222584_at	NM_018116																				
3.07	2.75	0.33	1.26E-02	2.18E-01	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	chr22q12.3-q13.1|22q13.1	217112_at	NM_002608 /// NM_033016																				
11.51	11.14	0.36	1.26E-02	2.18E-01	COX7C	cytochrome c oxidase subunit VIIc	chr5q14	201134_x_at	NM_001867																				

2.88	2.21	0.67	1.26E-02	2.18E-01	GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	chr22q13.31	1554670_at	NM_001001560 /// NM_001001561 /// NM_013365																				
2.45	2.15	0.31	1.26E-02	2.18E-01	---	---	---	242453_at	---																				
7.44	6.74	0.69	1.26E-02	2.18E-01	CHMP4A /// MDP-1	chromatin modifying protein 4A /// magnesium-dependent phosphatase 1	chr14q12	228764_s_at	NM_014169 /// NM_138476																				
5.68	5.17	0.52	1.26E-02	2.18E-01	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	chr2q11.2	204526_s_at	NM_001102426																				
5.70	5.14	0.56	1.27E-02	2.19E-01	RPL32P3	ribosomal protein L32 pseudogene 3	chr3q21.3	235314_at	NR_003111																				
5.41	4.66	0.75	1.27E-02	2.19E-01	NFS1	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	chr20q11.22	1554321_a_at	NM_021100																				
3.33	2.51	0.82	1.27E-02	2.19E-01	MYO16	myosin XVI	chr13q33.3	1557720_s_at	NM_015011																				
6.93	6.49	0.45	1.27E-02	2.19E-01	RNF113A	ring finger protein 113A	chrXq25-q26	209565_at	NM_006978																				
6.63	5.87	0.75	1.27E-02	2.19E-01	IFFO	intermediate filament family orphan	chr12p13.3	209721_s_at	NM_001039670 /// NM_080730 /// NM_080731																				
11.97	11.63	0.34	1.27E-02	2.19E-01	EEF2	eukaryotic translation elongation factor 2	chr19pter-q12	200094_s_at	NM_001961																				
4.98	4.53	0.46	1.28E-02	2.19E-01	ZNF133	zinc finger protein 133	chr20p11.23-p11.22	37254_at	NM_001083330 /// NM_003434																				
7.99	7.19	0.80	1.28E-02	2.19E-01	ZBED1	zinc finger, BED-type containing 1	chrXp22.33;Yp11	203043_at	NM_004729																				
7.20	6.55	0.65	1.28E-02	2.19E-01	TTC38	tetratricopeptide repeat domain 38	chr22q13	218272_at	NM_017931																				
5.79	4.86	0.93	1.28E-02	2.19E-01	---	---	---	239437_at	---																				
6.82	6.00	0.82	1.28E-02	2.19E-01	CXXC1	CXXC finger 1 (PHD domain)	chr18q12	218058_at	NM_001101654 /// NM_014593																				
7.01	6.35	0.66	1.28E-02	2.20E-01	BCS1L	BCS1-like (yeast)	chr2q33	207618_s_at	NM_001079866 /// NM_004328																				
6.01	5.13	0.87	1.28E-02	2.20E-01	C5orf13	chromosome 5 open reading frame 13	chr5q22.1	201309_x_at	NM_004772																				
7.81	7.34	0.47	1.28E-02	2.20E-01	TH1L	TH1-like (Drosophila)	chr20q13	225261_x_at	NM_198976																				
3.57	2.90	0.67	1.28E-02	2.20E-01	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	chr7q21.1	211442_x_at	NM_022820 /// NM_057095 /// NM_057096																				
3.53	2.31	1.21	1.28E-02	2.20E-01	C6orf141	chromosome 6 open reading frame 141	chr6p12.3	1552575_a_at	XR_040195 /// XR_040196 /// XR_040197 /// XR_040198 /// XR_040199 /// XR_040200																				
6.71	6.08	0.64	1.28E-02	2.20E-01	UBAC2	UBA domain containing 2	chr13q32.3	224298_s_at	NM_177967																				
4.88	4.07	0.82	1.29E-02	2.20E-01	IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble	chr2q33.3	242956_at	NM_005896																				
4.28	3.52	0.76	1.29E-02	2.20E-01	KIAA0495	KIAA0495	chr1p36.32	1569502_s_at	NM_207306																				
7.40	6.59	0.81	1.29E-02	2.20E-01	TRIM8	tripartite motif-containing 8	chr10q24.3	223132_s_at	NM_030912																				
4.56	3.96	0.59	1.29E-02	2.20E-01	---	---	---	236097_at	---																				
4.69	4.20	0.49	1.29E-02	2.21E-01	CENPN	centromere protein N	chr16q23.2	228559_at	NM_001100624 /// NM_001100625 /// NM_018455																				
6.33	5.08	1.24	1.29E-02	2.21E-01	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	chr11p15	209824_s_at	NM_001030272 /// NM_001030273 /// NM_001178																				
3.75	3.17	0.58	1.30E-02	2.21E-01	C13orf23	chromosome 13 open reading frame 23	chr13q13.3	218420_s_at	NM_025138 /// NM_170719																				
6.13	5.36	0.77	1.30E-02	2.21E-01	LOC339483	hypothetical LOC339483	chr1p35.1	228593_at	XR_040224 /// XR_040225 /// XR_040226																				
4.28	3.53	0.74	1.30E-02	2.22E-01	IRAK2	interleukin-1 receptor-associated kinase 2	chr3p25.3	231779_at	NM_001570																				

6.69	5.15	1.53	1.30E-02	2.22E-01	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	chr7q21.3-q22	202628_s_at	NM_000602																					
12.24	11.90	0.34	1.30E-02	2.22E-01	RPL28	ribosomal protein L28	chr19q13.4	200003_s_at	NM_000991																					
8.06	7.44	0.62	1.30E-02	2.22E-01	DGUOK	deoxyguanosine kinase	chr2p13	209549_s_at	NM_080916 /// NM_080918																					
4.03	3.26	0.76	1.31E-02	2.22E-01	---	---	---	242609_x_at	---																					
4.98	4.41	0.56	1.31E-02	2.22E-01	STAT5B	signal transducer and activator of transcription 5B	chr17q11.2	1555088_x_at	NM_012448																					
4.77	4.14	0.63	1.31E-02	2.22E-01	ZNF236	zinc finger protein 236	chr18q22-q23	47571_at	NM_007345																					
2.63	2.10	0.53	1.31E-02	2.22E-01	MKX	mohawk homeobox	chr10p12.1	241902_at	NM_173576																					
7.62	6.94	0.68	1.31E-02	2.22E-01	PNKP	polynucleotide kinase 3'-phosphatase	chr19q13.3-q13.4	218961_s_at	NM_007254																					
5.39	4.70	0.69	1.31E-02	2.22E-01	FHL3	four and a half LIM domains 3	chr1p34	218818_at	NM_004468																					
7.77	6.97	0.79	1.31E-02	2.22E-01	ZNRD1	zinc ribbon domain containing 1	chr6p21.3	228009_x_at	NM_014596 /// NM_170783																					
9.31	8.69	0.62	1.31E-02	2.23E-01	COMT	catechol-O-methyltransferase	chr22q11.21-q11.23|22q11.21	208817_at	NM_000754 /// NM_007310																					
6.73	6.16	0.57	1.32E-02	2.23E-01	MAGEF1	melanoma antigen family F, 1	chr3q13	218176_at	NM_022149																					
7.17	6.56	0.61	1.32E-02	2.23E-01	---	---	---	226347_at	---																					
7.26	6.72	0.54	1.32E-02	2.23E-01	LOC440957	similar to CG32736-PA	chr3p21.1	229826_at	NM_001124767 /// XM_001716881 /// XM_001717970 /// XM_001718706																					
8.96	8.40	0.57	1.32E-02	2.23E-01	HDGF	hepatoma-derived growth factor (high-mobility group protein 1-like)	chr1q21-q23	200896_x_at	NM_001126050 /// NM_001126051 /// NM_004494																					
3.80	2.47	1.32	1.32E-02	2.23E-01	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	chr11q22.3	235610_at	NM_138775																					
10.03	9.63	0.40	1.32E-02	2.23E-01	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	chr1q21	202243_s_at	NM_002796																					
5.64	5.04	0.60	1.32E-02	2.23E-01	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	chr6p22.2-p22.3	203608_at	NM_001080 /// NM_170740																					
6.13	5.24	0.89	1.32E-02	2.23E-01	KRT10	keratin 10	chr17q21	213287_s_at	NM_000421																					
4.29	3.36	0.94	1.33E-02	2.23E-01	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B	chr12q23.1	227440_at	NM_020140 /// NM_152788 /// NM_181670																					
6.86	6.17	0.69	1.33E-02	2.23E-01	41341	membrane-associated ring finger (C3HC4) 8	chr10q11.21	221824_s_at	NM_001002265 /// NM_001002266 /// NM_145021																					
3.08	2.59	0.48	1.33E-02	2.23E-01	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	chr3p22.1	239013_at	NM_004206 /// NM_032970																					
6.30	5.66	0.64	1.33E-02	2.23E-01	C10orf2	chromosome 10 open reading frame 2	chr10q23.3-q24.3	218590_at	NM_021830																					
3.88	3.30	0.58	1.33E-02	2.23E-01	---	---	---	224106_at	---																					
10.88	10.54	0.34	1.33E-02	2.23E-01	CIRBP	cold inducible RNA binding protein	chr19p13.3	200810_s_at	NM_001280 /// NR_023312 /// NR_023313																					
7.74	6.58	1.16	1.33E-02	2.23E-01	LOC100132430	hypothetical LOC100132430	chr14q22.1	214182_at	XR_038825 /// XR_038888 /// XR_039337																					
5.14	4.40	0.74	1.34E-02	2.24E-01	ATRNL1	attractin-like 1	chr10q26	1569796_s_at	NM_207303																					
8.15	6.81	1.33	1.34E-02	2.24E-01	TncRNA	trophoblast-derived noncoding RNA	chr11q13.1	224565_at	NR_002802																					
5.19	4.06	1.13	1.34E-02	2.24E-01	RAB40C	RAB40C, member RAS oncogene family	chr16p13.3	227698_s_at	NM_021168																					

4.78	3.61	1.17	1.34E-02	2.24E-01	C1orf79	chromosome 1 open reading frame 79	chr1p35.3	228990_at	XM_378848 /// XM_930434 /// XM_934809 /// XM_934810 /// XM_934811 /// XM_940389 /// XM_944565 /// XM_944566 /// XM_944567 /// XM_944569																				
6.14	5.47	0.67	1.34E-02	2.24E-01	ZDHHC5	zinc finger, DHHC-type containing 5	chr11q12.1	224868_at	NM_015457																				
8.86	7.95	0.91	1.34E-02	2.24E-01	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	chr12q23-q24.1	209186_at	NM_001681 /// NM_170665																				
8.73	7.67	1.07	1.34E-02	2.24E-01	HSPA1A /// HSPA1B	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	chr6p21.3	202581_at	NM_005345 /// NM_005346																				
5.88	5.22	0.66	1.34E-02	2.24E-01	---	---	---	221995_s_at	---																				
3.49	2.65	0.84	1.35E-02	2.24E-01	LOC727916	hypothetical protein LOC727916	chr6q12	1559322_at	XR_039953 /// XR_039954 /// XR_039955																				
6.01	5.40	0.61	1.35E-02	2.25E-01	MTERFD2	MTERF domain containing 2	chr2q37.3	1557965_at	NM_182501																				
5.86	4.74	1.12	1.35E-02	2.25E-01	AGRP	agouti related protein homolog (mouse)	chr16q22	207193_at	NM_001138 /// NM_007316																				
6.37	5.98	0.40	1.35E-02	2.25E-01	CDC2L1 /// CDC2L2	cell division cycle 2-like 1 (PITSLRE proteins) /// cell division cycle 2-like 2 (PITSLRE proteins)	chr1p36.33	211289_x_at	NM_024011 /// NM_033486 /// NM_033487 /// NM_033488 /// NM_033489 /// NM_033492 /// NM_033493 /// NM_033529 /// XM_001713735 /// XM_001713748 /// XM_001715985 /// XM_001716018 /// XM_001716037 /// XM_001716055																		
6.86	6.09	0.77	1.35E-02	2.25E-01	BAT5	HLA-B associated transcript 5	chr6p21.3	224756_s_at	NM_021160																				
3.80	3.27	0.53	1.35E-02	2.25E-01	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	chr18q12	219938_s_at	NM_024430																				
8.67	7.94	0.72	1.35E-02	2.25E-01	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	chr4q13-q21	201993_x_at	NM_031372 /// NR_003249																				
6.59	5.98	0.62	1.35E-02	2.25E-01	FAM89B	family with sequence similarity 89, member B	chr11q23	212484_at	NM_001098784 /// NM_001098785 /// NM_152832																				
7.50	6.55	0.95	1.36E-02	2.25E-01	NUDT16L1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	chr16p13.3	224477_s_at	NM_032349																				

5.97	5.44	0.53	1.36E-02	2.25E-01	CWF19L1	CWF19-like 1, cell cycle control (S. pombe)	chr10q24.2-q24.31	233568_x_at	NM_018294
8.12	7.66	0.46	1.36E-02	2.25E-01	UBE2Q1	ubiquitin-conjugating enzyme E2Q family member 1	chr1q21.3	217978_s_at	NM_017582
5.18	4.74	0.43	1.36E-02	2.25E-01	---	---	---	217313_at	---
6.59	6.03	0.56	1.36E-02	2.25E-01	POGK	pogo transposable element with KRAB domain	chr1q24.1	218229_s_at	NM_017542
6.86	6.17	0.69	1.36E-02	2.25E-01	PHF13	PHD finger protein 13	chr1p36.31	225005_at	NM_153812
5.79	5.18	0.61	1.36E-02	2.25E-01	THOC6	THO complex 6 homolog (Drosophila)	chr16p13.3	218848_at	NM_024339
10.98	10.46	0.52	1.36E-02	2.25E-01	OSAP	ovary-specific acidic protein	chr4q31.1	223734_at	NM_032623
8.25	7.64	0.61	1.36E-02	2.25E-01	CTSF	cathepsin F	chr11q13	203657_s_at	NM_003793
7.97	7.59	0.37	1.36E-02	2.25E-01	RPL26L1	ribosomal protein L26-like 1	chr5q35.2	218830_at	NM_016093
5.51	4.73	0.78	1.36E-02	2.25E-01	SLCO3A1	solute carrier organic anion transporter family, member 3A1	chr15q26	210542_s_at	NM_013272
6.36	5.46	0.90	1.36E-02	2.25E-01	RBM6	RNA binding motif protein 6	chr3p21.3	201967_at	NM_005777
6.82	6.29	0.54	1.36E-02	2.25E-01	PDRG1	p53 and DNA damage regulated 1	chr20q11.21	225075_at	NM_030815
8.47	7.74	0.72	1.36E-02	2.25E-01	WDR45	WD repeat domain 45	chrXp11.23	209216_at	NM_001029896 /// NM_007075
8.82	7.98	0.83	1.36E-02	2.25E-01	POM121 /// POM121C	POM121 membrane glycoprotein (rat) /// POM121 membrane glycoprotein C	chr7q11.2 /// chr7q11.23	213360_s_at	NM_001099415 /// NM_172020
9.64	9.14	0.50	1.37E-02	2.25E-01	C22orf32	chromosome 22 open reading frame 32	chr22q13.2	225794_s_at	NM_033318
7.14	6.20	0.95	1.37E-02	2.26E-01	TOB2	transducer of ERBB2, 2	chr22q13.2-q13.31	221496_s_at	NM_016272
2.64	2.31	0.33	1.38E-02	2.26E-01	BRP44L	Brain protein 44-like	chr6q27	240362_at	NM_016098
7.65	7.07	0.58	1.38E-02	2.26E-01	PDCD7	programmed cell death 7	chr15q22.31	231809_x_at	NM_005707
5.46	3.87	1.59	1.38E-02	2.26E-01	ANO4	anoctamin 4	chr12q23.1-q23.2	236420_s_at	NM_178826
5.69	5.09	0.60	1.38E-02	2.26E-01	C6orf89	chromosome 6 open reading frame 89	chr6p21.2	224987_at	NM_152734
5.14	4.18	0.95	1.38E-02	2.26E-01	---	---	---	236358_at	---
6.56	5.89	0.67	1.38E-02	2.26E-01	STX2	syntaxin 2	chr12q24.33	213434_at	NM_001980 /// NM_194356
8.04	7.19	0.84	1.38E-02	2.26E-01	CDC42SE1	CDC42 small effector 1	chr1q21.2	229120_s_at	NM_001038707 /// NM_020239
5.07	4.64	0.43	1.38E-02	2.26E-01	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	chr8p21.3	207000_s_at	NM_005605
5.77	3.11	2.66	1.38E-02	2.26E-01	CPLX3 /// LMAN1L	complexin 3 /// lectin, mannose-binding, 1 like	chr15q24.1	222927_s_at	NM_001030005 /// NM_021819
3.61	2.35	1.26	1.38E-02	2.26E-01	---	---	---	1563629_a_at	---
6.42	5.77	0.65	1.39E-02	2.26E-01	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	chr7q22.1	214526_x_at	NR_003613
8.21	7.39	0.82	1.39E-02	2.26E-01	C7orf55	chromosome 7 open reading frame 55	chr7q34	226780_s_at	NM_197964
11.35	10.95	0.40	1.39E-02	2.26E-01	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	chrXp22.32 and Yp11.3	212085_at	NM_001636
7.45	6.79	0.66	1.39E-02	2.26E-01	CKLF	chemokine-like factor	chr16q21	223451_s_at	NM_001040138 /// NM_016326 /// NM_016951 /// NM_181640 /// NM_181641
3.47	2.58	0.89	1.39E-02	2.26E-01	FAM117B	family with sequence similarity 117, member B	chr2q33.1	1553220_at	NM_173511
8.95	8.54	0.41	1.39E-02	2.26E-01	MRPL36	mitochondrial ribosomal protein L36	chr5p15.3	224331_s_at	NM_032479
6.02	5.18	0.84	1.39E-02	2.26E-01	TARBP2	TAR (HIV-1) RNA binding protein 2	chr12q12-q13	203677_s_at	NM_004178 /// NM_134323 /// NM_134324
2.52	2.17	0.36	1.39E-02	2.26E-01	---	---	---	239942_at	---
6.49	5.17	1.33	1.39E-02	2.26E-01	ATPIF1	ATPase inhibitory factor 1	---	223339_at	NM_016311 /// NM_178190 /// NM_178191
8.59	8.02	0.57	1.39E-02	2.26E-01	PIGY	phosphatidylinositol glycan anchor biosynthesis, class Y	chr4q22.1	224660_at	NM_001042616 /// NM_032906
5.03	4.50	0.53	1.39E-02	2.26E-01	IDS	iduronate 2-sulfatase	chrXq28	212223_at	NM_000202 /// NM_006123

7.15	5.15	2.00	1.39E-02	2.26E-01	LOC389895	hypothetical LOC389895	chrXq27.1	240312_at	XM_001721524 /// XM_372255 /// XM_936709
3.98	3.26	0.72	1.39E-02	2.26E-01	C12orf32	chromosome 12 open reading frame 32	chr12p13.33	225836_s_at	NM_031465
4.26	3.61	0.65	1.39E-02	2.26E-01	KRT7	keratin 7	chr12q12-q13	209016_s_at	NM_005556
6.71	6.39	0.31	1.39E-02	2.26E-01	DIAPH1	diaphanous homolog 1 (Drosophila)	chr5q31	209190_s_at	NM_001079812 /// NM_005219
4.05	3.69	0.36	1.39E-02	2.26E-01	---	---	---	221595_at	---
6.12	5.04	1.08	1.39E-02	2.26E-01	DAZAP1	DAZ associated protein 1	chr19p13.3	218443_s_at	NM_018959 /// NM_170711
7.19	6.61	0.58	1.39E-02	2.26E-01	EWSR1	Ewing sarcoma breakpoint region 1	chr22q12.2	210011_s_at	NM_005243 /// NM_013986
5.84	5.41	0.43	1.39E-02	2.26E-01	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)	chr3q21	220744_s_at	NM_018262 /// NM_052985 /// NM_052989 /// NM_052990
7.21	6.26	0.94	1.39E-02	2.26E-01	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	chr19p13.3	40837_at	NM_003260
9.30	8.74	0.56	1.40E-02	2.26E-01	UROD	uroporphyrinogen decarboxylase	chr1p34	208970_s_at	NM_000374
4.37	3.19	1.18	1.40E-02	2.26E-01	---	---	---	230787_at	---
6.67	6.19	0.48	1.40E-02	2.26E-01	BRD9	bromodomain containing 9	chr5p15.33	220155_s_at	NM_001009877 /// NM_023924
5.17	4.60	0.58	1.40E-02	2.26E-01	SLC2A11	solute carrier family 2 (facilitated glucose transporter), member 11	chr22q11.2	1558540_s_at	NM_001024938 /// NM_001024939 /// NM_030807
5.89	5.22	0.67	1.40E-02	2.26E-01	PARP12	poly (ADP-ribose) polymerase family, member 12	chr7q34	218543_s_at	NM_022750
7.38	6.55	0.83	1.40E-02	2.26E-01	MNT	MAX binding protein	chr17p13.3	204206_at	NM_020310
7.35	6.80	0.54	1.40E-02	2.26E-01	KEAP1	kelch-like ECH-associated protein 1	chr19p13.2	202417_at	NM_012289 /// NM_203500
7.74	7.13	0.61	1.40E-02	2.26E-01	JTV1	JTV1 gene	chr7p22	202138_x_at	NM_006303
6.59	6.10	0.50	1.40E-02	2.26E-01	KIF13B	kinesin family member 13B	chr8p21.1	202962_at	NM_015254
6.03	5.68	0.35	1.40E-02	2.26E-01	C3orf37	chromosome 3 open reading frame 37	chr3q21.3	201678_s_at	NM_001006109 /// NM_020187
4.35	3.64	0.71	1.40E-02	2.26E-01	MICALL1	MICAL-like 1	chr22q13.1-q13.2	55081_at	NM_033386
8.52	7.91	0.61	1.41E-02	2.26E-01	TRIM28	tripartite motif-containing 28	chr19q13.4	200990_at	NM_005762
4.34	3.72	0.63	1.41E-02	2.26E-01	DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	chr12q24.31	231843_at	NM_020936
5.28	4.61	0.67	1.41E-02	2.26E-01	MIB2	mindbomb homolog 2 (Drosophila)	chr1p36.33	228261_at	NM_080875
2.90	2.51	0.39	1.41E-02	2.27E-01	---	---	---	233149_at	---
6.15	5.53	0.62	1.41E-02	2.27E-01	HOMER3	homer homolog 3 (Drosophila)	chr19p13.11	204647_at	NM_004838
3.46	2.92	0.54	1.41E-02	2.27E-01	ANKRD6	ankyrin repeat domain 6	chr6q14.2-q16.1	204671_s_at	NM_014942
4.81	4.06	0.75	1.41E-02	2.27E-01	BIVM	basic, immunoglobulin-like variable motif containing	chr13q32-q33.1	222761_at	NM_017693
5.05	4.32	0.73	1.42E-02	2.28E-01	VWCE	von Willebrand factor C and EGF domains	chr11q12.2	242957_at	NM_152718
5.03	4.36	0.67	1.42E-02	2.28E-01	APOBEC3F /// APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F /// apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	chr22q13.1 /// chr22q13.1-q13.2	214995_s_at	NM_001006666 /// NM_021822 /// NM_145298
8.72	7.95	0.77	1.42E-02	2.28E-01	TMEM14C	transmembrane protein 14C	chr6p24.2	223106_at	NM_016462
8.53	7.98	0.55	1.43E-02	2.28E-01	HBXIP	hepatitis B virus x interacting protein	chr1p13.3	202299_s_at	NM_006402
7.63	6.63	1.00	1.43E-02	2.28E-01	TMEM128	transmembrane protein 128	chr4p16.2	225462_at	NM_032927
6.64	5.37	1.27	1.43E-02	2.28E-01	TDG	thymine-DNA glycosylase	chr12q24.1	203743_s_at	NM_003211
3.84	3.17	0.67	1.43E-02	2.28E-01	LOC441453 /// OR7E18P /// OR7E35P /// OR7E37P /// OR7E47P	similar to olfactory receptor, family 7, subfamily A, member 17 /// olfactory receptor, family 7, subfamily E, member 18 pseudogene /// olfactory receptor, family 7, subfamily E, member 35 pseudogene /// olfactory receptor, family 7, subfamily E, member 37 pseudogene /// olfactory receptor, family 7, subfamily E, member 47 pseudogene	chr11p15.1 /// chr12q13.13 /// chr13q14.11 /// chr19p13.2 /// chr4p16.1	216698_x_at	NR_002163 /// XR_041341 /// XR_041342 /// XR_041343 /// XR_042149
4.81	4.07	0.75	1.43E-02	2.28E-01	STK11IP	serine/threonine kinase 11 interacting protein	chr2q35	225713_at	NM_052902
6.32	5.83	0.49	1.43E-02	2.28E-01	TMEM43	transmembrane protein 43	chr3p25.1	222418_s_at	NM_024334
6.48	6.05	0.43	1.43E-02	2.28E-01	MED28	mediator complex subunit 28	chr4p16	218438_s_at	NM_025205
7.77	6.48	1.29	1.43E-02	2.28E-01	---	---	---	231274_s_at	---

3.04	2.44	0.59	1.43E-02	2.28E-01	EPPK1	epiplakin 1	chr8q24.3	208156_x_at	NM_031308
7.49	6.88	0.61	1.43E-02	2.28E-01	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	chr2p11.2	204929_s_at	NM_006634
8.85	8.35	0.50	1.44E-02	2.28E-01	CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11p11	221743_at	NM_001025596 /// NM_006560 /// NM_198700
4.67	4.32	0.35	1.44E-02	2.29E-01	SAMD11	sterile alpha motif domain containing 11	chr1p36.33	1560477_a_at	NM_152486
6.73	5.93	0.80	1.44E-02	2.29E-01	OCRL	oculocerebrorenal syndrome of Lowe	chrXq25-q26.1	203446_s_at	NM_000276 /// NM_001587
8.27	4.82	3.46	1.44E-02	2.29E-01	NR4A2	nuclear receptor subfamily 4, group A, member 2	chr2q22-q23	216248_s_at	NM_006186 /// NM_173171 /// NM_173172 /// NM_173173
7.19	6.51	0.68	1.44E-02	2.29E-01	TUSC4	tumor suppressor candidate 4	chr3p21.3	203246_s_at	NM_006545
7.48	6.83	0.64	1.44E-02	2.29E-01	HOXA7	homeobox A7	chr7p15-p14	235753_at	NM_006896
6.70	6.00	0.70	1.44E-02	2.29E-01	FAM118B	family with sequence similarity 118, member B	chr11q24.2	223386_at	NM_024556
7.40	6.85	0.54	1.45E-02	2.30E-01	ANAPC5	anaphase promoting complex subunit 5	chr12q24.31	208722_s_at	NM_016237
6.87	6.49	0.38	1.45E-02	2.30E-01	LAS1L	LAS1-like (S. cerevisiae)	chrXq12-q13	208117_s_at	NM_031206
4.41	3.35	1.07	1.45E-02	2.30E-01	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	chr14q11.2	236270_at	NM_004554
7.77	6.29	1.48	1.45E-02	2.30E-01	KIF5C	kinesin family member 5C	chr2q23.1	203130_s_at	NM_004522
8.27	7.72	0.56	1.46E-02	2.30E-01	NONO	non-POU domain containing, octamer-binding	chrXq13.1	208698_s_at	NM_007363
6.85	6.14	0.71	1.46E-02	2.30E-01	RPS17L4	ribosomal protein S17-like 4	chr6p12.3	216348_at	---
7.95	6.97	0.99	1.46E-02	2.31E-01	STK19	serine/threonine kinase 19	chr6p21.3	36019_at	NM_004197 /// NM_032454
7.39	6.54	0.85	1.47E-02	2.31E-01	CAMTA1	calmodulin binding transcription activator 1	chr1p36.31-p36.23	225692_at	NM_015215
6.13	5.43	0.70	1.47E-02	2.31E-01	WNT11	wingless-type MMTV integration site family, member 11	chr11q13.5	206737_at	NM_004626
7.65	7.17	0.48	1.47E-02	2.31E-01	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	chr3q26.33	225359_at	NM_145261
9.86	9.36	0.50	1.47E-02	2.31E-01	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	chr2q31.1	207507_s_at	NM_001002258 /// NM_001689
7.31	6.47	0.83	1.47E-02	2.31E-01	ILVBL	ilvB (bacterial acetolactate synthase)-like	chr19p13.1	202993_at	NM_006844
3.89	3.20	0.70	1.47E-02	2.31E-01	---	---	---	240454_at	---
3.50	2.92	0.58	1.47E-02	2.31E-01	PAQR6	progestin and adipoQ receptor family member VI	chr1q22	219236_at	NM_024897 /// NM_198406
4.31	3.62	0.68	1.48E-02	2.31E-01	LOC652993 /// PHLDA1	hypothetical LOC652993 /// pleckstrin homology-like domain, family A, member 1	chr12q15 /// chr12q21	217998_at	NM_007350 /// XR_018000 /// XR_042076
6.38	5.79	0.59	1.48E-02	2.31E-01	DNPEP	aspartyl aminopeptidase	chr2q35	201937_s_at	NM_012100
5.74	5.08	0.66	1.48E-02	2.31E-01	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	chr22q13.1	210647_x_at	NM_001004426 /// NM_003560
4.95	4.04	0.91	1.48E-02	2.31E-01	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	chr15q22	212770_at	NM_001105192 /// NM_005078 /// NM_020908
4.37	3.76	0.60	1.48E-02	2.31E-01	FGD6	FYVE, RhoGEF and PH domain containing 6	chr12q22	226799_at	NM_018351
4.34	3.86	0.47	1.48E-02	2.31E-01	LOC401320	Hypothetical LOC401320	chr7p15.1	233732_at	XM_379482 /// XM_380098 /// XM_938539
4.57	3.97	0.60	1.48E-02	2.31E-01	ZMYM3	zinc finger, MYM-type 3	chrXq13.1	1554172_a_at	NM_005096 /// NM_201599
6.20	5.15	1.05	1.48E-02	2.31E-01	CCNG2	cyclin G2	chr4q21.1	202770_s_at	NM_004354
5.39	4.38	1.01	1.48E-02	2.31E-01	WDR90	WD repeat domain 90	chr16p13.3	227894_at	NM_145294
3.28	2.89	0.39	1.48E-02	2.31E-01	---	---	---	236908_at	---
5.10	3.80	1.31	1.48E-02	2.31E-01	NEIL1	nei endonuclease VIII-like 1 (E. coli)	chr15q24.2	219396_s_at	NM_024608
7.03	6.59	0.44	1.49E-02	2.32E-01	SEPHS1	selenophosphate synthetase 1	chr10p14	208941_s_at	NM_012247
7.56	7.19	0.36	1.49E-02	2.32E-01	EIF3B	eukaryotic translation initiation factor 3, subunit B	chr7p22.2	211501_s_at	NM_001037283 /// NM_003751
3.94	3.46	0.48	1.49E-02	2.32E-01	C6orf153	Chromosome 6 open reading frame 153	chr6p21.1	235223_at	NM_033112
7.80	6.99	0.81	1.49E-02	2.32E-01	BSDC1	BSD domain containing 1	chr1p35.1	218004_at	NM_018045

6.30	5.61	0.69	1.49E-02	2.32E-01	SON	SON DNA binding protein	chr21q22.1-q22.2|21q22.11	213538_at	NM_032195 /// NM_138927																				
7.69	7.20	0.49	1.50E-02	2.32E-01	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	chr19p13.3	202355_s_at	NM_002096																				
5.36	4.39	0.97	1.50E-02	2.32E-01	ACPL2	acid phosphatase-like 2	chr3q23	226925_at	NM_001037172 /// NM_152282																				
3.89	3.37	0.52	1.51E-02	2.34E-01	---	---	---	217682_at	---																				
6.48	5.75	0.73	1.51E-02	2.34E-01	DUSP14	dual specificity phosphatase 14	chr17q12	203367_at	NM_007026																				
7.29	6.89	0.39	1.51E-02	2.34E-01	SLC15A4	solute carrier family 15, member 4	chr12q24.32	225043_at	NM_145648																				
3.92	3.31	0.61	1.51E-02	2.34E-01	SLC2A11	solute carrier family 2 (facilitated glucose transporter), member 11	chr22q11.2	232167_at	NM_001024938 /// NM_001024939 /// NM_030807																				
4.86	4.43	0.43	1.51E-02	2.34E-01	HPN	hepsin (transmembrane protease, serine 1)	chr19q11-q13.2	204934_s_at	NM_002151 /// NM_182983																				
7.37	6.64	0.74	1.51E-02	2.34E-01	AKT2	v-akt murine thymoma viral oncogene homolog 2	chr19q13.1-q13.2	225471_s_at	NM_001626																				
7.59	6.78	0.80	1.51E-02	2.34E-01	FAM125A	family with sequence similarity 125, member A	chr19p13.11	227864_s_at	NM_138401																				
3.02	2.38	0.64	1.52E-02	2.34E-01	TEX14	testis expressed 14	chr17q22	221035_s_at	NM_031272 /// NM_198393																				
4.03	3.21	0.82	1.52E-02	2.34E-01	SLC44A4	solute carrier family 44, member 4	chr6p21.3	1555203_s_at	NM_025257																				
8.09	7.55	0.54	1.53E-02	2.35E-01	IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	chr21q22.11	201642_at	NM_005534																				
6.81	6.13	0.68	1.53E-02	2.35E-01	ATG4B /// LOC727737	ATG4 autophagy related 4 homolog B (S. cerevisiae) /// similar to APG4 autophagy 4 homolog B	chr2q37.3	212280_x_at	NM_013325 /// NM_178326 /// XM_001126076 /// XM_001126088																				
5.45	4.80	0.65	1.53E-02	2.35E-01	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	chr20q11	238549_at	NM_001032999 /// NM_001039709 /// NM_005093																				
7.17	6.42	0.75	1.53E-02	2.35E-01	ZNRD1	zinc ribbon domain containing 1	chr6p21.3	223639_s_at	NM_014596 /// NM_170783																				
6.00	5.28	0.72	1.53E-02	2.35E-01	EEF2K	eukaryotic elongation factor-2 kinase	chr16p12.1	225546_at	NM_013302																				
3.67	3.05	0.62	1.53E-02	2.35E-01	PHLDA2	pleckstrin homology-like domain, family A, member 2	chr11p15.5	209803_s_at	NM_003311																				
2.96	2.45	0.51	1.53E-02	2.35E-01	NUDCD2	NudC domain containing 2	chr5q34	226643_s_at	NM_145266																				
5.69	5.22	0.47	1.53E-02	2.35E-01	XYLT2	xylosyltransferase II	chr17q21.3-q22	219401_at	NM_022167																				
6.39	5.81	0.58	1.54E-02	2.35E-01	HMG2L1	high-mobility group protein 2-like 1	chr22q13.1	212597_s_at	NM_001003681 /// NM_005487 /// NM_014250																				
10.75	10.35	0.40	1.54E-02	2.35E-01	COX7C	cytochrome c oxidase subunit VIIc	chr5q14	217491_x_at	NM_001867																				
9.60	8.30	1.30	1.54E-02	2.35E-01	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	chr16p12.1	203615_x_at	NM_001055 /// NM_177529 /// NM_177530 /// NM_177534 /// NM_177536																				
6.35	5.73	0.62	1.54E-02	2.35E-01	HMG20A	high-mobility group 20A	chr15q24	218152_at	NM_018200																				

4.33	3.64	0.69	1.54E-02	2.35E-01	C1orf79	chromosome 1 open reading frame 79	chr1p35.3	223774_at	XM_378848 /// XM_930434 /// XM_934809 /// XM_934810 /// XM_934811 /// XM_940389 /// XM_944565 /// XM_944566 /// XM_944567 /// XM_944569																				
6.00	5.27	0.74	1.54E-02	2.35E-01	ZFYVE27	zinc finger, FYVE domain containing 27	chr10q24.2	225218_at	NM_001002261 /// NM_001002262 /// NM_144588																				
4.28	3.55	0.72	1.54E-02	2.35E-01	WDR6	WD repeat domain 6	chr3p21.31	233573_s_at	NM_018031																				
7.26	6.51	0.76	1.54E-02	2.35E-01	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	chr3p21.31-p21.2	201419_at	NM_004656																				
5.62	4.96	0.66	1.54E-02	2.35E-01	NUPL2	nucleoporin like 2	chr7p15	204003_s_at	NM_007342																				
3.67	2.96	0.70	1.54E-02	2.35E-01	---	---	---	240174_at	---																				
5.11	4.18	0.94	1.54E-02	2.35E-01	FAM108C1	family with sequence similarity 108, member C1	chr15q25.1	225436_at	NM_021214																				
6.49	5.94	0.55	1.54E-02	2.35E-01	AKAP1	A kinase (PRKA) anchor protein 1	chr17q21-q23	201675_at	NM_003488																				
7.12	6.62	0.50	1.54E-02	2.35E-01	ASXL1	additional sex combs like 1 (Drosophila)	chr20q11.1	212234_at	NM_015338																				
5.73	4.79	0.93	1.54E-02	2.35E-01	ARHGAP9	Rho GTPase activating protein 9	chr12q14	224451_x_at	NM_001080156 /// NM_001080157 /// NM_032496																				
3.63	2.83	0.80	1.54E-02	2.35E-01	PRPSAP1	Phosphoribosyl pyrophosphate synthetase-associated protein 1	chr17q24-q25	1556715_at	NM_002766																				
5.74	4.90	0.84	1.54E-02	2.35E-01	IDUA	iduronidase, alpha-L-	chr4p16.3	205059_s_at	NM_000203																				
4.91	3.74	1.16	1.55E-02	2.35E-01	EPHA4	EPH receptor A4	chr2q36.1	229374_at	NM_004438																				
7.01	6.21	0.80	1.55E-02	2.35E-01	C1orf85	chromosome 1 open reading frame 85	chr1q22	1558693_s_at	NM_144580																				
4.40	3.51	0.89	1.55E-02	2.35E-01	BLNK	B-cell linker	chr10q23.2-q23.33	207655_s_at	NM_001114094 /// NM_013314																				
4.49	3.66	0.83	1.55E-02	2.35E-01	ZNF764	zinc finger protein 764	chr16p11.2	222120_at	NM_033410																				
5.59	4.50	1.09	1.55E-02	2.35E-01	---	---	---	227368_at	---																				
7.99	7.20	0.79	1.55E-02	2.35E-01	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	chr16p13.3	218368_s_at	NM_016639																				
7.61	7.07	0.54	1.55E-02	2.35E-01	MFF	mitochondrial fission factor	chr2q36.3	223354_x_at	NM_020194																				
7.62	7.25	0.37	1.55E-02	2.35E-01	C1orf123	chromosome 1 open reading frame 123	chr1p32.3	203197_s_at	NM_017887																				
4.92	4.15	0.77	1.55E-02	2.35E-01	C14orf181	chromosome 14 open reading frame 181	chr14q24.1	229054_at	NM_207442																				
7.90	7.27	0.63	1.55E-02	2.35E-01	PNKD	paroxysmal nonkinesigenic dyskinesia	chr2q35	225298_at	NM_001077399 /// NM_015488 /// NM_022572																				
4.71	3.81	0.90	1.55E-02	2.35E-01	CNKSR3	CNKSR family member 3	chr6q25.2	227481_at	NM_173515																				
8.00	7.36	0.64	1.55E-02	2.35E-01	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	chr17q21	208912_s_at	NM_033133																				
7.27	6.62	0.65	1.55E-02	2.35E-01	PPP4R1	protein phosphatase 4, regulatory subunit 1	chr18p11.22	201594_s_at	NM_001042388 /// NM_005134																				
5.24	4.56	0.68	1.55E-02	2.35E-01	---	---	---	213705_at	---																				
5.06	4.68	0.38	1.55E-02	2.35E-01	STX6	syntaxin 6	chr1q25.3	1552618_at	NM_005819																				
4.40	3.71	0.69	1.55E-02	2.35E-01	ZNF668	zinc finger protein 668	chr16p11.2	219047_s_at	NM_024706																				
6.41	5.79	0.61	1.55E-02	2.35E-01	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	chr4q21	211546_x_at	NM_000345 /// NM_007308																				
9.13	7.80	1.33	1.56E-02	2.35E-01	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	chr2p11.2	203217_s_at	NM_001042437 /// NM_003896																				
9.48	8.97	0.51	1.56E-02	2.35E-01	C2orf28	chromosome 2 open reading frame 28	chr2p23.3	219329_s_at	NM_016085 /// NM_080592																				
6.70	6.03	0.67	1.56E-02	2.35E-01	BRPF1	bromodomain and PHD finger containing, 1	chr3p26-p25	204481_at	NM_001003694 /// NM_004634																				
4.70	3.39	1.31	1.56E-02	2.35E-01	---	---	---	243509_at	---																				

6.58	6.13	0.45	1.56E-02	2.35E-01	CEP164	centrosomal protein 164kDa	chr11q23.3	1558953_s_at	NM_014956
7.42	6.58	0.84	1.56E-02	2.35E-01	C10orf72	chromosome 10 open reading frame 72	chr10q11.22	235471_at	NM_001031746 /// NM_144984
9.36	8.46	0.90	1.56E-02	2.36E-01	---	---	---	212812_at	---
6.10	5.66	0.45	1.56E-02	2.36E-01	NIPA2	Non imprinted in Prader-Willi/Angelman syndrome 2	chr15q11.2	212133_at	NM_001008860 /// NM_001008892 /// NM_001008894 /// NM_030922
5.54	4.84	0.70	1.57E-02	2.36E-01	ATP13A3	ATPase type 13A3	chr3q29	212297_at	NM_024524
3.92	2.79	1.13	1.57E-02	2.36E-01	SPIN3	spindlin family, member 3	chrXp11.1	1555882_at	NM_001010862
3.33	2.92	0.42	1.57E-02	2.36E-01	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	---	1553153_at	NM_152565
7.37	6.84	0.53	1.57E-02	2.36E-01	SIVA1	SIVA1, apoptosis-inducing factor	chr14q32.33	203489_at	NM_006427 /// NM_021709
7.25	6.33	0.92	1.57E-02	2.36E-01	CHIC2	cysteine-rich hydrophobic domain 2	chr4q11	219492_at	NM_012110
6.15	3.63	2.51	1.57E-02	2.36E-01	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	chr4q34-q35	211548_s_at	NM_000860
3.77	3.35	0.42	1.57E-02	2.36E-01	ENPP7	ectonucleotide pyrophosphatase/phosphodiesterase 7	chr17q25.3	238245_at	NM_178543
11.73	11.31	0.42	1.57E-02	2.36E-01	RPS19	ribosomal protein S19	chr19q13.2	202649_x_at	NM_001022
2.49	2.10	0.39	1.58E-02	2.36E-01	41530	septin 13	chr7p13	230355_at	XM_001126402 /// XM_001133108 /// XM_001717249 /// XM_001718865
6.12	5.60	0.52	1.58E-02	2.36E-01	PERLD1	per1-like domain containing 1	chr17q12	55616_at	NM_033419
7.51	6.81	0.70	1.58E-02	2.36E-01	SNRPA	small nuclear ribonucleoprotein polypeptide A	chr19q13.1	201770_at	NM_004596
5.68	4.26	1.42	1.58E-02	2.36E-01	NUSAP1	nucleolar and spindle associated protein 1	chr15q15.1	219978_s_at	NM_001129897 /// NM_016359 /// NM_018454
6.47	5.66	0.81	1.58E-02	2.36E-01	IL4R	interleukin 4 receptor	chr16p12.1-p11.2	203233_at	NM_000418 /// NM_001008699
8.37	7.86	0.50	1.58E-02	2.36E-01	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	chr3q27-qter	208625_s_at	NM_004953 /// NM_182917 /// NM_198241 /// NM_198242 /// NM_198244
3.58	3.15	0.43	1.58E-02	2.36E-01	LOC147299	Similar to hCG1996578	chr18q23	230477_at	---
4.30	3.58	0.72	1.58E-02	2.36E-01	---	---	---	242525_at	---
6.37	5.60	0.77	1.58E-02	2.36E-01	HOXA7	homeobox A7	chr7p15-p14	206847_s_at	NM_006896
3.41	2.88	0.53	1.58E-02	2.36E-01	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	chr11q12.3	213211_s_at	NM_006473
12.30	11.98	0.32	1.58E-02	2.36E-01	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	chr5q35.3	200651_at	NM_006098
2.39	2.03	0.36	1.58E-02	2.36E-01	VHL	von Hippel-Lindau tumor suppressor	chr3p26-p25	203844_at	NM_000551 /// NM_198156
2.59	2.26	0.34	1.58E-02	2.36E-01	IFI44	Interferon-induced protein 44	chr1p31.1	214059_at	NM_006417
7.33	6.53	0.80	1.59E-02	2.36E-01	C19orf66	chromosome 19 open reading frame 66	chr19p13.2	218429_s_at	NM_018381
5.06	4.66	0.40	1.59E-02	2.36E-01	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	chr3p25.3	209794_at	NM_001033117 /// NM_014850
8.82	8.34	0.48	1.59E-02	2.36E-01	ARF1	ADP-ribosylation factor 1	chr1q42	208750_s_at	NM_001024226 /// NM_001024227 /// NM_001024228 /// NM_001658
8.71	7.77	0.94	1.59E-02	2.36E-01	NDN	necdin homolog (mouse)	chr15q11.2-q12	209550_at	NM_002487
4.20	3.43	0.77	1.59E-02	2.36E-01	NPHP4	nephronophthisis 4	chr1p36.22	213471_at	NM_015102

6.86	5.59	1.26	1.59E-02	2.36E-01	FGF12	fibroblast growth factor 12	chr3q28	207501_s_at	NM_004113 /// NM_021032
4.83	4.13	0.70	1.59E-02	2.37E-01	DCUN1D2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	chr13q34	219116_s_at	NM_001014283
2.35	1.95	0.40	1.59E-02	2.37E-01	---	---	---	232397_at	---
11.99	11.68	0.31	1.60E-02	2.37E-01	TMSB4X /// TMSL3	thymosin beta 4, X-linked /// thymosin-like 3	chr4q22.1 /// chrXq21.3-q22	216438_s_at	NM_021109 /// NM_183049
8.11	7.71	0.40	1.60E-02	2.37E-01	EIF3B	eukaryotic translation initiation factor 3, subunit B	chr7p22.2	203462_x_at	NM_001037283 /// NM_003751
4.81	4.14	0.67	1.60E-02	2.37E-01	---	---	---	242733_at	---
5.44	4.96	0.47	1.60E-02	2.37E-01	MYCBP	c-myc binding protein	chr1p33-p32.2	203360_s_at	NM_012333
3.72	3.02	0.70	1.60E-02	2.37E-01	---	---	---	1555976_s_at	---
4.76	4.04	0.71	1.60E-02	2.37E-01	KIAA0841	KIAA0841	chr19q13.12	36888_at	NM_015302
7.11	6.33	0.78	1.60E-02	2.37E-01	---	---	---	228275_at	---
9.49	9.17	0.32	1.60E-02	2.37E-01	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	chr14q23.1	221952_x_at	NM_020810
3.76	2.65	1.12	1.60E-02	2.37E-01	---	---	---	237509_at	---
9.12	8.68	0.45	1.61E-02	2.37E-01	RRAGA	Ras-related GTP binding A	chr9p22.1	201628_s_at	NM_006570
7.22	6.80	0.42	1.61E-02	2.37E-01	UNQ1887	signal peptide peptidase 3	chr12q24.31	224639_at	NM_139015
4.44	3.81	0.64	1.61E-02	2.38E-01	HFE	hemochromatosis	chr6p21.3	235754_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
6.70	6.12	0.58	1.61E-02	2.38E-01	WDR57	WD repeat domain 57 (U5 snRNP specific)	chr1p35.2	215905_s_at	NM_004814
7.58	6.94	0.64	1.61E-02	2.38E-01	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	chr16q22.1	202659_at	NM_002801
4.95	4.53	0.42	1.61E-02	2.38E-01	PKNOX1	PBX/knotted 1 homeobox 1	chr21q22.3	204195_s_at	NM_004571
8.89	8.26	0.62	1.61E-02	2.38E-01	HLA-E	major histocompatibility complex, class I, E	chr6p21.3	200904_at	NM_005516
7.90	7.45	0.45	1.61E-02	2.38E-01	EIF2B2	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	chr14q24.3	202461_at	NM_014239
4.12	3.51	0.61	1.61E-02	2.38E-01	DAZAP2	DAZ associated protein 2	chr12q12	235704_at	NM_014764
5.76	5.03	0.73	1.62E-02	2.38E-01	SCUBE3	signal peptide, CUB domain, EGF-like 3	chr6p21.3	228407_at	NM_152753
7.03	6.12	0.91	1.62E-02	2.38E-01	ROGDI	rogdi homolog (Drosophila)	chr16p13.3	218394_at	NM_024589
7.77	7.40	0.37	1.62E-02	2.38E-01	OCIAD2	OCIA domain containing 2	chr4p12	225314_at	NM_001014446 /// NM_152398
6.73	4.26	2.47	1.62E-02	2.38E-01	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	chr4q34-q35	203914_x_at	NM_000860
7.89	7.38	0.51	1.62E-02	2.38E-01	AAMP	angio-associated, migratory cell protein	chr2q35	201511_at	NM_001087
6.86	6.14	0.72	1.62E-02	2.38E-01	TMEM216	transmembrane protein 216	chr11q13.1	223305_at	NM_016499
3.14	2.66	0.48	1.62E-02	2.38E-01	DCLK2	doublecortin-like kinase 2	chr4q31.3	227666_at	NM_001040260 /// NM_001040261
3.08	2.33	0.75	1.62E-02	2.38E-01	GATA3	GATA binding protein 3	chr10p15	209602_s_at	NM_001002295 /// NM_002051
7.28	6.58	0.70	1.62E-02	2.38E-01	MAN2B1	mannosidase, alpha, class 2B, member 1	chr19cen-q13.1	209166_s_at	NM_000528
5.89	5.17	0.72	1.63E-02	2.38E-01	FAM98C	family with sequence similarity 98, member C	chr19q13.2	227951_s_at	NM_174905
6.57	5.76	0.81	1.63E-02	2.38E-01	LOC284112	hypothetical protein LOC284112	chr17p13.2	230353_at	---
6.43	5.50	0.92	1.63E-02	2.38E-01	USP21	ubiquitin specific peptidase 21	chr1q22	232219_x_at	NM_001014443 /// NM_012475
8.79	7.93	0.86	1.63E-02	2.38E-01	SPATA20	spermatogenesis associated 20	chr17q21.33	218164_at	NM_022827
4.89	4.29	0.60	1.63E-02	2.38E-01	DEPDC5	DEP domain containing 5	chr22q12.3	205223_at	NM_001007188 /// NM_014662
5.17	4.32	0.85	1.63E-02	2.38E-01	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	chr22q13	204593_s_at	NM_019008
3.90	3.29	0.60	1.63E-02	2.38E-01	---	---	---	236192_at	---
3.92	2.30	1.62	1.63E-02	2.38E-01	USP34	ubiquitin specific peptidase 34	chr2p15	212980_at	NM_014709
8.07	7.47	0.60	1.63E-02	2.38E-01	SH3PXD2B	SH3 and PX domains 2B	chr5q35.1	231823_s_at	NM_001017995
9.40	9.02	0.38	1.64E-02	2.38E-01	RPS2	ribosomal protein S2	chr16p13.3	217466_x_at	NM_002952

3.55	3.16	0.39	1.64E-02	2.38E-01	PPP2R3C	protein phosphatase 2 (formerly 2A), regulatory subunit B", gamma	chr14q13.2	239188_at	NM_017917																				
6.71	6.09	0.63	1.64E-02	2.38E-01	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	chr7q22.1	217485_x_at	NR_003613																				
6.98	6.32	0.66	1.64E-02	2.38E-01	PRR14	proline rich 14	chr16p11.2	45687_at	NM_024031																				
8.76	8.33	0.43	1.64E-02	2.38E-01	MRPL27	mitochondrial ribosomal protein L27	chr17q21.3-q22	224330_s_at	NM_016504 /// NM_148570 /// NM_148571																				
3.33	2.93	0.39	1.64E-02	2.38E-01	TFAP2E	transcription factor AP-2 epsilon (activating enhancer binding protein 2 epsilon)	chr1p34.3	1555348_at	NM_178548																				
4.85	4.13	0.72	1.64E-02	2.38E-01	---	---	---	229371_at	---																				
6.85	6.07	0.79	1.64E-02	2.38E-01	GABPB1	GA binding protein transcription factor, beta subunit 2	chr15q21.2	227406_at	NM_002041 /// NM_005254 /// NM_016654 /// NM_016655 /// NM_181427																				
4.65	3.76	0.89	1.64E-02	2.38E-01	DNALI1	dynein, axonemal, light intermediate chain 1	chr1p35.1	227081_at	NM_003462																				
7.94	7.26	0.68	1.64E-02	2.38E-01	FAM91A2	family with sequence similarity 91, member A2	chr1q21.1	222001_x_at	XR_040635																				
5.25	4.56	0.69	1.64E-02	2.38E-01	C7orf31	chromosome 7 open reading frame 31	chr7p15.2	229146_at	NM_138811																				
5.59	4.65	0.94	1.64E-02	2.38E-01	C17orf62	chromosome 17 open reading frame 62	chr17q25.3	218130_at	NM_001033046 /// NM_001100407 /// NM_001100408																				
3.94	3.03	0.91	1.64E-02	2.38E-01	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	chr16q22.1	203579_s_at	NM_001076785 /// NM_003983																				
10.72	10.30	0.42	1.64E-02	2.38E-01	NPC2	Niemann-Pick disease, type C2	chr14q24.3	200701_at	NM_006432																				
9.17	8.54	0.63	1.64E-02	2.38E-01	C11orf31	chromosome 11 open reading frame 31	chr11q12.1	224677_x_at	NM_170746																				
7.39	6.46	0.92	1.65E-02	2.38E-01	RP1-93P18.1	hypothetical protein LOC126917	chr1p36.13	225615_at	XM_001714732 /// XM_001721924 /// XM_001722365																				
5.48	4.69	0.79	1.65E-02	2.38E-01	ASB6	ankyrin repeat and SOCS box-containing 6	---	222524_s_at	NM_017873 /// NM_177999																				
7.25	6.85	0.40	1.65E-02	2.38E-01	MRPS5	mitochondrial ribosomal protein S5	chr2p11.2-q11.2	224333_s_at	NM_031902																				
3.39	2.84	0.56	1.65E-02	2.38E-01	HOXD4	homeobox D4	chr2q31.1	1552337_s_at	NM_014621																				
7.38	6.78	0.60	1.65E-02	2.38E-01	TXNRD2	thioredoxin reductase 2	chr22q11.21	211177_s_at	NM_006440																				
6.06	5.56	0.50	1.65E-02	2.38E-01	ANTXR1	anthrax toxin receptor 1	chr2p13.1	227660_at	NM_018153 /// NM_032208 /// NM_053034																				
8.26	7.67	0.59	1.65E-02	2.39E-01	PLD3	phospholipase D family, member 3	chr19q13.2	201050_at	NM_001031696 /// NM_012268																				
4.47	3.94	0.53	1.65E-02	2.39E-01	FLJ22167	hypothetical protein FLJ22167	chr16q23.1	219182_at	NM_001077416 /// NM_001077418 /// NM_001077419																				
4.39	4.04	0.35	1.65E-02	2.39E-01	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	chr3p22.1	239056_at	NM_004206 /// NM_032970																				
2.87	2.43	0.44	1.65E-02	2.39E-01	UBE2Q1	ubiquitin-conjugating enzyme E2Q family member 1	chr1q21.3	222480_at	NM_017582																				
6.58	5.60	0.98	1.65E-02	2.39E-01	SCRN2	secernin 2	chr17q21.32	228730_s_at	NM_138355																				
8.15	7.59	0.56	1.65E-02	2.39E-01	TSPO	translocator protein (18kDa)	chr22q13.31	202096_s_at	NM_000714 /// NM_007311																				
5.06	4.44	0.62	1.66E-02	2.39E-01	ZNF783	zinc finger family member 783	chr7q36.1	221876_at	NM_001004302																				
4.01	3.43	0.59	1.66E-02	2.39E-01	LOC728537	hypothetical protein LOC728537	chr2q11.2	230941_at	XR_041702 /// XR_041703 /// XR_041704																				

9.02	8.42	0.61	1.66E-02	2.39E-01	ZNF706	zinc finger protein 706	chr8q22.3	218059_at	NM_001042510 /// NM_001042511 /// NM_016096																				
6.76	4.88	1.89	1.66E-02	2.39E-01	SFRS6	splicing factor, arginine/serine-rich 6	chr20q12-q13.1	206108_s_at	NM_006275																				
6.88	6.08	0.80	1.66E-02	2.39E-01	CHMP4A /// MDP-1	chromatin modifying protein 4A /// magnesium-dependent phosphatase 1	chr14q12	228763_at	NM_014169 /// NM_138476																				
7.60	6.08	1.52	1.66E-02	2.39E-01	ALCAM	activated leukocyte cell adhesion molecule	chr3q13.1	201952_at	NM_001627																				
3.56	3.14	0.42	1.67E-02	2.40E-01	KBTBD3	kelch repeat and BTB (POZ) domain containing 3	chr11q22.3	228777_at	NM_152433 /// NM_198439																				
6.43	5.62	0.81	1.67E-02	2.40E-01	HDAC5	histone deacetylase 5	chr17q21	202455_at	NM_001015053 /// NM_005474																				
12.97	12.69	0.28	1.68E-02	2.40E-01	RPL13A	ribosomal protein L13a	chr19q13.3	200716_x_at	NM_012423																				
7.99	7.60	0.40	1.68E-02	2.40E-01	WBSCR22	Williams Beuren syndrome chromosome region 22	---	207628_s_at	NM_017528																				
5.92	4.03	1.88	1.68E-02	2.40E-01	ID2 /// ID2B	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)	chr2p25 /// chr3p14.2	213931_at	NM_002166																				
7.32	6.32	1.01	1.68E-02	2.40E-01	CKB	creatine kinase, brain	chr14q32	200884_at	NM_001823																				
6.17	5.74	0.43	1.68E-02	2.40E-01	TTC4	tetratricopeptide repeat domain 4	chr1p32.3	218442_at	NM_004623 /// XM_001726392 /// XM_001726400 /// XM_001726506																				
9.12	8.50	0.62	1.68E-02	2.40E-01	CDK4	cyclin-dependent kinase 4	chr12q14	202246_s_at	NM_000075																				
7.55	6.94	0.61	1.68E-02	2.40E-01	MGAT1	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	chr5q35	201126_s_at	NM_001114617 /// NM_001114618 /// NM_001114619 /// NM_001114620 /// NM_002406																				
5.18	4.69	0.49	1.68E-02	2.40E-01	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	chr2q35	213098_at	NM_005444																				
5.81	5.16	0.65	1.68E-02	2.40E-01	LOC96610	Hypothetical gene LOC96610	chr22q11.22	233132_at	XR_040596																				
9.31	8.87	0.44	1.68E-02	2.40E-01	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	chr1pter-q24	202296_s_at	NM_007033																				
8.09	7.42	0.67	1.68E-02	2.40E-01	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	chr14q21	203102_s_at	NM_002408																				
2.99	2.60	0.39	1.68E-02	2.40E-01	---	---	---	229005_at	---																				
5.80	4.78	1.02	1.69E-02	2.40E-01	ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	chr6p21.1	213485_s_at	NM_033450																				
5.71	5.37	0.34	1.69E-02	2.40E-01	RPP38	ribonuclease P/MRP 38kDa subunit	chr10p13	205562_at	NM_001097590 /// NM_006414 /// NM_183005																				
3.81	3.41	0.40	1.69E-02	2.40E-01	---	---	---	243817_at	---																				
6.87	5.91	0.96	1.69E-02	2.40E-01	RNF44	ring finger protein 44	chr5q35.2	203286_at	NM_014901																				
4.44	3.51	0.93	1.69E-02	2.40E-01	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	230122_at	NM_001009569 /// NM_004641																				
3.72	3.07	0.64	1.69E-02	2.40E-01	JMJD2B	jumonji domain containing 2B	chr19p13.3	235789_at	NM_015015																				
5.72	4.98	0.74	1.69E-02	2.40E-01	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	chr15q26.1	44111_at	NM_018668																				
5.39	4.83	0.56	1.69E-02	2.40E-01	DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	chr17q21.31	203334_at	NM_004941																				
3.33	2.24	1.09	1.70E-02	2.41E-01	SLC44A5	solute carrier family 44, member 5	chr1p31.1	235763_at	NM_001130058 /// NM_152697																				
7.10	6.22	0.89	1.70E-02	2.41E-01	PPP1R16A	protein phosphatase 1, regulatory (inhibitor) subunit 16A	chr8q24.3	225203_at	NM_032902																				
3.80	3.06	0.74	1.70E-02	2.41E-01	CD300A	CD300a molecule	chr17q25.1	217078_s_at	NM_007261																				
3.82	3.07	0.75	1.70E-02	2.41E-01	SFI1	Sfi1 homolog, spindle assembly associated (yeast)	chr22q12.2	36545_s_at	NM_001007467 /// NM_014775																				
4.12	3.43	0.69	1.70E-02	2.41E-01	ULK2	unc-51-like kinase 2 (C. elegans)	chr17p11.2	1554112_a_at	NM_014683																				
6.60	6.03	0.58	1.70E-02	2.41E-01	CLK3	CDC-like kinase 3	chr15q24	202140_s_at	NM_001130028 /// NM_001292 /// NM_003992																				

7.00	5.77	1.24	1.70E-02	2.41E-01	ABAT	4-aminobutyrate aminotransferase	chr16p13.2	209460_at	NM_000663 /// NM_001127448 /// NM_020686																			
6.92	6.34	0.58	1.70E-02	2.41E-01	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	chr7p22	218927_s_at	NM_018641																			
8.60	5.65	2.94	1.71E-02	2.41E-01	NR4A2	nuclear receptor subfamily 4, group A, member 2	chr2q22-q23	204622_x_at	NM_006186 /// NM_173171 /// NM_173172 /// NM_173173																			
5.88	5.51	0.37	1.71E-02	2.41E-01	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	chr3p23-p21	201074_at	NM_003074																			
3.82	3.15	0.67	1.71E-02	2.41E-01	GPR143	G protein-coupled receptor 143	chrXp22.3	206696_at	NM_000273																			
6.99	5.46	1.53	1.71E-02	2.41E-01	NAV3	neuron navigator 3	chr12q14.3	204823_at	NM_014903																			
8.07	7.13	0.94	1.71E-02	2.41E-01	MERTK	c-mer proto-oncogene tyrosine kinase	chr2q14.1	206028_s_at	NM_006343																			
2.98	2.21	0.78	1.71E-02	2.41E-01	L3MBTL	l(3)mbt-like (Drosophila)	chr20q13.12	206822_s_at	NM_015478 /// NM_032107																			
7.92	7.36	0.56	1.71E-02	2.41E-01	PITRM1	pitrilysin metallopeptidase 1	chr10p15.2	205273_s_at	NM_014889																			
7.72	6.96	0.76	1.71E-02	2.41E-01	IRF9	interferon regulatory factor 9	chr14q11.2	203882_at	NM_006084																			
2.81	2.46	0.35	1.71E-02	2.41E-01	LOC283761	hypothetical protein LOC283761	chr15q26.1	1556452_a_at	---																			
6.80	6.06	0.74	1.71E-02	2.41E-01	GTF2IRD1	GTF2I repeat domain containing 1	chr7q11.23	218412_s_at	NM_005685 /// NM_016328																			
2.81	2.41	0.40	1.71E-02	2.41E-01	APAF1	apoptotic peptidase activating factor 1	chr12q23	204859_s_at	NM_001160 /// NM_013229 /// NM_181861 /// NM_181868 /// NM_181869																			
5.98	5.32	0.66	1.71E-02	2.41E-01	---	---	---	226223_at	---																			
7.31	6.98	0.33	1.71E-02	2.41E-01	MAP2K1	mitogen-activated protein kinase kinase 1	chr15q22.1-q22.33	202670_at	NM_002755																			
5.28	4.65	0.63	1.71E-02	2.41E-01	EPOR	erythropoietin receptor	chr19p13.3-p13.2	209963_s_at	NM_000121																			
3.35	2.83	0.52	1.72E-02	2.41E-01	---	---	---	241246_at	---																			
4.50	3.87	0.63	1.72E-02	2.41E-01	RPL10L	ribosomal protein L10-like	chr14q13-q21	217559_at	NM_080746																			
4.12	3.65	0.46	1.72E-02	2.41E-01	MTHFSD	methenyltetrahydrofolate synthetase domain containing	chr16q24.1	218879_s_at	NM_022764																			
5.79	5.09	0.69	1.72E-02	2.41E-01	MAP2K5	mitogen-activated protein kinase kinase 5	chr15q23	210482_x_at	NM_002757 /// NM_145160																			
6.88	6.11	0.76	1.72E-02	2.41E-01	SHC2	SHC (Src homology 2 domain containing) transforming protein 2	chr19p13.3	213464_at	NM_012435																			
6.29	5.35	0.93	1.72E-02	2.41E-01	MAP3K4	mitogen-activated protein kinase kinase kinase 4	chr6q26	216199_s_at	NM_005922 /// NM_006724																			
5.51	5.11	0.40	1.72E-02	2.41E-01	MBD1	methyl-CpG binding domain protein 1	chr18q21	226862_at	NM_002384 /// NM_015844 /// NM_015845 /// NM_015846 /// NM_015847																			
9.39	8.63	0.76	1.72E-02	2.41E-01	C14orf4	chromosome 14 open reading frame 4	chr14q24.3	223474_at	NM_024496																			
8.71	8.24	0.47	1.72E-02	2.41E-01	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	chr17p13	215464_s_at	NM_014604																			
6.46	5.71	0.75	1.72E-02	2.41E-01	RILPL1	Rab interacting lysosomal protein-like 1	chr12q24.31	226207_at	NM_178314																			
8.12	7.40	0.72	1.72E-02	2.41E-01	ST5	suppression of tumorigenicity 5	chr11p15	202440_s_at	NM_005418 /// NM_139157 /// NM_213618																			
8.49	7.96	0.53	1.72E-02	2.41E-01	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	chr19p13.2	201726_at	NM_001419																			
5.65	4.47	1.18	1.72E-02	2.41E-01	LOC729680	hypothetical protein LOC729680	chr13q12.11	228977_at	XR_040503																			

5.47	4.81	0.67	1.72E-02	2.41E-01	ING1	inhibitor of growth family, member 1	chr13q34	209808_x_at	NM_005537 /// NM_198217 /// NM_198218 /// NM_198219																				
5.70	4.86	0.84	1.72E-02	2.41E-01	EPOR	erythropoietin receptor	chr19p13.3-p13.2	209962_at	NM_000121																				
6.18	5.32	0.85	1.72E-02	2.41E-01	EIF1AD	eukaryotic translation initiation factor 1A domain containing	chr11q13.1	239377_at	NM_032325																				
4.97	4.21	0.76	1.73E-02	2.41E-01	MOV10	Mov10, Moloney leukemia virus 10, homolog (mouse)	chr1p13.2	223849_s_at	NM_001130079 /// NM_020963																				
2.46	1.94	0.52	1.73E-02	2.41E-01	BEST4	bestrophin 4	chr1p33-p32.3	1552296_at	NM_153274																				
7.09	6.37	0.72	1.73E-02	2.41E-01	TGFB1	transforming growth factor, beta 1	chr19q13.2|19q13.1	203085_s_at	NM_000660																				
7.43	5.35	2.08	1.73E-02	2.41E-01	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	chr19q13.32	202768_at	NM_001114171 /// NM_006732																				
5.61	4.15	1.46	1.73E-02	2.41E-01	PELI2	pellino homolog 2 (Drosophila)	chr14q21	219132_at	NM_021255																				
3.98	3.46	0.53	1.73E-02	2.41E-01	ERICH1	glutamate-rich 1	chr8p23.3	227017_at	NM_207332																				
4.76	4.06	0.70	1.73E-02	2.41E-01	RABL2A /// RABL2B	RAB, member of RAS oncogene family-like 2A /// RAB, member of RAS oncogene family-like 2B	chr22q13.33 /// chr2q13	220500_s_at	NM_001003789 /// NM_001130919 /// NM_001130920 /// NM_001130921 /// NM_001130922 /// NM_001130923 /// NM_007081 /// NM_007082 /// NM_013412																				
8.72	8.12	0.61	1.73E-02	2.41E-01	HMGN1	high-mobility group nucleosome binding domain 1	chr21q22.3|21q22.2	200944_s_at	NM_004965																				
7.96	7.16	0.80	1.73E-02	2.42E-01	BIN3	bridging integrator 3	chr8p21.3	222199_s_at	NM_018688																				
4.90	3.56	1.33	1.73E-02	2.42E-01	FAM110C	family with sequence similarity 110, member C	chr2p25.3	226863_at	NM_001077710																				
8.46	7.94	0.52	1.73E-02	2.42E-01	CTSC	cathepsin C	chr11q14.1-q14.3	201487_at	NM_001114173 /// NM_001814 /// NM_148170																				
4.12	2.78	1.34	1.74E-02	2.42E-01	EPHA4	EPH receptor A4	chr2q36.1	227449_at	NM_004438																				
5.86	4.93	0.93	1.74E-02	2.42E-01	USP20	ubiquitin specific peptidase 20	chr9q34.11	203965_at	NM_001008563 /// NM_001110303 /// NM_006676																				
4.24	2.63	1.61	1.74E-02	2.42E-01	---	---	---	242605_at	---																				
10.26	9.99	0.28	1.74E-02	2.42E-01	SAP18	Sin3A-associated protein, 18kDa	chr13q12.11	208742_s_at	NM_005870																				
7.82	7.24	0.58	1.74E-02	2.42E-01	PIH1D1	PIH1 domain containing 1	chr19q13.33	217872_at	NM_017916																				
7.91	7.25	0.66	1.74E-02	2.42E-01	EXOC7	exocyst complex component 7	chr17q25.1	212034_s_at	NM_001013839 /// NM_015219																				
4.02	3.64	0.38	1.74E-02	2.42E-01	LOC157562	hypothetical protein LOC157562	chr8q22.3	213776_at	---																				
5.41	3.58	1.83	1.75E-02	2.42E-01	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	chr6p21.31	203146_s_at	NM_001470 /// NM_021903 /// NM_021904 /// NM_021905																				
3.49	2.76	0.74	1.75E-02	2.42E-01	LOC285535	hypothetical protein LOC285535	chr4p16.1	229130_at	---																				
4.62	4.17	0.45	1.75E-02	2.43E-01	---	---	---	229577_at	---																				
6.92	6.07	0.85	1.75E-02	2.43E-01	FAM89B	family with sequence similarity 89, member B	chr11q23	32209_at	NM_001098784 /// NM_001098785 /// NM_152832																				
6.69	5.63	1.06	1.75E-02	2.43E-01	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	chr19q13.2	37028_at	NM_014330																				

7.50	6.51	0.99	1.75E-02	2.43E-01	TSPYL4	TSPY-like 4	chr6q22.1	212928_at	NM_021648																			
3.01	2.51	0.49	1.75E-02	2.43E-01	SESN3	sestrin 3	chr11q21	235683_at	NM_144665																			
5.90	5.30	0.59	1.75E-02	2.43E-01	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	chr14q24.3	222866_s_at	NM_017791																			
6.54	5.88	0.66	1.76E-02	2.43E-01	TRIM11	tripartite motif-containing 11	chr1q42.13	226566_at	NM_145214																			
6.42	5.68	0.74	1.76E-02	2.43E-01	---	---	---	1555833_a_at	---																			
12.68	12.37	0.31	1.76E-02	2.43E-01	RPL10	ribosomal protein L10	chrXq28	200725_x_at	NM_006013																			
3.31	2.30	1.02	1.76E-02	2.43E-01	MEGF10	multiple EGF-like-domains 10	chr5q33	236517_at	NM_032446																			
5.84	5.27	0.56	1.76E-02	2.43E-01	TNS1	tensin 1	chr2q35-q36	218864_at	NM_022648																			
7.86	6.55	1.31	1.76E-02	2.43E-01	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	chr7p15	225932_s_at	NM_002137 /// NM_031243																			
9.49	8.85	0.64	1.76E-02	2.43E-01	GNG5	guanine nucleotide binding protein (G protein), gamma 5	chr1p22	207157_s_at	NM_005274																			
3.33	2.29	1.03	1.77E-02	2.43E-01	PRR16	proline rich 16	chr5q23.1	220014_at	NM_016644																			
5.76	4.96	0.80	1.77E-02	2.43E-01	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	chr6p21.3	203577_at	NM_001517																			
5.88	4.98	0.89	1.77E-02	2.43E-01	SEDLP /// TRAPPC2 /// ZNF547	spondyloepiphyseal dysplasia, late, pseudogene /// trafficking protein particle complex 2 /// zinc finger protein 547	chr19q13.4 /// chr19q13.43 /// chrXp22	219351_at	NM_001011658 /// NM_001128835 /// NM_014563 /// NM_173631 /// NR_002166																			
10.30	9.72	0.59	1.77E-02	2.43E-01	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	chr3p21.2	201892_s_at	NM_000884																			
12.32	12.02	0.30	1.77E-02	2.43E-01	RPS15A	ribosomal protein S15a	chr16p	200781_s_at	NM_001019 /// NM_001030009																			
2.91	2.37	0.53	1.77E-02	2.43E-01	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	chr12q13.13	242069_at	NM_001127321 /// NM_001127322 /// NM_012117																			
5.46	5.04	0.43	1.77E-02	2.43E-01	SFRS15	splicing factor, arginine/serine-rich 15	chr21q22.1	226082_s_at	NM_020706																			
7.20	6.76	0.44	1.77E-02	2.44E-01	ANKRD13A	ankyrin repeat domain 13A	chr12q24.11	224810_s_at	NM_033121																			
2.49	2.09	0.40	1.77E-02	2.44E-01	---	---	---	243538_at	---																			
4.06	3.70	0.36	1.78E-02	2.44E-01	---	---	---	241371_at	---																			
8.19	7.41	0.78	1.78E-02	2.44E-01	HTRA1	HtrA serine peptidase 1	chr10q26.3	201185_at	NM_002775																			
8.06	7.06	0.99	1.78E-02	2.44E-01	FHL1	four and a half LIM domains 1	chrXq26	201540_at	NM_001449																			
2.97	2.33	0.64	1.78E-02	2.44E-01	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	chr12q13.1-q13.3	205676_at	NM_000785																			

3.73	2.65	1.08	1.78E-02	2.44E-01	hCG_2004593 /// hCG_39912 /// LOC100129657 /// LOC100132742 /// LOC442232 /// LOC643863 /// LOC727984 /// LOC729340 /// LOC729349 /// RPL17	ribosomal protein L17-like /// hCG39912 /// hypothetical protein LOC100129657 /// hypothetical protein LOC100132742 /// similar to hCG24487 /// similar to hCG39912 /// similar to hCG1641837 /// similar to hCG24487 /// similar to hCG24487 /// ribosomal protein L17	chr10q23.33 /// chr10q26.11 /// chr15q23 /// chr18q21 /// chr1p13.3 /// chr3p21.31 /// chr3q29 /// chr5q11.2 /// chr6q14.1	214291_at	NM_000985 /// NM_001035006 /// NM_001089592 /// NM_001093733 /// XM_001717156 /// XM_001717161 /// XM_001717890 /// XM_001719035 /// XM_001719497 /// XR_015259 /// XR_015954 /// XR_016559 /// XR_016732 /// XR_018484 /// XR_019623 /// XR_037946 /// XR_038148 /// XR_038230 /// XR_038636 /// XR_038666 /// XR_039281 /// XR_039489 /// XR_039650 /// XR_039688																				
6.79	6.12	0.67	1.78E-02	2.44E-01	GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	chr12q24.2	212139_at	NM_006836																				
7.96	7.42	0.54	1.78E-02	2.44E-01	JTV1	JTV1 gene	chr7p22	209971_x_at	NM_006303																				
2.52	2.20	0.31	1.78E-02	2.44E-01	ADRA1A	adrenergic, alpha-1A-, receptor	chr8p21-p11.2	211492_s_at	NM_000680 /// NM_033302 /// NM_033303 /// NM_033304																				
6.61	6.09	0.52	1.78E-02	2.44E-01	FN3KRP	fructosamine-3-kinase-related protein	chr17q25.3	218210_at	NM_024619																				
6.06	5.65	0.41	1.79E-02	2.44E-01	TSHZ1	teashirt zinc finger homeobox 1	chr18q22.3	223282_at	NM_005786																				
2.61	2.05	0.57	1.79E-02	2.44E-01	DPY19L2	dpy-19-like 2 (C. elegans)	chr12q14.2	230158_at	NM_173812																				
5.24	4.73	0.51	1.79E-02	2.44E-01	KLHL18	kelch-like 18 (Drosophila)	chr3p21.31	212882_at	NM_025010																				
4.51	3.56	0.95	1.79E-02	2.44E-01	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	chr12q15	226934_at	NM_007007																				
3.15	2.20	0.95	1.79E-02	2.44E-01	HINT1	histidine triad nucleotide binding protein 1	chr5q31.2	1555960_at	NM_005340																				
5.42	4.51	0.91	1.80E-02	2.44E-01	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	chr12q13.11-q13.3	218685_s_at	NM_014311																				
3.44	2.83	0.61	1.80E-02	2.44E-01	---	---	---	236566_at	---																				
4.05	3.42	0.63	1.80E-02	2.44E-01	LOC144305	hypothetical protein BC001437	chr12q24.22	223845_at	---																				
5.16	4.59	0.57	1.80E-02	2.44E-01	RFC5	replication factor C (activator 1) 5, 36.5kDa	chr12q24.23	203209_at	NM_001130112 /// NM_001130113 /// NM_007370 /// NM_181578																				

8.48	7.91	0.57	1.80E-02	2.44E-01	BOLA3	bolA homolog 3 (E. coli)	chr2p13.1	227291_s_at	NM_001035505 /// NM_212552
7.33	6.84	0.49	1.80E-02	2.44E-01	PPIH	peptidylprolyl isomerase H (cyclophilin H)	chr1p34.1	204228_at	NM_006347
4.29	3.79	0.50	1.80E-02	2.44E-01	CDK9	cyclin-dependent kinase 9	chr9q34.1	236023_at	NM_001261
7.22	6.55	0.68	1.80E-02	2.44E-01	CDC34	cell division cycle 34 homolog (S. cerevisiae)	chr19p13.3	212540_at	NM_004359
8.11	7.49	0.62	1.80E-02	2.44E-01	PHF23	PHD finger protein 23	chr17p13.1	223081_at	NM_024297
3.89	3.45	0.44	1.80E-02	2.44E-01	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	chr11q12.3	213209_at	NM_006473
3.62	2.34	1.28	1.80E-02	2.45E-01	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	chr11q14.3-q21	222161_at	NM_005467
7.12	6.28	0.83	1.81E-02	2.45E-01	FNTB	farnesyltransferase, CAAX box, beta	chr14q23-q24	225851_at	NM_002028
11.82	11.51	0.31	1.81E-02	2.45E-01	LOC100131713 /// RPL29 /// RPL29P4	similar to ribosomal protein L29 /// ribosomal protein L29 /// ribosomal protein L29 pseudogene 4	chr3p21.3-p21.2 /// chr3p22.2 /// chr6q22.2	200823_x_at	NM_000992 /// XM_001723470 /// XM_001723471 /// XM_001724270 /// XM_001724272 /// XM_001725513 /// XM_001725514
7.09	6.36	0.72	1.81E-02	2.45E-01	CRTAP	cartilage associated protein	chr3p22.3	201380_at	NM_006371
3.78	3.20	0.58	1.81E-02	2.45E-01	C16orf79	chromosome 16 open reading frame 79	chr16p13.3	1553990_at	NM_182563
5.47	4.87	0.61	1.81E-02	2.45E-01	KIAA1166	KIAA1166	chrXq11.1	225784_s_at	NM_018684
6.47	6.08	0.39	1.82E-02	2.45E-01	NFYC	nuclear transcription factor Y, gamma	chr1p32|1p32	211251_x_at	NM_014223
4.87	4.24	0.62	1.82E-02	2.45E-01	ADPGK	ADP-dependent glucokinase	chr15q24.1	224455_s_at	NM_031284 /// NR_023318 /// NR_023319
2.40	2.07	0.33	1.82E-02	2.45E-01	---	---	---	244399_at	---
6.38	5.59	0.79	1.82E-02	2.45E-01	LOC644096	hypothetical protein LOC644096	chr19q13.12	44669_at	NM_001042631
6.25	5.37	0.88	1.82E-02	2.45E-01	CCDC97	coiled-coil domain containing 97	chr19q13.2	225257_at	NM_052848
3.71	3.13	0.58	1.82E-02	2.45E-01	TMEM86A	transmembrane protein 86A	chr11p15.1	238710_at	NM_153347
5.04	3.14	1.91	1.82E-02	2.45E-01	CTH	cystathionase (cystathionine gamma-lyase)	chr1p31.1	217127_at	NM_001902 /// NM_153742
6.69	5.94	0.76	1.82E-02	2.45E-01	ZDHHC16	zinc finger, DHHC-type containing 16	chr10q24.1	223212_at	NM_032327 /// NM_198043 /// NM_198044 /// NM_198045 /// NM_198046
3.77	3.17	0.60	1.82E-02	2.45E-01	---	---	---	241601_at	---
7.42	6.95	0.47	1.83E-02	2.45E-01	GRB2	growth factor receptor-bound protein 2	chr17q24-q25	223049_at	NM_002086 /// NM_203506
6.82	5.64	1.17	1.83E-02	2.45E-01	THNSL2	threonine synthase-like 2 (S. cerevisiae)	chr2p11.2	219044_at	NM_018271
9.07	8.40	0.67	1.83E-02	2.45E-01	TMEM120A	transmembrane protein 120A	chr7q11.23	223482_at	NM_031925
4.34	3.17	1.17	1.83E-02	2.45E-01	ACAD11 /// NPHP3	acyl-Coenzyme A dehydrogenase family, member 11 /// nephronophthisis 3 (adolescent)	chr3q22.1	235410_at	NM_032169 /// NM_153240
6.99	6.21	0.78	1.83E-02	2.46E-01	TM2D3	TM2 domain containing 3	chr15q26.3	1552426_a_at	NM_025141 /// NM_078474
2.83	2.49	0.34	1.83E-02	2.46E-01	KNTC1	kinetochore associated 1	chr12q24.31	206316_s_at	NM_014708
6.38	5.77	0.60	1.83E-02	2.46E-01	DGUOK	deoxyguanosine kinase	chr2p13	203816_at	NM_080916 /// NM_080918
6.05	4.65	1.40	1.84E-02	2.46E-01	C13orf15	chromosome 13 open reading frame 15	chr13q14.11	218723_s_at	NM_014059
8.10	7.54	0.56	1.84E-02	2.46E-01	ANKHD1-EIF4EBP3 /// EIF4EBP3	ANKHD1-EIF4EBP3 /// eukaryotic translation initiation factor 4E binding protein 3	chr5q31.3	214919_s_at	NM_003732 /// NM_020690
5.97	4.81	1.17	1.84E-02	2.46E-01	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	chr3p21	216320_x_at	NM_020998
6.46	5.33	1.12	1.84E-02	2.46E-01	WIPI1	WD repeat domain, phosphoinositide interacting 1	chr17q24.2	213836_s_at	NM_017983
3.80	2.96	0.84	1.84E-02	2.46E-01	---	---	---	233090_at	---

6.01	5.37	0.64	1.84E-02	2.46E-01	MUTYH	mutY homolog (E. coli)	chr1p34.3-p32.1	207727_s_at	NM_001048171 /// NM_001048172 /// NM_001048173 /// NM_001048174 /// NM_001128425 /// NM_012222
3.80	3.33	0.46	1.84E-02	2.46E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	1554049_s_at	NM_015726
7.37	6.75	0.62	1.84E-02	2.46E-01	PHF5A	PHD finger protein 5A	chr22q13.2	225309_at	NM_032758
2.77	2.39	0.39	1.85E-02	2.46E-01	KLHL20	kelch-like 20 (Drosophila)	chr1q24.1-q24.3	210634_at	NM_014458
3.46	3.19	0.27	1.85E-02	2.46E-01	CASKIN1	CASK interacting protein 1	chr16p13.3	1552689_at	NM_020764
7.65	6.99	0.66	1.85E-02	2.46E-01	C11orf75	chromosome 11 open reading frame 75	chr11q13.3-q23.3	219806_s_at	NM_020179
6.59	5.85	0.74	1.85E-02	2.46E-01	HIP1R	huntingtin interacting protein 1 related	chr12q24	38340_at	NM_003959
5.94	5.02	0.92	1.85E-02	2.46E-01	APOC2 /// APOC4	apolipoprotein C-II /// apolipoprotein C-IV	chr19q13.2	204561_x_at	NM_000483 /// NM_001646
4.68	4.16	0.51	1.86E-02	2.47E-01	---	---	---	227125_at	---
3.77	3.36	0.41	1.86E-02	2.47E-01	---	---	---	230408_at	---
4.70	4.19	0.51	1.86E-02	2.47E-01	C20orf27	chromosome 20 open reading frame 27	chr20p13	50314_i_at	NM_001039140
7.58	6.61	0.97	1.86E-02	2.47E-01	---	---	---	228443_s_at	---
6.93	6.34	0.59	1.86E-02	2.47E-01	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	chr17p13.3	207088_s_at	NM_003562
3.72	3.06	0.66	1.86E-02	2.47E-01	CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	chr1p34-p12	1555497_a_at	NM_000779 /// NM_001099772
6.84	5.62	1.23	1.86E-02	2.47E-01	HLF	hepatic leukemia factor	chr17q22	204753_s_at	NM_002126
4.46	3.79	0.67	1.87E-02	2.47E-01	ROR2	receptor tyrosine kinase-like orphan receptor 2	chr9q22	205578_at	NM_004560
4.09	3.49	0.60	1.87E-02	2.47E-01	FBXL20	F-box and leucine-rich repeat protein 20	chr17q12	235089_at	NM_032875
4.57	3.62	0.95	1.87E-02	2.48E-01	TCTEX1D2 /// TM4SF19	Tctex1 domain containing 2 /// transmembrane 4 L six family member 19	chr3q29	228606_at	NM_138461 /// NM_152773
6.23	5.43	0.80	1.87E-02	2.48E-01	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	225992_at	NM_001009569 /// NM_004641
5.66	5.14	0.51	1.87E-02	2.48E-01	PURB	purine-rich element binding protein B	chr7p13	227718_at	NM_033224
5.05	4.58	0.47	1.88E-02	2.48E-01	CDC2L1 /// CDC2L2	cell division cycle 2-like 1 (PITSLRE proteins) /// cell division cycle 2-like 2 (PITSLRE proteins)	chr1p36.33	210474_s_at	NM_024011 /// NM_033486 /// NM_033487 /// NM_033488 /// NM_033489 /// NM_033492 /// NM_033493 /// NM_033529 /// XM_001713735 /// XM_001713748 /// XM_001715985 /// XM_001716018 /// XM_001716037 /// XM_001716055
6.21	5.54	0.67	1.88E-02	2.49E-01	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	chr6q25.1	225520_at	NM_015440
5.31	4.79	0.52	1.89E-02	2.49E-01	ZNF586	zinc finger protein 586	chr19q13.43	219711_at	NM_001077426 /// NM_017652
6.77	6.27	0.50	1.89E-02	2.49E-01	ELAC2	elaC homolog 2 (E. coli)	chr17p11.2	201767_s_at	NM_018127

11.56	11.17	0.39	1.89E-02	2.49E-01	RPS3	ribosomal protein S3	chr11q13.3-q13.5	208692_at	NM_001005																				
6.52	5.90	0.63	1.89E-02	2.49E-01	GTF2IRD2	GTF2I repeat domain containing 2	chr7q11.23	228765_at	NM_173537 /// XM_001721289 /// XM_001722115																				
4.54	4.01	0.53	1.89E-02	2.49E-01	MTMR15	myotubularin related protein 15	chr15q13.2-q13.3	203678_at	NM_014967																				
8.43	7.82	0.61	1.89E-02	2.49E-01	CLPTM1L	CLPTM1-like	chr5pter-p15.3	223020_at	NM_030782 /// XM_001722978																				
6.26	5.56	0.70	1.89E-02	2.49E-01	FBXL14	F-box and leucine-rich repeat protein 14	chr12p13.33	213145_at	NM_152441																				
12.69	12.36	0.32	1.89E-02	2.49E-01	RPS2	ribosomal protein S2	chr16p13.3	203107_x_at	NM_002952																				
3.18	2.81	0.37	1.89E-02	2.49E-01	GYG2	glycogenin 2	chrXp22.3	210964_s_at	NM_001079855 /// NM_003918																				
7.28	6.88	0.40	1.90E-02	2.50E-01	TMEM184C	transmembrane protein 184C	chr4q31.23	219074_at	NM_018241																				
5.61	4.38	1.23	1.90E-02	2.50E-01	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	chr12q12-q14	227527_at	NM_003482																				
6.93	5.62	1.31	1.90E-02	2.50E-01	BMP4	bone morphogenetic protein 4	chr14q22-q23	211518_s_at	NM_001202 /// NM_130850 /// NM_130851																				
3.97	3.43	0.54	1.90E-02	2.50E-01	KIAA2013	KIAA2013	chr1p36.22	1555933_at	NM_138346																				
7.56	7.00	0.56	1.90E-02	2.50E-01	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	chr6p25	213572_s_at	NM_030666																				
7.38	6.84	0.55	1.90E-02	2.50E-01	FAM134A	family with sequence similarity 134, member A	chr2q35	218037_at	NM_024293																				
3.16	2.44	0.72	1.90E-02	2.50E-01	---	---	---	226231_at	---																				
3.67	2.28	1.39	1.90E-02	2.50E-01	LOC389765	similar to KIF27C	chr9q21.33	230815_at	XM_001720643 /// XM_001721595 /// XM_001723166																				
3.01	2.49	0.51	1.91E-02	2.50E-01	TGIF1	TGFB-induced factor homeobox 1	chr18p11.3	1566901_at	NM_003244 /// NM_170695 /// NM_173207 /// NM_173208 /// NM_173209 /// NM_173210 /// NM_173211 /// NM_174886																				
6.73	5.97	0.75	1.91E-02	2.50E-01	LZTS2	leucine zipper, putative tumor suppressor 2	chr10q24	224473_x_at	NM_032429																				
9.38	8.94	0.44	1.91E-02	2.50E-01	SRI	sorcin	chr7q21.1	208921_s_at	NM_003130 /// NM_198901																				
7.24	6.67	0.57	1.91E-02	2.50E-01	ARPC4 /// TTLL3	actin related protein 2/3 complex, subunit 4, 20kDa /// tubulin tyrosine ligase-like family, member 3	chr3p25.3	217818_s_at	NM_001024959 /// NM_001024960 /// NM_001025930 /// NM_005718 /// NM_015644																				
6.13	5.66	0.47	1.92E-02	2.51E-01	KDSR	3-ketodihydrosphingosine reductase	chr18q21.3	202419_at	NM_002035																				
4.75	3.64	1.11	1.92E-02	2.51E-01	LOC100133197 /// PDXK	similar to Pyridoxal (pyridoxine, vitamin B6) kinase /// pyridoxal (pyridoxine, vitamin B6) kinase	chr21q22.3	1566671_a_at	NM_003681 /// XM_001719679 /// XM_001722695 /// XM_001726242																				
9.32	8.83	0.49	1.92E-02	2.51E-01	STARD7	StAR-related lipid transfer (START) domain containing 7	chr2q11.2	200028_s_at	NM_020151																				
7.39	6.99	0.41	1.92E-02	2.51E-01	MBTPS1	membrane-bound transcription factor peptidase, site 1	chr16|16q24	201620_at	NM_003791																				

7.69	7.14	0.55	1.93E-02	2.51E-01	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	chr19q13.2	208713_at	NM_007040 /// NM_144732																				
4.56	3.71	0.86	1.93E-02	2.51E-01	C11orf31	chromosome 11 open reading frame 31	chr11q12.1	1557801_x_at	NM_170746																				
4.58	4.06	0.53	1.93E-02	2.51E-01	PATL1	protein associated with topoisomerase II homolog 1 (yeast)	chr11q12.1	225468_at	NM_152716																				
5.74	5.30	0.43	1.93E-02	2.51E-01	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	chr12q13.12	40465_at	NM_004818																				
4.74	4.13	0.61	1.93E-02	2.51E-01	RERE	arginine-glutamic acid dipeptide (RE) repeats	chr1p36.2-p36.1	221643_s_at	NM_001042681 /// NM_001042682 /// NM_012102																				
7.88	7.17	0.72	1.93E-02	2.51E-01	IFI35	interferon-induced protein 35	chr17q21	209417_s_at	NM_005533																				
6.36	5.95	0.41	1.93E-02	2.51E-01	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	chr12q13.12	201440_at	NM_004818																				
3.59	3.07	0.52	1.93E-02	2.51E-01	---	---	---	238179_at	---																				
4.30	3.94	0.36	1.93E-02	2.51E-01	---	---	---	233378_at	---																				
4.55	4.02	0.53	1.94E-02	2.52E-01	GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	chr2p23.3	210620_s_at	NM_001035521 /// NM_001521																				
8.79	8.38	0.41	1.94E-02	2.52E-01	C1orf51 /// MRPS21	chromosome 1 open reading frame 51 /// mitochondrial ribosomal protein S21	chr1q21 /// chr1q21.2	222997_s_at	NM_018997 /// NM_031901 /// NM_144697																				
8.17	7.61	0.56	1.94E-02	2.52E-01	ILF2	interleukin enhancer binding factor 2, 45kDa	chr1q21.3	200052_s_at	NM_004515																				
4.57	4.15	0.42	1.94E-02	2.52E-01	CTPS	CTP synthase	chr1p34.1	202613_at	NM_001905																				
7.00	6.45	0.55	1.94E-02	2.52E-01	GOLGA3	golgi autoantigen, golgin subfamily a, 3	chr12q24.33	202106_at	NM_005895																				
5.48	4.96	0.52	1.94E-02	2.52E-01	RP3-377H14.5	hypothetical protein FLJ35429	chr6p22.1	222279_at	XR_039876 /// XR_039877 /// XR_039878 /// XR_039879 /// XR_039880																				
5.12	4.48	0.64	1.94E-02	2.52E-01	ZNF839	zinc finger protein 839	chr14q32.31	221709_s_at	NM_018335																				
4.28	3.33	0.95	1.94E-02	2.52E-01	DPP7	Dipeptidyl-peptidase 7	chr9q34.3	238012_at	NM_013379																				
6.11	5.43	0.68	1.94E-02	2.52E-01	JMJD3	jumonji domain containing 3, histone lysine demethylase	chr17p13.1	41386_i_at	NM_001080424																				
5.04	4.27	0.77	1.94E-02	2.52E-01	LOC100134053 /// LOC392713 /// LOC441259 /// POLR2J2 /// POLR2J4	similar to POLR2J4 protein /// similar to hCG1989139 /// PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like /// polymerase (RNA) II (DNA directed) polypeptide J2 /// polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13 /// chr7q11.23 /// chr7q22.1	1552622_s_at	NM_032959 /// NR_003655 /// XM_001713964 /// XM_001714277 /// XM_001717094 /// XM_001718001 /// XM_001718158 /// XR_042143 /// XR_042182																				
5.05	4.52	0.54	1.94E-02	2.52E-01	KIAA0753	KIAA0753	chr17p13.2	204711_at	NM_014804																				
6.82	5.92	0.91	1.94E-02	2.52E-01	ACCS	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	chr11p11	228264_at	NM_001127219 /// NM_032592																				
7.45	6.82	0.63	1.94E-02	2.52E-01	PPP2R5D	protein phosphatase 2, regulatory subunit B', delta isoform	chr6p21.1	202513_s_at	NM_006245 /// NM_180976 /// NM_180977																				
7.15	6.77	0.39	1.94E-02	2.52E-01	NSUN2	NOL1/NOP2/Sun domain family, member 2	chr5p15.31	223076_s_at	NM_017755																				
12.31	11.96	0.35	1.94E-02	2.52E-01	RPS5	ribosomal protein S5	chr19q13.4	200024_at	NM_001009																				
6.20	5.55	0.66	1.94E-02	2.52E-01	BMP1	bone morphogenetic protein 1	chr8p21.3	205574_x_at	NM_001199 /// NM_006128 /// NM_006129																				
5.77	5.25	0.52	1.95E-02	2.52E-01	ZBTB17	zinc finger and BTB domain containing 17	chr1p36.2-p36.1	203602_s_at	NM_003443																				
7.79	7.27	0.52	1.95E-02	2.52E-01	MDM4	Mdm4 p53 binding protein homolog (mouse)	chr1q32	235589_s_at	NM_002393																				

2.50	2.09	0.40	1.95E-02	2.52E-01	GNAS	GNAS complex locus	chr20q13.3	235851_s_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259																				
7.38	6.90	0.48	1.95E-02	2.52E-01	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	chr3q27-q28	201998_at	NM_003032 /// NM_173216 /// NM_173217																				
6.79	5.92	0.88	1.95E-02	2.52E-01	ZNF436	zinc finger protein 436	chr1p36	226113_at	NM_001077195 /// NM_030634																				
4.44	3.93	0.51	1.95E-02	2.52E-01	---	---	---	227076_at	---																				
2.77	2.19	0.58	1.95E-02	2.52E-01	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	chrXp11.4-p11.2	230652_at	NM_001654																				
7.38	6.88	0.50	1.96E-02	2.52E-01	DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	chr6p21.3	203694_s_at	NM_003587																				
5.01	3.40	1.61	1.96E-02	2.52E-01	BCAT1	branched chain aminotransferase 1, cytosolic	chr12p12.1	214452_at	NM_005504																				
7.20	6.52	0.68	1.96E-02	2.52E-01	COQ6	coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	chr14q24.3	218760_at	NM_182476 /// NM_182480																				
7.80	6.47	1.34	1.96E-02	2.52E-01	SLC25A37	solute carrier family 25, member 37	chr8p21.2	218136_s_at	NM_016612																				
5.73	4.69	1.05	1.96E-02	2.52E-01	RNF19B	ring finger protein 19B	chr1p35.1	213038_at	NM_001127361 /// NM_153341																				
4.10	3.04	1.06	1.96E-02	2.52E-01	CYB5R2	cytochrome b5 reductase 2	chr11p15.4	220230_s_at	NM_016229																				
7.10	6.56	0.54	1.96E-02	2.52E-01	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	chr14q12	220052_s_at	NM_001099274 /// NM_012461																				
7.96	7.42	0.54	1.96E-02	2.52E-01	RIC8A	resistance to inhibitors of cholinesterase 8 homolog A (C. elegans)	chr11p15.5	221647_s_at	NM_021932																				
6.09	5.19	0.90	1.96E-02	2.52E-01	TMEM61	transmembrane protein 61	chr1p32.3	230822_at	NM_182532																				
6.92	6.23	0.70	1.97E-02	2.52E-01	PARP6	poly (ADP-ribose) polymerase family, member 6	chr15q23	219639_x_at	NM_020214																				
5.93	4.85	1.08	1.97E-02	2.52E-01	PHF20L1	PHD finger protein 20-like 1	chr8q24.22	230098_at	NM_016018 /// NM_032205 /// NM_198513																				
5.70	4.99	0.71	1.97E-02	2.52E-01	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	chr19q13.1	203419_at	NM_014727																				
5.33	3.19	2.14	1.97E-02	2.52E-01	7A5	putative binding protein 7a5	chr7p15.3	232151_at	NM_182762																				
6.08	5.24	0.84	1.97E-02	2.52E-01	ANGEL2	angel homolog 2 (Drosophila)	chr1q32.3	221825_at	NM_144567																				
5.29	4.66	0.63	1.97E-02	2.52E-01	C19orf61	chromosome 19 open reading frame 61	chr19q13.31	221335_x_at	NM_019108																				
4.13	3.42	0.71	1.97E-02	2.52E-01	LOC100129022	Hypothetical protein LOC100129022	chr12q24.31	227332_at	XM_001714874 /// XM_001716591 /// XM_001719032																				
10.08	9.65	0.43	1.97E-02	2.52E-01	TUBB	tubulin, beta	chr6p21.33	209026_x_at	NM_178014																				
4.13	3.56	0.57	1.97E-02	2.53E-01	EP300	E1A binding protein p300	chr22q13.2	213579_s_at	NM_001429																				
4.47	3.95	0.53	1.98E-02	2.53E-01	EMILIN3	elastin microfibril interfacer 3	chr20q11.2-q12	228307_at	NM_052846																				
6.32	5.03	1.29	1.98E-02	2.53E-01	MGC21881	hypothetical locus MGC21881	chr9q21.11	1555874_x_at	NR_015363 /// XR_041522 /// XR_041523																				
8.64	8.14	0.50	1.98E-02	2.53E-01	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	chr14q24	201491_at	NM_012111																				
2.67	2.27	0.40	1.98E-02	2.53E-01	TCTE3	T-complex-associated-testis-expressed 3	chr6q27	1557945_at	NM_174910																				
10.81	10.34	0.47	1.99E-02	2.53E-01	RPL36	ribosomal protein L36	chr19p13.3	219762_s_at	NM_015414 /// NM_033643																				
2.73	2.38	0.35	1.99E-02	2.53E-01	C9orf66	chromosome 9 open reading frame 66	chr9p24.3	1552757_s_at	NM_152569																				
5.44	4.66	0.79	1.99E-02	2.53E-01	C14orf43	chromosome 14 open reading frame 43	chr14q24.3	225980_at	NM_001043318 /// NM_194278																				
4.51	3.56	0.95	1.99E-02	2.53E-01	HIC2	hypermethylated in cancer 2	chr22q11.21	212964_at	NM_015094																				

6.60	5.89	0.71	1.99E-02	2.53E-01	TYK2	tyrosine kinase 2	chr19p13.2	205546_s_at	NM_003331
3.02	2.59	0.43	1.99E-02	2.53E-01	BRUNOL6	bruno-like 6, RNA binding protein (Drosophila)	chr15q24	227775_at	NM_052840
9.59	9.20	0.38	1.99E-02	2.53E-01	HEBP1	heme binding protein 1	chr12p13.1	218450_at	NM_015987
5.38	4.76	0.61	1.99E-02	2.53E-01	CXorf34	chromosome X open reading frame 34	chrXq22.1	205238_at	NM_024917
6.52	5.64	0.87	1.99E-02	2.54E-01	KAT2A	K(lysine) acetyltransferase 2A	chr17q21	202182_at	NM_021078
4.09	3.52	0.57	1.99E-02	2.54E-01	ZNF509	zinc finger protein 509	chr4p16.2	229089_at	NM_145291
5.11	4.25	0.86	2.00E-02	2.54E-01	COL27A1	collagen, type XXVII, alpha 1	chr9q32	225293_at	NM_032888
4.97	4.25	0.72	2.00E-02	2.54E-01	C1orf38	chromosome 1 open reading frame 38	chr1p35.3	210785_s_at	NM_001039477 /// NM_001105556 /// NM_004848
4.37	3.81	0.56	2.01E-02	2.54E-01	CCR5 /// LOC727797	chemokine (C-C motif) receptor 5 /// C-C chemokine receptor type 5-like	chr3p21.31	206991_s_at	NM_000579 /// NM_001100168 /// NM_001105536
7.62	7.00	0.62	2.01E-02	2.54E-01	RREB1	ras responsive element binding protein 1	chr6p25	203704_s_at	NM_001003698 /// NM_001003699 /// NM_002955
7.46	6.97	0.48	2.01E-02	2.55E-01	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	chr14q22.3	212644_s_at	NM_144578
3.32	2.93	0.39	2.01E-02	2.55E-01	GAGE12B /// GAGE12C /// GAGE12D /// GAGE12E /// GAGE12F /// GAGE12G /// GAGE12H /// GAGE12I /// GAGE13 /// GAGE2A /// GAGE2B /// GAGE2C /// GAGE2E /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7	G antigen 12B /// G antigen 12C /// G antigen 12D /// G antigen 12E /// G antigen 12F /// G antigen 12G /// G antigen 12H /// G antigen 12I /// G antigen 13 /// G antigen 2A /// G antigen 2B /// G antigen 2C /// G antigen 2E /// G antigen 4 /// G antigen 5 /// G antigen 6 /// G antigen 7	chrXp11.23 /// chrXp11.4-p11.2	206640_x_at	NM_001085441 /// NM_001098405 /// NM_001098408 /// NM_001098409 /// NM_001098410 /// NM_001098411 /// NM_001098418 /// NM_001127199 /// NM_001127200 /// NM_001127212 /// NM_001127345 /// NM_001472 /// NM_001474 /// NM_001475 /// NM_001476 /// NM_001477 /// NM_021123 /// XM_001130991 /// XM_001713660 /// XM_001720189
4.71	4.22	0.49	2.01E-02	2.55E-01	MYOM2	myomesin (M-protein) 2, 165kDa	chr8p23.3	205826_at	NM_003970
7.23	6.08	1.15	2.02E-02	2.55E-01	FERMT1	fermitin family homolog 1 (Drosophila)	chr20p12.3	60474_at	NM_017671
5.56	4.77	0.79	2.02E-02	2.55E-01	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	chr2q37.3	201314_at	NM_006374
6.50	5.75	0.76	2.02E-02	2.55E-01	HDAC6	histone deacetylase 6	chrXp11.23	206846_s_at	NM_006044

5.06	4.57	0.49	2.02E-02	2.55E-01	MSTO1 /// MSTO2P	misato homolog 1 (Drosophila) /// misato homolog 2 pseudogene	chr1q22	218296_x_at	NM_018116 /// NR_024117 /// XM_001713716 /// XR_039074 /// XR_039412																			
6.01	5.64	0.37	2.02E-02	2.55E-01	AARSD1	alanyl-tRNA synthetase domain containing 1	chr17q21.31	222064_s_at	NM_025267																			
4.64	4.21	0.43	2.02E-02	2.55E-01	TDP1	tyrosyl-DNA phosphodiesterase 1	chr14q32.11	219715_s_at	NM_001008744 /// NM_018319																			
3.00	2.64	0.37	2.02E-02	2.55E-01	---	---	---	219881_s_at	---																			
12.27	11.99	0.28	2.03E-02	2.55E-01	RPL29 /// RPL29P4	ribosomal protein L29 /// ribosomal protein L29 pseudogene 4	chr3p21.3-p21.2 /// chr6q22.2	213969_x_at	NM_000992																			
6.01	4.91	1.10	2.03E-02	2.55E-01	LZTS2	leucine zipper, putative tumor suppressor 2	chr10q24	1555881_s_at	NM_032429																			
9.57	7.90	1.67	2.03E-02	2.55E-01	HOXA5	homeobox A5	chr7p15-p14	213844_at	NM_019102																			
4.97	4.39	0.58	2.03E-02	2.55E-01	C16orf84	chromosome 16 open reading frame 84	chr16q24.3	226410_at	NM_001012759 /// NM_001012762																			
3.63	3.22	0.41	2.03E-02	2.56E-01	---	---	---	238979_at	---																			
3.54	2.98	0.56	2.03E-02	2.56E-01	---	---	---	1558766_at	---																			
5.06	4.45	0.61	2.04E-02	2.56E-01	MUM1	melanoma associated antigen (mutated) 1	chr19p13.3	223348_x_at	NM_032853																			
6.80	6.23	0.57	2.04E-02	2.56E-01	BRD8	bromodomain containing 8	chr5q31	202227_s_at	NM_006696 /// NM_139199 /// NM_183359																			
5.16	4.44	0.72	2.04E-02	2.56E-01	SYNGR1	synaptogyrin 1	chr22q13.1	213854_at	NM_004711 /// NM_145731 /// NM_145738																			
6.88	6.28	0.60	2.04E-02	2.56E-01	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	213324_at	NM_005417 /// NM_198291																			
6.67	5.34	1.33	2.04E-02	2.56E-01	LOC388796	hypothetical LOC388796	chr20q11.23	225857_s_at	NR_015366 /// XM_001720823 /// XM_001720894 /// XM_001721371																			
6.02	5.21	0.81	2.04E-02	2.56E-01	PRCC	papillary renal cell carcinoma (translocation-associated)	chr1q21.1	208938_at	NM_005973 /// NM_199416																			
6.80	6.21	0.59	2.05E-02	2.57E-01	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	chr16q21-q23	221567_at	NM_003946																			
5.16	4.71	0.46	2.05E-02	2.57E-01	PHKA2	phosphorylase kinase, alpha 2 (liver)	chrXp22.2-p22.1	209438_at	NM_000292																			
4.21	3.81	0.40	2.05E-02	2.57E-01	LOC401320	Hypothetical LOC401320	chr7p15.1	1558459_s_at	XM_379482 /// XM_380098 /// XM_938539																			
5.97	5.35	0.62	2.05E-02	2.57E-01	ELMO2	engulfment and cell motility 2	chr20q13	55692_at	NM_133171 /// NM_182764																			
4.20	3.10	1.10	2.05E-02	2.57E-01	WDR8	WD repeat domain 8	chr1p36.3	236381_s_at	NM_017818																			
4.38	3.36	1.02	2.05E-02	2.57E-01	FAM153A /// FAM153B /// FAM153C	family with sequence similarity 153, member A /// family with sequence similarity 153, member B /// family with sequence similarity 153, member C	chr5q35.2 /// chr5q35.3	214945_at	NM_001079527 /// NM_001079529 /// NM_173663 /// XM_001716960																			
5.88	4.94	0.94	2.05E-02	2.57E-01	LARS2	leucyl-tRNA synthetase 2, mitochondrial	chr3p21.3	34764_at	NM_015340																			
3.49	3.05	0.44	2.06E-02	2.57E-01	---	---	---	236090_at	---																			
4.45	3.17	1.28	2.06E-02	2.57E-01	IFRD1	interferon-related developmental regulator 1	chr7q22-q31	202147_s_at	NM_001007245 /// NM_001550																			
5.46	3.87	1.59	2.06E-02	2.57E-01	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	chr2p13.3	219825_at	NM_019885																			

5.07	3.99	1.08	2.06E-02	2.57E-01	FNBP4	formin binding protein 4	chr11p11.2	229272_at	NM_015308
10.12	9.25	0.87	2.07E-02	2.58E-01	HSPA1A /// HSPA1B	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	chr6p21.3	200799_at	NM_005345 /// NM_005346
7.09	6.38	0.72	2.07E-02	2.58E-01	TMEM184B	transmembrane protein 184B	chr22q12	202027_at	NM_012264
3.73	3.16	0.57	2.07E-02	2.58E-01	C3orf31	chromosome 3 open reading frame 31	chr3p25.2	226815_at	NM_138807
6.73	6.13	0.59	2.07E-02	2.58E-01	MAN1B1	mannosidase, alpha, class 1B, member 1	chr9q34	65884_at	NM_016219
7.46	6.73	0.73	2.08E-02	2.58E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	210776_x_at	NM_003200
6.68	5.93	0.76	2.08E-02	2.58E-01	SLC31A2	solute carrier family 31 (copper transporters), member 2	chr9q31-q32	204204_at	NM_001860
5.41	4.27	1.14	2.08E-02	2.58E-01	SFRS18	splicing factor, arginine/serine-rich 18	chr6q16.3	212179_at	NM_015491 /// NM_032870
10.05	9.10	0.94	2.08E-02	2.58E-01	JUND	jun D proto-oncogene	chr19p13.2	203752_s_at	NM_005354
8.09	7.59	0.49	2.08E-02	2.58E-01	NOTCH2	Notch homolog 2 (Drosophila)	chr1p13-p11	202443_x_at	NM_024408
5.51	4.83	0.68	2.08E-02	2.58E-01	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	chr2q37.1	219997_s_at	NM_022730
2.54	2.27	0.27	2.08E-02	2.58E-01	---	---	---	243332_at	---
5.57	5.00	0.58	2.08E-02	2.58E-01	RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	chr11q13	209878_s_at	NM_021975
7.03	6.44	0.59	2.08E-02	2.58E-01	LYK5	protein kinase LYK5	chr17q23.3	52169_at	NM_001003786 /// NM_001003787 /// NM_001003788 /// NM_153335
5.71	4.87	0.85	2.09E-02	2.59E-01	CDC25B	cell division cycle 25 homolog B (S. pombe)	chr20p13	201853_s_at	NM_004358 /// NM_021872 /// NM_021873
3.26	2.22	1.04	2.09E-02	2.59E-01	C11orf31	chromosome 11 open reading frame 31	chr11q12.1	228331_at	NM_170746
6.62	5.89	0.72	2.09E-02	2.59E-01	SEPHS1	selenophosphate synthetase 1	chr10p14	208939_at	NM_012247
11.06	10.64	0.43	2.09E-02	2.59E-01	RNASEK	ribonuclease, RNase K	chr17p13.1	224573_at	NM_001004333
4.63	4.08	0.55	2.09E-02	2.59E-01	HRBL	HIV-1 Rev binding protein-like	chr7q22.1	206821_x_at	NM_006076
4.13	3.77	0.35	2.09E-02	2.59E-01	KIF3A	kinesin family member 3A	chr5q31	228680_at	NM_007054
7.20	6.41	0.79	2.09E-02	2.59E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	213730_x_at	NM_003200
8.83	8.29	0.54	2.09E-02	2.59E-01	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	chr19p13.3	223318_s_at	NM_032306
7.88	7.29	0.59	2.09E-02	2.59E-01	ISCA2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)	chr14q24.3	226007_at	NM_194279
5.84	5.37	0.47	2.09E-02	2.59E-01	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	chr7q22.1	222615_s_at	NM_024653
6.38	5.27	1.11	2.10E-02	2.59E-01	JUND	jun D proto-oncogene	chr19p13.2	214326_x_at	NM_005354
4.87	4.28	0.59	2.10E-02	2.59E-01	---	---	---	230446_at	---
5.86	5.12	0.74	2.10E-02	2.59E-01	---	---	---	228175_at	---
5.07	4.35	0.72	2.10E-02	2.59E-01	TAF1C	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	chr16q24	203938_s_at	NM_005679 /// NM_139353
8.24	7.03	1.22	2.10E-02	2.59E-01	SDC3	syndecan 3	chr1pter-p22.3	202898_at	NM_014654
4.81	4.10	0.71	2.10E-02	2.59E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	227199_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891
9.02	8.31	0.72	2.11E-02	2.59E-01	HLA-DMB	major histocompatibility complex, class II, DM beta	chr6p21.3	203932_at	NM_002118
3.57	3.14	0.43	2.11E-02	2.59E-01	---	---	---	232677_at	---
7.82	6.22	1.60	2.11E-02	2.59E-01	AVPI1	arginine vasopressin-induced 1	chr10q24.2	218631_at	NM_021732
3.76	3.23	0.53	2.11E-02	2.60E-01	CCDC90A	Coiled-coil domain containing 90A	chr6p24.3-p23	227451_s_at	NM_001031713
5.20	4.58	0.62	2.11E-02	2.60E-01	USP42	ubiquitin specific peptidase 42	chr7p22.1	226669_at	NM_032172
3.69	3.18	0.51	2.11E-02	2.60E-01	ZNF653	zinc finger protein 653	chr19p13.2	228864_at	NM_138783
3.98	3.46	0.51	2.12E-02	2.60E-01	---	---	---	228309_at	---
7.57	6.98	0.59	2.12E-02	2.60E-01	YIPF3	Yip1 domain family, member 3	chr6p21.1	216338_s_at	NM_015388
5.60	5.04	0.55	2.12E-02	2.60E-01	EGLN1	egl nine homolog 1 (C. elegans)	chr1q42.1	221497_x_at	NM_022051
3.47	2.46	1.01	2.12E-02	2.60E-01	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	chr2q23.3	206025_s_at	NM_007115
7.14	6.40	0.74	2.13E-02	2.60E-01	PRKCD	protein kinase C, delta	chr3p21.31	202545_at	NM_006254 /// NM_212539
5.31	4.12	1.19	2.13E-02	2.60E-01	FLJ21865	endo-beta-N-acetylglucosaminidase	chr17q25.3	220349_s_at	NM_001042573
5.66	5.02	0.64	2.13E-02	2.60E-01	CBR4	carbonyl reductase 4	chr4q32.3	213626_at	NM_032783
6.00	5.34	0.66	2.13E-02	2.60E-01	SETD2	SET domain containing 2	chr3p21.31	215038_s_at	NM_014159
8.23	7.74	0.49	2.13E-02	2.60E-01	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	chr18p11	1557820_at	NM_006796

7.39	6.86	0.53	2.13E-02	2.60E-01	C9orf23	chromosome 9 open reading frame 23	chr9p13.3	225403_at	NM_148178 /// NM_148179
3.92	3.24	0.68	2.13E-02	2.60E-01	---	---	---	1559948_at	---
3.00	2.55	0.45	2.14E-02	2.60E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	1561286_a_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891
4.13	3.62	0.51	2.14E-02	2.60E-01	ACTR3B	ARP3 actin-related protein 3 homolog B (yeast)	chr7q36.1	218868_at	NM_001040135 /// NM_020445
5.18	4.22	0.96	2.14E-02	2.60E-01	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	chr19q13.2	209498_at	NM_001024912 /// NM_001712
7.21	6.42	0.78	2.14E-02	2.60E-01	C15orf17	chromosome 15 open reading frame 17	chr15q24.1	224804_s_at	NM_020447
2.77	2.40	0.37	2.14E-02	2.60E-01	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	chr2q37.3	1554719_at	NM_004544
5.14	4.40	0.74	2.14E-02	2.60E-01	C9orf64	chromosome 9 open reading frame 64	chr9q21.32	235940_at	NM_032307
8.23	7.36	0.87	2.14E-02	2.61E-01	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	chr5q35.3	201031_s_at	NM_005520
5.42	4.62	0.80	2.14E-02	2.61E-01	---	---	---	229833_at	---
5.75	4.86	0.89	2.14E-02	2.61E-01	HLA-DOA	major histocompatibility complex, class II, DO alpha	chr6p21.3	226878_at	NM_002119
6.32	5.77	0.55	2.14E-02	2.61E-01	HYI	hydroxypyruvate isomerase homolog (E. coli)	chr1p34.2	221435_x_at	NM_031207
8.76	8.32	0.44	2.14E-02	2.61E-01	SEC13	SEC13 homolog (S. cerevisiae)	chr3p25-p24	207707_s_at	NM_183352
5.55	4.45	1.10	2.15E-02	2.61E-01	PLAUR	plasminogen activator, urokinase receptor	chr19q13	210845_s_at	NM_001005376 /// NM_001005377 /// NM_002659
5.18	4.52	0.66	2.15E-02	2.61E-01	---	---	---	227559_at	---
7.63	7.04	0.60	2.15E-02	2.61E-01	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	chr5q35	220189_s_at	NM_014275 /// NM_054013
6.76	6.05	0.71	2.15E-02	2.61E-01	RP3-402G11.5	selenoprotein O	chr22q13.33	233168_s_at	NM_031454
4.25	3.77	0.48	2.15E-02	2.61E-01	OTUD3	OTU domain containing 3	chr1p36.13	213216_at	NM_015207
5.75	5.13	0.62	2.16E-02	2.61E-01	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	chr14q12	202847_at	NM_001018073 /// NM_004563
8.47	7.69	0.79	2.16E-02	2.61E-01	TBX3	T-box 3	chr12q24.1	229576_s_at	NM_005996 /// NM_016569
3.29	2.78	0.51	2.16E-02	2.61E-01	ZNF280D	zinc finger protein 280D	chr15q21.3	1568951_at	NM_001002843 /// NM_001002844 /// NM_017661
6.73	6.13	0.60	2.16E-02	2.61E-01	SLBP	stem-loop binding protein	chr4p16.3	206052_s_at	NM_006527
3.55	2.92	0.63	2.16E-02	2.61E-01	FAM149A	family with sequence similarity 149, member A	chr4q35.2	214890_s_at	NM_001006655 /// NM_015398
8.00	7.61	0.39	2.16E-02	2.61E-01	HDAC1	histone deacetylase 1	chr1p34	201209_at	NM_004964
3.11	2.59	0.52	2.16E-02	2.61E-01	---	---	---	232107_at	---
3.24	2.54	0.70	2.16E-02	2.61E-01	SSBP1	single-stranded DNA binding protein 1	chr7q34	214060_at	NM_003143
7.03	6.46	0.57	2.16E-02	2.61E-01	TOP1MT	topoisomerase (DNA) I, mitochondrial	chr8q24.3	225802_at	NM_052963
5.58	4.95	0.63	2.17E-02	2.61E-01	MON1B	MON1 homolog B (yeast)	chr16q23.1	233557_s_at	NM_014940
5.98	5.46	0.52	2.17E-02	2.61E-01	TTC4	tetratricopeptide repeat domain 4	chr1p32.3	46167_at	NM_004623 /// XM_001726392 /// XM_001726400 /// XM_001726506
3.94	3.43	0.51	2.17E-02	2.61E-01	hCG_2033039	hypothetical protein BC006136	chr11q23.1	229989_at	NM_138378
8.04	7.52	0.52	2.17E-02	2.62E-01	SCAND1	SCAN domain containing 1	chr20q11.1-q11.23	231059_x_at	NM_016558 /// NM_033630
7.59	6.87	0.72	2.17E-02	2.62E-01	CTBP1	C-terminal binding protein 1	chr4p16	203392_s_at	NM_001012614 /// NM_001328
5.58	5.06	0.52	2.17E-02	2.62E-01	KIAA1166	KIAA1166	chrXq11.1	220040_x_at	NM_018684
7.28	6.75	0.53	2.18E-02	2.62E-01	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	chr5q35.3	217840_at	NM_016222
4.53	3.77	0.77	2.18E-02	2.62E-01	TMEM103	Transmembrane protein 103	chr3p21.31	229864_at	NM_001031703
7.01	6.56	0.45	2.18E-02	2.62E-01	JMJD1B	jumonji domain containing 1B	chr5q31	210878_s_at	NM_016604
3.84	2.97	0.86	2.18E-02	2.62E-01	---	---	---	235571_at	---

5.69	5.07	0.62	2.18E-02	2.62E-01	CCDC22	coiled-coil domain containing 22	chrXp11.23	206016_at	NM_014008																				
12.31	12.06	0.25	2.18E-02	2.62E-01	RPLP0	ribosomal protein, large, P0	chr12q24.2	208856_x_at	NM_001002 /// NM_053275																				
5.76	5.12	0.65	2.18E-02	2.62E-01	RASSF2	Ras association (RalGDS/AF-6) domain family member 2	chr20pter-p12.1	203185_at	NM_014737 /// NM_170774																				
3.53	3.13	0.39	2.18E-02	2.62E-01	YPEL4	yippee-like 4 (Drosophila)	chr11q12.1	235916_at	NM_145008																				
4.41	3.73	0.68	2.18E-02	2.62E-01	NOL3	Nucleolar protein 3 (apoptosis repressor with CARD domain)	chr16q21-q23	1558738_at	NM_003946																				
3.42	3.01	0.41	2.18E-02	2.62E-01	DEF6	differentially expressed in FDCP 6 homolog (mouse)	chr6p21.33-p21.1	226659_at	NM_022047																				
8.88	7.64	1.24	2.19E-02	2.62E-01	GADD45B	growth arrest and DNA-damage-inducible, beta	chr19p13.3	209304_x_at	NM_015675																				
4.54	3.68	0.86	2.19E-02	2.62E-01	---	---	---	229235_at	---																				
7.75	6.74	1.01	2.19E-02	2.62E-01	NLK	nemo-like kinase	chr17q11.2	222589_at	NM_016231																				
6.95	6.18	0.78	2.19E-02	2.62E-01	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	chr19p13.2-p13.11	211168_s_at	NM_002911																				
3.91	2.94	0.97	2.19E-02	2.62E-01	C4orf30	chromosome 4 open reading frame 30	chr4p15.32	228106_at	NM_017741																				
2.75	2.46	0.29	2.19E-02	2.62E-01	---	---	---	241341_at	---																				
3.15	2.33	0.82	2.19E-02	2.62E-01	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	chr16p13.3	1569867_at	NM_001010865																				
7.92	6.79	1.13	2.20E-02	2.63E-01	LONRF2	LON peptidase N-terminal domain and ring finger 2	chr2q11.2	225996_at	NM_198461																				
4.45	3.85	0.60	2.20E-02	2.63E-01	C5orf35	chromosome 5 open reading frame 35	chr5q11.2	238465_at	NM_153706																				
6.28	5.57	0.71	2.20E-02	2.63E-01	C1orf66	chromosome 1 open reading frame 66	chr1q23.1	218914_at	NM_015997																				
4.85	4.30	0.55	2.20E-02	2.63E-01	---	---	---	228639_at	---																				
9.19	8.72	0.48	2.20E-02	2.63E-01	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	chr16p13.3	213535_s_at	NM_003345 /// NM_194259 /// NM_194260 /// NM_194261																				
7.52	6.90	0.62	2.20E-02	2.63E-01	LOC644096	hypothetical protein LOC644096	chr19q13.12	221855_at	NM_001042631																				
7.01	6.52	0.49	2.20E-02	2.63E-01	NCSTN	nicastrin	chr1q22-q23	208759_at	NM_015331																				
2.41	1.88	0.53	2.20E-02	2.63E-01	SNORA72	small nucleolar RNA, H/ACA box 72	chr8q22	228047_at	NR_002581																				
7.10	6.75	0.34	2.20E-02	2.63E-01	MPZL1	myelin protein zero-like 1	chr1q24.2	201874_at	NM_003953 /// NM_024569																				
4.95	4.15	0.80	2.20E-02	2.63E-01	TRIM45	tripartite motif-containing 45	chr1p13.1	219923_at	NM_025188																				
8.79	8.23	0.56	2.20E-02	2.63E-01	ZBTB4	zinc finger and BTB domain containing 4	chr17p13.1	225629_s_at	NM_001128833 /// NM_020899																				
7.86	7.17	0.69	2.21E-02	2.63E-01	CTSB	cathepsin B	chr8p22	227961_at	NM_001908 /// NM_147780 /// NM_147781 /// NM_147782 /// NM_147783																				
5.84	4.70	1.14	2.21E-02	2.63E-01	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	chr3p21	205614_x_at	NM_020998																				
6.09	5.19	0.90	2.21E-02	2.63E-01	SLTM	SAFB-like, transcription modulator	chr15q22.1	217828_at	NM_001013843 /// NM_024755																				
5.44	4.55	0.89	2.21E-02	2.63E-01	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	chr14q24.3	219316_s_at	NM_017791																				
5.32	4.66	0.66	2.21E-02	2.63E-01	MFSD3	major facilitator superfamily domain containing 3	chr8q24.3	227296_at	NM_138431																				
7.67	6.95	0.72	2.21E-02	2.63E-01	MYD88	myeloid differentiation primary response gene (88)	chr3p22	209124_at	NM_002468																				
3.52	2.43	1.09	2.21E-02	2.63E-01	TFPI2	tissue factor pathway inhibitor 2	chr7q22	209277_at	NM_006528																				
6.96	6.33	0.62	2.21E-02	2.63E-01	C16orf53	chromosome 16 open reading frame 53	chr16p11.2	218300_at	NM_024516																				
3.02	2.69	0.33	2.21E-02	2.63E-01	NFYA	nuclear transcription factor Y, alpha	chr6p21.3	228433_at	NM_002505 /// NM_021705 /// XM_001716589 /// XM_001717592 /// XM_001718396																				
6.82	6.11	0.71	2.21E-02	2.63E-01	XBP1	X-box binding protein 1	chr22q12.1|22q12	200670_at	NM_001079539 /// NM_005080																				

3.71	3.02	0.69	2.22E-02	2.63E-01	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	chr19p13.3-p13.2	1555843_at	NM_005968 /// NM_031203																				
8.42	8.02	0.39	2.22E-02	2.63E-01	FAM32A	family with sequence similarity 32, member A	chr19pter-p13.3	201863_at	NM_014077																				
4.22	2.79	1.42	2.22E-02	2.63E-01	FAM178A	Family with sequence similarity 178, member A	chr10q24.31	235590_at	NM_018121																				
6.38	5.71	0.67	2.22E-02	2.63E-01	KIAA1545	KIAA1545 protein	chr12q24.33	225704_at	XM_001716046 /// XM_495939 /// XM_936428																				
5.48	4.86	0.62	2.22E-02	2.63E-01	ZNF324	zinc finger protein 324	chr19q13.43	205182_s_at	NM_014347																				
5.06	4.29	0.77	2.22E-02	2.63E-01	FLJ20674	hypothetical protein FLJ20674	chr12q24.23	1553991_s_at	NM_019086																				
2.74	2.35	0.39	2.23E-02	2.63E-01	RAB32	RAB32, member RAS oncogene family	chr6q24.3	228161_at	NM_006834																				
6.73	6.12	0.61	2.23E-02	2.63E-01	ILF3	interleukin enhancer binding factor 3, 90kDa	chr19p13.2	208931_s_at	NM_004516 /// NM_012218 /// NM_153464																				
3.81	2.98	0.83	2.23E-02	2.63E-01	PRPF39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	chr14q21.3	220553_s_at	NM_017922																				
4.44	3.81	0.63	2.23E-02	2.63E-01	URG4	up-regulated gene 4	chr7p13	244046_at	NM_001077663 /// NM_001077664 /// NM_017920																				
10.05	9.15	0.90	2.23E-02	2.64E-01	PEG10	paternally expressed 10	chr7q21	212094_at	NM_001040152 /// NM_015068																				
4.12	3.19	0.94	2.23E-02	2.64E-01	FOXC1	forkhead box C1	chr6p25	1553613_s_at	NM_001453																				
6.23	5.73	0.49	2.24E-02	2.64E-01	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10q25.3	216511_s_at	NM_030756																				
6.93	6.30	0.63	2.24E-02	2.64E-01	RBM15B	RNA binding motif protein 15B	chr3p21.2	202689_at	NM_013286																				
4.41	3.39	1.02	2.24E-02	2.64E-01	CCNJ	cyclin J	chr10pter-q26.12	229091_s_at	NM_001134375 /// NM_001134376 /// NM_019084																				
5.19	4.26	0.93	2.24E-02	2.64E-01	NCOA5	nuclear receptor coactivator 5	chr20q12-q13.12	225145_at	NM_020967																				
9.75	8.64	1.11	2.24E-02	2.64E-01	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	chr8q24.21	202431_s_at	NM_002467																				
2.33	2.06	0.27	2.24E-02	2.64E-01	FAM152A	family with sequence similarity 152, member A	chr1q44	222936_s_at	NM_016076																				
2.45	2.10	0.35	2.24E-02	2.64E-01	---	---	---	240597_at	---																				
4.64	4.03	0.61	2.24E-02	2.64E-01	---	---	---	235872_at	---																				
3.62	3.20	0.41	2.24E-02	2.64E-01	TTC21A	tetratricopeptide repeat domain 21A	chr3p22.2	230997_at	NM_001105513 /// NM_145755																				
3.03	2.49	0.54	2.25E-02	2.64E-01	---	---	---	230818_at	---																				
3.53	2.99	0.54	2.25E-02	2.64E-01	---	---	---	227927_at	---																				
5.44	4.88	0.56	2.25E-02	2.64E-01	APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	chr19p13.3	215148_s_at	NM_004886																				
8.61	8.05	0.56	2.25E-02	2.64E-01	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	chr20p13	209236_at	NM_005116 /// NM_203327																				
6.63	6.06	0.57	2.25E-02	2.64E-01	PWP2	PWP2 periodic tryptophan protein homolog (yeast)	chr21q22.3	209336_at	NM_005049																				
5.59	4.89	0.71	2.25E-02	2.64E-01	LOC642852	hypothetical LOC642852	chr21q22.3	243656_at	XM_001714922 /// XM_926249 /// XM_941790																				
7.67	7.23	0.44	2.25E-02	2.64E-01	LMAN2	lectin, mannose-binding 2	chr5q35.3	200805_at	NM_006816																				
6.86	6.35	0.51	2.26E-02	2.64E-01	PHACTR4	phosphatase and actin regulator 4	chr1p35.3	226823_at	NM_001048183 /// NM_023923																				
7.63	6.67	0.95	2.26E-02	2.65E-01	---	---	---	228854_at	---																				
6.76	6.23	0.54	2.26E-02	2.65E-01	PARP2	poly (ADP-ribose) polymerase 2	chr14q11.2-q12	215773_x_at	NM_001042618 /// NM_005484																				
6.11	5.58	0.54	2.26E-02	2.65E-01	HOMER3	homer homolog 3 (Drosophila)	chr19p13.11	215489_x_at	NM_004838																				
12.43	12.11	0.33	2.27E-02	2.65E-01	RPS28	ribosomal protein S28	chr19p13.2	208904_s_at	NM_001031																				
2.78	2.37	0.40	2.27E-02	2.65E-01	FLJ33706	hypothetical protein FLJ33706	chr20q11.21	1556721_at	XR_041128 /// XR_041129 /// XR_041130																				
5.00	4.12	0.88	2.27E-02	2.65E-01	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	chr7q31|14q24.2-q24.3	202843_at	NM_012328																				
5.17	4.63	0.54	2.27E-02	2.65E-01	C14orf104	chromosome 14 open reading frame 104	chr14q22.1	219166_at	NM_001083908 /// NM_018139																				

5.87	5.29	0.59	2.27E-02	2.65E-01	ZDHHC8	zinc finger, DHHC-type containing 8	chr22q11.21	225744_at	NM_013373
8.13	7.37	0.76	2.27E-02	2.65E-01	PI4KA /// PI4KAP1 /// PI4KAP2 /// PI4KAP2	phosphatidylinositol 4-kinase, catalytic, alpha /// phosphatidylinositol 4-kinase, catalytic, alpha pseudogene 1 /// phosphatidylinositol 4-kinase, catalytic, alpha pseudogene 2 /// Putative phosphatidylinositol 4-kinase alpha-like protein P2	chr22q11.21	213408_s_at	NM_002650 /// NM_058004 /// NR_003563 /// NR_003700 /// XM_001718688 /// XM_001721947 /// XR_042152 /// XR_042172
5.85	4.76	1.09	2.27E-02	2.65E-01	CREBZF	CREB/ATF bZIP transcription factor	chr11q14	202978_s_at	NM_001039618
5.95	5.24	0.71	2.27E-02	2.65E-01	---	---	---	225123_at	---
3.10	2.41	0.69	2.28E-02	2.66E-01	---	---	---	228826_at	---
7.42	6.96	0.46	2.29E-02	2.66E-01	XPO6	exportin 6	chr16p11.2	211982_x_at	NM_015171
7.89	7.26	0.63	2.29E-02	2.66E-01	C1orf85	chromosome 1 open reading frame 85	chr1q22	225401_at	NM_144580
9.36	9.00	0.36	2.29E-02	2.66E-01	RHEB	Ras homolog enriched in brain	chr7q36	201453_x_at	NM_005614
3.39	2.91	0.49	2.29E-02	2.66E-01	CAMK1	Calcium/calmodulin-dependent protein kinase I	chr3p25.3	1558556_at	NM_003656
2.78	2.47	0.31	2.29E-02	2.66E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	206462_s_at	NM_001007156 /// NM_001012338 /// NM_002530
5.27	3.27	2.00	2.30E-02	2.67E-01	XIST	X (inactive)-specific transcript (non-protein coding)	chrXq13.2	221728_x_at	NR_001564
4.80	4.19	0.61	2.30E-02	2.67E-01	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	chr12q13.13	217368_at	NM_001002031 /// NM_005176
2.40	2.09	0.30	2.30E-02	2.67E-01	LOC283666	hypothetical LOC283666	chr15q21.3	1562682_at	---
7.71	6.73	0.98	2.30E-02	2.67E-01	CLU	clusterin	chr8p21-p12	222043_at	NM_001831 /// NM_203339
2.34	1.92	0.42	2.30E-02	2.67E-01	CHD2	Chromodomain helicase DNA binding protein 2	chr15q26	230156_x_at	NM_001042572 /// NM_001271
7.49	6.99	0.51	2.30E-02	2.67E-01	RBM9	RNA binding motif protein 9	chr22q13.1	216215_s_at	NM_001031695 /// NM_001082576 /// NM_001082577 /// NM_001082578 /// NM_001082579 /// NM_014309
5.48	4.93	0.55	2.30E-02	2.67E-01	CDK10	cyclin-dependent kinase 10	chr16q24	203468_at	NM_001098533 /// NM_052987 /// NM_052988
4.79	4.27	0.52	2.31E-02	2.67E-01	ADC	arginine decarboxylase	chr1p33-p34.3	1554393_a_at	NM_052998
5.56	5.08	0.47	2.31E-02	2.67E-01	SVIP	small VCP/p97-interacting protein	chr11p14.2	226278_at	NM_148893
7.70	6.95	0.75	2.31E-02	2.67E-01	TMED4	transmembrane emp24 protein transport domain containing 4	chr7p13	1558487_a_at	NM_182547
3.92	3.23	0.69	2.31E-02	2.68E-01	TMTC4	transmembrane and tetratricopeptide repeat containing 4	chr13q32.3	1554101_a_at	NM_001079669 /// NM_032813
4.51	3.74	0.78	2.31E-02	2.68E-01	LOC400642	hypothetical LOC400642	chr18p11.31	215283_at	---
5.73	4.82	0.91	2.32E-02	2.68E-01	TTC31	tetratricopeptide repeat domain 31	chr2p13.1	218838_s_at	NM_022492
4.35	3.84	0.52	2.32E-02	2.68E-01	SMAD3	SMAD family member 3	chr15q22.33	205397_x_at	NM_005902
3.74	3.05	0.70	2.32E-02	2.68E-01	FAM119A	family with sequence similarity 119, member A	chr2q33.3	235931_at	NM_001127395 /// NM_145280
2.96	2.18	0.78	2.32E-02	2.68E-01	---	---	---	238501_at	---
3.72	2.66	1.06	2.32E-02	2.68E-01	TMEM35	transmembrane protein 35	chrXq22.1	219685_at	NM_021637
5.43	4.82	0.60	2.32E-02	2.68E-01	AGXT2L2	alanine-glyoxylate aminotransferase 2-like 2	chr5q35.3	226519_s_at	NM_153373
6.25	5.88	0.37	2.33E-02	2.68E-01	THADA	thyroid adenoma associated	chr2p21	54632_at	NM_001083953 /// NM_022065
4.78	3.41	1.37	2.33E-02	2.68E-01	BMPR1B	bone morphogenetic protein receptor, type IB	chr4q22-q24	242579_at	NM_001203

4.81	4.20	0.62	2.33E-02	2.68E-01	RNASEH1	Ribonuclease H1	chr2p25	241343_at	NM_002936
2.42	2.01	0.42	2.33E-02	2.68E-01	HIST1H2AG /// HIST1H2AH /// HIST1H2AI /// HIST1H2AJ /// HIST1H2AK /// HIST1H2AL /// HIST1H2AM	histone cluster 1, H2ag /// histone cluster 1, H2ah /// histone cluster 1, H2ai /// histone cluster 1, H2aj /// histone cluster 1, H2ak /// histone cluster 1, H2al /// histone cluster 1, H2am	chr6p21.33 /// chr6p22-p21.3 /// chr6p22.1	207156_at	NM_003509 /// NM_003510 /// NM_003511 /// NM_003514 /// NM_021064 /// NM_021066 /// NM_080596
5.90	5.47	0.43	2.33E-02	2.68E-01	HIATL2	hippocampus abundant gene transcript-like 2	chr9q22.33	224078_at	NR_002894
7.81	7.35	0.46	2.33E-02	2.68E-01	TMED4	transmembrane emp24 protein transport domain containing 4	chr7p13	224680_at	NM_182547
5.96	5.01	0.95	2.33E-02	2.68E-01	PLXNA1	plexin A1	chr3q21.3	221538_s_at	NM_032242
5.46	4.90	0.56	2.33E-02	2.68E-01	NOL9	nucleolar protein 9	chr1p36.31	1554082_a_at	NM_024654
7.36	6.49	0.87	2.33E-02	2.68E-01	PBX2	pre-B-cell leukemia homeobox 2	chr6p21.3	202876_s_at	NM_002586
6.59	6.15	0.44	2.34E-02	2.68E-01	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	chr14q22.2	225853_at	NM_198066
2.23	1.96	0.28	2.34E-02	2.69E-01	DYNLRB1	dynein, light chain, roadblock-type 1	chr20q11.21	1554568_at	NM_014183
2.84	2.56	0.29	2.34E-02	2.69E-01	CCNE1	Cyclin E1	chr19q12	242105_at	NM_001238 /// NM_057182
2.86	2.45	0.41	2.34E-02	2.69E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	213719_s_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072
2.70	2.34	0.37	2.34E-02	2.69E-01	DNHD2	dynein heavy chain domain 2	chr3p14.3	243802_at	NM_178504 /// XM_001134410 /// XM_001134433
5.03	3.78	1.25	2.34E-02	2.69E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	1559096_x_at	NM_012347 /// NM_033480 /// NM_033481
7.46	7.00	0.46	2.35E-02	2.69E-01	ERF	Ets2 repressor factor	chr19q13	203643_at	NM_006494
5.28	4.56	0.72	2.35E-02	2.69E-01	UCK2	uridine-cytidine kinase 2	chr1q23	209825_s_at	NM_012474
4.16	3.38	0.78	2.35E-02	2.69E-01	PCGF3	polycomb group ring finger 3	chr4p16.3	238084_at	NM_006315
2.65	2.27	0.38	2.35E-02	2.69E-01	ANXA3	annexin A3	chr4q13-q22	209369_at	NM_005139
2.53	2.04	0.49	2.35E-02	2.69E-01	---	---	---	235555_at	---
6.53	5.91	0.62	2.35E-02	2.69E-01	PNO1	partner of NOB1 homolog (S. cerevisiae)	chr2p14	203622_s_at	NM_020143
8.31	7.88	0.43	2.35E-02	2.69E-01	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	200073_s_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370
6.70	6.03	0.67	2.35E-02	2.69E-01	HMGN4	high mobility group nucleosomal binding domain 4	chr6p21.3	209786_at	NM_006353
2.54	2.17	0.37	2.35E-02	2.69E-01	---	---	---	241432_at	---
8.04	7.66	0.39	2.35E-02	2.69E-01	PTDSS1	phosphatidylserine synthase 1	chr8q22	201433_s_at	NM_014754
4.29	3.70	0.59	2.36E-02	2.69E-01	VASH1	Vasohibin 1	chr14q24.3	1556423_at	NM_014909
8.90	8.55	0.36	2.36E-02	2.69E-01	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	chr11p11.11	201740_at	NM_004551
4.14	3.48	0.66	2.36E-02	2.69E-01	PRR14	proline rich 14	chr16p11.2	1559397_s_at	NM_024031
3.38	2.35	1.04	2.36E-02	2.69E-01	---	---	---	236439_at	---
6.86	6.36	0.50	2.37E-02	2.69E-01	EXOSC4	exosome component 4	chr8q24.3	91684_g_at	NM_019037
5.66	5.21	0.46	2.37E-02	2.69E-01	RPS27L	ribosomal protein S27-like	chr15q22.2	222487_s_at	NM_015920
6.96	6.47	0.49	2.37E-02	2.69E-01	C2orf29	chromosome 2 open reading frame 29	chr2q11.2	224695_at	NM_017546
7.22	6.64	0.58	2.37E-02	2.69E-01	KIAA0141	KIAA0141	chr5q31.3	201978_s_at	NM_014773
6.53	6.17	0.36	2.37E-02	2.69E-01	PDCD11	programmed cell death 11	chr10q24.33	212424_at	NM_014976
5.91	5.42	0.49	2.37E-02	2.70E-01	ANGEL1	angel homolog 1 (Drosophila)	chr14q24.3	36865_at	NM_015305

2.97	2.63	0.35	2.38E-02	2.70E-01	LOC100130885	hypothetical protein LOC100130885	chr2q31.2	236213_at	XM_001716187 /// XM_001716652 /// XM_001718893																			
7.80	7.20	0.59	2.38E-02	2.70E-01	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	chr11q13.1	203188_at	NM_006876																			
9.54	8.38	1.16	2.38E-02	2.70E-01	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	chr16p12.1	215299_x_at	NM_001055 /// NM_177529 /// NM_177530 /// NM_177534 /// NM_177536																			
9.41	8.51	0.91	2.38E-02	2.70E-01	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	chr1q24	227556_at	NM_013330 /// NM_197972																			
5.52	5.03	0.49	2.38E-02	2.70E-01	CHRAC1	chromatin accessibility complex 1	chr8q24.3	231764_at	NM_017444 /// NR_023360																			
3.30	2.96	0.34	2.38E-02	2.70E-01	---	---	---	230786_at	---																			
7.55	6.92	0.63	2.38E-02	2.70E-01	MOCOS	molybdenum cofactor sulfurase	chr18q12	219959_at	NM_017947																			
7.84	6.44	1.40	2.38E-02	2.70E-01	RPRM	reprimo, TP53 dependent G2 arrest mediator candidate	chr2q23.3	219370_at	NM_019845																			
6.02	5.56	0.46	2.39E-02	2.70E-01	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	chr15q26.3	215722_s_at	NM_003090																			
7.62	6.84	0.78	2.39E-02	2.70E-01	MAML1	mastermind-like 1 (Drosophila)	chr5q35	202360_at	NM_014757																			
7.10	6.01	1.09	2.39E-02	2.70E-01	SLC25A37	solute carrier family 25, member 37	chr8p21.2	221920_s_at	NM_016612																			
8.92	8.57	0.35	2.40E-02	2.71E-01	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	chr1q21.2	200882_s_at	NM_002810																			
7.09	6.52	0.57	2.40E-02	2.71E-01	CRAT	carnitine acetyltransferase	chr9q34.1	209522_s_at	NM_000755 /// NM_004003																			
6.79	6.28	0.51	2.40E-02	2.71E-01	UQCC	ubiquinol-cytochrome c reductase complex chaperone	chr20q11.22	217935_s_at	NM_018244 /// NM_199487																			
7.45	6.84	0.61	2.40E-02	2.71E-01	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	chr21q22.3	218018_at	NM_003681																			
2.71	2.25	0.46	2.40E-02	2.71E-01	---	---	---	1558845_at	---																			
6.98	6.59	0.40	2.40E-02	2.71E-01	CRTAP	cartilage associated protein	chr3p22.3	226656_at	NM_006371																			
4.56	4.11	0.46	2.41E-02	2.71E-01	PKNOX1	PBX/knotted 1 homeobox 1	chr21q22.3	221883_at	NM_004571																			
6.27	5.55	0.73	2.41E-02	2.71E-01	---	---	---	227184_at	---																			
2.33	2.01	0.33	2.41E-02	2.71E-01	CNPY2	Canopy 2 homolog (zebrafish)	chr12q15	1557798_at	NM_014255																			
7.56	7.00	0.56	2.41E-02	2.71E-01	MYST1	MYST histone acetyltransferase 1	chr16p11.2	221820_s_at	NM_032188 /// NM_182958																			
3.10	2.79	0.31	2.41E-02	2.71E-01	LOC728902	hypothetical LOC728902	chr20q13.31	239981_x_at	XM_001132958 /// XM_001133409 /// XM_001723730																			
5.91	5.44	0.47	2.41E-02	2.71E-01	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	chr15q26.1	218415_at	NM_018668																			
4.54	4.20	0.35	2.41E-02	2.71E-01	---	---	---	228380_at	---																			
4.33	3.95	0.38	2.41E-02	2.71E-01	---	---	---	239355_at	---																			
6.09	4.33	1.76	2.41E-02	2.71E-01	CCL4	chemokine (C-C motif) ligand 4	chr17q12	204103_at	NM_002984																			
2.26	1.97	0.29	2.41E-02	2.71E-01	ZNF175	zinc finger protein 175	chr19q13.4	243128_at	NM_007147																			
5.94	5.37	0.57	2.42E-02	2.71E-01	MTERFD2	MTERF domain containing 2	chr2q37.3	1557966_x_at	NM_182501																			
6.73	6.20	0.53	2.42E-02	2.71E-01	SKIV2L	superkiller viralicidic activity 2-like (S. cerevisiae)	chr6p21	203727_at	NM_006929																			
4.35	3.38	0.97	2.42E-02	2.71E-01	LARP2	La ribonucleoprotein domain family, member 2	chr4q28.2	226750_at	NM_018078 /// NM_032239 /// NM_178043																			
9.84	9.39	0.45	2.42E-02	2.71E-01	CNPY2	canopy 2 homolog (zebrafish)	chr12q15	202857_at	NM_014255																			
8.11	7.69	0.42	2.42E-02	2.71E-01	RPS19BP1	ribosomal protein S19 binding protein 1	chr22q13.1	225148_at	NM_194326																			
6.48	5.65	0.83	2.42E-02	2.71E-01	DOM3Z	dom-3 homolog Z (C. elegans)	chr6p21.3	204522_at	NM_005510																			
6.73	5.93	0.80	2.42E-02	2.71E-01	TMEM107	transmembrane protein 107	chr17p13.1	238590_x_at	NM_032354 /// NM_183065																			
5.03	4.50	0.54	2.42E-02	2.71E-01	CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11p11	204113_at	NM_001025596 /// NM_006560 /// NM_198700																			

2.37	2.06	0.31	2.42E-02	2.71E-01	ALDH8A1	aldehyde dehydrogenase 8 family, member A1	chr6q23.2	220148_at	NM_022568 /// NM_170771																			
4.87	4.02	0.84	2.43E-02	2.71E-01	YPEL2	yippee-like 2 (Drosophila)	chr17q22	1556420_s_at	NM_001005404																			
7.70	6.90	0.80	2.43E-02	2.72E-01	LOC100132999	hypothetical protein LOC100132999	chr1q21.1	229872_s_at	XM_001722799																			
7.72	6.94	0.78	2.43E-02	2.72E-01	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	chr17q21	224784_at	NM_005937																			
5.30	4.08	1.21	2.43E-02	2.72E-01	ALCAM	activated leukocyte cell adhesion molecule	chr3q13.1	201951_at	NM_001627																			
7.10	6.49	0.61	2.43E-02	2.72E-01	THTPA	thiamine triphosphatase	chr14q11.2	218540_at	NM_001126339 /// NM_024328 /// NR_023314																			
7.17	6.48	0.69	2.43E-02	2.72E-01	DTX3	deltex 3 homolog (Drosophila)	chr12q13.3	235721_at	NM_178502																			
6.42	5.84	0.58	2.44E-02	2.72E-01	SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	chr17q25.3	223222_at	NM_001126121 /// NM_001126122 /// NM_021734																			
9.00	8.59	0.40	2.44E-02	2.72E-01	DYNLT1	dynein, light chain, Tctex-type 1	chr6q25.2-q25.3	201999_s_at	NM_006519																			
8.55	8.20	0.35	2.44E-02	2.72E-01	RANBP1	RAN binding protein 1	chr22q11.21	202483_s_at	NM_002882																			
9.79	9.15	0.64	2.44E-02	2.72E-01	C11orf10	chromosome 11 open reading frame 10	chr11q12-q13.1	218213_s_at	NM_014206																			
4.35	3.57	0.77	2.44E-02	2.72E-01	LOC653390	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	chr16p11.2	243124_at	NR_003369																			
7.55	6.77	0.78	2.44E-02	2.72E-01	HN1	hematological and neurological expressed 1	chr17q25.1	222396_at	NM_001002032 /// NM_001002033 /// NM_016185																			
10.44	10.11	0.32	2.44E-02	2.72E-01	NME1-NME2 /// NME2	NME1-NME2 /// non-metastatic cells 2, protein (NM23B) expressed in	chr17q21.3	201268_at	NM_001018136 /// NM_001018137 /// NM_001018138 /// NM_001018139 /// NM_002512																			
4.45	3.36	1.09	2.44E-02	2.72E-01	---	---	---	212444_at	---																			
4.39	3.33	1.06	2.45E-02	2.72E-01	SETD4	SET domain containing 4	chr21q22.13	219482_at	NM_001007259 /// NM_017438																			
8.97	8.42	0.55	2.45E-02	2.72E-01	HMGN3	high mobility group nucleosomal binding domain 3	chr6q14.1	209377_s_at	NM_004242 /// NM_138730																			
8.22	7.69	0.54	2.45E-02	2.73E-01	RBBP4	retinoblastoma binding protein 4	chr1p35.1	210371_s_at	NM_005610																			
8.06	7.42	0.64	2.45E-02	2.73E-01	CDC42SE1	CDC42 small effector 1	chr1q21.2	218157_x_at	NM_001038707 /// NM_020239																			
5.77	5.14	0.63	2.45E-02	2.73E-01	BRPF3	bromodomain and PHD finger containing, 3	chr6p21	225217_s_at	NM_015695																			
5.76	5.38	0.38	2.45E-02	2.73E-01	ITGA9	integrin, alpha 9	chr3p21.3	206009_at	NM_002207																			
5.53	4.77	0.76	2.45E-02	2.73E-01	SLC25A37	solute carrier family 25, member 37	chr8p21.2	218978_s_at	NM_016612																			
6.26	5.59	0.67	2.45E-02	2.73E-01	MUM1	melanoma associated antigen (mutated) 1	chr19p13.3	221290_s_at	NM_032853																			
4.14	3.16	0.97	2.45E-02	2.73E-01	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	chr12p	207100_s_at	NM_014231 /// NM_016830 /// NM_199245																			
6.54	6.02	0.53	2.46E-02	2.73E-01	COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	chr7q22.1	213504_at	NM_006833																			
4.80	4.17	0.64	2.46E-02	2.73E-01	ACTR5	ARP5 actin-related protein 5 homolog (yeast)	chr20q11.23	219623_at	NM_024855																			
5.88	4.90	0.98	2.46E-02	2.73E-01	SHF	Src homology 2 domain containing F	chr15q21.1	228922_at	NM_138356																			
7.09	6.62	0.47	2.46E-02	2.73E-01	UNC13B	unc-13 homolog B (C. elegans)	chr9p12-p11	202893_at	NM_006377																			
8.32	7.72	0.59	2.46E-02	2.73E-01	FAM91A2	family with sequence similarity 91, member A2	chr1q21.1	229429_x_at	XR_040635																			
10.22	9.92	0.30	2.46E-02	2.73E-01	COX6C	cytochrome c oxidase subunit VIc	chr8q22-q23	201754_at	NM_004374																			
7.61	7.23	0.38	2.47E-02	2.73E-01	PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	chr20q13.33	208880_s_at	NM_012469																			
5.18	4.59	0.60	2.47E-02	2.73E-01	NAB2	NGFI-A binding protein 2 (EGR1 binding protein 2)	chr12q13.3-q14.1	216017_s_at	NM_005967																			
7.14	6.83	0.31	2.47E-02	2.73E-01	THRAP3	thyroid hormone receptor associated protein 3	chr1p34.3	222440_s_at	NM_005119																			
2.85	2.10	0.75	2.48E-02	2.73E-01	DZIP1	DAZ interacting protein 1	chr13q32.1	204557_s_at	NM_014934 /// NM_198968																			
6.94	6.50	0.44	2.48E-02	2.73E-01	NUP43	nucleoporin 43kDa	chr6q25.1	219007_at	NM_198887																			
4.65	4.05	0.60	2.48E-02	2.74E-01	YJEFN3	YjeF N-terminal domain containing 3	chr19p13.11	229961_x_at	NM_198537																			

3.28	2.94	0.34	2.48E-02	2.74E-01	TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	chr6p21.1	1552494_at	NM_138572																				
8.79	8.06	0.73	2.48E-02	2.74E-01	STK19	serine/threonine kinase 19	chr6p21.3	204090_at	NM_004197 /// NM_032454																				
5.46	4.93	0.53	2.48E-02	2.74E-01	CLN5	ceroid-lipofuscinosis, neuronal 5	chr13q21.1-q32	214252_s_at	NM_006493																				
6.46	5.55	0.91	2.48E-02	2.74E-01	DKFZP586H2123	regeneration associated muscle protease	chr11p13	213661_at	NM_001001991 /// NM_015430																				
5.95	5.44	0.51	2.48E-02	2.74E-01	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	chr8q12.1	218642_s_at	NM_001011667 /// NM_001011668 /// NM_001011669 /// NM_001011670 /// NM_001011671 /// NM_024300																				
7.99	7.58	0.42	2.49E-02	2.74E-01	RUVBL2	RuvB-like 2 (E. coli)	chr19q13.3	201459_at	NM_006666																				
3.64	3.29	0.35	2.49E-02	2.74E-01	TERT	telomerase reverse transcriptase	chr5p15.33	207199_at	NM_198253 /// NM_198255																				
6.18	5.43	0.75	2.49E-02	2.74E-01	IL10RA	interleukin 10 receptor, alpha	chr11q23	204912_at	NM_001558																				
3.45	2.72	0.73	2.49E-02	2.74E-01	---	---	---	1556545_at	---																				
5.04	4.35	0.69	2.49E-02	2.74E-01	TYSND1	trypsin domain containing 1	chr10q22.1	238802_at	NM_001040273 /// NM_173555																				
6.30	5.97	0.33	2.49E-02	2.74E-01	PIM1	pim-1 oncogene	chr6p21.2	209193_at	NM_002648																				
6.10	5.20	0.90	2.49E-02	2.74E-01	USP21	ubiquitin specific peptidase 21	chr1q22	234735_s_at	NM_001014443 /// NM_012475																				
7.55	7.04	0.51	2.49E-02	2.74E-01	COMMD9	COMM domain containing 9	chr11p13	218072_at	NM_001101653 /// NM_014186																				
3.52	2.99	0.52	2.49E-02	2.74E-01	UQCC	ubiquinol-cytochrome c reductase complex chaperone	chr20q11.22	244795_at	NM_018244 /// NM_199487																				
5.00	3.95	1.05	2.49E-02	2.74E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	210916_s_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392																				
8.46	7.89	0.57	2.49E-02	2.74E-01	ARMET	arginine-rich, mutated in early stage tumors	chr3p21.1	202655_at	NM_006010																				
4.78	4.30	0.48	2.50E-02	2.74E-01	---	---	---	227591_at	---																				
2.38	2.06	0.33	2.50E-02	2.74E-01	---	---	---	230951_at	---																				
2.78	2.26	0.53	2.50E-02	2.74E-01	FAM80B	Family with sequence similarity 80, member B	chr12p13.31	226164_x_at	NM_020734																				
7.42	6.97	0.45	2.50E-02	2.74E-01	TUBGCP2	tubulin, gamma complex associated protein 2	chr10q26.3	202477_s_at	NM_006659																				
8.36	7.32	1.04	2.51E-02	2.74E-01	CLEC3B	C-type lectin domain family 3, member B	chr3p22-p21.3	205200_at	NM_003278																				
6.09	5.31	0.78	2.51E-02	2.74E-01	C10orf97	chromosome 10 open reading frame 97	chr10p13	218297_at	NM_024948																				
8.77	8.34	0.43	2.51E-02	2.74E-01	TMEM85	transmembrane protein 85	chr15q14	223043_at	NM_016454																				
3.75	3.11	0.64	2.51E-02	2.75E-01	---	---	---	242449_at	---																				
7.85	7.38	0.48	2.51E-02	2.75E-01	MAGED2	melanoma antigen family D, 2	chrXp11.2	213627_at	NM_014599 /// NM_177433 /// NM_201222																				
6.55	6.01	0.54	2.51E-02	2.75E-01	TBCD	tubulin folding cofactor D	chr17q25.3	211052_s_at	NM_005993																				
5.60	4.56	1.03	2.51E-02	2.75E-01	FAM43A	family with sequence similarity 43, member A	chr3q29	227410_at	NM_153690																				
6.84	6.10	0.74	2.51E-02	2.75E-01	PRMT5	protein arginine methyltransferase 5	chr14q11.2-q21	1564520_s_at	NM_001039619 /// NM_006109																				
5.12	4.57	0.55	2.52E-02	2.75E-01	ATF7	activating transcription factor 7	chr12q13	228830_s_at	NM_001130059 /// NM_001130060 /// NM_006856																				
2.68	2.31	0.38	2.52E-02	2.75E-01	ITGB5	Integrin, beta 5	chr3q21.2	214021_x_at	NM_002213																				
2.63	2.33	0.30	2.52E-02	2.75E-01	---	---	---	1559372_at	---																				

5.16	4.48	0.68	2.52E-02	2.75E-01	C19orf6	chromosome 19 open reading frame 6	chr19p13.3	213986_s_at	NM_001033026 /// NM_033420
4.78	4.11	0.67	2.52E-02	2.75E-01	GCA	grancalcin, EF-hand calcium binding protein	chr2q24.2	203765_at	NM_012198
5.94	5.23	0.71	2.52E-02	2.75E-01	EDC4	enhancer of mRNA decapping 4	chr16q22.1	202496_at	NM_014329
8.94	8.43	0.51	2.52E-02	2.75E-01	C3orf60	chromosome 3 open reading frame 60	chr3p21.31	209177_at	NM_199069 /// NM_199070 /// NM_199073 /// NM_199074 /// NM_199417
3.36	2.87	0.49	2.52E-02	2.75E-01	CIITA	class II, major histocompatibility complex, transactivator	chr16p13	205101_at	NM_000246
6.25	5.58	0.67	2.52E-02	2.75E-01	PFAS	phosphoribosylformylglycinamidine synthase	chr17p13.1	213302_at	NM_012393
9.27	8.74	0.53	2.53E-02	2.75E-01	CCDC56	coiled-coil domain containing 56	chr17q21	218026_at	NM_001040431
8.95	8.56	0.39	2.53E-02	2.75E-01	PSMD8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	chr19q13.2	200820_at	NM_002812
5.63	4.97	0.65	2.53E-02	2.75E-01	MOBKL2C	MOB1, Mps One Binder kinase activator-like 2C (yeast)	chr1p33	227066_at	NM_145279 /// NM_201403
8.21	7.32	0.88	2.53E-02	2.75E-01	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	chr2p22.1	214141_x_at	NM_001031684
6.94	6.38	0.56	2.53E-02	2.75E-01	NAT10	N-acetyltransferase 10	chr11p13	217884_at	NM_024662
3.84	3.26	0.58	2.53E-02	2.75E-01	41521	septin 4	chr17q22-q23	210348_at	NM_004574 /// NM_080415 /// NM_080416
4.44	3.65	0.79	2.53E-02	2.75E-01	CEP164	centrosomal protein 164kDa	chr11q23.3	204251_s_at	NM_014956
6.03	5.55	0.48	2.53E-02	2.75E-01	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	chr10q25.3	208453_s_at	NM_020383
5.32	4.82	0.49	2.54E-02	2.75E-01	C12orf26	chromosome 12 open reading frame 26	chr12q21.31	229018_at	NM_032230
7.69	6.79	0.91	2.54E-02	2.75E-01	ZDHHC2	zinc finger, DHHC-type containing 2	chr8p21.3-p22	222731_at	NM_016353
5.82	5.24	0.58	2.54E-02	2.75E-01	C18orf8	chromosome 18 open reading frame 8	chr18q11.2	221190_s_at	NM_013326
12.66	12.38	0.28	2.54E-02	2.75E-01	RPS11	ribosomal protein S11	chr19q13.3	200031_s_at	NM_001015
5.75	5.24	0.50	2.54E-02	2.75E-01	OTUD5	OTU domain containing 5	chrXp11.23	1555426_a_at	NM_017602
8.53	8.10	0.42	2.54E-02	2.75E-01	C3orf1	chromosome 3 open reading frame 1	chr3q13.33	223004_s_at	NM_016589
3.18	2.68	0.50	2.54E-02	2.75E-01	ZNHIT2	zinc finger, HIT type 2	chr11q13	222814_s_at	NM_014205
3.20	2.66	0.54	2.54E-02	2.75E-01	IL18	interleukin 18 (interferon-gamma-inducing factor)	chr11q22.2-q22.3	206295_at	NM_001562
5.39	4.81	0.58	2.54E-02	2.75E-01	---	---	---	231311_at	---
7.59	7.03	0.56	2.54E-02	2.75E-01	C20orf3	chromosome 20 open reading frame 3	chr20p11.22-p11.21	206656_s_at	NM_020531
7.22	6.60	0.62	2.55E-02	2.76E-01	UBE2Z	ubiquitin-conjugating enzyme E2Z	chr17q21.32	222395_s_at	NM_023079
5.94	4.84	1.10	2.55E-02	2.76E-01	NAP1L3	nucleosome assembly protein 1-like 3	chrXq21.3-q22	204749_at	NM_004538
7.23	6.91	0.33	2.55E-02	2.76E-01	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	chr10q	202406_s_at	NM_001033925 /// NM_003252
5.67	4.52	1.15	2.56E-02	2.76E-01	OLFM1	olfactomedin 1	chr9q34.3	205591_at	NM_006334 /// NM_014279
2.55	2.23	0.33	2.56E-02	2.76E-01	C6orf99 /// LOC100130967	chromosome 6 open reading frame 99 /// similar to hCG2044932	chr6q25.3	230487_at	XM_001716105 /// XM_001716695 /// XM_001726882
5.12	3.89	1.23	2.56E-02	2.76E-01	FUBP1	far upstream element (FUSE) binding protein 1	chr1p31.1	214093_s_at	NM_003902
6.69	6.00	0.69	2.56E-02	2.76E-01	PRDM2	PR domain containing 2, with ZNF domain	chr1p36.21	203057_s_at	NM_001007257 /// NM_012231 /// NM_015866
6.78	6.03	0.75	2.56E-02	2.76E-01	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	chr15q26.3	216977_x_at	NM_003090
5.78	4.87	0.91	2.56E-02	2.76E-01	ENOSF1	enolase superfamily member 1	chr18p11.32	213645_at	NM_001126123 /// NM_017512
6.46	5.92	0.54	2.56E-02	2.76E-01	ULK1	unc-51-like kinase 1 (C. elegans)	chr12q24.3	209333_at	NM_003565
2.76	2.20	0.56	2.56E-02	2.76E-01	PPOX	protoporphyrinogen oxidase	chr1q22	238117_at	NM_000309 /// NM_001122764

2.87	2.25	0.61	2.57E-02	2.77E-01	hCG_1815491	hCG1815491	chr16q12.2	238021_s_at	XR_042100 /// XR_042101 /// XR_042102																				
7.48	7.04	0.44	2.57E-02	2.77E-01	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	chr19q13.2	224913_s_at	NM_001001563																				
2.50	2.19	0.32	2.57E-02	2.77E-01	---	---	---	211667_x_at	---																				
10.89	10.58	0.31	2.57E-02	2.77E-01	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	chrXp22.32 and Yp11.3	212826_s_at	NM_001636																				
9.49	9.06	0.42	2.58E-02	2.77E-01	BAT1	HLA-B associated transcript 1	chr6p21.3	200041_s_at	NM_004640 /// NM_080598																				
2.97	2.43	0.54	2.58E-02	2.77E-01	NCAPG2	non-SMC condensin II complex, subunit G2	chr7q36.3	219588_s_at	NM_017760																				
5.37	4.70	0.66	2.58E-02	2.77E-01	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	chr17p11.2	223498_at	NM_001033553 /// NM_001033554 /// NM_001033555 /// NM_152904																				
5.25	4.51	0.74	2.58E-02	2.77E-01	EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)	chr16p12.1	1563796_s_at	NM_001083614 /// NR_003501																				
5.03	3.93	1.10	2.58E-02	2.77E-01	RGL3	ral guanine nucleotide dissociation stimulator-like 3	chr19p13.2	228877_at	NM_001035223																				
3.40	2.86	0.54	2.58E-02	2.77E-01	---	---	---	235884_at	---																				
8.08	7.60	0.48	2.59E-02	2.77E-01	SNX12	sorting nexin 12	chrXq13.1	224684_at	NM_013346																				
7.60	7.18	0.42	2.59E-02	2.77E-01	MRPL38	mitochondrial ribosomal protein L38	chr17q25.3	225103_at	NM_032478																				
5.81	4.93	0.88	2.59E-02	2.77E-01	TFAM	transcription factor A, mitochondrial	chr10q21	203177_x_at	NM_003201																				
6.24	5.59	0.65	2.59E-02	2.77E-01	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	chr5q12-q13	209624_s_at	NM_022132																				
7.18	6.52	0.65	2.59E-02	2.77E-01	RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	chr11q13	201783_s_at	NM_021975																				
7.00	6.60	0.40	2.59E-02	2.77E-01	DENND5A	DENN/MADD domain containing 5A	chr11p15.4	212561_at	NM_015213																				
6.95	6.24	0.71	2.59E-02	2.77E-01	COLEC11	collectin sub-family member 11	chr2p25.3	219873_at	NM_024027 /// NM_199235																				
2.81	2.19	0.62	2.60E-02	2.77E-01	---	---	---	226591_at	---																				
8.74	8.14	0.60	2.60E-02	2.77E-01	GLUL	glutamate-ammonia ligase (glutamine synthetase)	chr1q31	215001_s_at	NM_001033044 /// NM_001033056 /// NM_002065																				
9.29	8.96	0.33	2.60E-02	2.77E-01	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	chr14q11.2	212626_x_at	NM_001077442 /// NM_001077443 /// NM_004500 /// NM_031314																				
5.07	3.88	1.20	2.60E-02	2.77E-01	EPHA4	EPH receptor A4	chr2q36.1	206114_at	NM_004438																				
9.79	9.15	0.64	2.60E-02	2.77E-01	ZFP36L2	zinc finger protein 36, C3H type-like 2	chr2p22.3-p21	201368_at	NM_006887																				
6.02	5.66	0.36	2.60E-02	2.77E-01	CDK5RAP1	CDK5 regulatory subunit associated protein 1	chr20pter-q11.23	218315_s_at	NM_016082 /// NM_016408																				
4.29	3.60	0.69	2.60E-02	2.77E-01	RXRB	retinoid X receptor, beta	chr6p21.3	215099_s_at	NM_021976																				
8.42	7.65	0.78	2.60E-02	2.77E-01	FGD2	FYVE, RhoGEF and PH domain containing 2	chr6p21.2	1553906_s_at	NM_173558																				
2.46	2.04	0.42	2.61E-02	2.77E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	209151_x_at	NM_003200																				

7.43	6.54	0.89	2.61E-02	2.78E-01	CPNE1 /// RBM12	copine I /// RNA binding motif protein 12	chr20q11.21 /// chr20q11.22	212168_at	NM_003915 /// NM_006047 /// NM_152838 /// NM_152925 /// NM_152926 /// NM_152927 /// NM_152928 /// NM_152929 /// NM_152930 /// NM_152931																				
5.42	4.06	1.36	2.61E-02	2.78E-01	C1orf63	chromosome 1 open reading frame 63	chr1p36.13-p35.1	209006_s_at	NM_020317																				
4.22	3.51	0.72	2.61E-02	2.78E-01	ZNF550	zinc finger protein 550	chr19q13.43	228099_at	NM_001039654																				
6.18	4.90	1.28	2.61E-02	2.78E-01	MAT2A	methionine adenosyltransferase II, alpha	chr2p11.2	200769_s_at	NM_005911																				
7.80	7.35	0.45	2.62E-02	2.78E-01	NUBP2	nucleotide binding protein 2 (MinD homolog, E. coli)	chr16p13.3	218227_at	NM_012225																				
5.18	4.06	1.12	2.62E-02	2.78E-01	C15orf39	chromosome 15 open reading frame 39	chr15q24.2	215087_at	NM_015492																				
3.22	2.45	0.77	2.62E-02	2.78E-01	LOC100129196	similar to hCG2033298	chr1p35.2	1557558_s_at	XM_001724260 /// XM_001724594 /// XM_001724756																				
6.22	5.76	0.46	2.62E-02	2.78E-01	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	chr16q21-q22.3	209178_at	NM_014003																				
7.44	6.97	0.47	2.62E-02	2.78E-01	SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	chr19p13.11	226728_at	NM_198580																				
7.71	6.96	0.74	2.62E-02	2.78E-01	SSBP4	single stranded DNA binding protein 4	chr19p13.1	223226_x_at	NM_001009998 /// NM_032627																				
3.12	2.59	0.53	2.62E-02	2.78E-01	TRIM73 /// TRIM74	tripartite motif-containing 73 /// tripartite motif-containing 74	chr7q11.23	1554182_at	NM_198853 /// NM_198924																				
8.19	7.58	0.61	2.62E-02	2.78E-01	TM9SF1	transmembrane 9 superfamily member 1	chr14q11.2	209150_s_at	NM_001014842 /// NM_006405																				
6.57	5.67	0.90	2.63E-02	2.79E-01	---	---	---	229949_at	---																				
5.73	5.25	0.48	2.63E-02	2.79E-01	ENC1	ectodermal-neural cortex (with BTB-like domain)	chr5q12-q13.3	201341_at	NM_003633																				
4.66	4.23	0.43	2.63E-02	2.79E-01	SETD8	SET domain containing (lysine methyltransferase) 8	chr12q24.31	225118_at	NM_020382																				
5.90	5.37	0.53	2.63E-02	2.79E-01	C17orf70	chromosome 17 open reading frame 70	chr17q25.3	221800_s_at	NM_001109760 /// NM_025161																				
3.48	2.45	1.03	2.63E-02	2.79E-01	---	---	---	226848_at	---																				
7.59	7.02	0.57	2.63E-02	2.79E-01	C19orf22	chromosome 19 open reading frame 22	chr19p13.3	55705_at	NM_138774																				
3.95	3.54	0.41	2.63E-02	2.79E-01	DGKG	diacylglycerol kinase, gamma 90kDa	chr3q27.2-q27.3	206395_at	NM_001080744 /// NM_001080745 /// NM_001346																				
2.54	2.20	0.33	2.64E-02	2.79E-01	CHML	Choroideremia-like (Rab escort protein 2)	chr1q42-qter	1565947_a_at	NM_001821																				
2.52	1.91	0.60	2.64E-02	2.79E-01	LOC730051	similar to hCG2044798	chr19q13.43	60794_f_at	XM_001725674 /// XM_001725708 /// XM_001726286																				
7.54	7.21	0.33	2.64E-02	2.79E-01	OTUD5	OTU domain containing 5	chrXp11.23	224745_x_at	NM_017602																				
8.96	8.57	0.39	2.64E-02	2.79E-01	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	chr11q13	208714_at	NM_007103																				
3.31	2.79	0.53	2.64E-02	2.79E-01	STEAP2	six transmembrane epithelial antigen of the prostate 2	chr7q21	225871_at	NM_001040665 /// NM_001040666 /// NM_152999																				
6.85	6.26	0.59	2.65E-02	2.80E-01	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	chr12q13-q14	201320_at	NM_001130420 /// NM_003075 /// NM_139067																				
7.22	6.51	0.71	2.65E-02	2.80E-01	TXLNA	taxilin alpha	chr1p35.1	212300_at	NM_175852																				

2.95	2.64	0.31	2.65E-02	2.80E-01	DEFB119	defensin, beta 119	chr20q11.1	231155_at	NM_153289 /// NM_153323 /// NM_173460
8.08	7.54	0.55	2.65E-02	2.80E-01	SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	chr2p25.3	204019_s_at	NM_015677
8.26	7.80	0.46	2.65E-02	2.80E-01	GORASP2	golgi reassembly stacking protein 2, 55kDa	chr2q31.1-q31.2	207812_s_at	NM_015530
3.48	2.77	0.70	2.66E-02	2.80E-01	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	chr1p36.2	210847_x_at	NM_001039664 /// NM_003790 /// NM_148965 /// NM_148966 /// NM_148967 /// NM_148970
8.86	8.37	0.50	2.66E-02	2.80E-01	NAP1L1	nucleosome assembly protein 1-like 1	chr12q21.2	204528_s_at	NM_004537 /// NM_139207
6.58	5.75	0.84	2.66E-02	2.80E-01	EFNB2	ephrin-B2	chr13q33	202668_at	NM_004093
4.55	3.75	0.80	2.66E-02	2.80E-01	HOOK2	hook homolog 2 (Drosophila)	chr19p13.13	218780_at	NM_001100176 /// NM_013312
7.58	6.77	0.81	2.66E-02	2.81E-01	LOC646044 /// SSBP4	similar to single stranded DNA binding protein 4 /// single stranded DNA binding protein 4	chr18p11.21 /// chr19p13.1	229269_x_at	NM_001009998 /// NM_032627 /// XR_017055 /// XR_018999 /// XR_037328
8.38	7.93	0.45	2.67E-02	2.81E-01	TRIOBP	TRIO and F-actin binding protein	chr22q13.1	210276_s_at	NM_001039141 /// NM_007032 /// NM_138632
7.28	6.88	0.40	2.67E-02	2.81E-01	STX4	syntaxin 4	chr16p11.2	203530_s_at	NM_004604
6.59	5.97	0.63	2.67E-02	2.81E-01	MAP2K7	mitogen-activated protein kinase kinase 7	chr19p13.3-p13.2	226053_at	NM_145185
5.52	4.86	0.66	2.68E-02	2.81E-01	RUFY3	RUN and FYVE domain containing 3	chr4q13.3	227802_at	NM_001037442 /// NM_001130709 /// NM_014961
4.76	3.92	0.84	2.68E-02	2.81E-01	KIAA1712	KIAA1712	chr4q34	228334_x_at	NM_001040157
6.85	5.96	0.89	2.68E-02	2.82E-01	PTPRH	protein tyrosine phosphatase, receptor type, H	chr19q13.4	208300_at	NM_002842
3.30	2.92	0.38	2.68E-02	2.82E-01	WNT4	wingless-type MMTV integration site family, member 4	chr1p36.23-p35.1	1556689_a_at	NM_030761
6.11	5.31	0.80	2.68E-02	2.82E-01	GTPBP3	GTP binding protein 3 (mitochondrial)	chr19p13.11	213835_x_at	NM_001128855 /// NM_032620 /// NM_133644
2.86	2.38	0.48	2.68E-02	2.82E-01	STC1	stanniocalcin 1	chr8p21-p11.2	204597_x_at	NM_003155
3.02	2.65	0.36	2.69E-02	2.82E-01	hCG_1815491	hCG1815491	chr16q12.2	238022_at	XR_042100 /// XR_042101 /// XR_042102
7.25	6.67	0.59	2.69E-02	2.82E-01	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	chr17q12	201080_at	NM_003559
6.51	5.79	0.73	2.69E-02	2.82E-01	GYS1	glycogen synthase 1 (muscle)	chr19q13.3	201673_s_at	NM_002103
5.47	4.60	0.87	2.69E-02	2.82E-01	HOXA10	homeobox A10	chr7p15-p14	213150_at	NM_018951 /// NM_153715
4.37	3.65	0.72	2.69E-02	2.82E-01	SIVA1	SIVA1, apoptosis-inducing factor	chr14q32.33	222030_at	NM_006427 /// NM_021709
6.64	5.93	0.71	2.70E-02	2.82E-01	CHD2	chromodomain helicase DNA binding protein 2	chr15q26	225077_at	NM_001042572 /// NM_001271
4.28	3.87	0.41	2.70E-02	2.82E-01	EHBP1L1	EH domain binding protein 1-like 1	chr11q13.1	1557228_at	NM_001099409

5.80	5.46	0.34	2.70E-02	2.82E-01	PVR	poliovirus receptor	chr19q13.2	212662_at	NM_006505
6.64	6.18	0.46	2.70E-02	2.82E-01	ACVR1B	activin A receptor, type IB	chr12q13	213198_at	NM_004302 /// NM_020327 /// NM_020328
5.20	4.52	0.69	2.70E-02	2.82E-01	RASSF1	Ras association (RalGDS/AF-6) domain family member 1	chr3p21.3	204346_s_at	NM_007182 /// NM_170712 /// NM_170713 /// NM_170714
4.22	3.50	0.72	2.71E-02	2.82E-01	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	chrXq23	205584_at	NM_018466 /// XM_001713667 /// XM_001713668
7.81	7.20	0.61	2.71E-02	2.82E-01	CRLS1	cardiolipin synthase 1	chr20p13-p12.3	223978_s_at	NM_001127458 /// NM_019095
2.36	1.97	0.39	2.71E-02	2.82E-01	IMMP1L	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	chr11p13	230556_at	NM_144981
5.60	5.22	0.37	2.71E-02	2.82E-01	---	---	---	227252_at	---
2.84	2.37	0.47	2.71E-02	2.82E-01	BTG1	B-cell translocation gene 1, anti-proliferative	chr12q22	1559975_at	NM_001731
3.23	2.89	0.34	2.71E-02	2.82E-01	---	---	---	240826_at	---
3.82	3.32	0.50	2.71E-02	2.82E-01	GCKR	glucokinase (hexokinase 4) regulator	chr2p23	206867_at	NM_001486
7.62	7.09	0.53	2.72E-02	2.82E-01	ARF5	ADP-ribosylation factor 5	chr7q31.3	201526_at	NM_001662
8.40	7.95	0.45	2.72E-02	2.82E-01	TRAPPC5	trafficking protein particle complex 5	chr19p13.2	225870_s_at	NM_001042461 /// NM_001042462 /// NM_174894
4.53	3.42	1.11	2.72E-02	2.82E-01	JARID1C	jumonji, AT rich interactive domain 1C	chrXp11.22-p11.21	239207_at	NM_004187
5.48	4.84	0.64	2.72E-02	2.82E-01	FNTB	farnesyltransferase, CAAX box, beta	chr14q23-q24	204764_at	NM_002028
3.30	2.85	0.45	2.72E-02	2.82E-01	CKMT1A /// CKMT1B /// LOC100133623	creatine kinase, mitochondrial 1A /// creatine kinase, mitochondrial 1B /// similar to Creatine kinase, ubiquitous mitochondrial precursor (U-MtCK) (Mia-CK) (Acidic-type mitochondrial creatine kinase)	chr15q15	202712_s_at	NM_001015001 /// NM_020990 /// XM_001720241
7.59	7.12	0.48	2.72E-02	2.82E-01	THYN1	thymocyte nuclear protein 1	chr11q25	218491_s_at	NM_001037304 /// NM_001037305 /// NM_014174 /// NM_199297 /// NM_199298
7.07	6.53	0.54	2.72E-02	2.82E-01	ZNF384	zinc finger protein 384	chr12p12	212369_at	NM_001039916 /// NM_001039917 /// NM_001039918 /// NM_001039919 /// NM_001039920 /// NM_133476
6.12	5.50	0.61	2.73E-02	2.82E-01	WDR18	WD repeat domain 18	chr19p13.3	209461_x_at	NM_024100
9.25	8.97	0.28	2.73E-02	2.82E-01	HSBP1	heat shock factor binding protein 1	chr16q23.3	200942_s_at	NM_001537
5.76	5.25	0.51	2.73E-02	2.82E-01	ZNF587	zinc finger protein 587	chr19q13.43	219981_x_at	NM_032828
7.53	6.80	0.73	2.73E-02	2.82E-01	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	chr16p11.2	1565717_s_at	NM_004960

6.82	5.46	1.36	2.73E-02	2.82E-01	LOC652900 /// SEZ6L2	similar to seizure related 6 homolog (mouse)-like 2 isoform 1 /// seizure related 6 homolog (mouse)-like 2	chr16p11.2	218720_x_at	NM_001114099 /// NM_001114100 /// NM_012410 /// NM_201575 /// XM_001724912																				
4.03	3.69	0.34	2.73E-02	2.83E-01	---	---	---	240455_at	---																				
5.00	3.20	1.80	2.74E-02	2.83E-01	CNTN1	contactin 1	chr12q11-q12	211203_s_at	NM_001843 /// NM_175038																				
4.62	4.02	0.60	2.74E-02	2.83E-01	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	216503_s_at	NM_001009569 /// NM_004641																				
5.47	4.78	0.69	2.74E-02	2.83E-01	TUBG2	tubulin, gamma 2	chr17q21	203894_at	NM_016437																				
7.01	6.43	0.58	2.74E-02	2.83E-01	SLA	Src-like-adaptor	chr8q22.3-qter|8q24	203761_at	NM_001045556 /// NM_001045557 /// NM_006748																				
9.54	9.01	0.53	2.74E-02	2.83E-01	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	chr16p11.2	201253_s_at	NM_006319																				
4.07	3.29	0.79	2.74E-02	2.83E-01	---	---	---	214124_x_at	---																				
5.78	5.18	0.60	2.74E-02	2.83E-01	RCN2	reticulocalbin 2, EF-hand calcium binding domain	chr15q23	201486_at	NM_002902																				
7.21	6.33	0.88	2.75E-02	2.83E-01	OBSL1	obscurin-like 1	chr2q35	212776_s_at	NM_015311																				
2.97	2.56	0.42	2.75E-02	2.83E-01	MTMR1	myotubularin related protein 1	chrXq28	214975_s_at	NM_003828																				
5.42	5.06	0.37	2.75E-02	2.83E-01	CIAO1	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	chr2q11.2	217501_at	NM_004804																				
6.14	5.48	0.66	2.75E-02	2.83E-01	PARP16	poly (ADP-ribose) polymerase family, member 16	chr15q22.31	219034_at	NM_017851																				
4.06	3.22	0.85	2.75E-02	2.83E-01	AHI1	Abelson helper integration site 1	chr6q23.3	221569_at	NM_017651																				
5.35	4.92	0.43	2.75E-02	2.83E-01	PLEKHF1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	chr19q12	219566_at	NM_024310																				
7.18	6.81	0.37	2.76E-02	2.83E-01	GALNT11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	chr7q34-q36	219013_at	NM_022087																				
4.11	3.68	0.43	2.76E-02	2.83E-01	TIMELESS	timeless homolog (Drosophila)	chr12q12-q13	203046_s_at	NM_003920																				
7.17	6.58	0.59	2.76E-02	2.83E-01	FASTK	Fas-activated serine/threonine kinase	chr7q35	202676_x_at	NM_006712 /// NM_033015																				
4.53	3.54	0.98	2.76E-02	2.83E-01	BCAT1	branched chain aminotransferase 1, cytosolic	chr12p12.1	214390_s_at	NM_005504																				
8.91	8.29	0.62	2.76E-02	2.83E-01	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	chr1p35.1-p36.23	214259_s_at	NM_003689																				
7.81	6.79	1.03	2.77E-02	2.83E-01	DDR1	discoidin domain receptor tyrosine kinase 1	chr6p21.3	207169_x_at	NM_001954 /// NM_013993 /// NM_013994																				
6.26	5.65	0.61	2.77E-02	2.83E-01	MRRF	mitochondrial ribosome recycling factor	chr9q33.2	225126_at	NM_138777 /// NM_199177																				
6.16	5.43	0.73	2.77E-02	2.83E-01	EMP2	epithelial membrane protein 2	chr16p13.2	204975_at	NM_001424																				
6.17	5.41	0.76	2.77E-02	2.83E-01	TMEM55B	transmembrane protein 55B	chr14q11.2	225287_s_at	NM_001100814 /// NM_144568																				
3.05	2.78	0.26	2.77E-02	2.83E-01	---	---	---	238109_at	---																				
7.32	7.00	0.32	2.78E-02	2.84E-01	OS9	amplified in osteosarcoma	chr12q13	215399_s_at	NM_001017956 /// NM_001017957 /// NM_001017958 /// NM_006812																				
9.13	8.43	0.70	2.78E-02	2.84E-01	EBPL	emopamil binding protein-like	chr13q12-q13	223306_at	NM_032565																				
7.19	6.77	0.43	2.78E-02	2.84E-01	GPS1	G protein pathway suppressor 1	chr17q25.3	217782_s_at	NM_004127 /// NM_212492																				
5.69	4.29	1.40	2.78E-02	2.84E-01	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	chr9q32-q33.3	238669_at	NM_000962 /// NM_080591																				
2.96	2.58	0.39	2.79E-02	2.84E-01	C8orf50	chromosome 8 open reading frame 50	chr8p21.1	1556436_at	---																				
2.41	2.04	0.36	2.79E-02	2.84E-01	RHOB	ras homolog gene family, member B	chr2p24	1553965_x_at	NM_004040																				
6.71	6.13	0.58	2.79E-02	2.84E-01	UBL4A	ubiquitin-like 4A	chrXq28	221746_at	NM_014235																				
3.09	2.33	0.76	2.79E-02	2.84E-01	SCIN	scinderin	chr7p21.3	1552367_a_at	NM_001112706 /// NM_033128																				

8.95	8.50	0.45	2.79E-02	2.84E-01	CNIH4	cornichon homolog 4 (Drosophila)	chr1q42.11	223993_s_at	NM_014184
4.69	4.34	0.35	2.79E-02	2.84E-01	TXNDC17	thioredoxin domain containing 17	chr17p13.2	228743_at	NM_032731
6.46	5.84	0.62	2.79E-02	2.84E-01	KBTBD4 /// PTPMT1	kelch repeat and BTB (POZ) domain containing 4 /// protein tyrosine phosphatase, mitochondrial 1	chr11p11.2	218570_at	NM_016506 /// NM_018095 /// NM_175732
5.64	5.26	0.38	2.79E-02	2.84E-01	SRRD	SRR1 domain containing	chr22q12.1	213608_s_at	NM_001013694
4.83	4.49	0.34	2.79E-02	2.84E-01	HMCN2	hemicentin 2	chr9q34.11	1564117_at	XM_001715154 /// XM_001726942
9.82	9.40	0.42	2.80E-02	2.84E-01	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	chr14q11.2	201762_s_at	NM_002818
6.79	6.43	0.36	2.80E-02	2.84E-01	RPP30	ribonuclease P/MRP 30kDa subunit	chr10q23.31	203436_at	NM_001104546 /// NM_006413
6.34	5.86	0.48	2.80E-02	2.84E-01	MED10	mediator complex subunit 10	chr5p15.31	223247_at	NM_032286
9.59	9.20	0.39	2.80E-02	2.85E-01	C19orf56	chromosome 19 open reading frame 56	chr19p13.13	217780_at	NM_016145
7.10	6.53	0.58	2.80E-02	2.85E-01	ICAM2	intercellular adhesion molecule 2	chr17q23-q25	213620_s_at	NM_000873 /// NM_001099786 /// NM_001099787 /// NM_001099788 /// NM_001099789
6.04	5.31	0.73	2.81E-02	2.85E-01	SCRIB	scribbled homolog (Drosophila)	chr8q24.3	212556_at	NM_015356 /// NM_182706
4.66	3.26	1.40	2.81E-02	2.85E-01	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	chr9q32-q33.3	205127_at	NM_000962 /// NM_080591
4.29	3.90	0.39	2.82E-02	2.85E-01	UST	uronyl-2-sulfotransferase	chr6q25.1	205138_s_at	NM_005715
2.64	2.24	0.41	2.82E-02	2.85E-01	LOC401321	hypothetical LOC401321	chr7p14.3	232256_s_at	XM_001723040 /// XM_379483 /// XM_380099 /// XM_939915
4.69	3.65	1.04	2.82E-02	2.85E-01	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	chr4q21	204467_s_at	NM_000345 /// NM_007308
7.29	6.85	0.44	2.82E-02	2.85E-01	RY1	putative nucleic acid binding protein RY-1	chr2p14	212440_at	NM_006857
5.41	4.54	0.87	2.82E-02	2.85E-01	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	chr3p21.31-p21.2	1555735_a_at	NM_004656
8.08	7.46	0.63	2.82E-02	2.85E-01	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	chr16q24.2	208785_s_at	NM_022818
3.21	2.90	0.32	2.82E-02	2.85E-01	LOC27320 /// TNRC18	hypothetical protein LOC27320 /// trinucleotide repeat containing 18	chr7p22.1 /// chr7q11.21	1558949_at	NM_001080495 /// XM_376618 /// XM_499300
8.45	7.77	0.68	2.82E-02	2.85E-01	COPZ1	coatomer protein complex, subunit zeta 1	chr12q13.2-q13.3	222386_s_at	NM_016057
7.07	6.40	0.67	2.82E-02	2.85E-01	TBC1D2B	TBC1 domain family, member 2B	chr15q24.3-q25.1	212796_s_at	NM_015079 /// NM_144572
3.79	3.00	0.79	2.83E-02	2.86E-01	RTKN	rhotekin	chr2p13.1	225150_s_at	NM_001015055 /// NM_001015056 /// NM_033046
4.25	3.50	0.75	2.83E-02	2.86E-01	IRS1	insulin receptor substrate 1	chr2q36	242979_at	NM_005544
3.28	2.69	0.59	2.83E-02	2.86E-01	CSNK2B /// LY6G5B	casein kinase 2, beta polypeptide /// lymphocyte antigen 6 complex, locus G5B	chr6p21-p12|6p21.3 /// chr6p21.3	231777_at	NM_001320 /// NM_021221
3.95	2.85	1.10	2.84E-02	2.86E-01	HOXC10	homeobox C10	chr12q13.3	218959_at	NM_017409
5.96	5.46	0.50	2.84E-02	2.86E-01	INO80E	INO80 complex subunit E	chr16p11.2	227286_at	NM_173618

7.87	7.26	0.60	2.84E-02	2.86E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	212265_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855																				
6.27	5.66	0.61	2.84E-02	2.86E-01	FOXRED1	FAD-dependent oxidoreductase domain containing 1	chr11q24.2	223128_at	NM_017547																				
5.92	5.17	0.75	2.85E-02	2.86E-01	MAPK7	mitogen-activated protein kinase 7	chr17p11.2	207292_s_at	NM_002749 /// NM_139032 /// NM_139033 /// NM_139034																				
6.55	5.99	0.56	2.85E-02	2.86E-01	RBM10	RNA binding motif protein 10	chrXp11.23	217221_x_at	NM_005676 /// NM_152856																				
6.49	5.90	0.59	2.85E-02	2.86E-01	PRKD2	protein kinase D2	chr19q13.3	38269_at	NM_001079880 /// NM_001079881 /// NM_001079882 /// NM_016457																				
3.96	3.49	0.48	2.85E-02	2.86E-01	C6orf134	chromosome 6 open reading frame 134	chr6p21.33	218874_s_at	NM_001031722 /// NM_024909																				
2.94	2.64	0.30	2.85E-02	2.86E-01	CREBL1	cAMP responsive element binding protein-like 1	chr6p21.3	1554487_a_at	NM_004381																				
3.82	3.43	0.39	2.85E-02	2.86E-01	---	---	---	235477_at	---																				
7.99	7.61	0.38	2.85E-02	2.86E-01	EFTUD2	elongation factor Tu GTP binding domain containing 2	chr17q21.31	222398_s_at	NM_004247																				
5.40	4.94	0.47	2.85E-02	2.86E-01	HERPUD2	HERPUD family member 2	chr7p14.2	222751_at	NM_022373 /// XM_001716505 /// XM_001717741 /// XM_001717961 /// XM_001718593																				
4.43	3.93	0.50	2.86E-02	2.87E-01	FAM49A	family with sequence similarity 49, member A	chr2p24.3	230276_at	NM_030797																				
3.11	2.70	0.40	2.86E-02	2.87E-01	---	---	---	230527_at	---																				
9.63	8.29	1.34	2.86E-02	2.87E-01	FAM46A	family with sequence similarity 46, member A	chr6q14	221766_s_at	NM_017633																				
7.78	7.21	0.57	2.87E-02	2.87E-01	R3HDM2	R3H domain containing 2	chr12q13.3	203831_at	NM_014925																				
7.20	6.79	0.42	2.87E-02	2.87E-01	MRPL22	mitochondrial ribosomal protein L22	chr5q33.1-q33.3	218339_at	NM_001014990 /// NM_014180																				
7.34	6.57	0.77	2.87E-02	2.87E-01	ZMYM3	zinc finger, MYM-type 3	chrXq13.1	207559_s_at	NM_005096 /// NM_201599																				
5.25	4.57	0.68	2.87E-02	2.87E-01	LEMD2	LEM domain containing 2	chr6p21.31	224980_at	NM_181336																				
6.94	6.41	0.54	2.87E-02	2.87E-01	LOC348262	hypothetical protein LOC348262	chr17p13.3	225329_at	NM_001093767 /// NM_207368																				
5.47	4.94	0.54	2.87E-02	2.87E-01	C6orf192	chromosome 6 open reading frame 192	chr6q22.3-q23.3	226301_at	NM_052831																				
6.38	5.86	0.52	2.87E-02	2.87E-01	SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	chr1p36.33	226229_s_at	NM_014188																				
3.96	3.33	0.63	2.87E-02	2.87E-01	EML2	Echinoderm microtubule associated protein like 2	chr19q13.32	1569086_at	NM_012155																				
4.91	4.07	0.83	2.88E-02	2.87E-01	UCKL1	uridine-cytidine kinase 1-like 1	chr20q13.33	232675_s_at	NM_017859																				
4.73	3.29	1.44	2.88E-02	2.87E-01	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	chr3p12-q12	223218_s_at	NM_001005474 /// NM_031419																				
8.97	8.39	0.58	2.88E-02	2.87E-01	C21orf33	chromosome 21 open reading frame 33	chr21q22.3	202217_at	NM_004649 /// NM_198155																				
6.15	5.64	0.51	2.88E-02	2.87E-01	ZNF444	zinc finger protein 444	chr19q13.42	50376_at	NM_018337																				
4.68	4.31	0.37	2.88E-02	2.87E-01	---	---	---	239252_at	---																				
4.28	3.95	0.33	2.88E-02	2.87E-01	FTCD	formiminotransferase cyclodeaminase	chr21q22.3	220604_x_at	NM_006657 /// NM_206965																				

6.69	6.16	0.53	2.88E-02	2.87E-01	DEDD	death effector domain containing	chr1q23.3	215158_s_at	NM_001039711 /// NM_001039712 /// NM_032998																			
4.16	3.38	0.78	2.89E-02	2.87E-01	DNM3	dynamin 3	chr1q24.3	1558501_at	NM_015569																			
6.59	6.09	0.50	2.89E-02	2.87E-01	TMED1	transmembrane emp24 protein transport domain containing 1	chr19p13.2	203679_at	NM_006858																			
6.56	6.19	0.37	2.89E-02	2.88E-01	KIAA0090	KIAA0090	chr1p36.13	212396_s_at	NM_015047																			
7.43	6.97	0.46	2.89E-02	2.88E-01	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	chr11q12.1-q12.3	218408_at	NM_012456																			
2.53	2.26	0.28	2.89E-02	2.88E-01	HNRNPA1 /// HNRPA1L-2 /// HNRPA1P5 /// LOC100128836 /// LOC120364 /// LOC391670 /// LOC402112 /// LOC440125 /// LOC642817 /// LOC643033 /// LOC644037 /// LOC645001 /// LOC728170 /// LOC728643 /// LOC728732 /// LOC729102 /// LOC729366 /// LOC730246 /// RP11-78J21.1	heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1 pseudogene /// heterogeneous nuclear ribonucleoprotein A1 pseudogene 5 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC642817 /// similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed) /// hypothetical LOC644037 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1 pseudogene /// hypothetical LOC728732 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC730246 /// heterogeneous nuclear ribonucleoprotein A1-like	chr10q11.22 /// chr11p15.4 /// chr11q23.1 /// chr12q13.1 /// chr12q22 /// chr13q12.11 /// chr13q14.3 /// chr19p13.2 /// chr19q13.2 /// chr1q32.1 /// chr2q31.1 /// chr2q33.3 /// chr3p22.1 /// chr4q21.1 /// chr5q14.1 /// chr6p25.1 /// chr8q21.13 /// chrXq22 /// chrXq24	217353_at	NM_001011724 /// NM_001011725 /// NM_002136 /// NM_031157 /// NR_002944 /// NR_003277 /// XM_001718684 /// XM_062025 /// XM_937967 /// XR_015330 /// XR_015514 /// XR_015658 /// XR_015746 /// XR_015895 /// XR_015958 /// XR_015974 /// XR_016080 /// XR_016093 /// XR_016314 /// XR_016373 /// XR_016388 /// XR_017084 /// XR_017337 /// XR_017501 /// XR_018564 /// XR_019025 /// XR_019262 /// XR_019573 /// XR_038280 /// XR_038288 /// XR_038331 /// XR_038689 /// XR_038697 /// XR_038725 /// XR_038755 /// XR_038765 /// XR_038785 /// XR_038911 /// XR_039047 /// XR_039155 /// XR_039380 /// XR_039402 /// XR_039425 /// XR_039446 /// XR_039541																			
6.19	5.73	0.46	2.90E-02	2.88E-01	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	chr10q24.3	222416_at	NM_001017423 /// NM_002860																			
6.22	5.45	0.77	2.90E-02	2.88E-01	SYMPK	symplekin	chr19q13.3	1554595_at	NM_004819																			
2.95	2.62	0.33	2.90E-02	2.88E-01	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	chr6q22-q23	228952_at	NM_006208																			
3.80	2.60	1.20	2.90E-02	2.88E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	1559094_at	NM_012347 /// NM_033480 /// NM_033481																			
6.67	5.54	1.13	2.90E-02	2.88E-01	IRS1	Insulin receptor substrate 1	chr2q36	238933_at	NM_005544																			
6.85	5.86	0.99	2.90E-02	2.88E-01	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	chr1p32	204159_at	NM_001262 /// NM_078626																			

3.44	3.00	0.43	2.90E-02	2.88E-01	RGS9	regulator of G-protein signaling 9	chr17q23-q24	206518_s_at	NM_001081955 /// NM_003835																				
7.78	7.33	0.45	2.91E-02	2.88E-01	SAFB	scaffold attachment factor B	chr19p13.3-p13.2	201748_s_at	NM_002967																				
7.47	7.07	0.40	2.91E-02	2.88E-01	THYN1	thymocyte nuclear protein 1	chr11q25	223711_s_at	NM_001037304 /// NM_001037305 /// NM_014174 /// NM_199297 /// NM_199298																				
3.40	2.76	0.64	2.91E-02	2.88E-01	---	---	---	215029_at	---																				
5.16	4.38	0.78	2.91E-02	2.88E-01	HAMP	hepcidin antimicrobial peptide	chr19q13.1	220491_at	NM_021175																				
6.09	5.69	0.40	2.91E-02	2.88E-01	ABHD2	abhydrolase domain containing 2	chr15q26.1	205566_at	NM_007011 /// NM_152924																				
3.03	2.69	0.33	2.91E-02	2.88E-01	MRPS25	mitochondrial ribosomal protein S25	chr3p25	224873_s_at	NM_022497																				
5.25	4.67	0.58	2.91E-02	2.88E-01	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	chr6q21	212899_at	NM_015076																				
7.56	5.92	1.65	2.91E-02	2.88E-01	MCF2	MCF.2 cell line derived transforming sequence	chrXq27	208017_s_at	NM_001099855 /// NM_005369																				
3.70	3.07	0.63	2.92E-02	2.88E-01	NAF1	nuclear assembly factor 1 homolog (S. cerevisiae)	chr4q32.2	244828_x_at	NM_001128931 /// NM_138386																				
7.10	6.75	0.36	2.92E-02	2.88E-01	---	---	---	213604_at	---																				
3.57	2.98	0.59	2.92E-02	2.88E-01	LOC100131067	hypothetical protein LOC100131067	chr5q14.1	235443_at	XM_001720191 /// XM_001722264 /// XM_001723049																				
5.85	5.28	0.57	2.92E-02	2.88E-01	PMS2 /// PMS2CL	PMS2 postmeiotic segregation increased 2 (S. cerevisiae) /// PMS2 C-terminal like pseudogene	chr7p22.1 /// chr7p22.2	221206_at	NM_000535 /// NR_002217 /// NR_003085																				
6.15	5.57	0.58	2.92E-02	2.88E-01	---	---	---	229107_at	---																				
5.41	4.92	0.49	2.92E-02	2.88E-01	FBXO4	F-box protein 4	chr5p12	223493_at	NM_012176 /// NM_033484																				
5.92	5.15	0.77	2.93E-02	2.88E-01	KIAA0409	KIAA0409	chr11p15.4	203171_s_at	NM_015324																				
2.87	2.62	0.25	2.93E-02	2.89E-01	KIF6	kinesin family member 6	chr6p21.2	1556233_s_at	NM_145027																				
6.20	5.50	0.70	2.93E-02	2.89E-01	---	---	---	228292_at	---																				
10.60	9.91	0.69	2.93E-02	2.89E-01	CD9	CD9 molecule	chr12p13.3	201005_at	NM_001769																				
8.07	7.56	0.51	2.93E-02	2.89E-01	SCAND1	SCAN domain containing 1	chr20q11.1-q11.23	232652_x_at	NM_016558 /// NM_033630																				
7.68	7.11	0.57	2.94E-02	2.89E-01	MPST	mercaptopyruvate sulfurtransferase	chr22q13.1	203524_s_at	NM_001013436 /// NM_001013440 /// NM_001130517 /// NM_021126 /// NR_024038																				
5.90	5.13	0.77	2.94E-02	2.89E-01	CDADC1	cytidine and dCMP deaminase domain containing 1	chr13q14.2	233647_s_at	NM_030911																				
3.77	2.96	0.81	2.94E-02	2.89E-01	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	chr17p12-p11.2	227361_at	NM_006041																				
7.80	7.24	0.56	2.94E-02	2.89E-01	URG4	up-regulated gene 4	chr7p13	218601_at	NM_001077663 /// NM_001077664 /// NM_017920																				
4.52	3.67	0.85	2.95E-02	2.90E-01	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	chr15q21.1	203178_at	NM_001482																				
5.60	4.73	0.87	2.95E-02	2.90E-01	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	chr17q11-q21	228595_at	NM_000413																				
6.53	6.14	0.39	2.95E-02	2.90E-01	CLP1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	chr11q12	204370_at	NM_006831																				

5.59	4.58	1.01	2.96E-02	2.90E-01	APBB3	amyloid beta (A4) precursor protein-binding, family B, member 3	chr5q31	204650_s_at	NM_006051 /// NM_133172 /// NM_133173 /// NM_133174
5.83	4.94	0.88	2.96E-02	2.90E-01	NR1D1 /// THRA	nuclear receptor subfamily 1, group D, member 1 /// thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	chr17q11.2	204760_s_at	NM_003250 /// NM_021724 /// NM_199334
8.02	7.49	0.53	2.96E-02	2.90E-01	VPS52	vacuolar protein sorting 52 homolog (S. cerevisiae)	chr6p21.3	214585_s_at	NM_022553
3.98	3.40	0.58	2.96E-02	2.90E-01	SOX4	SRY (sex determining region Y)-box 4	chr6p22.3	213668_s_at	NM_003107
8.33	6.85	1.47	2.97E-02	2.90E-01	PTP4A1	protein tyrosine phosphatase type IVA, member 1	chr6q12	200730_s_at	NM_003463
5.70	5.26	0.44	2.97E-02	2.90E-01	KIAA1652	KIAA1652 protein	---	230880_at	---
3.41	2.86	0.54	2.97E-02	2.90E-01	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	---	235204_at	NM_020354
4.09	3.52	0.57	2.97E-02	2.90E-01	---	---	---	1567274_at	---
4.21	3.86	0.36	2.97E-02	2.90E-01	KIAA0329	KIAA0329	chr14q32.31	204307_at	NM_014844
9.90	9.52	0.38	2.98E-02	2.91E-01	RAB13	RAB13, member RAS oncogene family	chr1q21.2	202252_at	NM_002870
7.73	6.81	0.92	2.98E-02	2.91E-01	SMYD2	SET and MYND domain containing 2	chr1q41	212922_s_at	NM_020197
3.76	3.31	0.45	2.98E-02	2.91E-01	WHSC1	Wolf-Hirschhorn syndrome candidate 1	chr4p16.3	209053_s_at	NM_001042424 /// NM_007331 /// NM_133330 /// NM_133331 /// NM_133334 /// NM_133335
8.80	8.40	0.40	2.98E-02	2.91E-01	CYFIP1	cytoplasmic FMR1 interacting protein 1	chr15q11	208923_at	NM_001033028 /// NM_014608
5.26	4.69	0.57	2.98E-02	2.91E-01	DGCR8	DiGeorge syndrome critical region gene 8	chr22q11.2	218650_at	NM_022720
4.64	4.12	0.52	2.99E-02	2.91E-01	FLYWCH1	FLYWCH-type zinc finger 1	chr16p13.3	234106_s_at	NM_020912 /// NM_032296
6.45	6.03	0.43	2.99E-02	2.91E-01	---	---	---	228726_at	---
5.48	5.02	0.45	2.99E-02	2.91E-01	---	---	---	226262_at	---
6.09	5.54	0.55	3.00E-02	2.91E-01	PHKG2	phosphorylase kinase, gamma 2 (testis)	chr16p12.1-p11.2	203709_at	NM_000294
5.79	5.01	0.79	3.00E-02	2.91E-01	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	chr14q24.3	203981_s_at	NM_005050 /// NR_003256
7.48	7.08	0.40	3.00E-02	2.91E-01	SDF4	stromal cell derived factor 4	chr1p36.33	224472_x_at	NM_016176 /// NM_016547
6.73	5.60	1.13	3.00E-02	2.91E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	204490_s_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392
7.11	6.65	0.46	3.00E-02	2.92E-01	POLB	polymerase (DNA directed), beta	chr8p11.2	203616_at	NM_002690
6.42	5.79	0.63	3.00E-02	2.92E-01	ZNF672	zinc finger protein 672	chr1q44	218068_s_at	NM_024836
6.52	5.76	0.75	3.00E-02	2.92E-01	TRIM41	tripartite motif-containing 41	chr5q35.3	226445_s_at	NM_033549 /// NM_201627
7.57	4.79	2.77	3.01E-02	2.92E-01	TFPI2	tissue factor pathway inhibitor 2	chr7q22	209278_s_at	NM_006528
1.93	1.65	0.28	3.01E-02	2.92E-01	MIPOL1	mirror-image polydactyly 1	chr14q13.3-q21.1	1552572_a_at	NM_138731
7.22	6.83	0.39	3.01E-02	2.92E-01	NOTCH2	Notch homolog 2 (Drosophila)	chr1p13-p11	212377_s_at	NM_024408
7.02	6.54	0.48	3.01E-02	2.92E-01	RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr15q15.1	212301_at	NM_015138
7.17	6.56	0.61	3.01E-02	2.92E-01	ALKBH5	alkB, alkylation repair homolog 5 (E. coli)	chr17p11.2	1553101_a_at	NM_017758
12.12	11.53	0.59	3.01E-02	2.92E-01	CLU	clusterin	chr8p21-p12	208791_at	NM_001831 /// NM_203339
2.31	1.96	0.35	3.02E-02	2.92E-01	---	---	---	1562921_at	---
4.72	3.78	0.94	3.02E-02	2.92E-01	BPGM	2,3-bisphosphoglycerate mutase	chr7q31-q34	203502_at	NM_001724 /// NM_199186
4.32	3.76	0.56	3.02E-02	2.92E-01	BTBD12	BTB (POZ) domain containing 12	chr16p13.3	232147_at	NM_032444

4.56	4.11	0.46	3.02E-02	2.92E-01	DSCAM	Down syndrome cell adhesion molecule	chr21q22.2	211484_s_at	NM_001389
6.24	5.29	0.95	3.02E-02	2.92E-01	CROP	cisplatin resistance-associated overexpressed protein	chr17q21.33	220044_x_at	NM_006107 /// NM_016424
5.11	4.12	0.99	3.03E-02	2.92E-01	PLAGL1	pleiomorphic adenoma gene-like 1	chr6q24-q25	207943_x_at	NM_001080951 /// NM_001080952 /// NM_001080953 /// NM_001080954 /// NM_001080955 /// NM_001080956 /// NM_002656 /// NM_006718
8.56	8.02	0.54	3.03E-02	2.92E-01	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	chr14q12	223776_x_at	NM_001099274 /// NM_012461
8.96	7.90	1.06	3.03E-02	2.92E-01	S100A13	S100 calcium binding protein A13	chr1q21	202598_at	NM_001024210 /// NM_001024211 /// NM_001024212 /// NM_001024213 /// NM_005979 /// XM_001724603
4.25	3.82	0.43	3.03E-02	2.93E-01	PSTK	phosphoseryl-tRNA kinase	chr10q26.13	230129_at	NM_153336
2.90	2.61	0.29	3.03E-02	2.93E-01	ZNF235	zinc finger protein 235	chr19q13.2	220350_at	NM_004234
12.49	12.14	0.34	3.04E-02	2.93E-01	RPS19	ribosomal protein S19	chr19q13.2	213414_s_at	NM_001022
5.53	4.10	1.43	3.04E-02	2.93E-01	KIAA0146	KIAA0146	chr8q11.21	228325_at	NM_001080394
7.86	7.37	0.49	3.04E-02	2.93E-01	PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	chr1q21	210417_s_at	NM_002651
6.77	6.41	0.36	3.04E-02	2.93E-01	LOC389203	hypothetical gene supported by BC032431	chr4p15.2	225014_at	XR_040593 /// XR_040594 /// XR_040595
2.73	2.41	0.31	3.04E-02	2.93E-01	LOC440993	hypothetical gene supported by AK128346	chr3q29	1557293_at	XR_039810
6.69	6.21	0.47	3.04E-02	2.93E-01	UNQ1887	signal peptide peptidase 3	chr12q24.31	224640_at	NM_139015
7.56	6.88	0.68	3.04E-02	2.93E-01	TMEM93	transmembrane protein 93	chr17p13.3	221255_s_at	NM_001014764 /// NM_031298
5.31	4.53	0.78	3.05E-02	2.93E-01	GRAMD4	GRAM domain containing 4	chr22q13.31	212856_at	NM_015124
3.09	2.58	0.50	3.05E-02	2.93E-01	CARD14	caspase recruitment domain family, member 14	chr17q25	220599_s_at	NM_024110 /// NM_052819
2.67	2.36	0.32	3.05E-02	2.93E-01	C3orf33	chromosome 3 open reading frame 33	chr3q25.31	1554176_a_at	NM_173657
2.68	2.13	0.54	3.05E-02	2.93E-01	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	chr12p13.3	237058_x_at	NM_016615
4.67	3.88	0.78	3.06E-02	2.93E-01	ZNF599	zinc finger protein 599	chr19q13.11	228093_at	NM_001007248
5.83	4.93	0.90	3.06E-02	2.93E-01	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	chr16q22.1	224998_at	NM_178818 /// NM_181521
7.18	6.71	0.48	3.06E-02	2.94E-01	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	chr19q13.3	200922_at	NM_006801
10.07	9.44	0.62	3.06E-02	2.94E-01	C11orf31	chromosome 11 open reading frame 31	chr11q12.1	228332_s_at	NM_170746
7.43	6.71	0.72	3.06E-02	2.94E-01	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	chr11q13	228622_s_at	NM_005528
12.02	11.67	0.34	3.07E-02	2.94E-01	RPS2	ribosomal protein S2	chr16p13.3	212433_x_at	NM_002952
7.29	6.76	0.53	3.07E-02	2.94E-01	ATXN1L	ataxin 1-like	chr16q22.3	227373_at	XM_001724473 /// XM_001724532 /// XM_928464
5.22	3.79	1.43	3.07E-02	2.94E-01	TNIK	TRAF2 and NCK interacting kinase	chr3q26.2-q26.31	213107_at	NM_015028
4.94	3.95	0.99	3.07E-02	2.94E-01	GTPBP2	GTP binding protein 2	chr6p21-p12	221050_s_at	NM_019096
9.19	8.54	0.66	3.08E-02	2.94E-01	RAB34	RAB34, member RAS oncogene family	chr17q11.2	224710_at	NM_031934
5.38	4.37	1.01	3.08E-02	2.94E-01	SIN3B	SIN3 homolog B, transcription regulator (yeast)	chr19p13.11	209352_s_at	NM_015260

4.42	3.08	1.34	3.08E-02	2.94E-01	JOSD3	Josephin domain containing 3	chr11q21	218750_at	NM_024116
7.83	7.18	0.66	3.09E-02	2.95E-01	MBD1	methyl-CpG binding domain protein 1	chr18q21	203353_s_at	NM_002384 /// NM_015844 /// NM_015845 /// NM_015846 /// NM_015847
5.80	4.78	1.02	3.09E-02	2.95E-01	DPP10	dipeptidyl-peptidase 10	chr2q14.1	228598_at	NM_001004360 /// NM_020868
5.16	4.45	0.71	3.10E-02	2.95E-01	RFFL	ring finger and FYVE-like domain containing 1	chr17q12	228980_at	NM_001017368 /// NM_057178
4.66	4.18	0.48	3.10E-02	2.95E-01	FLJ20674	hypothetical protein FLJ20674	chr12q24.23	220137_at	NM_019086
2.69	2.32	0.37	3.10E-02	2.95E-01	AIM2	absent in melanoma 2	chr1q22	206513_at	NM_004833
7.91	6.44	1.47	3.10E-02	2.95E-01	FABP6	fatty acid binding protein 6, ileal	chr5q33.3-q34	210445_at	NM_001040442 /// NM_001130958 /// NM_001445
5.90	4.01	1.89	3.10E-02	2.95E-01	ANKRD10	Ankyrin repeat domain 10	chr13q34	227260_at	NM_017664
9.93	9.64	0.29	3.10E-02	2.95E-01	DAZAP2	DAZ associated protein 2	chr12q12	200794_x_at	NM_014764
7.84	7.29	0.55	3.10E-02	2.95E-01	PGD	phosphogluconate dehydrogenase	chr1p36.3-p36.13	201118_at	NM_002631
8.51	8.04	0.46	3.10E-02	2.95E-01	C7orf30	chromosome 7 open reading frame 30	chr7p15.3	226385_s_at	NM_138446
5.45	4.69	0.75	3.11E-02	2.95E-01	TARBP1	TAR (HIV-1) RNA binding protein 1	chr1q42.3	202813_at	NM_005646
8.43	7.07	1.36	3.11E-02	2.95E-01	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	chr1q32	201925_s_at	NM_000574 /// NM_001114752
8.95	8.42	0.53	3.11E-02	2.95E-01	CUEDC2	CUE domain containing 2	chr10q24.32	218097_s_at	NM_024040
5.40	4.22	1.17	3.11E-02	2.95E-01	CBLN3	cerebellin 3 precursor	chr14q12	235221_at	NM_001039771
5.47	5.05	0.42	3.11E-02	2.95E-01	GINS3	GINS complex subunit 3 (Psf3 homolog)	chr16q21	218719_s_at	NM_001126129 /// NM_001126130 /// NM_022770
5.80	5.36	0.43	3.11E-02	2.95E-01	DYNLL2	dynein, light chain, LC8-type 2	chr17q22	229106_at	NM_080677
7.57	7.18	0.39	3.12E-02	2.95E-01	MED31	mediator complex subunit 31	chr17p13.2	222867_s_at	NM_016060
3.21	2.75	0.46	3.12E-02	2.95E-01	HUS1	HUS1 checkpoint homolog (S. pombe)	chr7p13-p12	217618_x_at	NM_004507
3.37	2.80	0.57	3.12E-02	2.96E-01	SAP30L	SAP30-like	chr5q33.2	232135_at	NM_001131062 /// NM_001131063 /// NM_024632 /// NR_024084
6.47	5.89	0.58	3.12E-02	2.96E-01	TTC7A	tetratricopeptide repeat domain 7A	chr2p21	224912_at	NM_020458
3.92	3.49	0.44	3.12E-02	2.96E-01	TRERF1	transcriptional regulating factor 1	chr6p21.1-p12.1	229016_s_at	NM_033502
5.91	4.88	1.02	3.12E-02	2.96E-01	ALOX5	arachidonate 5-lipoxygenase	chr10q11.2	204446_s_at	NM_000698
3.57	2.63	0.94	3.12E-02	2.96E-01	HEMK1	HemK methyltransferase family member 1	chr3p21.3	218621_at	NM_016173
3.15	2.52	0.63	3.13E-02	2.96E-01	C17orf86	chromosome 17 open reading frame 86	chr17q25.2	221621_at	XR_041718 /// XR_041719 /// XR_041720
6.76	6.29	0.47	3.13E-02	2.96E-01	PARP2	poly (ADP-ribose) polymerase 2	chr14q11.2-q12	204752_x_at	NM_001042618 /// NM_005484
7.15	6.36	0.79	3.13E-02	2.96E-01	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	chr13q34	214323_s_at	NM_023011 /// NM_080687
6.63	5.89	0.74	3.13E-02	2.96E-01	---	---	---	227095_at	---
4.01	3.23	0.78	3.14E-02	2.96E-01	CEP192	centrosomal protein 192kDa	chr18p11.21	218827_s_at	NM_032142
3.96	3.14	0.82	3.14E-02	2.96E-01	LOC643224	similar to tubulin, beta 8	chr9q34.3	222361_at	XR_041477 /// XR_041478
3.20	2.70	0.50	3.14E-02	2.96E-01	PER3	period homolog 3 (Drosophila)	chr1p36.23	1555131_a_at	NM_016831
5.58	5.03	0.54	3.14E-02	2.96E-01	SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	chr5q33.1	213119_at	NM_078483
6.26	5.63	0.62	3.14E-02	2.96E-01	C8orf33	chromosome 8 open reading frame 33	chr8q24.3	222551_s_at	NM_023080
6.73	5.86	0.86	3.14E-02	2.96E-01	TREM2	triggering receptor expressed on myeloid cells 2	chr6p21.1	219725_at	NM_018965

3.67	3.28	0.39	3.15E-02	2.97E-01	SORBS1	sorbin and SH3 domain containing 1	chr10q23.3-q24.1	218087_s_at	NM_001034954 /// NM_001034955 /// NM_001034956 /// NM_001034957 /// NM_006434 /// NM_015385 /// NM_024991																			
6.43	5.77	0.66	3.15E-02	2.97E-01	ADCY9	adenylate cyclase 9	chr16p13.3	204497_at	NM_001116																			
8.15	7.65	0.50	3.15E-02	2.97E-01	KANK2	KN motif and ankyrin repeat domains 2	chr19p13.2	218418_s_at	NM_015493																			
4.87	4.09	0.78	3.15E-02	2.97E-01	HSPC157 /// LOC100128919	hypothetical LOC29092 /// similar to HSPC157	chr1p36.12	219865_at	NR_023918 /// NR_023919 /// XR_038476 /// XR_038890 /// XR_038986																			
3.65	3.12	0.53	3.15E-02	2.97E-01	GNAS	GNAS complex locus	chr20q13.3	229274_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259																			
4.14	3.65	0.49	3.16E-02	2.97E-01	ELMO2	engulfment and cell motility 2	chr20q13	220363_s_at	NM_133171 /// NM_182764																			
5.56	5.05	0.51	3.16E-02	2.97E-01	OSGEP	O-sialoglycoprotein endopeptidase	chr14q11.2	209450_at	NM_017807																			
4.08	3.69	0.39	3.16E-02	2.97E-01	PGBD2	piggyBac transposable element derived 2	chr1q44	238004_at	NM_001017434 /// NM_170725																			
5.16	4.57	0.59	3.16E-02	2.97E-01	SLC39A13	solute carrier family 39 (zinc transporter), member 13	chr11p11.2	1552295_a_at	NM_001128225 /// NM_152264																			
4.18	3.23	0.95	3.16E-02	2.97E-01	SLC20A1	Solute carrier family 20 (phosphate transporter), member 1	chr2q11-q14	230494_at	NM_005415																			
5.44	4.75	0.70	3.17E-02	2.98E-01	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	chr2q21	203664_s_at	NM_004805																			
4.82	4.23	0.59	3.17E-02	2.98E-01	ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)	chr11q24.2	219550_at	NM_022370																			
3.92	3.28	0.64	3.17E-02	2.98E-01	IL12RB1	interleukin 12 receptor, beta 1	chr19p13.1	1552584_at	NM_005535 /// NM_153701																			
7.94	7.31	0.64	3.17E-02	2.98E-01	SETD1B	SET domain containing 1B	chr12q24.31	213153_at	XM_001715003 /// XM_001719079 /// XM_037523																			
7.44	6.88	0.57	3.17E-02	2.98E-01	C7orf11	chromosome 7 open reading frame 11	chr7p14.1	225419_at	NM_138701																			
6.87	6.46	0.41	3.17E-02	2.98E-01	FAM103A1	family with sequence similarity 103, member A1	chr15q25.2	225208_s_at	NM_031452																			
4.05	3.62	0.44	3.18E-02	2.98E-01	---	---	---	1562013_a_at	---																			
3.94	3.26	0.68	3.18E-02	2.98E-01	ATG16L2	ATG16 autophagy related 16-like 2 (S. cerevisiae)	chr11q13.4	225883_at	NM_033388																			
3.11	2.77	0.34	3.18E-02	2.98E-01	LOC283666	hypothetical LOC283666	chr15q21.3	240163_at	---																			
5.49	4.14	1.35	3.18E-02	2.98E-01	AVPR1A	arginine vasopressin receptor 1A	chr12q14-q15	206252_s_at	NM_000706																			
6.54	6.07	0.46	3.18E-02	2.98E-01	TMEM103	transmembrane protein 103	chr3p21.31	229863_s_at	NM_001031703																			
8.31	7.81	0.50	3.18E-02	2.98E-01	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	chr2q12-q21	209389_x_at	NM_001079862 /// NM_001079863 /// NM_020548																			
5.57	5.09	0.48	3.19E-02	2.98E-01	TMEM185A	transmembrane protein 185A	chrXq28	1554105_at	NM_032508																			
3.24	2.86	0.39	3.19E-02	2.98E-01	GUCA1A	guanylate cyclase activator 1A (retina)	chr6p21.1	206062_at	NM_000409																			

5.47	5.01	0.45	3.19E-02	2.98E-01	---	---	---	1554599_x_at	---
5.03	4.42	0.61	3.19E-02	2.98E-01	---	---	---	237048_at	---
5.58	5.14	0.44	3.19E-02	2.98E-01	FLJ22222	hypothetical protein FLJ22222	chr17q25.3	64438_at	NM_024648 /// NM_175902
8.19	7.71	0.48	3.19E-02	2.99E-01	SLC25A28	solute carrier family 25, member 28	chr10q23-q24	223192_at	NM_031212
5.25	4.97	0.28	3.20E-02	2.99E-01	CWF19L1	CWF19-like 1, cell cycle control (S. pombe)	chr10q24.2-q24.31	218787_x_at	NM_018294
7.64	7.06	0.59	3.20E-02	2.99E-01	MAEA	macrophage erythroblast attacher	chr4p16.3	207922_s_at	NM_001017405 /// NM_005882
2.41	2.12	0.29	3.20E-02	2.99E-01	---	---	---	239209_at	---
5.72	5.21	0.51	3.20E-02	2.99E-01	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	chr22q11.21	209299_x_at	NM_014337 /// NM_148175 /// NM_148176
4.29	3.92	0.36	3.21E-02	2.99E-01	---	---	---	242951_at	---
3.40	2.79	0.61	3.21E-02	2.99E-01	C8orf31	chromosome 8 open reading frame 31	chr8q24.3	1552793_at	NM_173687
2.81	2.44	0.37	3.21E-02	2.99E-01	---	---	---	242983_at	---
6.25	5.08	1.17	3.21E-02	2.99E-01	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	chr12q13.11	204255_s_at	NM_000376 /// NM_001017535
4.01	3.58	0.43	3.22E-02	3.00E-01	CD86	CD86 molecule	chr3q21	205686_s_at	NM_006889 /// NM_175862
4.36	3.95	0.41	3.22E-02	3.00E-01	---	---	---	1555311_at	---
8.55	7.98	0.57	3.22E-02	3.00E-01	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	chr14q12	224809_x_at	NM_001099274 /// NM_012461
8.74	7.76	0.98	3.22E-02	3.00E-01	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	chr13q12	204174_at	NM_001629
2.20	1.90	0.31	3.22E-02	3.00E-01	---	---	---	243723_at	---
3.35	2.92	0.44	3.23E-02	3.00E-01	GALT	galactose-1-phosphate uridylyltransferase	chr9p13	242734_x_at	NM_000155
6.69	5.93	0.76	3.23E-02	3.00E-01	TMEM99	transmembrane protein 99	chr17q21.2	226565_at	NM_145274
5.69	5.15	0.54	3.23E-02	3.00E-01	COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	chr16p13.11-p12.3	210820_x_at	NM_016138
4.80	4.23	0.57	3.23E-02	3.00E-01	NARG1L	NMDA receptor regulated 1-like	chr13q14.11	219378_at	NM_001110798 /// NM_018527 /// NM_024561
6.44	5.75	0.69	3.24E-02	3.00E-01	AGBL5	ATP/GTP binding protein-like 5	chr2p23.3	218480_at	NM_001035507 /// NM_021831
6.13	5.25	0.89	3.24E-02	3.00E-01	VEGFA	vascular endothelial growth factor A	chr6p12	210513_s_at	NM_001025366 /// NM_001025367 /// NM_001025368 /// NM_001025369 /// NM_001025370 /// NM_001033756 /// NM_003376
4.18	3.82	0.36	3.24E-02	3.00E-01	---	---	---	91682_at	---
5.17	4.66	0.51	3.24E-02	3.00E-01	SP5	Sp5 transcription factor	chr2q31.1	235845_at	NM_001003845
7.70	7.00	0.70	3.24E-02	3.00E-01	TRIB2	tribbles homolog 2 (Drosophila)	chr2p25.1-p24.3	202478_at	NM_021643
3.60	2.84	0.76	3.24E-02	3.00E-01	---	---	---	243671_at	---
3.49	2.98	0.51	3.24E-02	3.00E-01	---	---	---	1559922_at	---
2.72	2.25	0.47	3.24E-02	3.00E-01	---	---	---	1558512_at	---
6.23	5.29	0.94	3.25E-02	3.00E-01	LONRF3	LON peptidase N-terminal domain and ring finger 3	chrXq24	242931_at	NM_001031855 /// NM_024778
3.06	2.49	0.57	3.25E-02	3.00E-01	LOC100130623	hypothetical protein LOC100130623	chr20q11.1	241803_s_at	XM_001713846 /// XM_001721157
6.89	6.46	0.44	3.25E-02	3.00E-01	HCFC1	host cell factor C1 (VP16-accessory protein)	chrXq28	202474_s_at	NM_005334
10.10	9.76	0.34	3.25E-02	3.00E-01	EIF3F	eukaryotic translation initiation factor 3, subunit F	chr11p15.4	200023_s_at	NM_003754
6.14	5.70	0.44	3.25E-02	3.00E-01	ASB6	ankyrin repeat and SOCS box-containing 6	---	221657_s_at	NM_017873 /// NM_177999

9.04	8.44	0.59	3.25E-02	3.00E-01	CKAP4	cytoskeleton-associated protein 4	chr12q23.3	200999_s_at	NM_006825
5.44	4.91	0.53	3.26E-02	3.00E-01	CNPY3	canopy 3 homolog (zebrafish)	chr6pter-p12.1	1552977_a_at	NM_006586
8.51	8.17	0.34	3.26E-02	3.01E-01	C14orf119	chromosome 14 open reading frame 119	chr14q11.2	223060_at	NM_017924
4.73	4.47	0.27	3.26E-02	3.01E-01	BTBD9	BTB (POZ) domain containing 9	chr6p21	235248_at	NM_001099272 /// NM_052893 /// NM_152733
6.03	5.51	0.52	3.26E-02	3.01E-01	---	---	---	64488_at	---
7.68	7.09	0.59	3.26E-02	3.01E-01	AP1M1	adaptor-related protein complex 1, mu 1 subunit	chr19p13.12	223024_at	NM_001130524 /// NM_032493
4.88	4.44	0.44	3.26E-02	3.01E-01	CLCN2	chloride channel 2	chr3q27-q28	213499_at	NM_004366
8.49	7.75	0.73	3.26E-02	3.01E-01	C2orf59 /// LOC541471	chromosome 2 open reading frame 59 /// hypothetical LOC541471	chr2p11.2 /// chr2q13	225799_at	XR_039885 /// XR_039886 /// XR_042051 /// XR_042052
3.70	2.62	1.07	3.26E-02	3.01E-01	---	---	---	242904_x_at	---
11.83	11.22	0.61	3.27E-02	3.01E-01	TIMP1	TIMP metallopeptidase inhibitor 1	chrXp11.3-p11.23	201666_at	NM_003254
2.43	2.08	0.35	3.27E-02	3.01E-01	SLFN13	schlafen family member 13	chr17q12	1558217_at	NM_144682
7.34	6.69	0.65	3.27E-02	3.01E-01	hCG_20857 /// RP11-544M22.4	hypothetical protein LOC100134860 /// KAT protein	chr1q21-q23 /// chr1q23.3	226482_s_at	NM_001113205 /// NM_001113206 /// NM_001113207 /// NM_001126312 /// XM_001722251 /// XM_001725725 /// XM_001725726
7.49	6.80	0.69	3.27E-02	3.01E-01	APEH	N-acylaminoacyl-peptide hydrolase	chr3p21.31	201284_s_at	NM_001640
5.43	4.89	0.54	3.27E-02	3.01E-01	IL20RA	interleukin 20 receptor, alpha	chr6q22.33-q23.1	222829_s_at	NM_014432
4.74	4.10	0.63	3.27E-02	3.01E-01	ETV6	ets variant gene 6 (TEL oncogene)	chr12p13	235056_at	NM_001987
2.90	2.52	0.38	3.27E-02	3.01E-01	---	---	---	243095_at	---
5.21	4.79	0.43	3.27E-02	3.01E-01	PKD1	polycystic kidney disease 1 (autosomal dominant)	chr16p13.3	202328_s_at	NM_000296 /// NM_001009944
2.89	2.32	0.58	3.27E-02	3.01E-01	---	---	---	239346_at	---
5.48	4.48	1.00	3.27E-02	3.01E-01	CSNK1E	casein kinase 1, epsilon	chr22q13.1	225756_at	NM_001894 /// NM_152221
4.23	3.83	0.40	3.27E-02	3.01E-01	FAM41C /// MGC70863 /// RPL23AP7	family with sequence similarity 41, member C /// similar to RPL23AP7 protein /// ribosomal protein L23a pseudogene 7	chr1p36.33 /// chr22q13.33 /// chr2q14	232899_at	NM_203302 /// NM_203477 /// NR_000029 /// XM_496333 /// XM_936761
3.89	3.31	0.58	3.28E-02	3.01E-01	FAM118B	family with sequence similarity 118, member B	chr11q24.2	230009_at	NM_024556
2.83	2.43	0.40	3.28E-02	3.01E-01	COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr3q13.33	1558346_at	NM_005694
6.26	5.78	0.48	3.29E-02	3.02E-01	RCL1	RNA terminal phosphate cyclase-like 1	chr9p24.1-p23	218544_s_at	NM_005772
7.52	7.11	0.41	3.29E-02	3.02E-01	EIF4E2	eukaryotic translation initiation factor 4E family member 2	chr2q37.1	213571_s_at	NM_004846
8.64	7.93	0.71	3.29E-02	3.02E-01	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	chr6p21.2	202284_s_at	NM_000389 /// NM_078467
8.22	7.86	0.36	3.29E-02	3.02E-01	TH1L	TH1-like (Drosophila)	chr20q13	225006_x_at	NM_198976
3.23	2.64	0.60	3.30E-02	3.02E-01	---	---	---	228632_at	---
3.94	3.50	0.44	3.30E-02	3.03E-01	IFRG15	interferon responsive gene 15	chr1q25.2	231719_at	NM_022347
2.72	2.40	0.33	3.30E-02	3.03E-01	C20orf74	chromosome 20 open reading frame 74	chr20p11.22	231826_at	NM_020343
6.87	6.11	0.76	3.31E-02	3.03E-01	TMEM51	transmembrane protein 51	chr1p36.21	218815_s_at	NM_018022
5.53	4.90	0.62	3.31E-02	3.03E-01	---	---	---	214857_at	---
4.00	3.67	0.33	3.31E-02	3.03E-01	FLJ35390	hypothetical LOC255031	chr7p13	1569090_x_at	---
12.37	12.10	0.27	3.31E-02	3.03E-01	RPS16	ribosomal protein S16	chr19q13.1	213890_x_at	NM_001020

4.82	4.28	0.54	3.32E-02	3.03E-01	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	chr8p12	223569_at	NM_001102559 /// NM_001102560 /// NM_032483																			
3.67	3.35	0.32	3.32E-02	3.03E-01	---	---	---	1568845_at	---																			
6.09	5.45	0.64	3.32E-02	3.03E-01	RPL13	ribosomal protein L13	chr16q24.3|17p11.2	229590_at	NM_000977 /// NM_033251																			
4.76	3.94	0.82	3.33E-02	3.04E-01	PAPOLG	poly(A) polymerase gamma	chr2p16.1	222839_s_at	NM_022894																			
3.35	2.97	0.38	3.33E-02	3.04E-01	DGCR11	DiGeorge syndrome critical region gene 11	chr22q11.21	215725_at	---																			
3.72	2.86	0.86	3.33E-02	3.04E-01	ZNF606	zinc finger protein 606	chr19q13.4	229707_at	NM_025027																			
6.80	5.67	1.13	3.34E-02	3.04E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	209835_x_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392																			
5.50	4.64	0.86	3.34E-02	3.04E-01	FRMD5	FERM domain containing 5	chr15q15.3	1569470_a_at	NM_032892																			
7.69	6.92	0.77	3.34E-02	3.04E-01	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	chr17p13.1	210314_x_at	NM_003808 /// NM_172087 /// NM_172088																			
5.39	4.62	0.77	3.34E-02	3.04E-01	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	chrXp11.23-p11.22	209326_at	NM_001032289 /// NM_001042498 /// NM_005660																			
6.67	6.19	0.48	3.34E-02	3.04E-01	LOC285053 /// LOC390354 /// RPL18A	similar to ribosomal protein L18a /// ribosomal protein L18a pseudogene /// ribosomal protein L18a	chr12q23.3 /// chr19p13 /// chr2p16.3	216383_at	NM_000980 /// NR_001593 /// XM_001725506 /// XM_001725508 /// XM_208281 /// XM_934020 /// XM_941835 /// XM_945469 /// XR_042140 /// XR_042141																			
5.99	5.26	0.74	3.35E-02	3.04E-01	DCP1A	DCP1 decapping enzyme homolog A (S. cerevisiae)	chr3p21.1	225443_at	NM_018403																			
6.65	6.06	0.59	3.35E-02	3.04E-01	SEC23B	Sec23 homolog B (S. cerevisiae)	chr20p11.23	210293_s_at	NM_006363 /// NM_032985 /// NM_032986																			
8.41	7.86	0.55	3.35E-02	3.04E-01	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	chr7q34	218201_at	NM_004546																			
6.78	6.13	0.64	3.35E-02	3.04E-01	AMPD2	adenosine monophosphate deaminase 2 (isoform L)	chr1p13.3	212360_at	NM_004037 /// NM_139156 /// NM_203404																			
5.71	5.07	0.64	3.35E-02	3.04E-01	RNASEH2A	ribonuclease H2, subunit A	chr19p13.13	203022_at	NM_006397																			
7.26	6.76	0.50	3.36E-02	3.04E-01	STX10	syntaxin 10	chr19p13.13	212625_at	NM_003765																			
6.76	6.22	0.54	3.36E-02	3.04E-01	WBSCR16	Williams-Beuren syndrome chromosome region 16	chr7q11.23	221247_s_at	NM_030798																			
7.42	6.71	0.71	3.36E-02	3.05E-01	TBRG1	transforming growth factor beta regulator 1	chr11q24.2	226318_at	NM_032811 /// NR_016021																			
5.11	4.50	0.61	3.36E-02	3.05E-01	ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	chr6p21.1	215873_x_at	NM_033450																			
9.73	9.32	0.42	3.36E-02	3.05E-01	SNX3	sorting nexin 3	chr6q21	213545_x_at	NM_003795																			

2.60	2.19	0.41	3.37E-02	3.05E-01	LOC100131731	hypothetical protein LOC100131731	chr14q11.2	1557262_at	XM_001714984 /// XM_001716923 /// XM_001717178																				
5.04	4.35	0.69	3.37E-02	3.05E-01	JMJD3	jumonji domain containing 3, histone lysine demethylase	chr17p13.1	1556067_a_at	NM_001080424																				
3.19	2.41	0.78	3.37E-02	3.05E-01	SNX5	sorting nexin 5	chr20p11	229981_at	NM_014426 /// NM_152227																				
4.28	3.92	0.36	3.37E-02	3.05E-01	CCHCR1	coiled-coil alpha-helical rod protein 1	chr6p21.3	37424_at	NM_001105563 /// NM_001105564 /// NM_019052																				
5.84	5.40	0.44	3.38E-02	3.05E-01	HSCB	HscB iron-sulfur cluster co-chaperone homolog (E. coli)	chr22q12.1	223647_x_at	NM_172002																				
5.45	4.57	0.88	3.38E-02	3.05E-01	TP53RK	TP53 regulating kinase	chr20q13.2	225402_at	NM_033550																				
3.29	2.75	0.54	3.38E-02	3.05E-01	FNDC3B	fibronectin type III domain containing 3B	chr3q26.31	229865_at	NM_022763																				
8.06	7.38	0.68	3.38E-02	3.05E-01	C5orf33	chromosome 5 open reading frame 33	chr5p13.2	228594_at	NM_001085411 /// NM_153013																				
2.49	2.14	0.35	3.38E-02	3.05E-01	---	---	---	241527_at	---																				
2.98	2.67	0.31	3.38E-02	3.05E-01	DNASE1L3	deoxyribonuclease I-like 3	chr3p21.1-p14.3	1561336_at	NM_004944																				
2.57	2.08	0.50	3.38E-02	3.05E-01	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	chr17q11.2	204995_at	NM_003885																				
5.26	4.50	0.75	3.38E-02	3.05E-01	YRDC	yrdC domain containing (E. coli)	chr1p34.3	222703_s_at	NM_024640																				
9.03	8.49	0.54	3.39E-02	3.05E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	212987_at	NM_012347 /// NM_033480 /// NM_033481																				
6.06	5.10	0.96	3.39E-02	3.05E-01	CDKN2AIP	CDKN2A interacting protein	chr4q35.1	218929_at	NM_017632																				
3.82	3.53	0.29	3.39E-02	3.05E-01	---	---	---	230959_at	---																				
7.17	6.39	0.78	3.39E-02	3.05E-01	FOXK2	forkhead box K2	chr17q25	203064_s_at	NM_004514																				
8.43	7.74	0.69	3.39E-02	3.05E-01	NISCH	nischarin	chr3p21.1	201591_s_at	NM_007184																				
8.09	7.49	0.60	3.39E-02	3.05E-01	---	---	---	225199_at	---																				
5.74	5.18	0.56	3.39E-02	3.05E-01	HAVCR2	hepatitis A virus cellular receptor 2	chr5q33.3	235458_at	NM_032782																				
5.30	4.58	0.72	3.39E-02	3.05E-01	ITGB5	Integrin, beta 5	chr3q21.2	214020_x_at	NM_002213																				
4.09	3.68	0.41	3.39E-02	3.05E-01	---	---	---	1566987_s_at	---																				
4.75	4.23	0.52	3.39E-02	3.05E-01	RBM28	RNA binding motif protein 28	chr7q32.1	218593_at	NM_018077																				
5.04	4.57	0.47	3.39E-02	3.05E-01	GMEB1	glucocorticoid modulatory element binding protein 1	chr1p35.3	235233_s_at	NM_006582 /// NM_024482																				
9.88	9.04	0.83	3.39E-02	3.05E-01	MT1X	metallothionein 1X	chr16q13	204326_x_at	NM_005952																				
5.93	5.59	0.34	3.40E-02	3.05E-01	TRIO	triple functional domain (PTPRF interacting)	chr5p15.2	209012_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929																				
6.93	6.21	0.72	3.40E-02	3.05E-01	FAM20C	family with sequence similarity 20, member C	chr7p22.3	226722_at	NM_020223																				
4.25	3.89	0.36	3.40E-02	3.05E-01	LOC123688	similar to RIKEN cDNA C630028N24 gene	chr15q25.1	236150_at	NM_001013619 /// NM_001083612																				
3.29	2.75	0.54	3.40E-02	3.06E-01	PAWR	PRKC, apoptosis, WT1, regulator	chr12q21	229515_at	NM_002583																				
4.59	4.10	0.48	3.40E-02	3.06E-01	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	chr11q13	208206_s_at	NM_001098670 /// NM_001098671 /// NM_153819																				
11.76	11.44	0.32	3.40E-02	3.06E-01	RPLP2	ribosomal protein, large, P2	chr11p15.5-p15.4	200909_s_at	NM_001004																				
6.22	4.93	1.29	3.40E-02	3.06E-01	LOC730101	hypothetical LOC730101	chr6p12.1	213248_at	XR_016069																				
12.07	11.83	0.24	3.41E-02	3.06E-01	RPL13A	ribosomal protein L13a	chr19q13.3	211942_x_at	NM_012423																				

5.35	4.43	0.92	3.41E-02	3.06E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	212999_x_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447																				
5.93	5.36	0.57	3.41E-02	3.06E-01	SERF1A /// SERF1B	small EDRK-rich factor 1A (telomeric) /// small EDRK-rich factor 1B (centromeric)	chr5q12.2-q13.3 /// chr5q13.2	223539_s_at	NM_021967 /// NM_022968 /// NM_022978 /// XM_001713905 /// XM_001720851 /// XM_001720856																				
8.78	8.50	0.28	3.41E-02	3.06E-01	U2AF1	U2 small nuclear RNA auxiliary factor 1	chr21q22.3	202858_at	NM_001025203 /// NM_001025204 /// NM_006758																				
6.23	5.76	0.48	3.41E-02	3.06E-01	FTSJD2	FtsJ methyltransferase domain containing 2	chr6p21.2	212380_at	NM_015050																				
4.23	3.64	0.59	3.42E-02	3.06E-01	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	chr15q15.3	223270_at	NM_016396																				
6.03	5.03	1.01	3.42E-02	3.06E-01	LOC25845	hypothetical LOC25845	chr5p15.33	225457_s_at	XR_017708 /// XR_017745 /// XR_040817																				
2.65	2.36	0.29	3.42E-02	3.06E-01	SH3RF2	SH3 domain containing ring finger 2	chr5q32	235768_at	NM_152550																				
9.23	8.90	0.33	3.42E-02	3.06E-01	OXA1L	oxidase (cytochrome c) assembly 1-like	chr14q11.2	208717_at	NM_005015																				

3.62	3.11	0.50	3.42E-02	3.06E-01	EDN3	endothelin 3	chr20q13.2-q13.3	208399_s_at	NM_000114 /// NM_207032 /// NM_207033 /// NM_207034																				
4.18	3.82	0.36	3.42E-02	3.06E-01	ERICH1	glutamate-rich 1	chr8p23.3	1563315_s_at	NM_207332																				
5.51	5.03	0.48	3.42E-02	3.06E-01	DZIP1	DAZ interacting protein 1	chr13q32.1	204556_s_at	NM_014934 /// NM_198968																				
6.12	5.56	0.56	3.42E-02	3.06E-01	GGCX	gamma-glutamyl carboxylase	chr2p12	214006_s_at	NM_000821																				
5.65	4.86	0.79	3.42E-02	3.06E-01	YRDC	yrdC domain containing (E. coli)	chr1p34.3	218647_s_at	NM_024640																				
6.37	5.88	0.49	3.43E-02	3.06E-01	HNRNPL	heterogeneous nuclear ribonucleoprotein L	chr19q13.2	202072_at	NM_001005335 /// NM_001533																				
5.19	4.58	0.61	3.43E-02	3.06E-01	THEM4	thioesterase superfamily member 4	chr1q21	229253_at	NM_053055																				
2.85	2.19	0.66	3.43E-02	3.06E-01	---	---	---	1557050_at	---																				
9.32	8.77	0.55	3.43E-02	3.06E-01	TBX3	T-box 3	chr12q24.1	225544_at	NM_005996 /// NM_016569																				
3.22	2.79	0.42	3.43E-02	3.06E-01	SYNC1	Syncoilin, intermediate filament 1	chr1p34.3-p33	237333_at	NM_030786																				
6.81	6.42	0.39	3.43E-02	3.06E-01	LRP3	low density lipoprotein receptor-related protein 3	chr19q13.11	204381_at	NM_002333																				
6.01	5.71	0.30	3.43E-02	3.06E-01	NIP30	NEFA-interacting nuclear protein NIP30	chr16q13	217896_s_at	NM_024946																				
6.49	5.97	0.52	3.43E-02	3.06E-01	RP9P	retinitis pigmentosa 9 pseudogene	chr7p14.3	227035_x_at	NR_003500																				
4.94	4.19	0.75	3.43E-02	3.06E-01	---	---	---	213685_at	---																				
7.77	7.23	0.54	3.44E-02	3.06E-01	FKBP4	FK506 binding protein 4, 59kDa	chr12p13.33	200895_s_at	NM_002014																				
7.47	6.91	0.56	3.44E-02	3.06E-01	VPS37C	vacuolar protein sorting 37 homolog C (S. cerevisiae)	chr11q12.2	1560060_s_at	NM_017966																				
8.24	7.60	0.64	3.44E-02	3.06E-01	EPDR1	ependymin related protein 1 (zebrafish)	chr7p14.1	223253_at	NM_017549																				
7.05	6.45	0.61	3.44E-02	3.07E-01	C2orf64	chromosome 2 open reading frame 64	chr2q11.2	225410_at	NM_001008215																				
5.83	5.16	0.67	3.45E-02	3.07E-01	ALKBH2	alkB, alkylation repair homolog 2 (E. coli)	chr12q24.11	225625_at	NM_001001655																				
5.65	5.18	0.47	3.45E-02	3.07E-01	C2orf76	chromosome 2 open reading frame 76	chr2q14.2	227840_at	NM_001017927																				
6.41	5.76	0.65	3.45E-02	3.07E-01	FAM160B2	family with sequence similarity 160, member B2	chr8p21.3	218337_at	NM_022749																				
4.87	3.92	0.95	3.46E-02	3.07E-01	RHBDL3	rhomboid, veinlet-like 3 (Drosophila)	chr17q11.2	230755_at	NM_138328																				
5.10	4.19	0.90	3.46E-02	3.07E-01	TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	chr20p12.3	233970_s_at	NM_015939																				
7.57	7.11	0.46	3.46E-02	3.07E-01	VPS4A	vacuolar protein sorting 4 homolog A (S. cerevisiae)	chr16q22.1	217913_at	NM_013245																				
6.02	5.51	0.51	3.46E-02	3.07E-01	C21orf2	chromosome 21 open reading frame 2	chr21q22.3	203994_s_at	NM_004928																				
4.36	3.64	0.71	3.46E-02	3.07E-01	STAT5B	signal transducer and activator of transcription 5B	chr17q11.2	1555086_at	NM_012448																				
6.46	5.96	0.50	3.46E-02	3.07E-01	NIPSNAP1	nipsnap homolog 1 (C. elegans)	chr22q12.2	201708_s_at	NM_003634																				
6.76	5.56	1.20	3.46E-02	3.07E-01	CLDN1	claudin 1	chr3q28-q29	218182_s_at	NM_021101																				
6.66	6.15	0.51	3.46E-02	3.07E-01	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	chr1q21.3	207838_x_at	NM_020524																				
3.42	2.87	0.55	3.46E-02	3.07E-01	RPL32P3	ribosomal protein L32 pseudogene 3	chr3q21.3	226877_at	NR_003111																				
7.83	7.25	0.58	3.47E-02	3.07E-01	DPF2	D4, zinc and double PHD fingers family 2	chr11q13	202116_at	NM_006268																				
7.62	7.06	0.56	3.47E-02	3.07E-01	TXNDC13	thioredoxin domain containing 13	chr20p12	201580_s_at	NM_021156																				
3.90	3.43	0.47	3.48E-02	3.08E-01	TBRG1	transforming growth factor beta regulator 1	chr11q24.2	242701_at	NM_032811 /// NR_016021																				
4.58	4.13	0.46	3.48E-02	3.08E-01	CUL4A	cullin 4A	chr13q34	201424_s_at	NM_001008895 /// NM_003589																				
2.95	2.54	0.41	3.48E-02	3.08E-01	FMNL3	formin-like 3	chr12q13.12	238823_at	NM_175736 /// NM_198900																				
9.49	7.50	1.98	3.49E-02	3.08E-01	NR4A1	nuclear receptor subfamily 4, group A, member 1	chr12q13	202340_x_at	NM_002135 /// NM_173157																				
6.05	5.77	0.27	3.49E-02	3.08E-01	USP39	ubiquitin specific peptidase 39	chr2p11.2	217829_s_at	NM_006590																				
5.77	4.76	1.01	3.49E-02	3.08E-01	TCERG1	transcription elongation regulator 1	chr5q31	202396_at	NM_001040006 /// NM_006706																				
6.43	5.53	0.90	3.49E-02	3.08E-01	CALML4	calmodulin-like 4	chr15q23	221879_at	NM_001031733 /// NM_033429																				

3.20	2.74	0.46	3.49E-02	3.08E-01	FAM72A /// FAM72B /// GCUD2	family with sequence similarity 72, member A /// family with sequence similarity 72, member B /// gastric cancer up-regulated-2	chr1p12 /// chr1q32.1	225834_at	NM_001100910 /// NM_001123168 /// NM_207418 /// XM_001133363 /// XM_001133364 /// XM_001133365																				
6.43	5.80	0.64	3.49E-02	3.08E-01	XIAP	X-linked inhibitor of apoptosis	chrXq25	228363_at	NM_001167																				
6.55	5.64	0.92	3.49E-02	3.08E-01	KHSRP	KH-type splicing regulatory protein	chr19p13.3	204372_s_at	NM_003685																				
4.61	3.59	1.02	3.49E-02	3.08E-01	MYO16	myosin XVI	chr13q33.3	215119_at	NM_015011																				
6.78	6.10	0.68	3.50E-02	3.08E-01	CUL7	cullin 7	chr6p21.1	36084_at	NM_014780																				
3.44	2.97	0.48	3.51E-02	3.08E-01	SPAG5	sperm associated antigen 5	chr17q11.2	203145_at	NM_006461																				
7.17	6.53	0.64	3.51E-02	3.08E-01	LSM10	LSM10, U7 small nuclear RNA associated	chr1p34.3	225593_at	NM_032881																				
6.38	5.61	0.77	3.51E-02	3.08E-01	NLK	nemo-like kinase	chr17q11.2	222590_s_at	NM_016231																				
7.58	6.96	0.63	3.51E-02	3.08E-01	LAGE3	L antigen family, member 3	chrXq28	219061_s_at	NM_006014																				
3.91	3.61	0.30	3.51E-02	3.09E-01	C11orf61	chromosome 11 open reading frame 61	chr11q24.2	221208_s_at	NM_024631																				
3.47	3.19	0.28	3.51E-02	3.09E-01	LOC728353	hypothetical protein LOC728353	chr14q11.2	1559927_a_at	XR_041035 /// XR_041036 /// XR_041037																				
7.77	7.19	0.58	3.52E-02	3.09E-01	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	chr1q21.3	212259_s_at	NM_020524																				
2.34	2.07	0.27	3.53E-02	3.09E-01	LOC440888	ARP3 actin-related protein 3 homolog B pseudogene	chr2p11.1	224426_s_at	---																				
2.46	2.11	0.35	3.53E-02	3.09E-01	CALML4	calmodulin-like 4	chr15q23	1568600_at	NM_001031733 /// NM_033429																				
3.91	3.03	0.88	3.53E-02	3.09E-01	---	---	---	239045_at	---																				
5.12	4.62	0.50	3.53E-02	3.09E-01	ABI2	abl interactor 2	chr2q33	209856_x_at	NM_005759																				
7.40	6.93	0.47	3.54E-02	3.09E-01	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	chrXq24-q25	201898_s_at	NM_003336 /// NM_181762 /// NM_181777																				
5.95	5.37	0.58	3.54E-02	3.09E-01	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	chr2p25.2	226702_at	NM_207315																				
6.56	5.46	1.10	3.54E-02	3.09E-01	CARD10	caspase recruitment domain family, member 10	chr22q13.1	210026_s_at	NM_014550																				
7.95	7.43	0.52	3.54E-02	3.09E-01	CREB3	cAMP responsive element binding protein 3	chr9pter-p22.1	209432_s_at	NM_006368																				
2.57	2.30	0.28	3.54E-02	3.10E-01	SCAND2	SCAN domain containing 2 pseudogene	chr15q25-q26	222177_s_at	NM_022050 /// NM_033633 /// NM_033634 /// NM_033635 /// NM_033636 /// NM_033640 /// NR_003654 /// NR_004859																				
4.95	3.89	1.06	3.54E-02	3.10E-01	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	chr3q25.32-q25.33	221872_at	NM_002888 /// NM_206963																				
2.25	1.99	0.26	3.55E-02	3.10E-01	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	chrXp11.22	217632_at	NM_019067																				
2.45	2.16	0.28	3.55E-02	3.10E-01	CBLL1	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	chr7q22.3	220018_at	NM_024814																				
8.00	7.04	0.96	3.55E-02	3.10E-01	DDR1	discoidin domain receptor tyrosine kinase 1	chr6p21.3	1007_s_at	NM_001954 /// NM_013993 /// NM_013994																				
3.78	3.00	0.78	3.56E-02	3.10E-01	NPAS2	neuronal PAS domain protein 2	chr2q11.2	39549_at	NM_002518																				
2.47	2.18	0.29	3.56E-02	3.10E-01	---	---	---	239120_at	---																				
5.24	4.56	0.69	3.56E-02	3.10E-01	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	chr2q37.1	203332_s_at	NM_001017915 /// NM_005541																				
7.20	6.48	0.72	3.56E-02	3.10E-01	TP53INP1	tumor protein p53 inducible nuclear protein 1	chr8q22	225912_at	NM_033285																				

5.43	4.16	1.27	3.57E-02	3.10E-01	FLJ42562	similar to echinoderm microtubule associated protein like 5	chr2p16.1	229656_s_at	XM_001725001 /// XM_001725002 /// XM_001725718 /// XM_001725719 /// XM_001726920 /// XM_001726921																				
5.89	5.52	0.37	3.57E-02	3.10E-01	FBXW2	F-box and WD repeat domain containing 2	chr9q34	218941_at	NM_012164																				
6.13	5.68	0.45	3.57E-02	3.10E-01	ALKBH3	alkB, alkylation repair homolog 3 (E. coli)	chr11p11.2	226127_at	NM_139178																				
4.81	3.84	0.97	3.57E-02	3.10E-01	BZRAP1	benzodiazapine receptor (peripheral) associated protein 1	chr17q22-q23	205839_s_at	NM_004758 /// NM_024418																				
4.18	3.79	0.39	3.57E-02	3.10E-01	---	---	---	239236_at	---																				
8.57	8.07	0.49	3.57E-02	3.10E-01	MRP63	mitochondrial ribosomal protein 63	chr13q12.11	204387_x_at	NM_024026																				
7.68	7.11	0.57	3.57E-02	3.10E-01	MOAP1	modulator of apoptosis 1	chr14q32	212508_at	NM_022151																				
4.62	4.02	0.60	3.57E-02	3.10E-01	C13orf33	chromosome 13 open reading frame 33	chr13q12.3	227058_at	NM_032849																				
5.56	4.84	0.72	3.57E-02	3.10E-01	ZNF697	zinc finger protein 697	chr1p12	227080_at	NM_001080470																				
6.19	5.51	0.68	3.57E-02	3.10E-01	ISYNA1	myo-inositol 1-phosphate synthase A1	chr19p13.11	222240_s_at	NM_016368																				
11.91	11.62	0.29	3.58E-02	3.10E-01	RPL18	ribosomal protein L18	chr19q13	200022_at	NM_000979																				
3.61	3.24	0.37	3.58E-02	3.11E-01	---	---	---	234663_at	---																				
5.07	4.57	0.51	3.58E-02	3.11E-01	AKAP1	A kinase (PRKA) anchor protein 1	chr17q21-q23	210625_s_at	NM_003488																				
7.06	6.44	0.62	3.58E-02	3.11E-01	SNX21	sorting nexin family member 21	chr20q13.12	1553961_s_at	NM_001042632 /// NM_001042633 /// NM_033421 /// NM_152897																				
5.40	3.70	1.69	3.58E-02	3.11E-01	RGS1	regulator of G-protein signaling 1	chr1q31	216834_at	NM_002922																				
5.09	4.48	0.61	3.59E-02	3.11E-01	ELF2	E74-like factor 2 (ets domain transcription factor)	chr4q28	203822_s_at	NM_006874 /// NM_201999																				
6.95	6.58	0.37	3.59E-02	3.11E-01	C10orf72	chromosome 10 open reading frame 72	chr10q11.22	244057_s_at	NM_001031746 /// NM_144984																				
6.65	6.13	0.52	3.59E-02	3.11E-01	MUL1	mitochondrial ubiquitin ligase activator of NFKB 1	chr1p36.12	218246_at	NM_024544																				
3.06	2.63	0.43	3.60E-02	3.11E-01	DTD1	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	chr20p11.23	1552718_at	NM_080820																				
8.77	8.24	0.54	3.60E-02	3.11E-01	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G	chr11q13.1	202306_at	NM_002696																				
6.59	5.91	0.68	3.60E-02	3.11E-01	LST1	leukocyte specific transcript 1	chr6p21.3	211581_x_at	NM_007161 /// NM_205837 /// NM_205838 /// NM_205839 /// NM_205840																				
7.44	6.82	0.62	3.60E-02	3.11E-01	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr7p14.3	211747_s_at	NM_001130710 /// NM_012322																				
6.87	6.24	0.63	3.60E-02	3.11E-01	BBS1	Bardet-Biedl syndrome 1	chr11q13.1	218471_s_at	NM_024649																				
4.07	3.61	0.46	3.60E-02	3.11E-01	FAM125B	family with sequence similarity 125, member B	chr9q33.3	221828_s_at	NM_001011703 /// NM_033446																				
7.03	6.30	0.73	3.60E-02	3.11E-01	RBBP6	retinoblastoma binding protein 6	chr16p12.2	223802_s_at	NM_006910 /// NM_018703 /// NM_032626																				
2.67	2.23	0.44	3.60E-02	3.11E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	60815_at	NR_003655 /// XR_042143 /// XR_042182																				
8.23	6.53	1.70	3.60E-02	3.11E-01	PDZRN3	PDZ domain containing ring finger 3	chr3p13	212915_at	NM_015009																				

7.23	6.42	0.81	3.61E-02	3.12E-01	BAX	BCL2-associated X protein	chr19q13.3-q13.4	211833_s_at	NM_004324 /// NM_138761 /// NM_138763 /// NM_138764 /// NM_138765
4.77	4.40	0.37	3.61E-02	3.12E-01	MR1	major histocompatibility complex, class I-related	chr1q25.3	207565_s_at	NM_001531
4.19	3.54	0.65	3.61E-02	3.12E-01	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	chr13q32	203196_at	NM_001105515 /// NM_005845
6.03	5.46	0.57	3.61E-02	3.12E-01	GGCX	gamma-glutamyl carboxylase	chr2p12	205351_at	NM_000821
7.84	7.35	0.50	3.62E-02	3.12E-01	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	chr11q12.1-q12.3	1555764_s_at	NM_012456
6.72	6.20	0.52	3.62E-02	3.12E-01	PXMP4	peroxisomal membrane protein 4, 24kDa	chr20q11.22	219428_s_at	NM_007238 /// NM_183397
5.97	5.29	0.68	3.62E-02	3.12E-01	NUDT2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	chr9p13	218609_s_at	NM_001161 /// NM_147172 /// NM_147173
4.36	3.83	0.54	3.62E-02	3.12E-01	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	chr8p11.2	209342_s_at	NM_001556
3.50	3.02	0.48	3.63E-02	3.12E-01	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	chr11q13-q14	209615_s_at	NM_001128620 /// NM_002576
7.92	7.57	0.35	3.63E-02	3.12E-01	TMEM43	transmembrane protein 43	chr3p25.1	217795_s_at	NM_024334
7.28	6.81	0.46	3.63E-02	3.12E-01	SF3A1	splicing factor 3a, subunit 1, 120kDa	chr22q12.2	201356_at	NM_001005409 /// NM_005877
2.93	2.47	0.46	3.63E-02	3.12E-01	---	---	---	1564479_a_at	---
7.37	6.92	0.45	3.63E-02	3.12E-01	RNF220	ring finger protein 220	chr1p34.1	219988_s_at	NM_018150
8.04	7.16	0.89	3.63E-02	3.12E-01	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	chr10q24.1-q25.1	208813_at	NM_002079
5.86	5.10	0.77	3.64E-02	3.12E-01	OPLAH	5-oxoprolinase (ATP-hydrolysing)	chr8q24.3	222025_s_at	NM_017570
10.17	9.84	0.33	3.64E-02	3.12E-01	SSR2	signal sequence receptor, beta (translocon-associated protein beta)	chr1q21-q23	200652_at	NM_003145
7.47	6.78	0.68	3.64E-02	3.12E-01	RHEB	Ras homolog enriched in brain	chr7q36	1555780_a_at	NM_005614
8.23	7.97	0.26	3.64E-02	3.12E-01	M6PR	mannose-6-phosphate receptor (cation dependent)	chr12p13	200901_s_at	NM_002355
5.22	4.48	0.73	3.64E-02	3.12E-01	C9orf127	chromosome 9 open reading frame 127	chr9p13.3	207839_s_at	NM_001042589 /// NM_001042590 /// NM_016446
8.09	7.12	0.96	3.64E-02	3.12E-01	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	chrXq13	209240_at	NM_181672 /// NM_181673
3.58	3.23	0.35	3.65E-02	3.13E-01	---	---	---	229279_at	---
7.19	6.80	0.39	3.65E-02	3.13E-01	RNF34	ring finger protein 34	chr12q24.31	219035_s_at	NM_025126 /// NM_194271
2.67	2.37	0.30	3.65E-02	3.13E-01	UNC5CL	Unc-5 homolog C (C. elegans)-like	chr6p21.1	231008_at	NM_173561
6.54	5.71	0.84	3.65E-02	3.13E-01	CCRK	cell cycle related kinase	chr9q22.1	205271_s_at	NM_001039803 /// NM_012119 /// NM_178432
6.64	6.01	0.62	3.65E-02	3.13E-01	DTYMK /// LOC727761	deoxythymidylate kinase (thymidylate kinase) /// similar to Deoxythymidylate kinase (thymidylate kinase)	chr2q37.3	1553984_s_at	NM_012145 /// XM_001126163 /// XM_001126184 /// XM_001126211
4.43	3.73	0.70	3.65E-02	3.13E-01	---	---	---	235459_at	---
6.46	5.17	1.29	3.65E-02	3.13E-01	RORA	RAR-related orphan receptor A	chr15q21-q22	210426_x_at	NM_002943 /// NM_134260 /// NM_134261 /// NM_134262

2.63	2.34	0.29	3.66E-02	3.13E-01	NF1	neurofibromin 1	chr17q11.2	243476_at	NM_000267 /// NM_001042492 /// NM_001128147																				
8.83	8.36	0.46	3.66E-02	3.13E-01	ANAPC11 /// LOC100131844	APC11 anaphase promoting complex subunit 11 /// similar to anaphase promoting complex subunit 11	chr17q25.3	226414_s_at	NM_001002244 /// NM_001002245 /// NM_001002246 /// NM_001002247 /// NM_001002248 /// NM_001002249 /// NM_016476 /// XM_001718759																				
6.92	5.89	1.03	3.66E-02	3.13E-01	IGFBP3	insulin-like growth factor binding protein 3	chr7p13-p12	210095_s_at	NM_000598 /// NM_001013398																				
6.41	5.32	1.09	3.67E-02	3.13E-01	HLF	hepatic leukemia factor	chr17q22	204755_x_at	NM_002126																				
7.77	7.46	0.32	3.67E-02	3.13E-01	HARS	histidyl-tRNA synthetase	chr5q31.3	202042_at	NM_002109																				
5.64	5.24	0.40	3.67E-02	3.13E-01	E4F1	E4F transcription factor 1	chr16p13.3	218524_at	NM_004424																				
3.96	3.52	0.43	3.67E-02	3.13E-01	ZNF74	zinc finger protein 74	chr22q11.2|22q11.21	205881_at	NM_003426 /// NR_003253																				
5.71	5.16	0.55	3.67E-02	3.13E-01	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	chr8q13	202625_at	NM_001111097 /// NM_002350																				
6.01	5.21	0.80	3.67E-02	3.13E-01	CPEB2	cytoplasmic polyadenylation element binding protein 2	chr4p15.33	226939_at	NM_182485 /// NM_182646																				
2.90	2.50	0.40	3.67E-02	3.13E-01	JUB	Jub, ajuba homolog (Xenopus laevis)	chr14q11.2	243446_at	NM_032876 /// NM_198086																				
3.70	3.21	0.50	3.68E-02	3.14E-01	WNT6	wingless-type MMTV integration site family, member 6	chr2q35	71933_at	NM_006522																				
8.42	7.94	0.48	3.68E-02	3.14E-01	CARKD	carbohydrate kinase domain containing	chr13q34	217940_s_at	NM_018210																				
7.60	7.08	0.52	3.68E-02	3.14E-01	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	chr8q13.1	209567_at	NM_015169																				
6.27	5.74	0.53	3.68E-02	3.14E-01	CNBP	CCHC-type zinc finger, nucleic acid binding protein	chr3q21	227731_at	NM_001127192 /// NM_001127193 /// NM_001127194 /// NM_001127195 /// NM_001127196 /// NM_003418																				
3.34	2.93	0.40	3.68E-02	3.14E-01	KIAA1751	KIAA1751	chr1p36.33	216807_at	NM_001080484																				
6.66	6.09	0.57	3.68E-02	3.14E-01	KIAA1244	KIAA1244	chr6q23.3	227479_at	NM_020340																				
4.89	4.27	0.62	3.68E-02	3.14E-01	---	---	---	226542_at	---																				
8.57	8.00	0.57	3.68E-02	3.14E-01	C1QBP	complement component 1, q subcomponent binding protein	chr17p13.3	214214_s_at	NM_001212																				
3.29	2.93	0.36	3.68E-02	3.14E-01	---	---	---	215196_at	---																				
2.73	2.20	0.52	3.68E-02	3.14E-01	---	---	---	229934_at	---																				
9.81	9.41	0.40	3.69E-02	3.14E-01	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	chr10q23.2-q23.33	201227_s_at	NM_005004																				
4.27	3.67	0.60	3.69E-02	3.14E-01	ZNF853	zinc finger protein 853	chr7p22.1	232884_s_at	XM_001715278 /// XM_001716278 /// XM_001716628 /// XM_001723503																				

2.94	2.60	0.35	3.69E-02	3.14E-01	LOC100128288	hypothetical protein LOC100128288	chr17p13.1	1559045_at	XM_001721372 /// XM_001724933 /// XM_001725953																			
3.15	2.84	0.31	3.69E-02	3.14E-01	GATA4	GATA binding protein 4	chr8p23.1-p22	205517_at	NM_002052																			
3.72	2.91	0.81	3.69E-02	3.14E-01	HECTD2	HECT domain containing 2	chr10q23.32	227568_at	NM_173497 /// NM_182765																			
7.02	6.09	0.93	3.70E-02	3.14E-01	KALRN	kalirin, RhoGEF kinase	chr3q21.1-q21.2	227750_at	NM_001024660 /// NM_003947 /// NM_007064																			
4.48	3.99	0.49	3.70E-02	3.14E-01	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1	chr3q21	226442_at	NM_032548 /// NM_172027 /// NM_172028																			
5.89	5.09	0.80	3.70E-02	3.14E-01	TPM2	tropomyosin 2 (beta)	chr9p13.2-p13.1	212654_at	NM_003289 /// NM_213674																			
2.38	2.07	0.31	3.70E-02	3.14E-01	---	---	---	243714_at	---																			
8.36	7.62	0.74	3.71E-02	3.14E-01	---	---	---	227167_s_at	---																			
5.44	5.02	0.42	3.71E-02	3.14E-01	PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	chr1q21	206139_at	NM_002651																			
5.54	5.20	0.33	3.71E-02	3.14E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	208793_x_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072																			
7.57	6.76	0.81	3.71E-02	3.14E-01	JMJD2B	jumonji domain containing 2B	chr19p13.3	212496_s_at	NM_015015																			
8.14	7.78	0.36	3.71E-02	3.14E-01	EIF3B	eukaryotic translation initiation factor 3, subunit B	chr7p22.2	208688_x_at	NM_001037283 /// NM_003751																			
5.09	4.50	0.59	3.71E-02	3.14E-01	---	---	---	238611_at	---																			
3.51	3.12	0.39	3.72E-02	3.14E-01	RNF149	Ring finger protein 149	chr2q11.2	235536_at	NM_173647																			
7.10	6.27	0.84	3.72E-02	3.14E-01	HSD3B1 /// HSD3B2 /// LOC128102 /// LOC391081	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 /// hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 /// 3-beta-hydroxysteroid dehydrogenase, tissue-type heart /// similar to 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1 (3-beta-HSD I)	chr1p12 /// chr1p13.1	215665_at	NM_000198 /// NM_000862 /// XR_017445 /// XR_019377 /// XR_039185																			
5.29	4.84	0.45	3.72E-02	3.14E-01	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	chr12q24.13	219372_at	NM_014055 /// NM_031473																			
6.37	5.99	0.37	3.73E-02	3.14E-01	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	chr11p11.2	225901_at	NM_175732																			
7.18	6.79	0.39	3.73E-02	3.14E-01	C4orf14	chromosome 4 open reading frame 14	chr4q12	223157_at	NM_032313																			
5.83	5.44	0.39	3.73E-02	3.14E-01	---	---	---	226468_at	---																			
6.27	5.72	0.56	3.73E-02	3.14E-01	LMAN2L	lectin, mannose-binding 2-like	chr2q11.2	221274_s_at	NM_030805																			
6.15	5.54	0.60	3.73E-02	3.14E-01	ZNF282	zinc finger protein 282	chr7q36.1	212892_at	NM_003575																			
8.07	7.70	0.37	3.73E-02	3.14E-01	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	chr5q31	201055_s_at	NM_006805																			
3.24	2.72	0.51	3.73E-02	3.14E-01	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	chr7q21.3	231966_at	NM_017650																			
4.97	4.43	0.54	3.73E-02	3.14E-01	LPIN2	lipin 2	chr18p11.31	202459_s_at	NM_014646																			
6.79	6.19	0.60	3.73E-02	3.15E-01	RANGAP1	Ran GTPase activating protein 1	chr22q13	1553535_a_at	NM_002883																			
10.07	9.57	0.50	3.74E-02	3.15E-01	---	---	---	228297_at	---																			
6.96	6.46	0.51	3.74E-02	3.15E-01	BAD	BCL2-associated agonist of cell death	chr11q13.1	209364_at	NM_004322 /// NM_032989																			
3.39	3.07	0.32	3.74E-02	3.15E-01	UHRF1	ubiquitin-like with PHD and ring finger domains 1	chr19p13.3	225655_at	NM_001048201 /// NM_013282																			
2.97	2.12	0.85	3.74E-02	3.15E-01	---	---	---	234759_at	---																			
2.87	2.62	0.24	3.74E-02	3.15E-01	LPCAT4	lysophosphatidylcholine acyltransferase 4	chr15q14	239609_s_at	NM_153613																			

6.40	5.41	0.99	3.75E-02	3.15E-01	RFC3	replication factor C (activator 1) 3, 38kDa	chr13q12.3-q13	204127_at	NM_002915 /// NM_181558																				
6.97	6.31	0.66	3.76E-02	3.15E-01	NAP1L1	nucleosome assembly protein 1-like 1	chr12q21.2	208754_s_at	NM_004537 /// NM_139207																				
8.42	8.07	0.36	3.76E-02	3.15E-01	DAZAP2	DAZ associated protein 2	chr12q12	214334_x_at	NM_014764																				
9.32	8.82	0.51	3.76E-02	3.15E-01	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	chr16q22.1	201633_s_at	NM_030579																				
7.75	7.20	0.55	3.76E-02	3.15E-01	VPS25	vacuolar protein sorting 25 homolog (S. cerevisiae)	chr17q21.31	224608_s_at	NM_032353																				
2.82	2.46	0.36	3.76E-02	3.16E-01	---	---	---	236333_at	---																				
3.42	3.11	0.31	3.76E-02	3.16E-01	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	chr14q32.12	1568922_at	NM_153646 /// NM_153647 /// NM_153648																				
5.18	4.68	0.51	3.76E-02	3.16E-01	DUS3L	dihydrouridine synthase 3-like (S. cerevisiae)	chr19p13.3	224966_s_at	NM_020175																				
3.28	2.73	0.55	3.77E-02	3.16E-01	C6orf134	chromosome 6 open reading frame 134	chr6p21.33	228510_at	NM_001031722 /// NM_024909																				
4.74	3.80	0.94	3.77E-02	3.16E-01	TUB	tubby homolog (mouse)	chr11p15.5	228882_at	NM_003320 /// NM_177972																				
7.21	6.89	0.32	3.77E-02	3.16E-01	GEMIN6	gem (nuclear organelle) associated protein 6	chr2p22.1	219539_at	NM_024775																				
6.99	6.20	0.79	3.77E-02	3.16E-01	---	---	---	231550_at	---																				
2.91	2.67	0.24	3.77E-02	3.16E-01	EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	chr3q27.1	1558050_at	NM_003907																				
4.71	4.13	0.58	3.77E-02	3.16E-01	USP30	ubiquitin specific peptidase 30	chr12q24.11	223602_at	NM_032663																				
6.70	6.30	0.40	3.77E-02	3.16E-01	ZNF740	zinc finger protein 740	chr12q13.13	227331_at	NM_001004304																				
7.13	6.75	0.39	3.77E-02	3.16E-01	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	chr13q32.2	201910_at	NM_001001715 /// NM_005766																				
4.20	3.69	0.51	3.77E-02	3.16E-01	LOC90379	hypothetical protein BC002926	chr19p13.12	91952_at	NM_138353																				
7.24	5.80	1.44	3.78E-02	3.16E-01	AMFR	autocrine motility factor receptor	chr16q21	202203_s_at	NM_001144																				
2.61	2.33	0.28	3.78E-02	3.16E-01	MOCS1	molybdenum cofactor synthesis 1	chr6p21.3	1555127_at	NM_001075098 /// NM_005942 /// NM_005943 /// NM_138928																				
2.58	2.06	0.52	3.78E-02	3.16E-01	---	---	---	238142_at	---																				
10.71	10.02	0.70	3.78E-02	3.16E-01	ACADVL	acyl-Coenzyme A dehydrogenase, very long chain	chr17p13-p11	200710_at	NM_000018 /// NM_001033859																				
6.70	6.02	0.68	3.78E-02	3.16E-01	FLJ12529	pre-mRNA cleavage factor I, 59 kDa subunit	chr11q12.2	217866_at	NM_024811																				
5.88	5.40	0.48	3.78E-02	3.16E-01	CDYL	chromodomain protein, Y-like	chr6p25.1	203098_at	NM_004824 /// NM_170751 /// NM_170752																				
7.80	7.23	0.57	3.78E-02	3.16E-01	MTX1	metaxin 1	chr1q21	210386_s_at	NM_002455 /// NM_198883																				
6.44	5.79	0.66	3.79E-02	3.16E-01	LTBP3	latent transforming growth factor beta binding protein 3	chr11q12	227308_x_at	NM_001130144 /// NM_021070																				
4.91	4.40	0.51	3.79E-02	3.16E-01	FLJ46875	hypothetical LOC440918	chr2q24.1	230203_at	XM_498914 /// XM_943663																				
10.13	9.75	0.39	3.79E-02	3.16E-01	TUBB	tubulin, beta	chr6p21.33	211714_x_at	NM_178014																				
6.55	4.37	2.18	3.79E-02	3.16E-01	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6	chr5q23.3	219932_at	NM_001017372 /// NM_014031																				
4.36	3.53	0.83	3.79E-02	3.16E-01	CCBE1	collagen and calcium binding EGF domains 1	chr18q21.32	243805_at	NM_133459																				
2.51	2.24	0.27	3.79E-02	3.16E-01	FLJ26056 /// LOC284861 /// LOC729461	hypothetical protein LOC375127 /// hypothetical gene supported by BC039313 /// hypothetical LOC729461	chr22q11.21	233338_at	XM_001126757 /// XM_001130329 /// XM_001715190 /// XM_001715905																				

6.05	5.16	0.88	3.80E-02	3.16E-01	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	chr5q33.2	230906_at	NM_017540 /// NM_198321																				
4.91	4.26	0.65	3.80E-02	3.17E-01	MEX3C	mex-3 homolog C (C. elegans)	chr18q21.2	218247_s_at	NM_016626																				
11.21	10.46	0.75	3.80E-02	3.17E-01	MT1X	metallothionein 1X	chr16q13	208581_x_at	NM_005952																				
8.21	6.98	1.23	3.80E-02	3.17E-01	BHLHB2	basic helix-loop-helix domain containing, class B, 2	chr3p26	201170_s_at	NM_003670																				
5.36	4.86	0.50	3.80E-02	3.17E-01	TAF4	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	chr20q13.33	213090_s_at	NM_003185																				
6.68	5.78	0.90	3.81E-02	3.17E-01	PHLPP	PH domain and leucine rich repeat protein phosphatase	chr18q21.33	212719_at	NM_194449																				
5.54	5.04	0.50	3.81E-02	3.17E-01	ARIH2	ariadne homolog 2 (Drosophila)	chr3p21.2-p21.3	216008_s_at	NM_006321																				
3.35	2.74	0.61	3.82E-02	3.17E-01	---	---	---	229548_at	---																				
5.89	5.26	0.63	3.82E-02	3.17E-01	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	chr20cen-q13	232011_s_at	NM_032514 /// NM_181509																				
8.80	8.34	0.46	3.82E-02	3.17E-01	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	chr1q21.3	214177_s_at	NM_020524																				
6.74	6.13	0.61	3.82E-02	3.17E-01	METTL1	methyltransferase like 1	chr12q13	204027_s_at	NM_005371 /// NM_023033																				
7.06	5.85	1.21	3.83E-02	3.18E-01	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	chr12q24.31	221704_s_at	NM_024667																				
2.81	2.53	0.29	3.83E-02	3.18E-01	---	---	---	221137_at	---																				
6.29	5.68	0.61	3.83E-02	3.18E-01	CMC1	COX assembly mitochondrial protein homolog (S. cerevisiae)	chr3p24.1	228283_at	NM_182523																				
7.74	7.21	0.53	3.83E-02	3.18E-01	KIAA0247	KIAA0247	chr14q24.1	202181_at	NM_014734																				
7.17	6.73	0.44	3.84E-02	3.18E-01	PES1	pescadillo homolog 1, containing BRCT domain (zebrafish)	chr22q12.1	202212_at	NM_014303																				
7.59	6.96	0.62	3.84E-02	3.18E-01	PAQR5	progestin and adipoQ receptor family member V	chr15q23	242871_at	NM_001104554 /// NM_017705																				
4.84	4.25	0.59	3.84E-02	3.18E-01	TMEM80	transmembrane protein 80	chr11p15.5	65630_at	NM_001042463 /// NM_174940																				
5.86	5.13	0.72	3.84E-02	3.18E-01	VARS	valyl-tRNA synthetase	chr6p21.3	201797_s_at	NM_006295																				
6.10	5.70	0.41	3.84E-02	3.18E-01	USE1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	chr19p13.11	221706_s_at	NM_018467																				
5.77	5.17	0.60	3.84E-02	3.18E-01	MED29	mediator complex subunit 29	chr19q13.2	225708_at	NM_017592																				
6.28	5.75	0.53	3.85E-02	3.18E-01	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	chr1q23.1	208114_s_at	NM_030980																				
5.14	4.01	1.13	3.85E-02	3.18E-01	HOXA11	homeobox A11	chr7p15-p14	213823_at	NM_005523																				
2.87	2.52	0.35	3.85E-02	3.18E-01	RDH10	retinol dehydrogenase 10 (all-trans)	chr8q21.11	1552378_s_at	NM_172037																				
3.70	3.27	0.43	3.85E-02	3.18E-01	CENPH	centromere protein H	chr5p15.2	231772_x_at	NM_022909																				
7.39	6.90	0.49	3.85E-02	3.18E-01	FUBP1	far upstream element (FUSE) binding protein 1	chr1p31.1	203091_at	NM_003902																				
5.55	5.17	0.38	3.85E-02	3.18E-01	INO80	INO80 homolog (S. cerevisiae)	chr15q15.1	225357_s_at	NM_017553																				
7.13	6.47	0.66	3.85E-02	3.18E-01	MGRN1	mahogunin, ring finger 1	chr16p13.3	212576_at	NM_015246																				
2.65	2.35	0.29	3.85E-02	3.18E-01	---	---	---	1570064_at	---																				
7.62	6.58	1.04	3.85E-02	3.18E-01	---	---	---	239105_at	---																				
6.60	6.02	0.57	3.86E-02	3.18E-01	ANKRD11	ankyrin repeat domain 11	chr16q24.3	226012_at	NM_013275																				
3.35	2.79	0.56	3.86E-02	3.18E-01	SCPEP1	serine carboxypeptidase 1	chr17q22	1560665_at	NM_021626																				
4.92	4.56	0.36	3.86E-02	3.18E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	208875_s_at	NM_002577																				
6.28	5.58	0.70	3.86E-02	3.18E-01	TTC39C	tetratricopeptide repeat domain 39C	chr18q11.2	1552307_a_at	NM_153211																				
2.42	2.16	0.25	3.87E-02	3.18E-01	PXT1	peroxisomal, testis specific 1	chr6p21.31	1552599_at	NM_152990																				
7.60	6.96	0.64	3.87E-02	3.19E-01	RNF11	ring finger protein 11	chr1pter-p22.1	208924_at	NM_014372																				
3.09	2.84	0.25	3.87E-02	3.19E-01	---	---	---	217125_at	---																				
2.87	2.61	0.27	3.88E-02	3.19E-01	TTC23L	tetratricopeptide repeat domain 23-like	chr5p13.2	1557003_at	NM_144725																				
5.57	4.88	0.68	3.88E-02	3.19E-01	---	---	---	230728_at	---																				
2.66	2.40	0.26	3.88E-02	3.19E-01	---	---	---	232758_s_at	---																				
6.57	6.22	0.34	3.88E-02	3.19E-01	RPP14	ribonuclease P/MRP 14kDa subunit	chr3p14.3	204245_s_at	NM_001098783 /// NM_007042																				
3.40	2.63	0.77	3.88E-02	3.19E-01	BTBD11	BTB (POZ) domain containing 11	chr12q23.3	228570_at	NM_001017523 /// NM_001018072																				
5.37	4.80	0.57	3.88E-02	3.19E-01	MTFMT	mitochondrial methionyl-tRNA formyltransferase	chr15q22.31	235689_at	NM_139242																				
4.84	3.84	1.00	3.89E-02	3.19E-01	FANCG /// VCP	Fanconi anemia, complementation group G /// valosin-containing protein	chr9p13 /// chr9p13.3	203564_at	NM_004629 /// NM_007126																				
3.35	2.93	0.42	3.89E-02	3.19E-01	NR2C1	nuclear receptor subfamily 2, group C, member 1	chr12q22	210530_s_at	NM_001032287 /// NM_001127362 /// NM_003297																				
7.50	7.13	0.38	3.89E-02	3.19E-01	PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	chr19p13	202927_at	NM_006221																				

6.45	5.88	0.57	3.89E-02	3.19E-01	ING4	inhibitor of growth family, member 4	chr12p13.31	48825_at	NM_001127582 /// NM_001127583 /// NM_001127584 /// NM_001127585 /// NM_001127586 /// NM_016162																				
7.38	6.63	0.75	3.89E-02	3.19E-01	FAM60A	family with sequence similarity 60, member A	chr12p11	220147_s_at	NM_021238																				
5.75	5.25	0.49	3.89E-02	3.19E-01	TMEM136	transmembrane protein 136	chr11q23.3	230186_at	NM_174926																				
3.38	2.40	0.98	3.90E-02	3.19E-01	FUBP1	Far upstream element (FUSE) binding protein 1	chr1p31.1	212847_at	NM_003902																				
5.36	5.02	0.33	3.90E-02	3.19E-01	KIAA0406	KIAA0406	chr20q11.23	212898_at	NM_014657																				
3.11	2.76	0.35	3.90E-02	3.19E-01	INTS10	integrator complex subunit 10	chr8p21.3	229633_at	NM_018142																				
6.41	5.84	0.57	3.90E-02	3.19E-01	FOXJ2	forkhead box J2	chr12p13.31	203734_at	NM_018416																				
6.09	5.46	0.63	3.91E-02	3.20E-01	LOC728554 /// THOC3	similar to THO complex 3 /// THO complex 3	chr5q35.2 /// chr5q35.3	224623_at	NM_032361 /// NR_003615 /// XM_001723779																				
10.31	9.91	0.40	3.91E-02	3.20E-01	LOC100128731	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	chr2p23.3	224637_at	NM_001134693 /// XM_001717663 /// XM_001717721 /// XM_001720035																				
5.20	4.73	0.48	3.91E-02	3.20E-01	CDR2	cerebellar degeneration-related protein 2, 62kDa	chr16p12.3	209501_at	NM_001802																				
6.52	5.82	0.70	3.92E-02	3.20E-01	CTBP2	C-terminal binding protein 2	chr10q26.13	201218_at	NM_001083914 /// NM_001329 /// NM_022802																				
5.80	5.17	0.63	3.92E-02	3.20E-01	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	chr1p33-p32.3	224728_at	NM_001042546 /// NM_022745																				
6.79	6.29	0.49	3.92E-02	3.20E-01	CHKA	choline kinase alpha	chr11q13.2	204233_s_at	NM_001277 /// NM_212469																				
2.22	1.93	0.29	3.92E-02	3.20E-01	LHCGR	luteinizing hormone/choriogonadotropin receptor	chr2p21	207240_s_at	NM_000233																				
8.20	7.61	0.59	3.92E-02	3.20E-01	DAP	death-associated protein	chr5p15.2	201095_at	NM_004394																				
8.23	7.67	0.57	3.93E-02	3.20E-01	CSNK1D	casein kinase 1, delta	chr17q25	208774_at	NM_001893 /// NM_139062																				
2.66	2.36	0.30	3.93E-02	3.20E-01	---	---	---	217521_at	---																				
2.63	2.34	0.29	3.93E-02	3.20E-01	C4orf28	chromosome 4 open reading frame 28	chr4p15.31	235259_at	NM_001130727 /// NM_145048																				
6.24	5.67	0.58	3.93E-02	3.20E-01	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	chr12q24.32	204088_at	NM_002560																				
6.68	6.25	0.42	3.93E-02	3.20E-01	ZCCHC14	zinc finger, CCHC domain containing 14	chr16q24.2	212655_at	NM_015144																				
4.22	3.48	0.74	3.93E-02	3.20E-01	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	chr21q22.11	212996_s_at	NM_014825																				
6.91	6.47	0.44	3.93E-02	3.20E-01	DEAF1	deformed epidermal autoregulatory factor 1 (Drosophila)	chr11p15.5	209407_s_at	NM_021008																				
4.27	3.77	0.50	3.93E-02	3.20E-01	BAHCC1	BAH domain and coiled-coil containing 1	chr17q25.3	1559048_at	NM_001080519																				
8.50	7.63	0.87	3.94E-02	3.20E-01	NR0B1	nuclear receptor subfamily 0, group B, member 1	chrXp21.3-p21.2	206645_s_at	NM_000475																				
10.10	9.39	0.71	3.94E-02	3.20E-01	HSPA1A /// HSPA1B	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	chr6p21.3	200800_s_at	NM_005345 /// NM_005346																				
4.78	4.17	0.61	3.94E-02	3.20E-01	C2orf68	chromosome 2 open reading frame 68	chr2p11.2	232145_at	NM_001013649																				
6.59	5.98	0.62	3.94E-02	3.20E-01	MAN2C1	mannosidase, alpha, class 2C, member 1	chr15q11-q13	203668_at	NM_006715																				
2.87	2.44	0.43	3.95E-02	3.20E-01	---	---	---	1558208_at	---																				
4.65	3.82	0.84	3.95E-02	3.21E-01	C6orf57	chromosome 6 open reading frame 57	chr6q13	238504_at	NM_145267																				
7.06	6.61	0.45	3.95E-02	3.21E-01	PHF21A	PHD finger protein 21A	chr11p11.2	203278_s_at	NM_001101802 /// NM_016621																				
7.77	7.16	0.61	3.95E-02	3.21E-01	TSFM	Ts translation elongation factor, mitochondrial	chr12q13-q14	212656_at	NM_005726																				
3.60	3.15	0.46	3.95E-02	3.21E-01	FLJ45803	FLJ45803 protein	chr11q23.1	230956_at	NM_207429																				
5.19	4.40	0.79	3.96E-02	3.21E-01	ETNK1	ethanolamine kinase 1	chr12p12.1	219017_at	NM_001039481 /// NM_018638																				

7.30	6.91	0.39	3.96E-02	3.21E-01	MAX	MYC associated factor X	chr14q23	209331_s_at	NM_002382 /// NM_145112 /// NM_145113 /// NM_145114 /// NM_145116 /// NM_197957																				
3.46	3.04	0.42	3.97E-02	3.21E-01	CLDN2	claudin 2	chrXq22.3-q23	223509_at	NM_020384																				
2.22	1.91	0.32	3.97E-02	3.21E-01	LOC729291	hypothetical protein LOC729291	chr12p11.22	1570572_at	XR_041492 /// XR_041493 /// XR_041494																				
6.51	5.85	0.66	3.97E-02	3.21E-01	ANKRD54	ankyrin repeat domain 54	chr22q13.1	231847_at	NM_138797																				
6.98	6.55	0.43	3.97E-02	3.21E-01	TRAPPC6A	trafficking protein particle complex 6A	chr19q13.32	204985_s_at	NM_024108																				
7.55	7.09	0.46	3.98E-02	3.22E-01	CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1	chr22q13.1	204693_at	NM_007061 /// NM_152243																				
7.97	7.62	0.36	3.98E-02	3.22E-01	DERL2	Der1-like domain family, member 2	chr17p13.2	218333_at	NM_016041																				
3.60	3.27	0.33	3.98E-02	3.22E-01	LOC440296	hypothetical LOC440296	chr15q25.2	244498_x_at	XM_496082																				
6.05	5.52	0.52	3.98E-02	3.22E-01	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	chr1p36.2	203879_at	NM_005026																				
5.28	4.62	0.66	3.98E-02	3.22E-01	SH3GLB2	SH3-domain GRB2-like endophilin B2	chr9q34	218813_s_at	NM_020145																				
5.84	5.39	0.45	3.98E-02	3.22E-01	TSEN54	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	chr17q25.1	1558304_s_at	NM_207346																				
4.46	3.67	0.79	3.99E-02	3.22E-01	LONP2	Lon peptidase 2, peroxisomal	chr16q12.1	221833_at	NM_031490																				
6.90	5.91	0.99	3.99E-02	3.22E-01	RUSC1	RUN and SH3 domain containing 1	chr1q21-q22	206949_s_at	NM_001105203 /// NM_001105204 /// NM_001105205 /// NM_014328																				
8.14	7.69	0.45	3.99E-02	3.22E-01	TRIOBP	TRIO and F-actin binding protein	chr22q13.1	202795_x_at	NM_001039141 /// NM_007032 /// NM_138632																				
2.71	2.33	0.39	3.99E-02	3.22E-01	RAD52	RAD52 homolog (S. cerevisiae)	chr12p13-p12.2	210630_s_at	NM_134424																				
6.05	5.43	0.61	3.99E-02	3.22E-01	---	---	---	225256_at	---																				
7.95	7.42	0.53	3.99E-02	3.22E-01	RASSF5	Ras association (RalGDS/AF-6) domain family member 5	chr1q32.1	223322_at	NM_182663 /// NM_182664 /// NM_182665																				
6.50	5.84	0.66	3.99E-02	3.22E-01	HEMK1	HemK methyltransferase family member 1	chr3p21.3	52159_at	NM_016173																				
5.87	5.35	0.52	4.00E-02	3.22E-01	---	---	---	235282_at	---																				
2.68	2.33	0.35	4.00E-02	3.22E-01	---	---	---	238463_at	---																				
7.09	6.52	0.57	4.00E-02	3.22E-01	PLCG1	phospholipase C, gamma 1	chr20q12-q13.1	202789_at	NM_002660 /// NM_182811																				
9.18	8.41	0.77	4.00E-02	3.22E-01	TSPAN13	tetraspanin 13	chr7p21.1	217979_at	NM_014399																				
4.70	4.27	0.43	4.01E-02	3.22E-01	JMJD7 /// LOC100137047-PLA2G4B /// PLA2G4B	jumonji domain containing 7 /// hypothetical protein LOC8681 /// phospholipase A2, group IVB (cytosolic)	chr15q11.2-q21.3 /// chr15q15.1	222256_s_at	NM_001114632 /// NM_001114633 /// NM_005090 /// NR_015346 /// XM_001720570 /// XM_001723659 /// XM_001725545																				
4.47	4.14	0.33	4.01E-02	3.22E-01	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	chr16q13-q21	216282_x_at	NM_032940																				
4.20	3.53	0.67	4.01E-02	3.22E-01	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	chr8p23	229958_at	NM_018941																				
3.00	2.60	0.40	4.01E-02	3.22E-01	RPAIN	RPA interacting protein	chr17p13.2	216962_at	NM_001033002																				
4.56	2.86	1.70	4.01E-02	3.22E-01	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	chr4q34-q35	203913_s_at	NM_000860																				
6.99	6.09	0.90	4.01E-02	3.22E-01	RBM3	RNA binding motif (RNP1, RRM) protein 3	chrXp11.2	208319_s_at	NM_006743																				

7.83	7.28	0.55	4.02E-02	3.22E-01	PEX10	peroxisomal biogenesis factor 10	chr1p36.32	206352_s_at	NM_002617 /// NM_153818																					
7.73	7.25	0.49	4.02E-02	3.23E-01	AMFR	autocrine motility factor receptor	chr16q21	202204_s_at	NM_001144																					
5.13	4.52	0.61	4.02E-02	3.23E-01	---	---	---	238719_at	---																					
4.56	3.94	0.62	4.02E-02	3.23E-01	---	---	---	240339_at	---																					
3.26	2.89	0.37	4.02E-02	3.23E-01	C19orf15	chromosome 19 open reading frame 15	chr19q13.1	231261_at	NM_021185																					
5.64	5.03	0.60	4.02E-02	3.23E-01	LOC728568	hypothetical LOC728568	chr12q23.3	226943_at	NR_024026 /// XR_042054 /// XR_042055 /// XR_042056																					
2.44	2.11	0.33	4.03E-02	3.23E-01	---	---	---	243742_at	---																					
6.78	6.25	0.52	4.04E-02	3.23E-01	MLYCD	malonyl-CoA decarboxylase	chr16q24	218869_at	NM_012213																					
3.81	3.04	0.77	4.04E-02	3.23E-01	---	---	---	1559410_at	---																					
7.38	6.85	0.53	4.05E-02	3.23E-01	VPS37C	vacuolar protein sorting 37 homolog C (S. cerevisiae)	chr11q12.2	219053_s_at	NM_017966																					
6.76	6.38	0.38	4.06E-02	3.24E-01	MEMO1	mediator of cell motility 1	chr2p22-p21	219065_s_at	NM_015955																					
4.00	3.00	1.00	4.06E-02	3.24E-01	---	---	---	214373_at	---																					
4.01	3.62	0.39	4.06E-02	3.24E-01	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	chr8p21.3	32541_at	NM_005605																					
3.14	2.81	0.34	4.07E-02	3.24E-01	---	---	---	238645_at	---																					
6.27	5.61	0.65	4.07E-02	3.24E-01	---	---	---	217591_at	---																					
9.35	8.99	0.36	4.07E-02	3.24E-01	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	chr14q22.3	212643_at	NM_144578																					
6.86	6.20	0.66	4.07E-02	3.24E-01	---	---	---	228159_at	---																					
4.43	4.01	0.42	4.07E-02	3.24E-01	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7	chr2q37.3	201213_at	NM_002712																					
9.39	8.94	0.45	4.07E-02	3.24E-01	---	---	---	212952_at	---																					
3.37	3.01	0.35	4.08E-02	3.24E-01	TTLL4	tubulin tyrosine ligase-like family, member 4	chr2p24.3-p24.1	203703_s_at	NM_014640																					
7.49	7.07	0.42	4.08E-02	3.24E-01	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	chr1q32	201460_at	NM_004759 /// NM_032960																					
2.69	2.33	0.35	4.08E-02	3.24E-01	---	---	---	239682_at	---																					
5.72	5.14	0.58	4.08E-02	3.24E-01	MYO18A /// TIAF1	myosin XVIIIA /// TGFB1-induced anti-apoptotic factor 1	chr17q11.2	202039_at	NM_004740 /// NM_078471 /// NM_203318																					
3.34	2.60	0.74	4.08E-02	3.24E-01	---	---	---	224185_at	---																					
12.10	11.54	0.57	4.08E-02	3.24E-01	CLU	clusterin	chr8p21-p12	208792_s_at	NM_001831 /// NM_203339																					
2.74	2.35	0.39	4.09E-02	3.24E-01	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	chr2p21	227148_at	NM_172069																					
9.79	9.24	0.55	4.09E-02	3.24E-01	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	chrXp11.2	202282_at	NM_001037811 /// NM_004493																					
2.73	2.43	0.30	4.09E-02	3.24E-01	MUC12	mucin 12, cell surface associated	chr7q22	1557906_at	XM_001714400 /// XM_001724943 /// XM_379904 /// XM_936315																					
7.21	6.82	0.39	4.09E-02	3.24E-01	KAT5	K(lysine) acetyltransferase 5	chr11q13	209192_x_at	NM_006388 /// NM_182709 /// NM_182710																					
10.00	9.54	0.45	4.09E-02	3.24E-01	SCD5	stearoyl-CoA desaturase 5	chr4q21.22	224901_at	NM_001037582 /// NM_024906																					
3.81	2.86	0.96	4.09E-02	3.24E-01	---	---	---	1560525_at	---																					
7.91	7.15	0.75	4.10E-02	3.25E-01	SLC39A10	solute carrier family 39 (zinc transporter), member 10	chr2q32.3	225295_at	NM_001127257 /// NM_020342																					
2.49	1.98	0.51	4.10E-02	3.25E-01	---	---	---	1557383_a_at	---																					
2.22	1.93	0.29	4.10E-02	3.25E-01	41340	Membrane-associated ring finger (C3HC4) 7	chr2q24.2	1557704_a_at	NM_022826																					
7.76	7.27	0.50	4.10E-02	3.25E-01	METTL11A	methyltransferase like 11A	chr9q34.11	223369_at	NM_014064																					
7.73	7.18	0.54	4.11E-02	3.25E-01	ZC3H4	zinc finger CCCH-type containing 4	chr19q13.32	213390_at	NM_015168																					
8.91	8.48	0.43	4.11E-02	3.25E-01	CSDA	cold shock domain protein A	chr12p13.1	201160_s_at	NM_003651																					
2.95	2.44	0.51	4.11E-02	3.25E-01	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	chr10p14	228747_at	NM_018144																					

3.84	3.03	0.81	4.11E-02	3.25E-01	RNF207	ring finger protein 207	chr1p36.31	1555870_at	NM_207396 /// XM_001716213 /// XM_001718203 /// XM_001719665																				
7.29	6.90	0.39	4.12E-02	3.25E-01	TOR1A	torsin family 1, member A (torsin A)	chr9q34	202349_at	NM_000113																				
10.99	9.90	1.09	4.12E-02	3.25E-01	DUSP1	dual specificity phosphatase 1	chr5q34	201041_s_at	NM_004417																				
4.36	3.73	0.63	4.12E-02	3.25E-01	RAD51L3	RAD51-like 3 (S. cerevisiae)	chr17q11	209965_s_at	NM_002878 /// NM_133629																				
7.12	6.58	0.54	4.12E-02	3.25E-01	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	chr12q15	202469_s_at	NM_007007																				
6.84	6.45	0.39	4.12E-02	3.25E-01	EI24	etoposide induced 2.4 mRNA	chr11q24	208289_s_at	NM_001007277 /// NM_004879																				
7.30	6.73	0.57	4.13E-02	3.26E-01	ZFYVE21	zinc finger, FYVE domain containing 21	chr14q32.33	224445_s_at	NM_024071																				
5.32	4.35	0.97	4.13E-02	3.26E-01	SNHG11	small nucleolar RNA host gene (non-protein coding) 11	chr20q11.23	226149_at	NR_003239																				
3.60	2.89	0.71	4.13E-02	3.26E-01	ZNF33B	zinc finger protein 33B	chr10q11.2	1558586_at	NM_006955																				
6.89	5.91	0.98	4.13E-02	3.26E-01	FAM178A	family with sequence similarity 178, member A	chr10q24.31	203482_at	NM_018121																				
3.72	3.26	0.46	4.14E-02	3.26E-01	ZMYM5	zinc finger, MYM-type 5	chr13q12	215948_x_at	NM_001039649 /// NM_001039650																				
8.35	8.10	0.25	4.14E-02	3.26E-01	H2AFV	H2A histone family, member V	chr7p13	202487_s_at	NM_012412 /// NM_138635 /// NM_201436 /// NM_201516 /// NM_201517																				
4.44	4.10	0.34	4.14E-02	3.26E-01	SETD8	SET domain containing (lysine methyltransferase) 8	chr12q24.31	220200_s_at	NM_020382																				
9.18	8.88	0.30	4.14E-02	3.26E-01	UBL5	ubiquitin-like 5	chr19p13.3	218011_at	NM_001048241 /// NM_024292																				
4.44	3.88	0.56	4.14E-02	3.26E-01	LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	chrXq23	227688_at	NM_020871																				
4.20	3.32	0.88	4.15E-02	3.27E-01	TRAF5	TNF receptor-associated factor 5	chr1q32	204352_at	NM_001033910 /// NM_004619 /// NM_145759																				
11.62	11.35	0.27	4.15E-02	3.27E-01	RPL19	ribosomal protein L19	chr17q11.2-q12	200029_at	NM_000981																				
3.48	3.18	0.30	4.15E-02	3.27E-01	SIRT5	Sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	chr6p23	222081_at	NM_012241 /// NM_031244																				
7.27	6.62	0.65	4.15E-02	3.27E-01	ERRFI1	ERBB receptor feedback inhibitor 1	chr1p36	224657_at	NM_018948																				
4.25	3.65	0.60	4.15E-02	3.27E-01	ETV4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	chr17q21	1554576_a_at	NM_001079675 /// NM_001986																				
8.35	7.95	0.40	4.15E-02	3.27E-01	ILK	integrin-linked kinase	chr11p15.5-p15.4	201234_at	NM_001014794 /// NM_001014795 /// NM_004517																				
4.45	4.02	0.43	4.15E-02	3.27E-01	HAVCR2	hepatitis A virus cellular receptor 2	chr5q33.3	1554285_at	NM_032782																				
6.27	5.29	0.99	4.16E-02	3.27E-01	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	chr9q13	205632_s_at	NM_003558																				
6.40	5.79	0.61	4.16E-02	3.27E-01	ASCC1	activating signal cointegrator 1 complex subunit 1	chr10pter-q25.3	219336_s_at	NM_015947																				
8.09	7.76	0.33	4.16E-02	3.27E-01	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	chr11p12-p13	201267_s_at	NM_002804																				
6.21	5.59	0.62	4.17E-02	3.27E-01	UIMC1	ubiquitin interaction motif containing 1	chr5q35.2	220746_s_at	NM_016290																				
4.97	4.64	0.33	4.17E-02	3.27E-01	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	chr22q12.2	211392_s_at	NM_014323 /// NM_032050 /// NM_032051 /// NM_032052																				

3.51	2.77	0.74	4.17E-02	3.27E-01	LOC441876 /// RPS16	similar to Rps16 protein /// ribosomal protein S16	chr19q13.1 /// chr1p36.21	226130_at	NM_001020 /// XM_001718374 /// XM_497657 /// XM_942704
6.73	6.43	0.30	4.18E-02	3.27E-01	ZNFX1	zinc finger, NFX1-type containing 1	chr20q13.13	225076_s_at	NM_021035
6.47	5.92	0.55	4.18E-02	3.27E-01	OPRS1	opioid receptor, sigma 1	chr9p13.3	214484_s_at	NM_005866 /// NM_147157
8.52	8.03	0.49	4.18E-02	3.27E-01	PRKAR2A	Protein kinase, cAMP-dependent, regulatory, type II, alpha	chr3p21.3-p21.2	225000_at	NM_004157
6.88	6.21	0.67	4.18E-02	3.27E-01	PISD	phosphatidylserine decarboxylase	chr22q12.2	202392_s_at	NM_014338
5.08	4.55	0.53	4.19E-02	3.28E-01	LRRC37B	leucine rich repeat containing 37B	---	229231_at	NM_052888
4.42	3.46	0.95	4.19E-02	3.28E-01	CENPT	centromere protein T	chr16q22.1	218148_at	NM_025082
6.27	5.85	0.42	4.19E-02	3.28E-01	LYPLA2	lysophospholipase II	chr1p36.12-p35.1	215566_x_at	NM_007260
4.93	4.51	0.42	4.19E-02	3.28E-01	LIG3	ligase III, DNA, ATP-dependent	chr17q11.2-q12	204123_at	NM_002311 /// NM_013975
7.42	7.12	0.30	4.20E-02	3.28E-01	ANAPC7	anaphase promoting complex subunit 7	chr12q24.11	225554_s_at	NM_016238
2.87	2.33	0.54	4.20E-02	3.28E-01	---	---	---	237075_at	---
4.09	3.64	0.46	4.21E-02	3.28E-01	CANT1	calcium activated nucleotidase 1	chr17q25.3	1554327_a_at	NM_138793
5.57	4.94	0.63	4.21E-02	3.28E-01	TYSND1	trypsin domain containing 1	chr10q22.1	225877_at	NM_001040273 /// NM_173555
5.24	4.17	1.07	4.21E-02	3.29E-01	C12orf68	chromosome 12 open reading frame 68	chr12q13.11	229626_at	NM_001013635
4.15	3.70	0.44	4.22E-02	3.29E-01	KLHL36	kelch-like 36 (Drosophila)	chr16q24.1	219453_at	NM_024731
3.29	2.72	0.57	4.22E-02	3.29E-01	C2orf3	chromosome 2 open reading frame 3	chr2p11.2-p11.1	210175_at	NM_003203
4.73	4.16	0.57	4.22E-02	3.29E-01	LIG1	ligase I, DNA, ATP-dependent	chr19q13.2-q13.3	202726_at	NM_000234
8.09	7.65	0.44	4.22E-02	3.29E-01	YTHDF1	YTH domain family, member 1	chr20q13.33	221741_s_at	NM_017798
4.46	4.04	0.43	4.22E-02	3.29E-01	BCL9	B-cell CLL/lymphoma 9	chr1q21	204129_at	NM_004326
6.45	5.57	0.89	4.23E-02	3.29E-01	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	chr2q33-q35	212190_at	NM_006216
5.98	5.65	0.34	4.23E-02	3.29E-01	CRTC1	CREB regulated transcription coactivator 1	chr19p13.11	207159_x_at	NM_001098482 /// NM_015321
7.04	6.33	0.71	4.24E-02	3.30E-01	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	chr17p13	203871_at	NM_015670
6.72	6.26	0.46	4.24E-02	3.30E-01	RNF185	ring finger protein 185	chr22q12.2	224750_at	NM_152267
7.11	6.54	0.57	4.24E-02	3.30E-01	GAK	cyclin G associated kinase	chr4p16	40225_at	NM_005255
7.56	6.92	0.64	4.25E-02	3.30E-01	INO80B /// WBP1	INO80 complex subunit B /// WW domain binding protein 1	chr2p12 /// chr2p13.1	223072_s_at	NM_012477 /// NM_031288
7.84	7.16	0.68	4.25E-02	3.30E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	225368_at	NM_001113239 /// NM_022740
10.23	9.87	0.36	4.25E-02	3.30E-01	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	chrXq24-q26	200657_at	NM_001152
7.00	6.67	0.33	4.25E-02	3.30E-01	RNF114	ring finger protein 114	chr20q13.13	200868_s_at	NM_018683
4.87	4.29	0.58	4.26E-02	3.30E-01	CHMP4C	chromatin modifying protein 4C	chr8q21.13	226803_at	NM_152284
6.26	5.91	0.35	4.26E-02	3.30E-01	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	208913_at	NM_015044
3.63	2.76	0.87	4.26E-02	3.30E-01	---	---	---	227793_at	---
3.36	2.74	0.62	4.26E-02	3.30E-01	---	---	---	244240_at	---
5.03	4.41	0.61	4.26E-02	3.30E-01	SPRED1	sprouty-related, EVH1 domain containing 1	chr15q14	226837_at	NM_152594
8.17	7.83	0.35	4.26E-02	3.30E-01	TH1L	TH1-like (Drosophila)	chr20q13	225865_x_at	NM_198976
6.91	6.46	0.45	4.26E-02	3.30E-01	LOC653562 /// SLC6A10P /// SLC6A8	hypothetical LOC653562 /// solute carrier family 6 (neurotransmitter transporter, creatine), member 10 (pseudogene) /// solute carrier family 6 (neurotransmitter transporter, creatine), member 8	chr16p11.2 /// chrXq28	215812_s_at	NM_005629 /// NR_003083 /// XR_017514 /// XR_037879 /// XR_042169
12.32	12.10	0.22	4.26E-02	3.30E-01	RPLP0	ribosomal protein, large, P0	chr12q24.2	201033_x_at	NM_001002 /// NM_053275
5.36	3.93	1.43	4.26E-02	3.30E-01	VSNL1	visinin-like 1	chr2p24.3	203798_s_at	NM_003385
8.76	7.29	1.48	4.26E-02	3.30E-01	---	---	---	242680_at	---
3.22	2.99	0.23	4.26E-02	3.30E-01	TMEM86B	transmembrane protein 86B	chr19q13.42	229736_at	NM_173804
7.28	6.76	0.52	4.27E-02	3.30E-01	TMEM80	transmembrane protein 80	chr11p15.5	221951_at	NM_001042463 /// NM_174940
4.64	4.11	0.52	4.27E-02	3.31E-01	RBM19	RNA binding motif protein 19	chr12q24.13-q24.21	205115_s_at	NM_016196

8.05	7.69	0.37	4.27E-02	3.31E-01	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	chr16p13.3	218537_at	NM_001002017 /// NM_001002018 /// NM_017885																				
6.46	6.03	0.43	4.28E-02	3.31E-01	AIP	aryl hydrocarbon receptor interacting protein	chr11q13.3	201781_s_at	NM_003977																				
7.32	6.53	0.79	4.28E-02	3.31E-01	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	chr2q31.2	211929_at	NM_194247																				
3.17	2.60	0.57	4.28E-02	3.31E-01	RAD52	RAD52 homolog (S. cerevisiae)	chr12p13-p12.2	205647_at	NM_134424																				
6.15	5.65	0.51	4.29E-02	3.31E-01	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	chr16p13.3	213178_s_at	NM_001040439 /// NM_015133																				
5.46	4.84	0.62	4.29E-02	3.31E-01	GEMIN4	gem (nuclear organelle) associated protein 4	chr17p13	217099_s_at	NM_015721																				
3.86	3.44	0.43	4.29E-02	3.31E-01	---	---	---	235543_at	---																				
6.07	5.38	0.70	4.30E-02	3.32E-01	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	chr1q21.3	205661_s_at	NM_025207 /// NM_201398																				
2.24	1.92	0.33	4.30E-02	3.32E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	1556488_s_at	NM_033364																				
2.74	2.34	0.40	4.30E-02	3.32E-01	---	---	---	239953_at	---																				
3.28	3.02	0.26	4.30E-02	3.32E-01	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	chr20q11	209145_s_at	NM_001032999 /// NM_001039709 /// NM_005093																				
7.63	7.17	0.46	4.31E-02	3.32E-01	PPIA	peptidylprolyl isomerase A (cyclophilin A)	chr7p13	226336_at	NM_021130																				
6.03	5.50	0.53	4.31E-02	3.32E-01	CLCN6	chloride channel 6	chr1p36	203950_s_at	NM_001286 /// NM_021735 /// NM_021736 /// NM_021737																				
7.20	6.74	0.45	4.31E-02	3.32E-01	C1orf86	chromosome 1 open reading frame 86	chr1p36.33	229113_s_at	NM_182533 /// XM_001718861																				
3.36	3.07	0.28	4.32E-02	3.32E-01	OBP2A /// OBP2B	odorant binding protein 2A /// odorant binding protein 2B	chr9q34	233860_s_at	NM_014581 /// NM_014582																				
5.02	4.34	0.69	4.32E-02	3.32E-01	LCAT	lecithin-cholesterol acyltransferase	chr16q22.1	204428_s_at	NM_000229																				
7.66	7.28	0.38	4.33E-02	3.32E-01	C19orf63	chromosome 19 open reading frame 63	chr19q13.33	224727_at	NM_175063 /// NM_206538																				
5.56	5.19	0.36	4.33E-02	3.32E-01	EXT2	exostoses (multiple) 2	chr11p12-p11	202013_s_at	NM_000401 /// NM_207122																				
6.56	6.06	0.49	4.33E-02	3.32E-01	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	chr2p24.3-p11.2	218504_at	NM_016044																				
6.76	6.19	0.57	4.33E-02	3.32E-01	C17orf90	chromosome 17 open reading frame 90	chr17q25.3	50374_at	NM_001039842																				
11.24	10.94	0.30	4.34E-02	3.33E-01	COX4I1	cytochrome c oxidase subunit IV isoform 1	chr16q22-qter	202698_x_at	NM_001861																				
3.22	2.28	0.94	4.34E-02	3.33E-01	CREBZF	CREB/ATF bZIP transcription factor	chr11q14	225595_at	NM_001039618																				
3.34	2.83	0.51	4.34E-02	3.33E-01	GDNF	glial cell derived neurotrophic factor	chr5p13.1-p12	230090_at	NM_000514 /// NM_199231 /// NM_199234																				
9.68	9.22	0.46	4.35E-02	3.33E-01	SEC61B	Sec61 beta subunit	chr9q22.32-q31.3	203133_at	NM_006808																				
3.61	3.12	0.50	4.35E-02	3.33E-01	TRAF4	TNF receptor-associated factor 4	chr17q11-q12	211899_s_at	NM_004295																				
8.33	7.95	0.38	4.36E-02	3.33E-01	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	chr1q23.3	202004_x_at	NM_001035511 /// NM_001035512 /// NM_001035513 /// NM_003001																				
3.42	2.99	0.43	4.36E-02	3.33E-01	WDR73	WD repeat domain 73	chr15q25.2	230612_at	NM_032856																				
2.10	1.87	0.22	4.36E-02	3.33E-01	---	---	---	232477_at	---																				
2.21	1.88	0.32	4.36E-02	3.33E-01	MATN3	matrilin 3	chr2p24-p23	206091_at	NM_002381																				
6.48	5.96	0.53	4.37E-02	3.34E-01	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	chr1p36	223234_at	NM_001127325 /// NM_006341																				
5.33	4.88	0.46	4.37E-02	3.34E-01	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	chr17p11.2	227304_at	NM_144775																				
6.89	6.24	0.65	4.37E-02	3.34E-01	FAM100B	family with sequence similarity 100, member B	chr17q25.1	224783_at	NM_182565																				
7.45	6.96	0.48	4.38E-02	3.34E-01	---	---	---	214801_at	---																				

2.84	2.56	0.29	4.38E-02	3.34E-01	CSH1 /// CSH2 /// FCHO2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// FCH domain only 2 /// growth hormone 1	chr17q24.2 /// chr5q13.2	211739_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645 /// NM_138782																			
2.94	2.58	0.36	4.38E-02	3.34E-01	DNAH7	dynein, axonemal, heavy chain 7	chr2q32.3	234476_at	NM_018897																				
3.92	3.03	0.89	4.39E-02	3.34E-01	CXCR7	chemokine (C-X-C motif) receptor 7	chr2q37.3	212977_at	NM_020311																				
9.10	8.71	0.40	4.39E-02	3.34E-01	LARP1	La ribonucleoprotein domain family, member 1	chr5q33.2	212137_at	NM_015315 /// NM_033551																				
3.93	3.21	0.72	4.39E-02	3.34E-01	LOC284576	hypothetical protein LOC284576	chr1q32.1	1561281_a_at	---																				
4.80	4.19	0.61	4.39E-02	3.34E-01	PHF15	PHD finger protein 15	chr5q31.1	208202_s_at	NM_015288																				
5.96	5.48	0.47	4.39E-02	3.34E-01	PMM2	phosphomannomutase 2	chr16p13.3-p13.2	203201_at	NM_000303																				
7.12	6.50	0.62	4.40E-02	3.34E-01	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	chr3p21.31	204355_at	NM_014966 /// NM_138615																				
4.77	3.74	1.03	4.40E-02	3.34E-01	ORMDL1	ORM1-like 1 (S. cerevisiae)	chr2q32	227548_at	NM_001128150 /// NM_016467																				
8.32	7.42	0.90	4.40E-02	3.34E-01	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	chr20q13.1-q13.2	221485_at	NM_004776																				
6.72	6.02	0.70	4.40E-02	3.34E-01	BCL10	B-cell CLL/lymphoma 10	chr1p22	205263_at	NM_003921																				
4.87	4.29	0.58	4.40E-02	3.34E-01	MAP3K12	mitogen-activated protein kinase kinase kinase 12	chr12q13	205447_s_at	NM_006301																				
4.66	4.02	0.64	4.40E-02	3.34E-01	HRBL	HIV-1 Rev binding protein-like	chr7q22.1	222362_at	NM_006076																				
6.31	5.46	0.85	4.40E-02	3.34E-01	HSPC159	galectin-related protein	chr2p14	219998_at	NM_014181																				
8.27	7.73	0.54	4.41E-02	3.35E-01	NOB1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	chr16q22.3	223018_at	NM_014062																				
6.97	6.22	0.75	4.41E-02	3.35E-01	ILVBL	ilvB (bacterial acetolactate synthase)-like	chr19p13.1	210624_s_at	NM_006844																				
4.89	4.37	0.52	4.41E-02	3.35E-01	TBCD	tubulin folding cofactor D	chr17q25.3	229192_s_at	NM_005993																				
7.86	7.04	0.81	4.41E-02	3.35E-01	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	chr17q22	230682_x_at	NM_003786																				
2.16	1.95	0.21	4.42E-02	3.35E-01	CDC20B	Cell division cycle 20 homolog B (S. cerevisiae)	chr5q11.2	240161_s_at	NM_152623																				
7.33	6.68	0.65	4.42E-02	3.35E-01	CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	chr8q24.23	201639_s_at	NM_013291																				
2.92	2.29	0.63	4.42E-02	3.35E-01	MAP3K8	mitogen-activated protein kinase kinase kinase 8	chr10p11.23	205027_s_at	NM_005204																				
6.97	6.52	0.45	4.43E-02	3.35E-01	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	chr19p13.12	44702_at	NM_033025																				
7.19	6.72	0.46	4.43E-02	3.35E-01	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	chr11p11.2	223808_s_at	NM_175732																				
6.21	5.27	0.94	4.43E-02	3.35E-01	GATA3	GATA binding protein 3	chr10p15	209604_s_at	NM_001002295 /// NM_002051																				
5.58	5.17	0.41	4.43E-02	3.35E-01	---	---	---	235640_at	---																				
3.83	3.40	0.42	4.43E-02	3.35E-01	N4BP2L2	NEDD4 binding protein 2-like 2	chr13q13.1	214748_at	NM_014887 /// NM_033111																				
2.45	2.15	0.30	4.43E-02	3.35E-01	---	---	---	1559462_at	---																				
5.34	4.32	1.02	4.43E-02	3.35E-01	FAM19A4	family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	chr3p14.1	242348_at	NM_001005527 /// NM_182522																				
10.96	10.64	0.32	4.44E-02	3.36E-01	PNN	pinin, desmosome associated protein	chr14q21.1	210183_x_at	NM_002687																				

4.19	3.47	0.72	4.44E-02	3.36E-01	DMD	dystrophin	chrXp21.2	208086_s_at	NM_000109 /// NM_004006 /// NM_004007 /// NM_004009 /// NM_004010 /// NM_004011 /// NM_004012 /// NM_004013 /// NM_004014 /// NM_004015 /// NM_004016 /// NM_004017 /// NM_004018 /// NM_004019 /// NM_004020 /// NM_004021 /// NM_004022 /// NM_004023																			
7.90	7.04	0.85	4.44E-02	3.36E-01	SUOX	sulfite oxidase	chr12q13.2	204067_at	NM_000456 /// NM_001032386 /// NM_001032387																			
8.13	7.27	0.86	4.44E-02	3.36E-01	CBX4	chromobox homolog 4 (Pc class homolog, Drosophila)	chr17q25.3	227558_at	NM_003655																			
4.27	3.69	0.58	4.45E-02	3.36E-01	SDC3	syndecan 3	chr1pter-p22.3	1554864_a_at	NM_014654																			
6.52	5.98	0.53	4.45E-02	3.36E-01	SRF	serum response factor (c-fos serum response element-binding transcription factor)	chr6p21.1	202401_s_at	NM_003131																			
4.90	4.53	0.37	4.45E-02	3.36E-01	C3orf37	Chromosome 3 open reading frame 37	chr3q21.3	201677_at	NM_001006109 /// NM_020187																			
3.59	3.20	0.39	4.45E-02	3.36E-01	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	chr2q11.2	208363_s_at	NM_001134224 /// NM_001134225 /// NM_001566 /// NM_004027																			
6.26	5.67	0.59	4.45E-02	3.36E-01	KLF13	Kruppel-like factor 13	chr15q12	225390_s_at	NM_015995																			
3.04	2.69	0.36	4.45E-02	3.36E-01	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	chr2q11.2	241017_at	NM_001102426																			
3.54	2.92	0.62	4.46E-02	3.36E-01	ATAD2B	ATPase family, AAA domain containing 2B	chr2p24.1-p23.3	213387_at	NM_017552																			
4.80	4.30	0.50	4.46E-02	3.36E-01	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	chrXq11.1	203263_s_at	NM_015185																			
3.27	2.70	0.56	4.46E-02	3.36E-01	PSPH	phosphoserine phosphatase	chr7p15.2-p15.1	205194_at	NM_004577																			
4.87	4.64	0.23	4.46E-02	3.36E-01	ZCWPW1	zinc finger, CW type with PWWP domain 1	chr7q22.1	223992_x_at	NM_017984																			
3.04	2.45	0.60	4.47E-02	3.37E-01	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	chr19p13.2	227612_at	NM_001420 /// NM_032281																			
6.03	5.59	0.44	4.47E-02	3.37E-01	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	chr8q22.2	213243_at	NM_015243 /// NM_017890 /// NM_152564 /// NM_181661																			
4.01	3.46	0.55	4.48E-02	3.37E-01	PDE12	phosphodiesterase 12	chr3p14.3	1554915_a_at	NM_177966																			

2.22	1.98	0.24	4.48E-02	3.37E-01	RLN1 /// RLN2	relaxin 1 /// relaxin 2	chr9p24.1	214519_s_at	NM_005059 /// NM_006911 /// NM_134441																				
3.35	3.04	0.31	4.48E-02	3.37E-01	---	---	---	228209_at	---																				
7.56	6.96	0.60	4.48E-02	3.37E-01	WSB1	WD repeat and SOCS box-containing 1	chr17q11.1	210561_s_at	NM_015626 /// NM_134265																				
3.30	2.74	0.56	4.48E-02	3.37E-01	TMEM170A	transmembrane protein 170A	chr16q23.1	228505_s_at	NM_145254																				
3.62	3.11	0.51	4.48E-02	3.37E-01	C20orf39	chromosome 20 open reading frame 39	chr20p11.21	219310_at	NM_024893																				
7.83	7.42	0.42	4.49E-02	3.37E-01	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	chr16p13.3	45714_at	NM_001002017 /// NM_001002018 /// NM_017885																				
3.06	2.62	0.45	4.49E-02	3.37E-01	FAM153A /// FAM153B	family with sequence similarity 153, member A /// family with sequence similarity 153, member B	chr5q35.2 /// chr5q35.3	215133_s_at	NM_001079529 /// NM_173663																				
5.67	4.78	0.89	4.49E-02	3.37E-01	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	chr4q13.3	238762_at	NM_001004346																				
3.16	2.84	0.32	4.49E-02	3.37E-01	SEC16B	SEC16 homolog B (S. cerevisiae)	chr1q25.2	1555289_at	NM_033127																				
3.72	2.65	1.07	4.50E-02	3.37E-01	---	---	---	239577_at	---																				
10.75	10.34	0.41	4.50E-02	3.37E-01	PHB2	prohibitin 2	chr12p13	201600_at	NM_007273																				
4.42	3.47	0.94	4.50E-02	3.37E-01	---	---	---	1567101_at	---																				
4.40	3.69	0.71	4.50E-02	3.37E-01	LOC283050	hypothetical LOC283050	chr10q22.3	1563745_a_at	XM_378238 /// XM_944265																				
4.83	4.27	0.56	4.50E-02	3.37E-01	A2LD1	AIG2-like domain 1	chr13q32.3	232422_at	NM_033110 /// XM_001714498 /// XM_001714769 /// XM_001715756																				
2.62	2.33	0.29	4.50E-02	3.37E-01	---	---	---	1559679_a_at	---																				
9.07	8.61	0.46	4.50E-02	3.37E-01	RABAC1	Rab acceptor 1 (prenylated)	chr19q13.2	203136_at	NM_006423																				
5.81	5.05	0.76	4.50E-02	3.37E-01	GCHFR	GTP cyclohydrolase I feedback regulator	chr15q15	204867_at	NM_005258																				
7.99	7.04	0.95	4.50E-02	3.37E-01	CCDC8	coiled-coil domain containing 8	chr19q13.32	223495_at	NM_032040																				
6.26	5.66	0.61	4.51E-02	3.37E-01	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	chr19q13.2	226437_at	NM_001039671 /// NM_001039672 /// NM_001039673 /// NM_033557																				
6.88	6.31	0.58	4.51E-02	3.37E-01	VPS72	vacuolar protein sorting 72 homolog (S. cerevisiae)	chr1q21	202261_at	NM_005997																				
7.04	6.57	0.48	4.51E-02	3.37E-01	TTC15	tetratricopeptide repeat domain 15	chr2p25.3	203122_at	NM_016030																				
2.79	2.41	0.38	4.52E-02	3.37E-01	MGC14425	hypothetical protein MGC14425	chr10q21.3	1552665_at	XM_928066 /// XM_938414																				
5.26	4.83	0.43	4.52E-02	3.38E-01	TTPAL	tocopherol (alpha) transfer protein-like	chr20q13.12	228031_at	NM_001039199 /// NM_024331																				
6.33	5.64	0.69	4.52E-02	3.38E-01	ZNF641	Zinc finger protein 641	chr12q13.11	229897_at	NM_152320																				
5.00	4.63	0.38	4.52E-02	3.38E-01	---	---	---	216806_at	---																				
2.86	2.62	0.24	4.52E-02	3.38E-01	---	---	---	241239_at	---																				
4.59	3.82	0.77	4.53E-02	3.38E-01	KCTD13	potassium channel tetramerisation domain containing 13	chr16p11.2	45653_at	NM_178863																				
4.35	4.00	0.36	4.53E-02	3.38E-01	HISPPD2A	histidine acid phosphatase domain containing 2A	chr15q15.3	1555255_a_at	NM_001024463 /// NM_001130858 /// NM_001130859 /// NM_014659 /// XM_001723275																				
5.23	4.65	0.58	4.53E-02	3.38E-01	AMIGO3 /// GMPPB	adhesion molecule with Ig-like domain 3 /// GDP-mannose pyrophosphorylase B	chr3p21 /// chr3p21.31	229717_at	NM_013334 /// NM_021971 /// NM_198722																				
2.55	2.28	0.27	4.53E-02	3.38E-01	---	---	---	243961_at	---																				

8.25	7.01	1.24	4.53E-02	3.38E-01	AKAP7	A kinase (PRKA) anchor protein 7	chr6q23	205771_s_at	NM_004842 /// NM_016377 /// NM_138633																				
3.28	2.64	0.64	4.53E-02	3.38E-01	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	chr2p13	201449_at	NM_022037 /// NM_022173																				
3.54	3.24	0.31	4.53E-02	3.38E-01	C14orf28	chromosome 14 open reading frame 28	chr14q21.3	238647_at	NM_001017923																				
7.33	6.91	0.41	4.54E-02	3.38E-01	DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12	chr10q22.1	202866_at	NM_001002762 /// NM_017626																				
2.70	1.89	0.81	4.54E-02	3.38E-01	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	chr11q14.3-q21	1554507_at	NM_005467																				
3.85	3.51	0.35	4.54E-02	3.38E-01	MDM2	Mdm2 p53 binding protein homolog (mouse)	chr12q14.3-q15	217373_x_at	NM_002392 /// NM_006878 /// NM_006879 /// NM_006881 /// NM_006882																				
7.39	7.05	0.35	4.54E-02	3.38E-01	MRPS17	mitochondrial ribosomal protein S17	chr7p11	218982_s_at	NM_015969																				
2.32	2.08	0.23	4.55E-02	3.38E-01	UNC84A	unc-84 homolog A (C. elegans)	chr7p22.3	230210_at	NM_001130965 /// NM_025154																				
2.96	2.36	0.60	4.56E-02	3.38E-01	ZNF518A	zinc finger protein 518A	chr10q23.33	204291_at	NM_014803																				
4.24	3.64	0.59	4.56E-02	3.38E-01	PATL1	protein associated with topoisomerase II homolog 1 (yeast)	chr11q12.1	235234_at	NM_152716																				
6.55	5.97	0.58	4.56E-02	3.38E-01	NFYC	nuclear transcription factor Y, gamma	chr1p32|1p32	202215_s_at	NM_014223																				
4.63	4.03	0.60	4.56E-02	3.39E-01	YPEL2	yippee-like 2 (Drosophila)	chr17q22	229060_at	NM_001005404																				
4.63	3.48	1.14	4.56E-02	3.39E-01	EPN3	epsin 3	chr17q21.33	220318_at	NM_017957																				
8.54	8.09	0.45	4.56E-02	3.39E-01	POLDIP2	polymerase (DNA-directed), delta interacting protein 2	chr17q11.2	222425_s_at	NM_015584																				
7.01	6.41	0.60	4.56E-02	3.39E-01	CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	chr8q24.23	33132_at	NM_013291																				
6.33	5.89	0.44	4.57E-02	3.39E-01	KLHL5	kelch-like 5 (Drosophila)	chr4p14	226001_at	NM_001007075 /// NM_015990 /// NM_199039																				
4.07	2.97	1.10	4.57E-02	3.39E-01	CHRDL1	chordin-like 1	chrXq22.3	209763_at	NM_145234																				
7.12	6.66	0.46	4.57E-02	3.39E-01	CIAO1	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	chr2q11.2	203536_s_at	NM_004804																				
2.60	2.36	0.24	4.58E-02	3.39E-01	RNF7	ring finger protein 7	chr3q22-q24	224394_at	NM_014245 /// NM_183237																				
2.47	2.05	0.42	4.58E-02	3.39E-01	FLJ25006	hypothetical protein FLJ25006	chr17q11.2	1553292_s_at	NM_144610																				
9.71	9.37	0.34	4.58E-02	3.39E-01	ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	chr10q26.2-q26.3	201135_at	NM_004092																				
6.92	6.35	0.58	4.58E-02	3.39E-01	FBXO31	F-box protein 31	chr16q24.2	224162_s_at	NM_024735																				
7.43	6.98	0.45	4.58E-02	3.39E-01	ITGAE	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	chr17p13	205055_at	NM_002208																				
8.16	7.78	0.38	4.58E-02	3.39E-01	C11orf2	chromosome 11 open reading frame2	chr11q13	217969_at	NM_013265																				
4.05	2.88	1.17	4.58E-02	3.39E-01	SOX7	SRY (sex determining region Y)-box 7	chr8p22	228698_at	NM_031439																				
7.18	6.29	0.89	4.58E-02	3.39E-01	---	---	---	228850_s_at	---																				
8.57	7.22	1.34	4.59E-02	3.39E-01	PSAT1	phosphoserine aminotransferase 1	chr9q21.2	223062_s_at	NM_021154 /// NM_058179																				
3.00	2.42	0.59	4.59E-02	3.39E-01	COL11A1	collagen, type XI, alpha 1	chr1p21	37892_at	NM_001854 /// NM_080629 /// NM_080630																				
6.31	5.80	0.51	4.59E-02	3.39E-01	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	chr8q11	208694_at	NM_001081640 /// NM_006904																				
5.50	4.52	0.98	4.59E-02	3.39E-01	FAM178A	family with sequence similarity 178, member A	chr10q24.31	203481_at	NM_018121																				
6.43	6.04	0.39	4.59E-02	3.39E-01	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	chr4q24	209239_at	NM_003998																				
6.10	5.55	0.55	4.59E-02	3.39E-01	KIAA0831	KIAA0831	chr14q22.3	204568_at	NM_014924																				
6.19	5.74	0.45	4.60E-02	3.39E-01	FBXL15	F-box and leucine-rich repeat protein 15	chr10q24.32	218938_at	NM_024326																				
10.29	10.02	0.27	4.60E-02	3.39E-01	HINT1	histidine triad nucleotide binding protein 1	chr5q31.2	208826_x_at	NM_005340																				
7.48	6.99	0.49	4.60E-02	3.39E-01	XTP3TPA	XTP3-transactivated protein A	chr16p11.2	218069_at	NM_024096																				

5.19	4.54	0.65	4.60E-02	3.40E-01	LOC391132	similar to hCG2041276	chr1q24.2	216177_at	XR_017287 /// XR_018883 /// XR_038069																				
12.61	12.34	0.27	4.61E-02	3.40E-01	RPS10	ribosomal protein S10	chr6p21.31	200095_x_at	NM_001014																				
2.46	2.12	0.34	4.61E-02	3.40E-01	---	---	---	237791_at	---																				
9.33	9.05	0.28	4.61E-02	3.40E-01	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	chr14q11.2	214737_x_at	NM_001077442 /// NM_001077443 /// NM_004500 /// NM_031314																				
6.69	6.23	0.46	4.61E-02	3.40E-01	WWP2	WW domain containing E3 ubiquitin protein ligase 2	chr16q22.1	204022_at	NM_007014 /// NM_199423 /// NM_199424																				
2.88	2.61	0.27	4.62E-02	3.40E-01	C1orf215	chromosome 1 open reading frame 215	chr1p36.11	1552803_a_at	XR_042017 /// XR_042018 /// XR_042019																				
3.12	2.64	0.48	4.62E-02	3.40E-01	LOC283508	hypothetical protein LOC283508	chr13q13.3	227415_at	---																				
8.00	7.08	0.92	4.62E-02	3.40E-01	DDR1	discoidin domain receptor tyrosine kinase 1	chr6p21.3	210749_x_at	NM_001954 /// NM_013993 /// NM_013994																				
5.62	5.11	0.51	4.62E-02	3.40E-01	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	chr22q11.21	214986_x_at	NM_014337 /// NM_148175 /// NM_148176																				
6.59	6.13	0.46	4.62E-02	3.40E-01	ZNF511	zinc finger protein 511	chr10q26.3	225307_at	NM_145806																				
6.22	5.41	0.81	4.62E-02	3.40E-01	---	---	---	242705_x_at	---																				
4.30	3.86	0.45	4.63E-02	3.40E-01	LOC642826	hypothetical LOC642826	chr10q11.22	240230_s_at	XR_041405																				
5.71	4.78	0.93	4.63E-02	3.40E-01	CRKRS	Cdc2-related kinase, arginine/serine-rich	chr17q12	225694_at	NM_015083 /// NM_016507																				
7.01	6.39	0.62	4.63E-02	3.40E-01	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	chr14q24.3-q31	203127_s_at	NM_004863																				
3.77	3.31	0.46	4.63E-02	3.40E-01	FAM87A /// FAM87B /// LOC100134357	family with sequence similarity 87, member A /// family with sequence similarity 87, member B /// similar to hCG1735895	chr1p36.33 /// chr8p23.3	1559140_at	XM_001713962 /// XM_001719631 /// XM_001719643 /// XM_001719709 /// XM_001719721 /// XM_001721137 /// XM_001721145																				
9.00	8.60	0.40	4.63E-02	3.40E-01	SELS	selenoprotein S	chr15q26.3	223209_s_at	NM_018445 /// NM_203472																				
6.26	5.57	0.69	4.63E-02	3.40E-01	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	chr1p36.13-q31.3	1554417_s_at	NM_001077628 /// NM_016022																				
5.13	4.71	0.41	4.63E-02	3.40E-01	ZNF498	zinc finger protein 498	chr7q22.1	228138_at	NM_145115																				
7.02	6.70	0.33	4.63E-02	3.40E-01	HADH	hydroxyacyl-Coenzyme A dehydrogenase	chr4q22-q26	201035_s_at	NM_005327																				
4.85	4.37	0.48	4.63E-02	3.40E-01	NBEAL2	neurobeachin-like 2	chr3p21.31	212443_at	NM_015175																				
5.79	5.08	0.71	4.64E-02	3.40E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	202250_s_at	NM_015726																				
3.56	3.12	0.44	4.64E-02	3.40E-01	---	---	---	237081_at	---																				
2.44	2.18	0.26	4.64E-02	3.40E-01	FLJ35848	Hypothetical protein FLJ35848	chr17q21.31	1564075_a_at	NM_001033659																				
3.25	2.96	0.28	4.65E-02	3.40E-01	---	---	---	219987_at	---																				
4.20	3.11	1.09	4.65E-02	3.40E-01	---	---	---	235803_at	---																				
5.86	5.20	0.67	4.66E-02	3.40E-01	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	chr2p23	204087_s_at	NM_021095																				
8.09	7.65	0.44	4.66E-02	3.40E-01	CHMP1B	chromatin modifying protein 1B	chr18p11.21	218178_s_at	NM_020412																				
6.79	6.22	0.57	4.66E-02	3.40E-01	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	chr16q21-q23	59625_at	NM_003946																				

5.59	5.25	0.34	4.66E-02	3.40E-01	GRSF1	G-rich RNA sequence binding factor 1	chr4q13	215030_at	NM_001098477 /// NM_002092																				
6.88	6.26	0.62	4.66E-02	3.40E-01	RCCD1	RCC1 domain containing 1	chr15q26.1	226488_at	NM_001017919 /// NM_033544																				
6.94	6.53	0.40	4.66E-02	3.40E-01	SEC14L1	SEC14-like 1 (S. cerevisiae)	chr17q25.1-q25.2	202083_s_at	NM_001039573 /// NM_003003																				
5.59	4.93	0.66	4.66E-02	3.40E-01	DUSP12	dual specificity phosphatase 12	chr1q21-q22	218576_s_at	NM_007240																				
6.78	6.19	0.59	4.66E-02	3.40E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	213720_s_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072																				
4.28	3.69	0.59	4.67E-02	3.40E-01	RAF1	V-raf-1 murine leukemia viral oncogene homolog 1	chr3p25	1557675_at	NM_002880																				
4.00	3.31	0.69	4.67E-02	3.40E-01	---	---	---	237299_at	---																				
4.65	3.48	1.18	4.67E-02	3.40E-01	FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	chr9q34.3	207804_s_at	NM_004108 /// NM_015837																				
7.50	7.06	0.43	4.67E-02	3.40E-01	PGCP	plasma glutamate carboxypeptidase	chr8q22.2	203501_at	NM_016134																				
5.23	3.76	1.47	4.67E-02	3.40E-01	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	chr6p21.3	209480_at	NM_002123 /// XM_001722253 /// XM_001723447																				
4.26	3.09	1.17	4.67E-02	3.40E-01	SYN2	synapsin II	chr3p25	210247_at	NM_003178 /// NM_133625																				
5.20	4.68	0.52	4.69E-02	3.41E-01	TYMP	thymidine phosphorylase	chr22q13|22q13.33	204858_s_at	NM_001113755 /// NM_001113756 /// NM_001953																				
2.09	1.81	0.28	4.69E-02	3.41E-01	MCM6	minichromosome maintenance complex component 6	chr2q21	238977_at	NM_005915																				
10.55	10.15	0.40	4.69E-02	3.41E-01	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	chr4q28.2-q31.1	203478_at	NM_002494																				
2.54	2.13	0.41	4.69E-02	3.41E-01	---	---	---	1556301_at	---																				
7.60	6.99	0.61	4.70E-02	3.41E-01	ATPIF1	ATPase inhibitory factor 1	---	223338_s_at	NM_016311 /// NM_178190 /// NM_178191																				
6.87	6.16	0.71	4.70E-02	3.41E-01	BANP	BTG3 associated nuclear protein	chr16q24.2-q24.3	219966_x_at	NM_017869 /// NM_079837 /// XM_001718410																				
5.04	4.57	0.47	4.70E-02	3.41E-01	---	---	---	222294_s_at	---																				

3.98	3.59	0.39	4.70E-02	3.41E-01	LOC128192 /// LOC131691 /// LOC202227 /// LOC256374 /// LOC342541 /// LOC391532 /// LOC439953 /// LOC440063 /// LOC643997 /// LOC654188 /// PPIA /// tcag7.873	similar to peptidyl-Pro cis trans isomerase /// similar to peptidyl-Pro cis trans isomerase /// hypothetical LOC202227 /// similar to peptidyl-Pro cis trans isomerase /// similar to peptidyl-Pro cis trans isomerase /// hypothetical LOC391532 /// similar to peptidylprolyl isomerase A-like /// similar to peptidylprolyl isomerase A-like /// similar to peptidylprolyl isomerase A-like /// similar to peptidylprolyl isomerase A isoform 1 /// peptidylprolyl isomerase A (cyclophilin A) /// hypothetical LOC402644	chr10p11.22 /// chr11q22.1 /// chr15q24.2 /// chr17q23.3 /// chr1p34.1 /// chr2q31.1 /// chr3p14.2 /// chr3q22.3 /// chr5q12.3 /// chr7p13 /// chr7p15.1	217346_at	NM_001126493 /// NM_021130 /// XM_001717377 /// XM_001717840 /// XM_001717979 /// XM_001718507 /// XM_001721772 /// XM_001721978 /// XM_001725191 /// XM_001726050 /// XM_060887 /// XM_170597 /// XM_292596 /// XM_292963 /// XM_939418 /// XM_939860 /// XM_941423 /// XM_941618 /// XR_016123 /// XR_016767 /// XR_017375 /// XR_017653 /// XR_018309 /// XR_018394 /// XR_019278 /// XR_037629 /// XR_037862 /// XR_038864 /// XR_039333 /// XR_039651																					
11.13	10.25	0.87	4.71E-02	3.41E-01	MT1E	metallothionein 1E	chr16q13	212859_x_at	NM_175617																				
4.76	3.85	0.92	4.71E-02	3.41E-01	CNTN6	contactin 6	chr3p26-p25	207195_at	NM_014461																				
4.91	4.19	0.72	4.71E-02	3.41E-01	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	chr16p13.3	218686_s_at	NM_022450																				
7.44	6.79	0.65	4.71E-02	3.41E-01	MRPL9	mitochondrial ribosomal protein L9	chr1q21	209609_s_at	NM_031420																				
6.59	6.08	0.51	4.71E-02	3.41E-01	C7orf26	chromosome 7 open reading frame 26	chr7p22.1	47083_at	NM_024067																				
8.22	7.36	0.86	4.72E-02	3.41E-01	SDC4	syndecan 4	chr20q12	202071_at	NM_002999																				
6.88	5.94	0.94	4.72E-02	3.41E-01	DUSP5	dual specificity phosphatase 5	chr10q25	209457_at	NM_004419																				
3.55	3.15	0.40	4.72E-02	3.41E-01	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	chr1q21	202914_s_at	NM_014784 /// NM_198236																				
7.23	6.39	0.84	4.73E-02	3.42E-01	SEC16A	SEC16 homolog A (S. cerevisiae)	chr9q34.3	215696_s_at	NM_014866																				
3.46	3.04	0.42	4.74E-02	3.42E-01	---	---	---	228828_at	---																				
7.47	6.47	1.01	4.74E-02	3.42E-01	NDEL1	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	chr17p13.1	208093_s_at	NM_001025579 /// NM_030808																				
2.92	2.32	0.60	4.74E-02	3.42E-01	C6orf26 /// MSH5	chromosome 6 open reading frame 26 /// mutS homolog 5 (E. coli)	chr6p21.3 /// chr6p21.33	212913_at	NM_001039651 /// NM_002441 /// NM_025259 /// NM_172165 /// NM_172166																				
6.43	5.37	1.05	4.74E-02	3.42E-01	PGM2	phosphoglucomutase 2	chr4p14	225367_at	NM_018290																				
7.88	7.15	0.73	4.74E-02	3.42E-01	BMI1	BMI1 polycomb ring finger oncogene	chr10p11.23	202265_at	NM_005180																				
6.78	5.96	0.82	4.74E-02	3.42E-01	C12orf34	chromosome 12 open reading frame 34	chr12q24.11	226487_at	NM_032829																				

7.94	6.32	1.62	4.75E-02	3.42E-01	CCNL1	cyclin L1	chr3q25.32	220046_s_at	NM_020307
8.59	8.23	0.36	4.75E-02	3.42E-01	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	chr1q23.3	210131_x_at	NM_001035511 /// NM_001035512 /// NM_001035513 /// NM_003001
9.96	9.65	0.32	4.75E-02	3.42E-01	SNX3	sorting nexin 3	chr6q21	200067_x_at	NM_003795
3.02	2.53	0.49	4.75E-02	3.42E-01	SLC6A16	solute carrier family 6, member 16	chr19q13.1-q13.4	219820_at	NM_014037
4.13	2.80	1.33	4.75E-02	3.42E-01	7A5	putative binding protein 7a5	chr7p15.3	1559361_at	NM_182762
8.20	7.66	0.54	4.75E-02	3.42E-01	TMEM50B	transmembrane protein 50B	chr21q22.11	225182_at	NM_006134
3.12	2.57	0.55	4.76E-02	3.42E-01	---	---	---	219880_at	---
5.83	4.88	0.95	4.76E-02	3.42E-01	PRKD1	protein kinase D1	chr14q11	205880_at	NM_002742
8.19	7.64	0.55	4.77E-02	3.43E-01	GALM	galactose mutarotase (aldose 1-epimerase)	chr2p22.1	235256_s_at	NM_138801
9.00	8.48	0.52	4.77E-02	3.43E-01	MAPRE2	microtubule-associated protein, RP/EB family, member 2	chr18q12.1	202501_at	NM_014268
2.39	2.10	0.29	4.78E-02	3.43E-01	GABRR3	gamma-aminobutyric acid (GABA) receptor, rho 3	chr3q11.2	234410_at	NM_001105580
4.58	4.05	0.52	4.78E-02	3.43E-01	ZSWIM7	zinc finger, SWIM-type containing 7	chr17p12	228719_at	NM_001042697 /// NM_001042698
5.81	5.41	0.40	4.78E-02	3.43E-01	RNMT	RNA (guanine-7-) methyltransferase	chr18p11.22-p11.23	202683_s_at	NM_003799
5.07	4.59	0.48	4.78E-02	3.43E-01	JMJD4	jumonji domain containing 4	chr1q42.13	222671_s_at	NM_023007
5.78	5.27	0.51	4.79E-02	3.43E-01	CRTC2	CREB regulated transcription coactivator 2	chr1q21.3	226307_at	NM_181715
2.97	2.74	0.23	4.79E-02	3.43E-01	LOC283867	hypothetical protein LOC283867	chr16q21	231518_at	NM_001101346
5.35	4.52	0.83	4.80E-02	3.44E-01	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	chr2p22-p21	202715_at	NM_004341
7.62	6.94	0.68	4.80E-02	3.44E-01	HDDC3	HD domain containing 3	chr15q26.1	227008_at	NM_198527
7.20	6.78	0.42	4.80E-02	3.44E-01	COG8 /// PDF	component of oligomeric golgi complex 8 /// peptide deformylase (mitochondrial)	chr16q22.1	219575_s_at	NM_022341 /// NM_032382
8.30	6.73	1.56	4.80E-02	3.44E-01	DUSP1	dual specificity phosphatase 1	chr5q34	201044_x_at	NM_004417
4.50	3.93	0.57	4.80E-02	3.44E-01	FAM86C	family with sequence similarity 86, member C	chr11q13.4	220353_at	NM_001099653 /// NM_018172 /// NM_152563
6.69	6.14	0.55	4.80E-02	3.44E-01	TMEM115	transmembrane protein 115	chr3p21.3	216267_s_at	NM_007024
3.84	3.41	0.43	4.81E-02	3.44E-01	CA5BL	Carbonic anhydrase VB-like	chrXp22.2	239106_at	XM_001715245 /// XM_001716189 /// XM_001719208 /// XM_001719213
8.79	8.11	0.67	4.81E-02	3.44E-01	C8orf33	chromosome 8 open reading frame 33	chr8q24.3	218187_s_at	NM_023080
3.33	2.77	0.56	4.81E-02	3.44E-01	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	chr10p14	219499_at	NM_018144
6.50	5.53	0.98	4.81E-02	3.44E-01	ISOC1	isochorismatase domain containing 1	chr5q22.1-q33.3	218170_at	NM_016048
3.66	3.18	0.48	4.81E-02	3.44E-01	C5orf28	chromosome 5 open reading frame 28	chr5p12	219029_at	NM_022483
4.80	4.25	0.56	4.81E-02	3.44E-01	TMEM2	transmembrane protein 2	chr9q13-q21	218113_at	NM_013390
6.33	5.90	0.42	4.82E-02	3.44E-01	ZNF317	zinc finger protein 317	---	225296_at	NM_020933
2.99	2.60	0.39	4.82E-02	3.44E-01	C11orf70	chromosome 11 open reading frame 70	chr11q22.1	224463_s_at	NM_032930
4.06	3.69	0.37	4.83E-02	3.44E-01	WIPF1	WAS/WASL interacting protein family, member 1	chr2q31.1	202663_at	NM_001077269 /// NM_003387
4.42	4.12	0.30	4.83E-02	3.44E-01	HAVCR2	hepatitis A virus cellular receptor 2	chr5q33.3	1555628_a_at	NM_032782
5.53	5.21	0.33	4.83E-02	3.45E-01	C3orf23	chromosome 3 open reading frame 23	chr3p21.33-p21.32	1555906_s_at	NM_001029839 /// NM_001029840 /// NM_173826
6.17	5.76	0.41	4.84E-02	3.45E-01	RNF126	ring finger protein 126	chr19p13.3	205748_s_at	NM_194460
3.57	2.78	0.80	4.84E-02	3.45E-01	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	chr10q24.3	1562573_at	NM_000102
5.20	4.52	0.67	4.84E-02	3.45E-01	LOC645212	hypothetical LOC645212	chr15q15.3	235124_at	XM_001719119 /// XM_928252 /// XM_939117
3.61	2.86	0.75	4.85E-02	3.45E-01	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	chr16p13.3	1569868_s_at	NM_001010865
2.98	2.56	0.42	4.85E-02	3.45E-01	---	---	---	242818_x_at	---
5.67	5.07	0.60	4.85E-02	3.45E-01	C1orf51	chromosome 1 open reading frame 51	chr1q21.2	227285_at	NM_144697
7.37	6.87	0.50	4.85E-02	3.45E-01	41339	membrane-associated ring finger (C3HC4) 6	chr5p15.2	201736_s_at	NM_005885

7.39	6.80	0.59	4.85E-02	3.45E-01	RAB5B	RAB5B, member RAS oncogene family	chr12q13	201276_at	NM_002868																			
12.32	12.10	0.21	4.86E-02	3.45E-01	RPLP0	ribosomal protein, large, P0	chr12q24.2	211720_x_at	NM_001002 /// NM_053275																			
3.63	3.06	0.57	4.86E-02	3.45E-01	STC1	stanniocalcin 1	chr8p21-p11.2	204595_s_at	NM_003155																			
6.13	5.71	0.42	4.86E-02	3.45E-01	RNF114	ring finger protein 114	chr20q13.13	200867_at	NM_018683																			
4.08	3.37	0.72	4.86E-02	3.45E-01	C14orf138	chromosome 14 open reading frame 138	chr14q22.1	218940_at	NM_001040662 /// NM_024558																			
6.76	6.44	0.32	4.87E-02	3.45E-01	LASS5	LAG1 homolog, ceramide synthase 5	chr12q13.13	224951_at	NM_147190																			
8.05	7.52	0.53	4.87E-02	3.45E-01	HYOU1	hypoxia up-regulated 1	chr11q23.1-q23.3	200825_s_at	NM_001130991 /// NM_006389																			
2.64	2.25	0.39	4.87E-02	3.45E-01	DNPEP	aspartyl aminopeptidase	chr2q35	215135_at	NM_012100																			
2.85	2.54	0.31	4.87E-02	3.45E-01	LOC283887	hypothetical protein LOC283887	chr16p12.1	1564373_a_at	XM_929898																			
3.73	2.95	0.79	4.88E-02	3.45E-01	LOC440944	Hypothetical gene supported by AK128398	chr3p25.3	1555860_x_at	XR_017845 /// XR_017949 /// XR_041324																			
6.58	5.91	0.67	4.88E-02	3.45E-01	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	chr22q13	204594_s_at	NM_019008																			
9.33	8.79	0.53	4.88E-02	3.45E-01	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	chr5q31	201054_at	NM_006805																			
2.85	2.51	0.34	4.88E-02	3.46E-01	ZNF333	zinc finger protein 333	chr19p13	1552375_at	NM_032433																			
5.69	4.78	0.91	4.89E-02	3.46E-01	CREM	cAMP responsive element modulator	chr10p11.21	228092_at	NM_001881 /// NM_181571 /// NM_182717 /// NM_182718 /// NM_182719 /// NM_182720 /// NM_182721 /// NM_182722 /// NM_182723 /// NM_182724 /// NM_182725 /// NM_182769 /// NM_182770 /// NM_182771 /// NM_182772 /// NM_182850 /// NM_182853 /// NM_183011 /// NM_183012 /// NM_183013 /// NM_183060																			
4.33	3.80	0.54	4.89E-02	3.46E-01	LOC645676	hypothetical LOC645676	chr1q22	1554057_at	XR_040468 /// XR_040469 /// XR_040470																			
4.35	3.99	0.35	4.90E-02	3.46E-01	MYH14	myosin, heavy chain 14	chr19q13.33	234290_x_at	NM_001077186 /// NM_024729																			
7.91	7.40	0.51	4.90E-02	3.46E-01	GPR177	G protein-coupled receptor 177	chr1p31.3	221958_s_at	NM_001002292 /// NM_024911																			
4.37	3.98	0.39	4.90E-02	3.46E-01	N4BP1	NEDD4 binding protein 1	chr16q12.1	32069_at	NM_153029																			

3.39	2.81	0.59	4.90E-02	3.46E-01	KIFC2	kinesin family member C2	chr8q24.3	226791_at	NM_145754
4.70	4.30	0.39	4.90E-02	3.46E-01	C2orf81	chromosome 2 open reading frame 81	chr2p13.1	236070_at	XM_001726549 /// XM_371503 /// XM_942034
5.09	4.44	0.65	4.90E-02	3.46E-01	C16orf67	chromosome 16 open reading frame 67	chr16p11.2	219442_at	NR_024034 /// XM_001714859 /// XM_001714976 /// XM_001717906
3.79	3.38	0.42	4.91E-02	3.46E-01	IL9R /// LOC729486	interleukin 9 receptor /// similar to hCG1790853	chr16p13.3 /// chrXq28 and Yq12	217212_s_at	NM_002186 /// NM_176786 /// NR_024033 /// XR_042290 /// XR_042385 /// XR_042402
2.92	2.56	0.36	4.91E-02	3.46E-01	---	---	---	238227_at	---
3.02	2.68	0.34	4.91E-02	3.46E-01	---	---	---	241443_at	---
2.37	2.05	0.32	4.91E-02	3.46E-01	ARMCX4	armadillo repeat containing, X-linked 4	chrXq22.1	1552327_at	NM_152583
2.85	2.30	0.55	4.91E-02	3.47E-01	---	---	---	232453_at	---
5.77	5.16	0.61	4.91E-02	3.47E-01	CCNE1	cyclin E1	chr19q12	213523_at	NM_001238 /// NM_057182
6.75	6.17	0.58	4.91E-02	3.47E-01	QSOX1	quiescin Q6 sulfhydryl oxidase 1	chr1q24	201482_at	NM_001004128 /// NM_002826
3.71	3.30	0.41	4.92E-02	3.47E-01	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	chr16p11.2	212808_at	NM_032815
3.46	2.58	0.88	4.92E-02	3.47E-01	---	---	---	235274_at	---
7.10	6.58	0.52	4.92E-02	3.47E-01	HMG20B	high-mobility group 20B	chr19p13.3	210719_s_at	NM_006339
2.16	1.92	0.24	4.93E-02	3.47E-01	---	---	---	1559534_at	---
6.03	5.44	0.60	4.93E-02	3.47E-01	MAP2K5	mitogen-activated protein kinase kinase 5	chr15q23	211370_s_at	NM_002757 /// NM_145160
8.15	7.69	0.46	4.93E-02	3.47E-01	CASC3	cancer susceptibility candidate 3	chr17q11-q21.3	207842_s_at	NM_007359
6.54	6.07	0.47	4.93E-02	3.47E-01	PGK1	phosphoglycerate kinase 1	chrXq13	227068_at	NM_000291
7.28	6.73	0.55	4.93E-02	3.47E-01	HEPH	hephaestin	chrXq11-q12	203903_s_at	NM_001130860 /// NM_014799 /// NM_138737
7.39	6.41	0.98	4.94E-02	3.47E-01	FLRT2	fibronectin leucine rich transmembrane protein 2	chr14q24-q32	204359_at	NM_013231
3.10	2.82	0.28	4.94E-02	3.47E-01	---	---	---	1559116_s_at	---
6.74	6.31	0.43	4.94E-02	3.47E-01	FARSA	phenylalanyl-tRNA synthetase, alpha subunit	chr19p13.2	216602_s_at	NM_004461
8.85	7.73	1.12	4.94E-02	3.47E-01	JUNB	jun B proto-oncogene	chr19p13.2	201473_at	NM_002229
2.82	2.41	0.42	4.94E-02	3.47E-01	BMPR1B	bone morphogenetic protein receptor, type IB	chr4q22-q24	210523_at	NM_001203
7.47	6.98	0.49	4.95E-02	3.47E-01	PSMD3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	chr17q12-q21.1	201388_at	NM_002809
6.37	5.68	0.70	4.95E-02	3.47E-01	HCST	hematopoietic cell signal transducer	chr19q13.1	223640_at	NM_001007469 /// NM_014266
7.14	6.62	0.52	4.95E-02	3.47E-01	KIAA2013	KIAA2013	chr1p36.22	224706_at	NM_138346
8.68	8.17	0.51	4.95E-02	3.47E-01	TXN	thioredoxin	chr9q31	208864_s_at	NM_003329
6.63	6.24	0.39	4.95E-02	3.47E-01	C20orf4	chromosome 20 open reading frame 4	chr20pter-q12	218089_at	NM_015511
6.46	5.95	0.51	4.95E-02	3.47E-01	THAP7	THAP domain containing 7	chr22q11.2	218492_s_at	NM_001008695 /// NM_030573
3.04	2.75	0.30	4.95E-02	3.47E-01	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	chr3q29	204210_s_at	NM_005017
4.25	3.73	0.52	4.95E-02	3.47E-01	MXD1	MAX dimerization protein 1	chr2p13-p12	228846_at	NM_002357
5.48	4.91	0.57	4.95E-02	3.47E-01	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	chr9q22.33	226586_at	NM_173551
4.36	3.69	0.67	4.95E-02	3.47E-01	NR0B1	nuclear receptor subfamily 0, group B, member 1	chrXp21.3-p21.2	206644_at	NM_000475
3.78	3.34	0.44	4.95E-02	3.47E-01	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	chr7q21.1	211441_x_at	NM_022820 /// NM_057095 /// NM_057096
9.98	9.54	0.44	4.96E-02	3.47E-01	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	chr17q25	200923_at	NM_005567
2.17	1.96	0.21	4.96E-02	3.47E-01	SCGB2A2	secretoglobin, family 2A, member 2	chr11q13	206378_at	NM_002411

5.34	4.64	0.70	4.96E-02	3.47E-01	IER5L	immediate early response 5-like	chr9q34.11	226552_at	NM_203434
6.37	5.89	0.48	4.96E-02	3.47E-01	TMPO	thymopoietin	chr12q22	224944_at	NM_001032283 /// NM_001032284 /// NM_003276
6.96	6.46	0.51	4.96E-02	3.47E-01	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	chr17p13.1	202725_at	NM_000937
3.96	3.15	0.80	4.96E-02	3.47E-01	---	---	---	222280_at	---
6.39	5.79	0.60	4.96E-02	3.47E-01	TM2D1	TM2 domain containing 1	chr1p31.3	213883_s_at	NM_032027
6.11	5.38	0.73	4.97E-02	3.48E-01	C20orf72	chromosome 20 open reading frame 72	chr20p11.23	225890_at	NM_052865
5.51	4.92	0.59	4.97E-02	3.48E-01	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	chr7q36.3	1558511_s_at	NM_020728
6.57	5.60	0.97	4.97E-02	3.48E-01	SFRS12	splicing factor, arginine/serine-rich 12	chr5q12.3	212721_at	NM_001077199 /// NM_139168
2.88	2.48	0.39	4.99E-02	3.48E-01	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	chr20p13	1554692_at	NM_005116 /// NM_203327
6.30	5.80	0.50	4.99E-02	3.48E-01	C11orf71	chromosome 11 open reading frame 71	chr11q14.2-q14.3	222743_s_at	NM_019021
5.59	5.16	0.43	4.99E-02	3.48E-01	---	---	---	231431_s_at	---
3.41	2.90	0.52	5.00E-02	3.48E-01	LOC100134089 /// PPP2R3B	similar to protein phosphatase 2 (formerly 2A), regulatory subunit B, beta /// protein phosphatase 2 (formerly 2A), regulatory subunit B", beta	chrXp22.33; Yp11.3	219264_s_at	NM_013239 /// NM_199326 /// XM_001720606 /// XR_038350
4.49	3.63	0.86	5.00E-02	3.48E-01	---	---	---	240392_at	---
7.79	7.05	0.74	5.00E-02	3.48E-01	ZSWIM7	zinc finger, SWIM-type containing 7	chr17p12	229119_s_at	NM_001042697 /// NM_001042698
7.99	7.52	0.48	5.00E-02	3.48E-01	C19orf10	chromosome 19 open reading frame 10	chr19p13.3	221739_at	NM_019107
7.41	6.84	0.57	5.00E-02	3.48E-01	DERL1	Der1-like domain family, member 1	chr8q24.13	222543_at	NM_001134671 /// NM_024295
6.52	6.06	0.46	5.00E-02	3.48E-01	GAA	glucosidase, alpha; acid	chr17q25.2-q25.3	202812_at	NM_000152 /// NM_001079803 /// NM_001079804
6.38	5.83	0.55	5.00E-02	3.48E-01	GEMIN7	gem (nuclear organelle) associated protein 7	chr19q13.32	222821_s_at	NM_001007269 /// NM_001007270 /// NM_024707
12.34	12.12	0.22	5.01E-02	3.48E-01	RPLP0	ribosomal protein, large, P0	chr12q24.2	211972_x_at	NM_001002 /// NM_053275
10.83	9.71	1.11	5.01E-02	3.48E-01	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	chr9p13	228498_at	NM_001497
3.95	3.46	0.48	5.01E-02	3.48E-01	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	chr16p11.2	231108_at	NM_004960
6.02	5.41	0.61	5.01E-02	3.48E-01	LOC653506 /// METRNL	similar to meteorin, glial cell differentiation regulator-like /// meteorin, glial cell differentiation regulator-like	chr17q25.3	225955_at	NM_001004431 /// XM_001714390 /// XM_927769
8.35	7.86	0.49	5.02E-02	3.48E-01	HMGN1	high-mobility group nucleosome binding domain 1	chr21q22.3|21q22.2	200943_at	NM_004965
5.27	4.98	0.28	5.02E-02	3.48E-01	ST7	suppression of tumorigenicity 7	chr7q31.1-q31.3	207524_at	NM_018412 /// NM_021908
6.77	5.55	1.22	5.02E-02	3.48E-01	LOC652900 /// SEZ6L2	similar to seizure related 6 homolog (mouse)-like 2 isoform 1 /// seizure related 6 homolog (mouse)-like 2	chr16p11.2	233337_s_at	NM_001114099 /// NM_001114100 /// NM_012410 /// NM_201575 /// XM_001724912
4.77	4.19	0.58	5.02E-02	3.48E-01	CEP76	centrosomal protein 76kDa	chr18p11.21	219311_at	NM_024899

4.40	3.82	0.57	5.02E-02	3.48E-01	IL11RA	interleukin 11 receptor, alpha	chr9p13	1552646_at	NM_004512 /// NM_147162
2.69	2.34	0.35	5.02E-02	3.49E-01	LOC553158 /// PRR5	PRR5-ARHGAP8 fusion /// proline rich 5 (renal)	chr22q13	1555162_at	NM_001017528 /// NM_001017529 /// NM_001017530 /// NM_015366 /// NM_181333 /// NM_181334
2.33	2.02	0.31	5.02E-02	3.49E-01	---	---	---	215475_at	---
6.85	6.09	0.76	5.03E-02	3.49E-01	CORO1A	coronin, actin binding protein, 1A	chr16p11.2	209083_at	NM_007074
8.81	7.98	0.84	5.03E-02	3.49E-01	RHOBTB3	Rho-related BTB domain containing 3	chr5q15	225202_at	NM_014899
5.94	5.36	0.57	5.03E-02	3.49E-01	ORC5L	origin recognition complex, subunit 5-like (yeast)	chr7q22.1	204957_at	NM_002553 /// NM_181747
9.12	8.49	0.63	5.03E-02	3.49E-01	RAB34	RAB34, member RAS oncogene family	chr17q11.2	1555630_a_at	NM_031934
4.89	4.44	0.45	5.03E-02	3.49E-01	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	chr19p13.3	227400_at	NM_002501
8.60	8.05	0.55	5.04E-02	3.49E-01	MAP2K2	mitogen-activated protein kinase kinase 2	chr19p13.3	202424_at	NM_030662
2.42	2.18	0.25	5.04E-02	3.49E-01	---	---	---	1559524_at	---
7.81	7.34	0.47	5.04E-02	3.49E-01	C6orf108	chromosome 6 open reading frame 108	chr6p21.1	204238_s_at	NM_006443 /// NM_199184
4.72	4.08	0.64	5.04E-02	3.49E-01	SFXN2	sideroflexin 2	chr10q24.32	227560_at	NM_178858
4.02	3.39	0.63	5.04E-02	3.49E-01	C2orf68	chromosome 2 open reading frame 68	chr2p11.2	238768_at	NM_001013649
5.61	4.78	0.83	5.04E-02	3.49E-01	SMAD7	SMAD family member 7	chr18q21.1	204790_at	NM_005904
8.27	7.85	0.42	5.05E-02	3.49E-01	NENF	neuron derived neurotrophic factor	chr1q32.3	218407_x_at	NM_013349
4.54	4.25	0.30	5.05E-02	3.49E-01	---	---	---	240698_s_at	---
6.04	5.56	0.48	5.05E-02	3.49E-01	TMEM143	transmembrane protein 143	chr19q13.32	222905_s_at	NM_018273
6.31	5.95	0.36	5.05E-02	3.49E-01	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	chr7q31.1-q31.33	222561_at	NM_018697
7.16	6.76	0.40	5.05E-02	3.49E-01	PFDN6	prefoldin subunit 6	chr6p21.3	233588_x_at	NM_014260
7.63	7.06	0.56	5.05E-02	3.49E-01	SLC35B2	solute carrier family 35, member B2	chr6p12.1-p11.2	224716_at	NM_178148
6.49	5.97	0.52	5.05E-02	3.49E-01	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	chr11q13	206782_s_at	NM_005528
3.96	3.11	0.86	5.06E-02	3.49E-01	NAT11	N-acetyltransferase 11	chr11q13.1	222369_at	NM_024771
5.34	4.24	1.10	5.06E-02	3.49E-01	HBEGF	heparin-binding EGF-like growth factor	chr5q23	203821_at	NM_001945
8.96	8.50	0.46	5.06E-02	3.49E-01	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	chr7p22.1	200700_s_at	NM_001100603 /// NM_006854
10.11	9.70	0.41	5.07E-02	3.49E-01	PFN1	profilin 1	chr17p13.3	200634_at	NM_005022
7.31	6.48	0.83	5.07E-02	3.49E-01	FAM174A	family with sequence similarity 174, member A	chr5q21.1	226752_at	NM_198507
7.32	6.76	0.56	5.07E-02	3.49E-01	ZDHHC5	zinc finger, DHHC-type containing 5	chr11q12.1	224858_at	NM_015457
8.43	7.91	0.52	5.07E-02	3.49E-01	LAPTM4B	lysosomal protein transmembrane 4 beta	chr8q22.1	208029_s_at	NM_018407
6.87	6.39	0.48	5.07E-02	3.49E-01	RBM10	RNA binding motif protein 10	chrXp11.23	215089_s_at	NM_005676 /// NM_152856
2.50	2.02	0.48	5.07E-02	3.49E-01	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	chr6q22	232737_s_at	NM_005021
5.57	5.14	0.43	5.08E-02	3.50E-01	TELO2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	chr16p13.3	209528_s_at	NM_016111
6.05	5.69	0.37	5.08E-02	3.50E-01	MCAM	melanoma cell adhesion molecule	chr11q23.3	211042_x_at	NM_006500
5.99	5.47	0.51	5.09E-02	3.50E-01	CHMP1B	chromatin modifying protein 1B	chr18p11.21	218177_at	NM_020412
5.77	5.40	0.37	5.09E-02	3.50E-01	RRP1B	ribosomal RNA processing 1 homolog B (S. cerevisiae)	chr21q22.3	212846_at	NM_015056
10.02	9.66	0.36	5.09E-02	3.50E-01	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	chr7p21.3	217773_s_at	NM_002489
2.77	2.44	0.32	5.09E-02	3.50E-01	---	---	---	230267_at	---
6.99	6.61	0.39	5.09E-02	3.50E-01	PANK2	pantothenate kinase 2	chr20p13	218809_at	NM_024960 /// NM_153638 /// NM_153640
9.94	9.67	0.27	5.09E-02	3.50E-01	NDUFB8 /// SEC31B	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa /// SEC31 homolog B (S. cerevisiae)	chr10q23.2-q23.33 /// chr10q24.31	201226_at	NM_005004 /// NM_015490
7.98	7.55	0.42	5.09E-02	3.50E-01	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	chr6q12	217249_x_at	NM_001865
8.17	7.86	0.30	5.10E-02	3.50E-01	MFF	mitochondrial fission factor	chr2q36.3	222832_s_at	NM_020194
9.50	9.17	0.32	5.10E-02	3.50E-01	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	chr17q21.3	200758_s_at	NM_003204
4.22	3.64	0.59	5.11E-02	3.50E-01	ICAM1	intercellular adhesion molecule 1	chr19p13.3-p13.2	202638_s_at	NM_000201
6.15	5.73	0.42	5.11E-02	3.50E-01	ZNF689	zinc finger protein 689	chr16p11.2	227294_at	NM_138447
6.75	5.86	0.89	5.11E-02	3.51E-01	FLRT2	fibronectin leucine rich transmembrane protein 2	chr14q24-q32	204358_s_at	NM_013231
7.09	6.71	0.38	5.11E-02	3.51E-01	COQ4	coenzyme Q4 homolog (S. cerevisiae)	chr9q34.11	218328_at	NM_016035
5.48	4.63	0.85	5.12E-02	3.51E-01	BCL9L	B-cell CLL/lymphoma 9-like	chr11q23.3	228065_at	NM_182557
4.43	4.07	0.36	5.13E-02	3.51E-01	SRCAP	Snf2-related CREBBP activator protein	chr16p11.2	38766_at	NM_006662

3.42	2.97	0.45	5.13E-02	3.52E-01	KHDRBS2	KH domain containing, RNA binding, signal transduction associated 2	chr6q11.1	215527_at	NM_152688																			
6.16	5.66	0.49	5.13E-02	3.52E-01	KLHL29	kelch-like 29 (Drosophila)	chr2p24.1	229310_at	XM_001717454 /// XM_001717533 /// XM_940375																			
8.58	8.10	0.48	5.14E-02	3.52E-01	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	chr1p36.13-q31.3	218389_s_at	NM_001077628 /// NM_016022																			
5.61	5.13	0.48	5.14E-02	3.52E-01	DND1	dead end homolog 1 (zebrafish)	chr5q31.3	57739_at	NM_194249																			
5.99	4.92	1.07	5.14E-02	3.52E-01	PHF20L1	PHD finger protein 20-like 1	chr8q24.22	226942_at	NM_016018 /// NM_032205 /// NM_198513																			
3.30	2.85	0.45	5.14E-02	3.52E-01	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	chr10q22	214322_at	NM_001222 /// NM_172169 /// NM_172170 /// NM_172171 /// NM_172173																			
3.28	2.62	0.66	5.14E-02	3.52E-01	CSAD	cysteine sulfinic acid decarboxylase	chr12q13.11-q14.3	1568620_at	NM_015989																			
4.23	3.71	0.52	5.15E-02	3.52E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	202547_s_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735																			
3.06	2.69	0.37	5.15E-02	3.52E-01	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	chr16q22.1	203578_s_at	NM_001076785 /// NM_003983																			
4.50	3.77	0.73	5.15E-02	3.52E-01	MTAP	methylthioadenosine phosphorylase	chr9p21	231984_at	NM_002451																			
4.44	3.95	0.50	5.16E-02	3.52E-01	---	---	---	1566144_at	---																			
7.92	7.42	0.50	5.16E-02	3.52E-01	ABHD14B	abhydrolase domain containing 14B	chr3p21.1	224821_at	NM_032750																			
12.59	12.37	0.22	5.16E-02	3.52E-01	RPS16	ribosomal protein S16	chr19q13.1	226131_s_at	NM_001020																			
7.23	6.49	0.74	5.17E-02	3.52E-01	PNMAL1	PNMA-like 1	chr19q13.32	218824_at	NM_001103149 /// NM_018215																			
7.29	6.76	0.53	5.17E-02	3.52E-01	TPD52L2	tumor protein D52-like 2	chr20q13.2-q13.3	201379_s_at	NM_003288 /// NM_199359 /// NM_199360 /// NM_199361 /// NM_199362 /// NM_199363																			
5.59	4.97	0.62	5.17E-02	3.52E-01	EFNB2	ephrin-B2	chr13q33	202669_s_at	NM_004093																			
4.55	3.93	0.62	5.17E-02	3.52E-01	C16orf52	chromosome 16 open reading frame 52	chr16p12.1	230721_at	NR_024104 /// XM_001126460 /// XM_001132387 /// XM_001724381																			
5.49	4.95	0.54	5.17E-02	3.52E-01	STEAP3	STEAP family member 3	chr2q14.2	218424_s_at	NM_001008410 /// NM_018234 /// NM_182915																			
3.49	3.04	0.45	5.17E-02	3.52E-01	---	---	---	235407_at	---																			
4.73	4.25	0.48	5.18E-02	3.53E-01	C9orf25	chromosome 9 open reading frame 25	chr9p13.3	225146_at	NM_147202																			
2.64	2.31	0.33	5.18E-02	3.53E-01	C2orf68	chromosome 2 open reading frame 68	chr2p11.2	65472_at	NM_001013649																			

7.11	6.43	0.68	5.19E-02	3.53E-01	LOC100128443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	chr5q12.3	225611_at	NM_015183 /// NM_198828 /// XM_001720470 /// XM_001720479 /// XM_001722488																				
6.69	6.20	0.49	5.19E-02	3.53E-01	MAD2L1BP	MAD2L1 binding protein	chr6p21.1	203094_at	NM_001003690 /// NM_014628																				
2.73	2.31	0.42	5.19E-02	3.53E-01	LOC441528	hypothetical protein LOC441528	chrXp22.33	1558045_a_at	XR_041386																				
5.50	5.05	0.45	5.19E-02	3.53E-01	TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	chr22q13	213634_s_at	NM_018006																				
4.02	3.28	0.74	5.19E-02	3.53E-01	---	---	---	240467_at	---																				
2.71	2.44	0.27	5.20E-02	3.53E-01	ZNF131	Zinc finger protein 131	chr5p12-p11	232070_at	NM_003432																				
5.77	5.40	0.37	5.20E-02	3.53E-01	METAP1	methionyl aminopeptidase 1	chr4q23	212673_at	NM_015143																				
6.90	6.16	0.75	5.20E-02	3.53E-01	C6orf145	chromosome 6 open reading frame 145	chr6p25.2	212923_s_at	NM_183373																				
2.73	2.48	0.25	5.20E-02	3.53E-01	C7orf46	chromosome 7 open reading frame 46	chr7p15.3	228600_x_at	NM_001127364 /// NM_001127365 /// NM_199136																				
2.73	2.24	0.49	5.20E-02	3.53E-01	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	chr3p21.31	1556144_at	NM_014966 /// NM_138615																				
6.99	6.41	0.59	5.21E-02	3.54E-01	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	chr12q13.2	223420_at	NM_032364																				
4.84	4.13	0.71	5.21E-02	3.54E-01	ARSD	arylsulfatase D	chrXp22.3	232423_at	NM_001669 /// NM_009589																				
4.63	4.08	0.55	5.21E-02	3.54E-01	LOC440957	similar to CG32736-PA	chr3p21.1	238207_at	NM_001124767 /// XM_001716881 /// XM_001717970 /// XM_001718706																				
8.37	7.53	0.84	5.21E-02	3.54E-01	DKK3	dickkopf homolog 3 (Xenopus laevis)	chr11p15.2	214247_s_at	NM_001018057 /// NM_013253 /// NM_015881																				
6.95	6.25	0.70	5.21E-02	3.54E-01	PSMG4	proteasome (prosome, macropain) assembly chaperone 4	chr6p25.2	228217_s_at	NM_001128591 /// NM_001128592 /// XR_017743 /// XR_017905 /// XR_041314																				
6.24	5.71	0.52	5.22E-02	3.54E-01	RUFY3	RUN and FYVE domain containing 3	chr4q13.3	213437_at	NM_001037442 /// NM_001130709 /// NM_014961																				
5.60	5.20	0.40	5.22E-02	3.54E-01	CSF3R	colony stimulating factor 3 receptor (granulocyte)	chr1p35-p34.3	1553297_a_at	NM_000760 /// NM_156038 /// NM_156039 /// NM_172313																				
8.19	7.57	0.62	5.22E-02	3.54E-01	TSPAN31	tetraspanin 31	chr12q13.3	203227_s_at	NM_005981																				
4.89	4.01	0.88	5.22E-02	3.54E-01	OSMR	oncostatin M receptor	chr5p13.1	1554008_at	NM_003999																				
2.78	2.48	0.30	5.22E-02	3.54E-01	---	---	---	1566728_at	---																				
7.19	6.60	0.59	5.23E-02	3.54E-01	SYVN1	synovial apoptosis inhibitor 1, synoviolin	chr11q13	225090_at	NM_032431 /// NM_172230																				

5.89	5.32	0.58	5.23E-02	3.54E-01	BRWD1	bromodomain and WD repeat domain containing 1	chr21q22.2	225446_at	NM_001007246 /// NM_018963 /// NM_033656																				
5.03	4.13	0.89	5.23E-02	3.54E-01	SFRP4	secreted frizzled-related protein 4	chr7p14.1	204051_s_at	NM_003014																				
6.14	5.73	0.41	5.23E-02	3.54E-01	RP11-529I10.4	deleted in a mouse model of primary ciliary dyskinesia	chr10q24.32	1553976_a_at	NM_015448																				
7.88	7.08	0.80	5.24E-02	3.54E-01	ING2	inhibitor of growth family, member 2	chr4q35.1	205981_s_at	NM_001564																				
4.97	4.37	0.60	5.24E-02	3.54E-01	C1orf213	chromosome 1 open reading frame 213	chr1p36.12	229086_at	NM_001008896 /// NM_138479																				
2.44	2.18	0.26	5.24E-02	3.55E-01	TPP2	tripeptidyl peptidase II	chr13q32-q33	1569856_at	NM_003291																				
5.08	4.55	0.53	5.25E-02	3.55E-01	KANK3	KN motif and ankyrin repeat domains 3	chr19p13.2	213715_s_at	NM_198471																				
4.74	4.29	0.46	5.25E-02	3.55E-01	ARIH2	ariadne homolog 2 (Drosophila)	chr3p21.2-p21.3	201228_s_at	NM_006321																				
7.22	6.63	0.59	5.26E-02	3.55E-01	BAT4	HLA-B associated transcript 4	chr6p21.3	225472_at	NM_033177																				
5.07	4.57	0.50	5.26E-02	3.55E-01	C19orf52	chromosome 19 open reading frame 52	chr19p13.2	231901_at	NM_138358																				
5.82	5.20	0.62	5.26E-02	3.55E-01	ANAPC2	anaphase promoting complex subunit 2	chr9q34.3	218555_at	NM_013366																				
7.46	7.12	0.34	5.26E-02	3.55E-01	VPS11	vacuolar protein sorting 11 homolog (S. cerevisiae)	chr11q23	203292_s_at	NM_021729																				
6.80	6.32	0.47	5.26E-02	3.55E-01	MED16	mediator complex subunit 16	chr19p13.3	43544_at	NM_005481																				
6.71	6.26	0.45	5.27E-02	3.55E-01	PET112L	PET112-like (yeast)	chr4q27-q28	204300_at	NM_004564																				
7.34	7.01	0.32	5.27E-02	3.55E-01	STX16	syntaxin 16	chr20q13.32	221499_s_at	NM_001001433 /// NM_003763																				
2.57	2.25	0.32	5.27E-02	3.55E-01	SNAP25	Synaptosomal-associated protein, 25kDa	chr20p12-p11.2	1556629_a_at	NM_003081 /// NM_130811																				
8.51	8.05	0.46	5.27E-02	3.55E-01	IRS2	insulin receptor substrate 2	chr13q34	209184_s_at	NM_003749																				
4.35	3.79	0.56	5.27E-02	3.55E-01	---	---	---	221590_s_at	---																				
3.93	3.09	0.84	5.28E-02	3.55E-01	---	---	---	228121_at	---																				
5.45	4.99	0.46	5.28E-02	3.55E-01	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	chr10q26.13	226247_at	NM_001001974 /// NM_021622																				
2.39	2.05	0.34	5.28E-02	3.55E-01	MPHOSPH6	M-phase phosphoprotein 6	chr16q23.3	1554906_a_at	NM_005792																				
3.58	3.27	0.31	5.28E-02	3.55E-01	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	chr8p21	1552648_a_at	NM_003844																				
2.75	2.27	0.49	5.28E-02	3.55E-01	LOC256021	hypothetical protein LOC256021	chr12q21.33	1564150_a_at	---																				
6.63	5.96	0.67	5.29E-02	3.55E-01	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	chr17p13.3	209003_at	NM_003562																				
2.47	2.16	0.31	5.29E-02	3.55E-01	PGM5	phosphoglucomutase 5	chr9q13	1554560_at	NM_021965																				
4.34	3.94	0.40	5.29E-02	3.55E-01	EXOC3	exocyst complex component 3	chr5p15.33	228847_at	NM_007277																				
3.91	3.52	0.39	5.29E-02	3.55E-01	C10orf76	chromosome 10 open reading frame 76	chr10q24.32	1568733_at	NM_024541																				
8.95	8.50	0.45	5.29E-02	3.55E-01	TMED9	transmembrane emp24 protein transport domain containing 9	chr5q35.3	205812_s_at	NM_017510																				
4.29	3.93	0.36	5.29E-02	3.55E-01	C14orf128	chromosome 14 open reading frame 128	chr14q12	228889_at	XR_040876 /// XR_040877 /// XR_040878																				
4.34	3.77	0.57	5.30E-02	3.55E-01	PCIF1	PDX1 C-terminal inhibiting factor 1	chr20q13.12	222044_at	NM_022104																				
5.92	4.80	1.12	5.30E-02	3.55E-01	---	---	---	235392_at	---																				
7.72	7.29	0.42	5.31E-02	3.55E-01	TRIM4	tripartite motif-containing 4	chr7q22-q31.1	223384_s_at	NM_033017 /// NM_033091																				
4.57	4.10	0.47	5.31E-02	3.55E-01	---	---	---	238032_at	---																				
6.99	6.48	0.51	5.31E-02	3.55E-01	TRADD	TNFRSF1A-associated via death domain	chr16q22	1729_at	NM_003789																				
7.15	6.60	0.55	5.31E-02	3.56E-01	MRPL4	mitochondrial ribosomal protein L4	chr19p13.2	223743_s_at	NM_015956 /// NM_146387 /// NM_146388																				
6.69	6.18	0.50	5.31E-02	3.56E-01	NT5C1B /// RDH14	5'-nucleotidase, cytosolic IB /// retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	chr2p24.2	222203_s_at	NM_001002006 /// NM_020905 /// NM_033253																				
2.57	2.34	0.22	5.31E-02	3.56E-01	---	---	---	241456_at	---																				
2.80	2.47	0.34	5.31E-02	3.56E-01	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	chr6q23.2	235050_at	NM_145176																				
3.72	3.44	0.28	5.31E-02	3.56E-01	CXorf34	chromosome X open reading frame 34	chrXq22.1	1554279_a_at	NM_024917																				
3.73	2.87	0.86	5.31E-02	3.56E-01	---	---	---	241464_s_at	---																				

5.25	4.74	0.51	5.32E-02	3.56E-01	BCOR	BCL6 co-repressor	chrXp21.2-p11.4	219433_at	NM_001123383 /// NM_001123384 /// NM_001123385 /// NM_001130139 /// NM_017745 /// NM_020926																				
4.61	3.94	0.67	5.32E-02	3.56E-01	LOC440348	similar to nuclear pore complex interacting protein	chr16q22.3	221992_at	NM_001018059																				
3.24	2.75	0.49	5.32E-02	3.56E-01	MAP3K14	mitogen-activated protein kinase kinase kinase 14	chr17q21	205192_at	NM_003954																				
5.09	4.28	0.81	5.32E-02	3.56E-01	CRIPAK	cysteine-rich PAK1 inhibitor	chr4p16.3	228318_s_at	NM_175918																				
5.60	5.02	0.58	5.33E-02	3.56E-01	SSH2	slingshot homolog 2 (Drosophila)	chr17q11.2	226080_at	NM_033389																				
6.23	5.65	0.58	5.33E-02	3.56E-01	C7orf26	chromosome 7 open reading frame 26	chr7p22.1	219261_at	NM_024067																				
7.82	7.35	0.47	5.33E-02	3.56E-01	FBXL7	F-box and leucine-rich repeat protein 7	chr5p15.1	213249_at	NM_012304																				
6.51	6.14	0.37	5.33E-02	3.56E-01	C17orf71	chromosome 17 open reading frame 71	chr17q22	218514_at	NM_018149																				
3.63	3.34	0.29	5.34E-02	3.56E-01	GTF2IRD2 /// GTF2IRD2B /// LOC100133748	GTF2I repeat domain containing 2 /// GTF2I repeat domain containing 2B /// similar to GTF2IRD2 protein	chr7q11.23	215569_at	NM_001003795 /// NM_173537 /// XM_001717948 /// XM_001721289 /// XM_001722115																				
3.79	3.15	0.64	5.34E-02	3.56E-01	---	---	---	238299_at	---																				
6.76	6.31	0.45	5.34E-02	3.56E-01	C22orf30	chromosome 22 open reading frame 30	chr22q12.2-q12.3	1558097_at	NM_173566																				
4.64	3.79	0.86	5.34E-02	3.56E-01	NALCN	sodium leak channel, non-selective	chr13q32.3	228608_at	NM_052867																				
2.42	2.17	0.25	5.34E-02	3.56E-01	---	---	---	1556226_at	---																				
9.72	9.25	0.47	5.34E-02	3.56E-01	UQCR	ubiquinol-cytochrome c reductase, 6.4kDa subunit	chr19p13.3	202090_s_at	NM_006830																				
3.58	3.00	0.58	5.34E-02	3.56E-01	---	---	---	239448_at	---																				
3.09	2.57	0.52	5.34E-02	3.56E-01	---	---	---	221973_at	---																				
5.93	5.39	0.54	5.35E-02	3.56E-01	PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	chr9p13.3	209998_at	NM_032634 /// NM_152850																				
6.90	6.19	0.71	5.35E-02	3.56E-01	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	chr5q33.2	212256_at	NM_017540 /// NM_198321																				
2.53	2.26	0.27	5.35E-02	3.56E-01	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	chr3q24-q25	234940_s_at	NM_024621																				
3.76	3.13	0.62	5.35E-02	3.56E-01	ZBED1	zinc finger, BED-type containing 1	chrXp22.33;Yp11	1554821_a_at	NM_004729																				
5.44	4.36	1.08	5.36E-02	3.56E-01	IMMP1L	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	chr11p13	229025_s_at	NM_144981																				
3.22	2.89	0.33	5.36E-02	3.56E-01	PREP	Prolyl endopeptidase	chr6q22	229644_at	NM_002726																				
7.05	6.40	0.65	5.36E-02	3.56E-01	RBM16	RNA binding motif protein 16	chr6q25.1-q25.3	203250_at	NM_014892																				
4.69	3.85	0.84	5.37E-02	3.57E-01	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	chr1q25	240440_at	NM_030769																				
6.60	6.15	0.44	5.37E-02	3.57E-01	PCGF2	polycomb group ring finger 2	chr17q12	213551_x_at	NM_007144																				
11.77	11.20	0.58	5.37E-02	3.57E-01	MT2A	metallothionein 2A	chr16q13	212185_x_at	NM_005953																				
3.27	2.97	0.30	5.38E-02	3.57E-01	ZNF589	zinc finger protein 589	chr3p21	210062_s_at	NM_016089																				
5.27	4.62	0.65	5.38E-02	3.57E-01	BIRC7	baculoviral IAP repeat-containing 7	chr20q13.3	220451_s_at	NM_022161 /// NM_139317																				
7.11	6.40	0.72	5.38E-02	3.57E-01	CALHM2	calcium homeostasis modulator 2	chr10pter-q26.12	57715_at	NM_015916																				
3.06	2.78	0.28	5.38E-02	3.57E-01	LPCAT2	lysophosphatidylcholine acyltransferase 2	chr16q12.2	222833_at	NM_017839																				
6.83	6.36	0.47	5.39E-02	3.57E-01	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	chrXq28	204928_s_at	NM_019848																				
2.51	2.20	0.31	5.39E-02	3.57E-01	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	chr1p31.1-p22.1	230465_at	NM_001134492 /// NM_012262																				
6.04	5.50	0.55	5.39E-02	3.57E-01	DNAL4	dynein, axonemal, light chain 4	chr22q13.1	204008_at	NM_005740																				
2.41	2.12	0.29	5.39E-02	3.57E-01	---	---	---	236242_at	---																				
2.73	2.45	0.29	5.40E-02	3.57E-01	---	---	---	227754_at	---																				
5.58	5.13	0.44	5.40E-02	3.57E-01	UBTF	upstream binding transcription factor, RNA polymerase I	chr17q21.3	214881_s_at	NM_001076683 /// NM_001076684 /// NM_014233																				
7.85	7.34	0.50	5.40E-02	3.57E-01	EXOSC4	exosome component 4	chr8q24.3	58696_at	NM_019037																				
6.09	5.33	0.76	5.40E-02	3.57E-01	GLIPR2	GLI pathogenesis-related 2	chr9p13-p12	225604_s_at	NM_022343																				

2.35	2.05	0.30	5.40E-02	3.57E-01	C3orf65	chromosome 3 open reading frame 65	chr3q27.2	1562694_at	NM_001039788
2.32	2.01	0.31	5.40E-02	3.57E-01	---	---	---	1556097_at	---
6.98	6.45	0.53	5.40E-02	3.57E-01	---	---	---	226348_at	---
7.77	7.31	0.46	5.41E-02	3.57E-01	ADIPOR1	adiponectin receptor 1	chr1p36.13-q41	217748_at	NM_001127687 /// NM_015999
2.12	1.91	0.21	5.41E-02	3.57E-01	---	---	---	1563771_a_at	---
4.66	4.11	0.55	5.41E-02	3.57E-01	LAMA5	Laminin, alpha 5	chr20q13.2-q13.3	229570_at	NM_005560
5.81	5.21	0.60	5.41E-02	3.57E-01	GORASP1	golgi reassembly stacking protein 1, 65kDa	chr3p22-p21.33	215749_s_at	NM_031899
6.38	5.90	0.48	5.41E-02	3.57E-01	DUSP11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	chr2p13.2	202703_at	NM_003584
3.01	2.52	0.48	5.42E-02	3.57E-01	TTC18	tetratricopeptide repeat domain 18	chr10q22.2	229169_at	NM_145170
9.20	8.92	0.28	5.42E-02	3.57E-01	SNRPE	small nuclear ribonucleoprotein polypeptide E	chr1q32	203316_s_at	NM_003094
7.23	5.70	1.53	5.42E-02	3.57E-01	DACH1	dachshund homolog 1 (Drosophila)	chr13q22	205471_s_at	NM_004392 /// NM_080759 /// NM_080760
2.66	2.37	0.29	5.42E-02	3.57E-01	LOC100130360	Hypothetical protein LOC100130360	chr6p22.3	243179_at	XM_001717221 /// XM_001718619 /// XM_001718724
6.14	5.55	0.59	5.43E-02	3.57E-01	FLJ36031	hypothetical protein FLJ36031	chr7q22.3	229521_at	NM_175884
3.07	2.49	0.58	5.43E-02	3.57E-01	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	chr20q13.2	205286_at	NM_003222
8.31	7.38	0.93	5.43E-02	3.57E-01	IFI27	interferon, alpha-inducible protein 27	chr14q32	202411_at	NM_001130080 /// NM_005532
4.74	4.45	0.30	5.43E-02	3.57E-01	NRF1	nuclear respiratory factor 1	chr7q32	204652_s_at	NM_001040110 /// NM_005011
7.85	7.46	0.39	5.43E-02	3.57E-01	ZNF207	zinc finger protein 207	chr17q11.2	200829_x_at	NM_001032293 /// NM_001098507 /// NM_003457
2.78	2.41	0.38	5.43E-02	3.57E-01	CDKN2AIPNL	CDKN2A interacting protein N-terminal like	chr5q31.1	1554348_s_at	NM_080656
2.86	2.56	0.31	5.43E-02	3.57E-01	---	---	---	238155_at	---
5.79	5.21	0.58	5.43E-02	3.57E-01	CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	chr6p22.3	212554_at	NM_006366
7.29	6.92	0.37	5.43E-02	3.57E-01	HNRNPL	heterogeneous nuclear ribonucleoprotein L	chr19q13.2	35201_at	NM_001005335 /// NM_001533
4.41	3.79	0.63	5.44E-02	3.57E-01	ANKRD16	ankyrin repeat domain 16	chr10p15.1	229058_at	NM_001009941 /// NM_001009942 /// NM_001009943 /// NM_019046
8.48	7.85	0.63	5.44E-02	3.57E-01	C14orf124	chromosome 14 open reading frame 124	chr14q12	213398_s_at	NM_020195
6.05	5.68	0.37	5.44E-02	3.58E-01	BTD	biotinidase	chr3p25	204167_at	NM_000060
4.74	4.32	0.41	5.45E-02	3.58E-01	GNB5	guanine nucleotide binding protein (G protein), beta 5	chr15q21.2	211871_x_at	NM_006578 /// NM_016194
5.53	4.85	0.69	5.45E-02	3.58E-01	---	---	---	213448_at	---
3.26	2.76	0.50	5.45E-02	3.58E-01	ZFAND5	Zinc finger, AN1-type domain 5	chr9q13-q21	229368_s_at	NM_001102420 /// NM_001102421 /// NM_006007
8.00	7.05	0.95	5.45E-02	3.58E-01	PID1	phosphotyrosine interaction domain containing 1	chr2q36.3	219093_at	NM_001100818 /// NM_017933
7.82	7.21	0.61	5.45E-02	3.58E-01	CRTAP	cartilage associated protein	chr3p22.3	1554464_a_at	NM_006371
4.77	4.01	0.76	5.45E-02	3.58E-01	---	---	---	238477_at	---
7.95	7.48	0.47	5.46E-02	3.58E-01	TMEM214	transmembrane protein 214	chr2p23.3	217899_at	NM_001083590 /// NM_017727

4.19	3.80	0.39	5.46E-02	3.58E-01	RFC5	replication factor C (activator 1) 5, 36.5kDa	chr12q24.23	203210_s_at	NM_001130112 /// NM_001130113 /// NM_007370 /// NM_181578																			
3.93	3.38	0.55	5.46E-02	3.58E-01	C20orf59	chromosome 20 open reading frame 59	chr20q13.33	219559_at	NM_022082																			
5.40	4.86	0.54	5.46E-02	3.58E-01	CSNK1E	Casein kinase 1, epsilon	chr22q13.1	222015_at	NM_001894 /// NM_152221																			
7.13	6.59	0.54	5.46E-02	3.58E-01	BMP1	bone morphogenetic protein 1	chr8p21.3	202701_at	NM_001199 /// NM_006128 /// NM_006129																			
7.05	6.22	0.83	5.46E-02	3.58E-01	ZNRF3	zinc and ring finger 3	chr22q12.1	226360_at	NM_032173																			
5.41	4.91	0.49	5.46E-02	3.58E-01	ZNF691	zinc finger protein 691	chr1p34.2	232780_s_at	NM_015911																			
3.68	3.33	0.35	5.47E-02	3.58E-01	---	---	---	243626_at	---																			
3.17	2.83	0.34	5.47E-02	3.58E-01	---	---	---	1569807_at	---																			
6.95	6.30	0.65	5.48E-02	3.58E-01	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	chr7q36.1	222415_at	NM_170606																			
9.40	8.91	0.48	5.48E-02	3.58E-01	SAT1	spermidine/spermine N1-acetyltransferase 1	chrXp22.1	213988_s_at	NM_002970																			
8.15	7.50	0.65	5.48E-02	3.58E-01	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	chr13q11-q12	227013_at	NM_014572																			
8.15	7.83	0.32	5.48E-02	3.58E-01	LOC391833 /// LOC728791 /// LOC730187 /// RPS10	similar to hCG2000485 /// similar to ribosomal protein S10 /// similar to ribosomal protein S10 /// ribosomal protein S10	chr2p14 /// chr3q13.31 /// chr5q31.1 /// chr6p21.31	216505_x_at	NM_001014 /// XR_015547 /// XR_015651 /// XR_038633 /// XR_038708 /// XR_038743 /// XR_038761 /// XR_042354 /// XR_042409 /// XR_042419																			
6.95	6.47	0.48	5.49E-02	3.58E-01	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	chr16q21-q23	221566_s_at	NM_003946																			
10.17	9.69	0.48	5.49E-02	3.58E-01	DYNLL1	dynein, light chain, LC8-type 1	chr12q24.23	200703_at	NM_001037494 /// NM_001037495 /// NM_003746																			
5.46	4.99	0.47	5.49E-02	3.58E-01	MARK3	MAP/microtubule affinity-regulating kinase 3	chr14q32.3	202569_s_at	NM_001128918 /// NM_001128919 /// NM_001128920 /// NM_001128921 /// NM_002376																			
4.88	4.02	0.86	5.49E-02	3.58E-01	VEGFA	vascular endothelial growth factor A	chr6p12	211527_x_at	NM_001025366 /// NM_001025367 /// NM_001025368 /// NM_001025369 /// NM_001025370 /// NM_001033756 /// NM_003376																			
7.90	7.49	0.41	5.50E-02	3.58E-01	MRPL12	mitochondrial ribosomal protein L12	chr17q25	203931_s_at	NM_002949																			
2.28	2.01	0.28	5.50E-02	3.59E-01	CCDC150	coiled-coil domain containing 150	chr2q33.1	232398_at	NM_001080539																			
5.38	4.63	0.76	5.50E-02	3.59E-01	HDAC4	histone deacetylase 4	chr2q37.3	204225_at	NM_006037																			

3.47	3.17	0.30	5.50E-02	3.59E-01	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	chr22q13.1	235827_at	NM_006116 /// NM_153497																				
3.20	2.91	0.29	5.50E-02	3.59E-01	RP6-213H19.1	serine/threonine protein kinase MST4	chrXq26.2	218499_at	NM_001042452 /// NM_001042453 /// NM_016542																				
3.38	2.80	0.58	5.50E-02	3.59E-01	---	---	---	238766_at	---																				
6.36	5.74	0.62	5.52E-02	3.59E-01	---	---	---	241600_at	---																				
8.59	6.39	2.20	5.52E-02	3.59E-01	NR4A2	nuclear receptor subfamily 4, group A, member 2	chr2q22-q23	204621_s_at	NM_006186 /// NM_173171 /// NM_173172 /// NM_173173																				
7.74	7.31	0.43	5.52E-02	3.59E-01	WDR68	WD repeat domain 68	chr17q23.3	224748_at	NM_005828																				
6.89	5.99	0.91	5.52E-02	3.59E-01	SIX5	SIX homeobox 5	chr19q13.32	229009_at	NM_175875																				
2.81	2.57	0.24	5.53E-02	3.59E-01	NEK6	NIMA (never in mitosis gene a)-related kinase 6	chr9q33.3-q34.11	237761_at	NM_014397																				
4.63	4.18	0.45	5.53E-02	3.59E-01	LOC552889	hypothetical LOC552889	chr12q21	212113_at	NR_015371 /// XR_040493 /// XR_040494 /// XR_040495																				
4.07	3.50	0.57	5.53E-02	3.59E-01	ATP8B1	ATPase, class I, type 8B, member 1	chr18q21-q22|18q21.31	226302_at	NM_005603																				
2.80	2.53	0.28	5.53E-02	3.59E-01	CNR1	cannabinoid receptor 1 (brain)	chr6q14-q15	207940_x_at	NM_016083 /// NM_033181																				
5.31	5.01	0.30	5.53E-02	3.59E-01	RHEB	Ras homolog enriched in brain	chr7q36	227633_at	NM_005614																				
8.05	7.43	0.62	5.53E-02	3.59E-01	ZNF410	zinc finger protein 410	chr14q24.3	209944_at	NM_021188																				
5.02	4.09	0.93	5.53E-02	3.59E-01	ATF3	activating transcription factor 3	chr1q32.3	1554980_a_at	NM_001030287 /// NM_001040619 /// NM_001674 /// NM_004024																				
6.48	6.05	0.43	5.54E-02	3.59E-01	C14orf109	chromosome 14 open reading frame 109	chr14q32.12	213246_at	NM_001098621 /// NM_015676																				
2.92	2.45	0.47	5.54E-02	3.60E-01	SNHG10	small nucleolar RNA host gene 10 (non-protein coding)	chr14q32.13	244786_at	NR_001459 /// NR_003138																				
7.21	6.78	0.43	5.54E-02	3.60E-01	HPRT1	hypoxanthine phosphoribosyltransferase 1	chrXq26.1	202854_at	NM_000194																				
5.35	4.28	1.07	5.54E-02	3.60E-01	CCDC8	coiled-coil domain containing 8	chr19q13.32	223496_s_at	NM_032040																				
8.45	7.95	0.50	5.55E-02	3.60E-01	LOC642393 /// MRPL20	similar to mitochondrial ribosomal protein L20 /// mitochondrial ribosomal protein L20	chr1p36.3-p36.2	220526_s_at	NM_017971 /// XM_001724426 /// XM_001724427 /// XM_001724428 /// XM_001724433																				
3.92	3.43	0.49	5.55E-02	3.60E-01	---	---	---	240908_at	---																				
9.76	9.56	0.21	5.55E-02	3.60E-01	SUMO2	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	chr17q25.1	208739_x_at	NM_001005849 /// NM_006937																				
5.06	4.23	0.83	5.55E-02	3.60E-01	CENTB5	centaurin, beta 5	---	225529_at	NM_030649																				
3.49	3.11	0.39	5.55E-02	3.60E-01	---	---	---	244550_at	---																				
6.39	5.61	0.78	5.56E-02	3.60E-01	C6orf136	chromosome 6 open reading frame 136	chr6p21.33	227456_s_at	NM_001109938 /// NM_145029																				
6.51	6.14	0.36	5.56E-02	3.60E-01	CSNK2A1	casein kinase 2, alpha 1 polypeptide	chr20p13	206075_s_at	NM_001895 /// NM_177559 /// NM_177560																				
3.17	2.05	1.12	5.58E-02	3.61E-01	CCNE2	cyclin E2	chr8q22.1	205034_at	NM_057749																				
2.55	2.30	0.25	5.58E-02	3.61E-01	LOC285045	hypothetical LOC285045	chr2p22.3	1556999_at	---																				

8.05	7.63	0.42	5.58E-02	3.61E-01	D4S234E /// GPS2	DNA segment on chromosome 4 (unique) 234 expressed sequence /// G protein pathway suppressor 2	chr17p13 /// chr4p16.3	209350_s_at	NM_001040101 /// NM_004489 /// NM_014392																				
4.21	3.78	0.42	5.58E-02	3.61E-01	LOC791120 /// ZNF783	hypothetical LOC791120 /// zinc finger family member 783	chr7q36.1	1569473_s_at	NM_001004302 /// NR_015357 /// XR_039872 /// XR_039873 /// XR_039874 /// XR_039875																				
3.49	3.09	0.40	5.58E-02	3.61E-01	SDHALP1	succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1	chr3q29	239022_at	NR_003264 /// XR_042174																				
6.60	6.24	0.35	5.59E-02	3.61E-01	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide	chr1p36.3-p36.2	203277_at	NM_004401 /// NM_213566																				
6.68	6.05	0.63	5.59E-02	3.61E-01	ANKFY1	ankyrin repeat and FYVE domain containing 1	chr17p13.3	224900_at	NM_016376 /// NM_020740																				
8.33	7.37	0.96	5.59E-02	3.61E-01	SLC25A37	solute carrier family 25, member 37	chr8p21.2	222529_at	NM_016612																				
2.58	2.36	0.21	5.59E-02	3.61E-01	---	---	---	1561089_at	---																				
7.08	6.25	0.84	5.59E-02	3.61E-01	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	chr8p21.3	219049_at	NM_001130518 /// NM_018371 /// NR_024040																				
10.41	10.14	0.27	5.59E-02	3.61E-01	AP2M1	adaptor-related protein complex 2, mu 1 subunit	chr3q28	200613_at	NM_001025205 /// NM_004068																				
8.46	7.92	0.54	5.59E-02	3.61E-01	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	chr7q32	222421_at	NM_003344 /// NM_182697																				
3.31	2.97	0.34	5.59E-02	3.61E-01	RTP3	receptor (chemosensory) transporter protein 3	chr3p21.3	1552568_at	NM_031440																				
4.45	4.09	0.36	5.60E-02	3.61E-01	CUL4A	cullin 4A	chr13q34	227757_at	NM_001008895 /// NM_003589																				
5.68	4.82	0.86	5.60E-02	3.61E-01	LAT2	linker for activation of T cells family, member 2	chr7q11.23	221581_s_at	NM_014146 /// NM_032463 /// NM_032464																				
6.58	6.17	0.41	5.60E-02	3.61E-01	TSSC1	tumor suppressing subtransferable candidate 1	chr2p25.3	217968_at	NM_003310																				
6.08	5.57	0.51	5.61E-02	3.61E-01	TMEM186	transmembrane protein 186	chr16p13.13-p12.3	204676_at	NM_015421																				
9.07	8.69	0.38	5.61E-02	3.61E-01	PCBP1	poly(rC) binding protein 1	chr2p13-p12	208620_at	NM_006196																				
8.81	8.39	0.42	5.61E-02	3.61E-01	TXNDC17	thioredoxin domain containing 17	chr17p13.2	224511_s_at	NM_032731																				
3.91	3.38	0.53	5.61E-02	3.61E-01	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	chr3p21.1	219689_at	NM_020163																				
6.39	5.79	0.60	5.61E-02	3.61E-01	GTPBP1	GTP binding protein 1	chr22q13.1	219357_at	NM_004286																				
4.83	4.35	0.48	5.61E-02	3.61E-01	RIBC1	RIB43A domain with coiled-coils 1	chrXp11.22	235946_at	NM_001031745 /// NM_144968																				
3.56	3.02	0.54	5.61E-02	3.61E-01	---	---	---	240347_at	---																				
7.42	5.95	1.47	5.62E-02	3.61E-01	JAM2	junctional adhesion molecule 2	chr21q21.2	219213_at	NM_021219																				
4.29	4.03	0.26	5.62E-02	3.61E-01	DGCR14	DiGeorge syndrome critical region gene 14	chr22q11.21|22q11.2	217285_at	NM_022719																				
4.29	3.58	0.71	5.62E-02	3.61E-01	HIG2	hypoxia-inducible protein 2	chr7q32.1	218507_at	NM_001098786 /// NM_013332																				
7.66	6.90	0.77	5.62E-02	3.61E-01	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	chr5q31	208950_s_at	NM_001182																				
6.03	5.77	0.26	5.62E-02	3.61E-01	TRSPAP1	tRNA selenocysteine associated protein 1	chr1p35.3	218977_s_at	NM_017846 /// NR_003109																				
7.55	5.98	1.57	5.63E-02	3.61E-01	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	chr12q	222857_s_at	NM_014505																				

2.27	1.98	0.28	5.63E-02	3.62E-01	SNRPN	small nuclear ribonucleoprotein polypeptide N	chr15q11.2	1559546_s_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																				
11.10	10.78	0.32	5.63E-02	3.62E-01	USMG5	up-regulated during skeletal muscle growth 5 homolog (mouse)	chr10q24.33	225413_at	NM_032747																			
4.93	4.44	0.49	5.64E-02	3.62E-01	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	chr5q33.2	220296_at	NM_017540 /// NM_198321																			
5.82	5.45	0.37	5.64E-02	3.62E-01	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	chrXq24	204587_at	NM_003951 /// NM_022810																			
2.28	1.97	0.31	5.64E-02	3.62E-01	---	---	---	1565576_at	---																			
8.33	7.67	0.67	5.64E-02	3.62E-01	TMEM14B	transmembrane protein 14B	chr6p25.1-p23	221452_s_at	NM_001127711 /// NM_030969																			
7.33	7.00	0.33	5.65E-02	3.62E-01	SUMO2 /// SUMO4	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) /// SMT3 suppressor of mif two 3 homolog 4 (S. cerevisiae)	chr17q25.1 /// chr6q25	215452_x_at	NM_001002255 /// NM_001005849 /// NM_006937																			
12.46	12.23	0.23	5.65E-02	3.62E-01	RPS27	ribosomal protein S27	chr1q21	200741_s_at	NM_001030																			
4.99	4.32	0.67	5.65E-02	3.62E-01	SS18L1	synovial sarcoma translocation gene on chromosome 18-like 1	chr20q13.3	213140_s_at	NM_198935																			
7.56	7.03	0.53	5.66E-02	3.62E-01	CXXC1	CXXC finger 1 (PHD domain)	chr18q12	48580_at	NM_001101654 /// NM_014593																			
6.60	6.22	0.38	5.66E-02	3.62E-01	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	chr7q22.1	214756_x_at	NR_003613																			

6.50	5.99	0.51	5.66E-02	3.62E-01	PCID2	PCI domain containing 2	chr13q34	219940_s_at	NM_018386 /// XM_001721381 /// XM_001721407 /// XM_001722771																			
5.83	5.36	0.47	5.66E-02	3.62E-01	SFRS1	splicing factor, arginine/serine-rich 1	chr17q21.3-q22	227164_at	NM_001078166 /// NM_006924																			
4.18	3.40	0.77	5.66E-02	3.62E-01	AURKA	aurora kinase A	chr20q13.2-q13.3	204092_s_at	NM_003600 /// NM_198433 /// NM_198434 /// NM_198435 /// NM_198436 /// NM_198437																			
6.95	6.21	0.74	5.66E-02	3.62E-01	PHF6	PHD finger protein 6	chrXq26.3	225501_at	NM_001015877 /// NM_032335 /// NM_032458																			
6.50	6.01	0.49	5.67E-02	3.62E-01	ITPRIP	inositol 1,4,5-triphosphate receptor interacting protein	chr10q25.1	225582_at	NM_033397																			
2.68	2.32	0.36	5.67E-02	3.62E-01	EGLN3	egl nine homolog 3 (C. elegans)	chr14q13.1	219232_s_at	NM_022073																			
4.54	3.68	0.86	5.68E-02	3.62E-01	---	---	---	226197_at	---																			
4.89	4.12	0.77	5.68E-02	3.62E-01	MGC16121	hypothetical protein MGC16121	chrXq26.3	227488_at	XM_001128419 /// XM_001715787 /// XM_001715872																			
2.73	2.34	0.39	5.69E-02	3.62E-01	---	---	---	1555261_at	---																			
12.25	12.04	0.21	5.69E-02	3.62E-01	RPL27	ribosomal protein L27	chr17q21.1-q21.2	200025_s_at	NM_000988																			
2.87	2.53	0.34	5.69E-02	3.63E-01	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	chr1q21	217048_at	NM_001130040 /// NM_001130041 /// NM_003029 /// NM_183001																			
5.09	4.49	0.60	5.70E-02	3.63E-01	MCM5	minichromosome maintenance complex component 5	chr22q13.1	216237_s_at	NM_006739																			
5.41	4.92	0.49	5.70E-02	3.63E-01	C2CD2L	C2CD2-like	chr11q23.3	204757_s_at	NM_014807																			
12.04	11.80	0.24	5.70E-02	3.63E-01	RPS21	ribosomal protein S21	chr20q13.3	200834_s_at	NM_001024																			
6.00	5.55	0.46	5.70E-02	3.63E-01	TM2D1	TM2 domain containing 1	chr1p31.3	211703_s_at	NM_032027																			
6.74	6.12	0.62	5.70E-02	3.63E-01	LST1	leukocyte specific transcript 1	chr6p21.3	210629_x_at	NM_007161 /// NM_205837 /// NM_205838 /// NM_205839 /// NM_205840																			
5.33	4.85	0.48	5.70E-02	3.63E-01	EIF2C2	Eukaryotic translation initiation factor 2C, 2	chr8q24	225569_at	NM_012154																			
5.00	4.49	0.50	5.70E-02	3.63E-01	CCDC49	coiled-coil domain containing 49	chr17q12	218655_s_at	NM_017748																			
3.93	3.53	0.40	5.70E-02	3.63E-01	MESDC2	mesoderm development candidate 2	chr15q13	224672_x_at	NM_015154																			
7.94	7.41	0.53	5.71E-02	3.63E-01	RERE	arginine-glutamic acid dipeptide (RE) repeats	chr1p36.2-p36.1	200940_s_at	NM_001042681 /// NM_001042682 /// NM_012102																			
4.56	3.98	0.58	5.72E-02	3.63E-01	IQCE	IQ motif containing E	chr7p22.2	204202_at	NM_001100390 /// NM_152558																			
3.11	2.71	0.40	5.72E-02	3.63E-01	---	---	---	235378_at	---																			
6.81	6.21	0.60	5.73E-02	3.64E-01	C2orf24	chromosome 2 open reading frame 24	chr2q35	207511_s_at	NM_015680																			
5.72	5.29	0.42	5.73E-02	3.64E-01	C17orf39	chromosome 17 open reading frame 39	chr17p11.2	228452_at	NM_024052																			

2.81	2.17	0.64	5.73E-02	3.64E-01	SCARF1	scavenger receptor class F, member 1	chr17p13.3	206995_x_at	NM_003693 /// NM_145349 /// NM_145350 /// NM_145351 /// NM_145352																				
8.29	8.01	0.28	5.73E-02	3.64E-01	TCEAL3	transcription elongation factor A (SII)-like 3	chrXq22.2	227279_at	NM_001006933 /// NM_032926																				
3.87	3.33	0.55	5.73E-02	3.64E-01	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	chr15q15.1	219270_at	NM_024111																				
6.25	5.68	0.57	5.74E-02	3.64E-01	HEATR2	HEAT repeat containing 2	chr7p22.3	218460_at	NM_017802																				
4.35	3.87	0.48	5.74E-02	3.64E-01	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide	chr6q13-q15	210653_s_at	NM_000056 /// NM_183050																				
4.06	3.60	0.46	5.75E-02	3.64E-01	C13orf23	chromosome 13 open reading frame 23	chr13q13.3	225887_at	NM_025138 /// NM_170719																				
4.16	3.59	0.57	5.76E-02	3.64E-01	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	chr22q13.1	215938_s_at	NM_001004426 /// NM_003560																				
4.43	3.48	0.95	5.76E-02	3.64E-01	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	chr2p23.3	227859_at	NM_016544																				
4.67	4.04	0.62	5.76E-02	3.64E-01	ANAPC1	anaphase promoting complex subunit 1	chr2q12.1	231973_s_at	NM_022662																				
8.04	7.52	0.52	5.77E-02	3.65E-01	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	chr19p13.3	227878_s_at	NM_032306																				
5.96	5.61	0.35	5.77E-02	3.65E-01	PELI3	pellino homolog 3 (Drosophila)	chr11q13.1	235431_s_at	NM_001098510 /// NM_145065																				
6.16	5.57	0.59	5.77E-02	3.65E-01	NECAP1	NECAP endocytosis associated 1	chr12p13.31	209300_s_at	NM_015509																				
4.62	4.28	0.34	5.78E-02	3.65E-01	DGCR8	DiGeorge syndrome critical region gene 8	chr22q11.2	64474_g_at	NM_022720																				
6.74	6.03	0.71	5.78E-02	3.65E-01	APOBEC3F /// APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F /// apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	chr22q13.1 /// chr22q13.1-q13.2	204205_at	NM_001006666 /// NM_021822 /// NM_145298																				
2.83	2.44	0.39	5.79E-02	3.65E-01	USP27X	ubiquitin specific peptidase 27, X-linked	chrXp11.23	217605_at	XM_001714049 /// XM_372213 /// XM_937860																				
10.83	10.52	0.31	5.79E-02	3.65E-01	UCRC	ubiquinol-cytochrome c reductase complex (7.2 kD)	chr22cen-q12.3	218190_s_at	NM_001003684 /// NM_013387																				
2.68	2.45	0.23	5.79E-02	3.65E-01	---	---	---	234770_at	---																				
5.81	5.51	0.30	5.80E-02	3.65E-01	TK2	thymidine kinase 2, mitochondrial	chr16q22-q23.1	204227_s_at	NM_004614																				
4.17	3.78	0.39	5.80E-02	3.65E-01	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	chr8p11.2-p11.1	213003_s_at	NM_005195																				
3.90	3.15	0.75	5.80E-02	3.65E-01	GSTT1	Glutathione S-transferase theta 1	chr22q11.23	232193_at	NM_000853																				
7.84	7.13	0.70	5.80E-02	3.65E-01	FKBP11	FK506 binding protein 11, 19 kDa	chr12q13.12	219117_s_at	NM_016594																				
6.03	5.56	0.48	5.80E-02	3.65E-01	PAQR7	progestin and adipoQ receptor family member VII	chr1p36.11	242123_at	NM_178422																				
7.08	6.20	0.88	5.80E-02	3.65E-01	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	chr17q24.2	219155_at	NM_012417 /// NM_181671																				
7.65	7.36	0.30	5.80E-02	3.65E-01	AOF2	amine oxidase (flavin containing) domain 2	chr1p36.12	212348_s_at	NM_015013																				
5.14	4.57	0.56	5.81E-02	3.65E-01	BID	BH3 interacting domain death agonist	chr22q11.1	227143_s_at	NM_001196 /// NM_197966 /// NM_197967																				
7.03	6.62	0.41	5.81E-02	3.66E-01	SDF4	stromal cell derived factor 4	chr1p36.33	221972_s_at	NM_016176 /// NM_016547																				
4.54	4.28	0.26	5.82E-02	3.66E-01	SETDB1	SET domain, bifurcated 1	chr1q21	214197_s_at	NM_012432																				
6.20	5.79	0.41	5.82E-02	3.66E-01	NDNL2	necdin-like 2	chr15q13.1	226008_at	NM_138704																				
7.77	7.08	0.70	5.82E-02	3.66E-01	PLSCR3	phospholipid scramblase 3	chr17p13.1	56197_at	NM_020360																				
6.60	6.17	0.43	5.83E-02	3.66E-01	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	chr20q13.13	221780_s_at	NM_017895																				
3.34	2.96	0.38	5.83E-02	3.66E-01	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	chr8q22	216832_at	NM_004349 /// NM_175634 /// NM_175635 /// NM_175636																				
5.27	4.58	0.69	5.83E-02	3.66E-01	CCDC76	coiled-coil domain containing 76	chr1pter-q31.3	219130_at	NM_019083																				

5.14	4.89	0.25	5.83E-02	3.66E-01	LOC390998	similar to hCG1644589	chr1p36.22	216589_at	XM_001716257 /// XM_372759 /// XM_938288																				
6.62	6.02	0.61	5.84E-02	3.67E-01	---	---	---	225227_at	---																				
4.08	3.85	0.24	5.84E-02	3.67E-01	---	---	---	242813_at	---																				
8.73	8.15	0.58	5.85E-02	3.67E-01	KIAA0152	KIAA0152	chr12q24.31	200617_at	NM_014730																				
2.33	1.99	0.34	5.85E-02	3.67E-01	---	---	---	241049_at	---																				
5.62	5.13	0.50	5.85E-02	3.67E-01	CAPRIN1	cell cycle associated protein 1	chr11p13	226285_at	NM_005898 /// NM_203364																				
7.55	7.10	0.45	5.86E-02	3.67E-01	HSPB11	heat shock protein family B (small), member 11	chr1p32.1-p33	215691_x_at	NM_016126																				
3.07	2.51	0.56	5.86E-02	3.67E-01	LY6G5C	lymphocyte antigen 6 complex, locus G5C	chr6p21.33	219860_at	NM_025262																				
8.39	7.71	0.68	5.86E-02	3.67E-01	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	chr16q22.1	224984_at	NM_001113178 /// NM_006599 /// NM_138713 /// NM_138714 /// NM_173214																				
8.51	8.02	0.49	5.86E-02	3.67E-01	WTAP	Wilms tumor 1 associated protein	chr6q25-q27	229630_s_at	NM_004906 /// NM_152857 /// NM_152858																				
4.88	4.16	0.72	5.87E-02	3.68E-01	LOC400657	hypothetical LOC400657	chr18q22.3	226924_at	XR_039912 /// XR_039913 /// XR_039914																				
2.98	2.62	0.36	5.88E-02	3.68E-01	NOS1AP	Nitric oxide synthase 1 (neuronal) adaptor protein	chr1q23.3	1563512_at	NM_001126060 /// NM_014697																				
2.23	1.99	0.24	5.88E-02	3.68E-01	---	---	---	233039_at	---																				
8.72	8.44	0.28	5.89E-02	3.68E-01	SARS	seryl-tRNA synthetase	chr1p13.3-p13.1	200802_at	NM_006513																				
4.43	3.78	0.65	5.89E-02	3.68E-01	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	chr15q22.31	222606_at	NM_017975 /// NR_003105																				
7.57	7.13	0.43	5.90E-02	3.68E-01	NEK9	NIMA (never in mitosis gene a)- related kinase 9	chr14q24.3	212299_at	NM_033116																				
4.96	4.31	0.65	5.90E-02	3.68E-01	SNRPA1	Small nuclear ribonucleoprotein polypeptide A'	chr15q26.3	242146_at	NM_003090																				
2.53	2.26	0.27	5.90E-02	3.68E-01	TRIM40	tripartite motif-containing 40	chr6p21.33	1553079_at	NM_138700																				
10.52	10.04	0.48	5.90E-02	3.68E-01	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	chr20q13.1	212501_at	NM_005194																				
3.23	2.79	0.44	5.91E-02	3.68E-01	BICC1	bicaudal C homolog 1 (Drosophila)	chr10q21.1	220580_at	NM_001080512																				
4.74	4.32	0.41	5.91E-02	3.68E-01	---	---	---	231078_at	---																				
4.84	3.97	0.87	5.91E-02	3.68E-01	SLFN12	schlafen family member 12	chr17q12	219885_at	NM_018042																				
5.87	5.49	0.38	5.91E-02	3.68E-01	KIAA1147	KIAA1147	chr7q34	223162_s_at	NM_001080392																				
4.73	4.20	0.53	5.91E-02	3.69E-01	KIAA0467	KIAA0467	chr1p34.2	215364_s_at	NM_015284																				
9.26	8.61	0.65	5.92E-02	3.69E-01	SGCE	sarcoglycan, epsilon	chr7q21-q22	204688_at	NM_001099400 /// NM_001099401 /// NM_003919																				
2.70	2.48	0.22	5.92E-02	3.69E-01	---	---	---	236115_at	---																				
2.93	2.57	0.36	5.93E-02	3.69E-01	ARTN	artemin	chr1p33-p32	207675_x_at	NM_003976 /// NM_057090 /// NM_057091 /// NM_057160																				
8.26	7.96	0.30	5.93E-02	3.69E-01	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	chr14q32.3-qter|14q32	211928_at	NM_001376																				
5.36	4.82	0.54	5.93E-02	3.69E-01	SMYD4	SET and MYND domain containing 4	chr17p13.3	229175_at	NM_052928																				
4.94	4.26	0.68	5.93E-02	3.69E-01	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	chr19p13.3	204431_at	NM_003260																				
4.00	3.52	0.48	5.93E-02	3.69E-01	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	chr8p21	231775_at	NM_003844																				
7.48	7.05	0.43	5.93E-02	3.69E-01	GTF3C1	general transcription factor IIIC, polypeptide 1, alpha 220kDa	chr16p12	35671_at	NM_001520																				

2.51	2.25	0.26	5.93E-02	3.69E-01	C12orf28	chromosome 12 open reading frame 28	chr12q15	1556267_at	XM_001716650 /// XM_001718058 /// XM_001718908																				
7.60	7.21	0.39	5.93E-02	3.69E-01	C10orf104	chromosome 10 open reading frame 104	chr10q22.1	229145_at	NM_173473																				
5.29	4.86	0.44	5.94E-02	3.69E-01	CLIP2	CAP-GLY domain containing linker protein 2	chr7q11.23	211031_s_at	NM_003388 /// NM_032421																				
3.58	3.22	0.36	5.94E-02	3.69E-01	RFWD3	ring finger and WD repeat domain 3	chr16q22.3	218564_at	NM_018124																				
8.18	7.83	0.35	5.94E-02	3.69E-01	ASCC3L1	activating signal cointegrator 1 complex subunit 3-like 1	chr2q11.2	200058_s_at	NM_014014																				
11.43	11.15	0.28	5.94E-02	3.69E-01	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	chr17p13	211787_s_at	NM_001416																				
5.25	4.52	0.73	5.94E-02	3.69E-01	WDR85	WD repeat domain 85	chr9q34.3	225586_at	NM_138778																				
6.90	6.50	0.40	5.94E-02	3.69E-01	C14orf179	chromosome 14 open reading frame 179	chr14q24.3	226195_at	NM_001102564 /// NM_052873																				
6.73	6.33	0.40	5.94E-02	3.69E-01	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	chr16p13.3	221769_at	NM_080861																				
6.08	5.23	0.84	5.95E-02	3.69E-01	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	chr2p13.1	201761_at	NM_001040409 /// NM_006636																				
2.22	1.97	0.25	5.95E-02	3.69E-01	---	---	---	1561513_at	---																				
7.75	7.18	0.56	5.95E-02	3.69E-01	AKAP11	A kinase (PRKA) anchor protein 11	chr13q14.11	203156_at	NM_016248																				
4.22	3.87	0.35	5.95E-02	3.69E-01	---	---	---	229821_at	---																				
4.88	4.18	0.70	5.96E-02	3.69E-01	LOC100129282	Hypothetical protein LOC100129282	chr3p13	238165_at	XM_001714218 /// XM_001714248																				
8.35	7.86	0.49	5.96E-02	3.69E-01	TMEM70	transmembrane protein 70	chr8q21.11	219449_s_at	NM_001040613 /// NM_017866																				
4.78	4.14	0.64	5.96E-02	3.69E-01	IGSF21	immunoglobin superfamily, member 21	chr1p36.13	227154_at	NM_032880																				
5.68	4.83	0.84	5.96E-02	3.69E-01	U2AF2	U2 small nuclear RNA auxiliary factor 2	chr19q13.42	218381_s_at	NM_001012478 /// NM_007279																				
4.15	3.61	0.54	5.97E-02	3.69E-01	SYMPK	symplekin	chr19q13.3	32402_s_at	NM_004819																				
3.88	3.55	0.34	5.99E-02	3.70E-01	C1orf174	chromosome 1 open reading frame 174	chr1p36.32	238010_at	NM_207356																				
8.95	8.59	0.36	5.99E-02	3.70E-01	JAGN1	jagunal homolog 1 (Drosophila)	chr3p25.2	223104_at	NM_032492																				
5.92	5.25	0.67	5.99E-02	3.70E-01	ADCK2	aarF domain containing kinase 2	chr7q32-q34	221893_s_at	NM_052853																				
11.90	11.67	0.22	5.99E-02	3.70E-01	RPL8	ribosomal protein L8	chr8q24.3	200936_at	NM_000973 /// NM_033301																				
4.73	4.28	0.45	5.99E-02	3.70E-01	KIAA0556	KIAA0556	chr16p12.1-p11.2	213185_at	NM_015202																				
8.58	8.23	0.35	5.99E-02	3.70E-01	MRPS18C	mitochondrial ribosomal protein S18C	chr4q21.23	228019_s_at	NM_016067																				
5.25	4.75	0.50	5.99E-02	3.70E-01	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	chr12q24.31	44617_at	NM_024623																				
6.54	5.96	0.58	6.00E-02	3.70E-01	RANGAP1	Ran GTPase activating protein 1	chr22q13	212125_at	NM_002883																				
5.28	4.97	0.31	6.00E-02	3.70E-01	SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	chr11q23.3	217289_s_at	NM_001467																				
3.16	2.61	0.55	6.00E-02	3.70E-01	---	---	---	237451_x_at	---																				
10.81	10.21	0.60	6.00E-02	3.70E-01	MT1P2	metallothionein 1 pseudogene 2	chr1q43	211456_x_at	---																				
3.08	2.82	0.26	6.01E-02	3.70E-01	MAGEA9 /// MAGEA9B	melanoma antigen family A, 9 /// melanoma antigen family A, 9B	chrXq28	210437_at	NM_001080790 /// NM_005365																				
4.54	4.03	0.51	6.01E-02	3.70E-01	---	---	---	228435_at	---																				
2.63	2.14	0.49	6.01E-02	3.70E-01	TGFB2	transforming growth factor, beta 2	chr1q41	209909_s_at	NM_003238																				
7.52	6.60	0.92	6.01E-02	3.71E-01	MOXD1	monooxygenase, DBH-like 1	chr6q23.1-q23.3	209708_at	NM_015529																				
3.90	3.43	0.47	6.02E-02	3.71E-01	LRP5L	low density lipoprotein receptor-related protein 5-like	chr22q11.23	214873_at	NM_182492 /// XM_001720417 /// XM_001723035 /// XM_001726196																				
4.29	3.77	0.52	6.02E-02	3.71E-01	FOXRED2	FAD-dependent oxidoreductase domain containing 2	chr22q12.3	220707_s_at	NM_001102371 /// NM_024955																				
2.82	2.47	0.35	6.02E-02	3.71E-01	FAM113A	family with sequence similarity 113, member A	chr20p13	231965_at	NM_022760																				
7.16	6.64	0.53	6.02E-02	3.71E-01	COMMD4	COMM domain containing 4	chr15q24.2	209132_s_at	NM_017828																				
5.02	4.41	0.61	6.03E-02	3.71E-01	C19orf6	chromosome 19 open reading frame 6	chr19p13.3	212574_x_at	NM_001033026 /// NM_033420																				
4.10	3.82	0.28	6.03E-02	3.71E-01	C7orf63	chromosome 7 open reading frame 63	chr7q21.13	219455_at	NM_001039706																				

3.43	3.12	0.31	6.04E-02	3.71E-01	---	---	---	237204_at	---
3.18	2.78	0.40	6.04E-02	3.71E-01	BDNF	brain-derived neurotrophic factor	chr11p13	239367_at	NM_001709 /// NM_170731 /// NM_170732 /// NM_170733 /// NM_170734 /// NM_170735
3.34	2.83	0.51	6.05E-02	3.71E-01	---	---	---	1557192_at	---
6.80	6.21	0.59	6.05E-02	3.72E-01	MFF	mitochondrial fission factor	chr2q36.3	219137_s_at	NM_020194
5.87	4.92	0.95	6.05E-02	3.72E-01	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	chr19q13.2	202014_at	NM_014330
3.04	2.75	0.29	6.06E-02	3.72E-01	ZNF197	zinc finger protein 197	chr3p21	205855_at	NM_001024855 /// NM_006991
3.88	3.41	0.46	6.06E-02	3.72E-01	ZNF777	zinc finger protein 777	chr7q36.1	1553172_at	NM_015694
7.11	6.73	0.38	6.06E-02	3.72E-01	RXRB	retinoid X receptor, beta	chr6p21.3	209148_at	NM_021976
3.18	2.82	0.36	6.07E-02	3.72E-01	---	---	---	242424_at	---
4.05	3.26	0.80	6.07E-02	3.72E-01	---	---	---	243491_at	---
5.98	5.19	0.79	6.08E-02	3.72E-01	SP2	Sp2 transcription factor	chr17q21.32	204367_at	NM_003110
3.71	3.13	0.58	6.08E-02	3.72E-01	S100P	S100 calcium binding protein P	chr4p16	204351_at	NM_005980
4.31	3.85	0.46	6.09E-02	3.72E-01	RAB43	RAB43, member RAS oncogene family	chr3q21.3	229894_s_at	NM_198490
5.49	4.74	0.75	6.09E-02	3.72E-01	STK36	serine/threonine kinase 36, fused homolog (Drosophila)	chr2q35	234005_x_at	NM_015690
7.04	6.18	0.86	6.09E-02	3.72E-01	EXOSC6	exosome component 6	chr16q22.1	227696_at	NM_058219
3.20	2.83	0.37	6.10E-02	3.72E-01	KIAA1161	KIAA1161	chr9p13.3	232244_at	NM_020702
4.12	3.57	0.55	6.10E-02	3.72E-01	LOC729120 /// THEM4	hypothetical LOC729120 /// thioesterase superfamily member 4	chr15q21.3 /// chr1q21	243492_at	NM_053055 /// XM_001133026 /// XM_001133204 /// XM_001726232
10.72	10.17	0.55	6.10E-02	3.73E-01	MAGED1	melanoma antigen family D, 1	chrXp11.23	209014_at	NM_001005332 /// NM_001005333 /// NM_006986
3.12	2.78	0.34	6.10E-02	3.73E-01	---	---	---	238376_at	---
2.36	2.08	0.27	6.10E-02	3.73E-01	---	---	---	237516_at	---
5.27	4.85	0.43	6.10E-02	3.73E-01	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	chr21q22.3	226209_at	NM_001001503 /// NM_021075
4.98	4.65	0.33	6.11E-02	3.73E-01	LRRC23	leucine rich repeat containing 23	chr12p13	206076_at	NM_006992 /// NM_201650
2.89	2.55	0.35	6.11E-02	3.73E-01	---	---	---	1556398_a_at	---
3.84	3.36	0.48	6.11E-02	3.73E-01	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	chr4p16.3	209570_s_at	NM_001040101 /// NM_014392
4.28	3.79	0.49	6.11E-02	3.73E-01	ARID2	AT rich interactive domain 2 (ARID, RFX-like)	chr12q12	231090_s_at	NM_152641
10.12	9.75	0.36	6.11E-02	3.73E-01	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	chr9q22.32	201306_s_at	NM_006401
5.81	5.41	0.40	6.12E-02	3.73E-01	CUEDC1	CUE domain containing 1	chr17q23.2	227667_at	NM_017949
8.37	7.94	0.43	6.12E-02	3.73E-01	GPAA1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	chr8q24.3	211060_x_at	NM_003801
6.45	5.64	0.80	6.12E-02	3.73E-01	ZNF266	zinc finger protein 266	chr19p13.2	214686_at	NM_006631 /// NM_198058
5.04	3.94	1.10	6.12E-02	3.73E-01	NUP62CL	nucleoporin 62kDa C-terminal like	chrXq22.3	220520_s_at	NM_017681
5.36	4.84	0.52	6.12E-02	3.73E-01	---	---	---	226457_at	---
3.50	2.95	0.55	6.13E-02	3.73E-01	VMO1	vitelline membrane outer layer 1 homolog (chicken)	chr17p13.2	235751_s_at	NM_182566
8.43	7.36	1.07	6.14E-02	3.73E-01	CCL2	chemokine (C-C motif) ligand 2	chr17q11.2-q12	216598_s_at	NM_002982
2.26	2.01	0.25	6.14E-02	3.73E-01	HSPB11	heat shock protein family B (small), member 11	chr1p32.1-p33	214163_at	NM_016126
4.68	4.02	0.67	6.14E-02	3.73E-01	CCDC14	coiled-coil domain containing 14	chr3q21.1	225017_at	NM_022757
4.72	3.90	0.82	6.14E-02	3.73E-01	LOC147650	hypothetical protein LOC147650	chr19q13.33	227992_s_at	XR_041605 /// XR_041606 /// XR_041607
4.53	4.22	0.31	6.14E-02	3.73E-01	SFT2D1	SFT2 domain containing 1	chr6q27	226836_at	NM_145169

6.36	5.81	0.54	6.14E-02	3.73E-01	LOC646808	hypothetical LOC646808	chr9p13.3	222338_x_at	XR_017339 /// XR_018782 /// XR_037491																			
4.77	4.14	0.62	6.15E-02	3.74E-01	PARVG	parvin, gamma	chr22q13.2-q13	223562_at	NM_022141																			
6.80	6.33	0.46	6.15E-02	3.74E-01	MKNK1	MAP kinase interacting serine/threonine kinase 1	chr1p33	209467_s_at	NM_003684 /// NM_198973																			
3.05	2.69	0.35	6.15E-02	3.74E-01	LTB4R	leukotriene B4 receptor	chr14q11.2-q12	236172_at	NM_181657																			
7.88	7.47	0.41	6.16E-02	3.74E-01	---	---	---	230795_at	---																			
6.45	5.80	0.65	6.16E-02	3.74E-01	TNFSF12 /// TNFSF12-TNFSF13 /// TNFSF13	tumor necrosis factor (ligand) superfamily, member 12 /// TNFSF12-TNFSF13 /// tumor necrosis factor (ligand) superfamily, member 13	chr17p13 /// chr17p13.1	209499_x_at	NM_003808 /// NM_003809 /// NM_172087 /// NM_172088 /// NM_172089																			
6.91	6.14	0.77	6.16E-02	3.74E-01	DEF8	differentially expressed in FDCP 8 homolog (mouse)	chr16q24.3	225637_at	NM_017702 /// NM_207514																			
4.14	3.18	0.97	6.17E-02	3.74E-01	ORMDL1	ORM1-like 1 (S. cerevisiae)	chr2q32	228801_at	NM_001128150 /// NM_016467																			
7.08	6.74	0.34	6.17E-02	3.74E-01	C11orf60	chromosome 11 open reading frame 60	chr11q23.3	218483_s_at	NM_020153																			
7.71	6.98	0.72	6.17E-02	3.74E-01	HSPA12A	heat shock 70kDa protein 12A	chr10q26.12	214434_at	NM_025015																			
12.55	12.32	0.23	6.17E-02	3.74E-01	RPS10	ribosomal protein S10	chr6p21.31	200817_x_at	NM_001014																			
7.19	6.31	0.88	6.18E-02	3.75E-01	RBM39	RNA binding motif protein 39	chr20q11.22	207941_s_at	NM_004902 /// NM_184234																			
3.59	3.23	0.36	6.18E-02	3.75E-01	RTEL1 /// TNFRSF6B	regulator of telomere elongation helicase 1 /// tumor necrosis factor receptor superfamily, member 6b, decoy	chr20q13.3	206467_x_at	NM_003823 /// NM_016434 /// NM_032945 /// NM_032957																			
6.31	4.49	1.82	6.18E-02	3.75E-01	CCL3 /// CCL3L1 /// CCL3L3 /// LOC728830	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3 /// similar to C-C motif chemokine 3-like 1 precursor (Small-inducible cytokine A3-like 1) (Tonsillar lymphocyte LD78 beta protein) (LD78-beta(1-70)) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (PAT 464.2)	chr17q11-q21 /// chr17q21.1	205114_s_at	NM_001001437 /// NM_002983 /// NM_021006 /// XM_001133177																			
8.21	7.76	0.46	6.19E-02	3.75E-01	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	chr20q12-q13.1	202732_at	NM_007066 /// NM_181804 /// NM_181805																			
5.48	4.93	0.55	6.19E-02	3.75E-01	RAP2C	RAP2C, member of RAS oncogene family	chrXq25	218668_s_at	NM_021183																			
3.81	2.90	0.91	6.19E-02	3.75E-01	ADAMTSL1	ADAMTS-like 1	chr9p22.2-p22.1	237217_at	NM_001040272 /// NM_052866																			
7.02	6.27	0.75	6.20E-02	3.75E-01	ZRANB2	zinc finger, RAN-binding domain containing 2	chr1p31	223716_s_at	NM_005455 /// NM_203350																			
7.16	6.92	0.24	6.20E-02	3.75E-01	NIP30	NEFA-interacting nuclear protein NIP30	chr16q13	224248_x_at	NM_024946																			
7.21	6.72	0.50	6.20E-02	3.75E-01	DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11	chr1p36.31	215792_s_at	NM_018198																			
9.86	9.40	0.47	6.20E-02	3.75E-01	COMT	catechol-O-methyltransferase	chr22q11.21-q11.23|22q11.21	208818_s_at	NM_000754 /// NM_007310																			
7.86	7.25	0.61	6.20E-02	3.75E-01	SETD5	SET domain containing 5	chr3p25.3	221806_s_at	NM_001080517																			
4.42	4.05	0.37	6.20E-02	3.75E-01	POLE	polymerase (DNA directed), epsilon	chr12q24.3	216026_s_at	NM_006231																			
7.88	7.19	0.69	6.21E-02	3.76E-01	CKAP4	cytoskeleton-associated protein 4	chr12q23.3	200998_s_at	NM_006825																			

8.11	7.53	0.58	6.22E-02	3.76E-01	MAX	MYC associated factor X	chr14q23	209332_s_at	NM_002382 /// NM_145112 /// NM_145113 /// NM_145114 /// NM_145116 /// NM_197957
5.82	4.62	1.20	6.23E-02	3.76E-01	CLK1	CDC-like kinase 1	chr2q33	214683_s_at	NM_004071
8.14	7.77	0.37	6.23E-02	3.76E-01	ADD1	adducin 1 (alpha)	chr4p16.3	214736_s_at	NM_001119 /// NM_014189 /// NM_014190 /// NM_176801
4.40	3.99	0.41	6.23E-02	3.76E-01	LOC284939	hypothetical protein LOC284939	chr22q13.33	1556001_at	---
4.35	3.86	0.48	6.23E-02	3.76E-01	LOC145783	hypothetical LOC145783	chr15q21.3	229013_at	XM_934388
2.36	2.02	0.34	6.23E-02	3.76E-01	---	---	---	244503_at	---
3.54	3.29	0.25	6.24E-02	3.76E-01	---	---	---	1556400_at	---
2.87	2.56	0.31	6.24E-02	3.76E-01	SYNGR4	synaptogyrin 4	chr19q13.3	206719_at	NM_012451
3.71	2.92	0.79	6.24E-02	3.76E-01	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	chr17p12-p11.2	205873_at	NM_004278
3.68	3.26	0.42	6.24E-02	3.76E-01	C3orf10	chromosome 3 open reading frame 10	chr3p25.3	224023_s_at	NM_018462
2.93	2.62	0.30	6.24E-02	3.76E-01	PVT1	Pvt1 oncogene (non-protein coding)	chr8q24	1562153_a_at	NR_003367
4.87	3.83	1.04	6.26E-02	3.76E-01	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	chr4q34-q35	211549_s_at	NM_000860
2.80	2.41	0.38	6.26E-02	3.76E-01	UQCRB	ubiquinol-cytochrome c reductase binding protein	chr8q22	244293_at	NM_006294
5.44	4.92	0.52	6.26E-02	3.76E-01	SPIN2A /// SPIN2B	spindlin family, member 2A /// spindlin family, member 2B	chrXp11.1	211704_s_at	NM_001006681 /// NM_001006682 /// NM_001006683 /// NM_019003
4.59	4.21	0.38	6.27E-02	3.77E-01	CXorf38	chromosome X open reading frame 38	chrXp11.4	230532_at	NM_144970
7.21	6.88	0.33	6.28E-02	3.77E-01	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	chr19q13.11-q13.13	201252_at	NM_006503 /// NM_153001
5.19	4.38	0.81	6.29E-02	3.77E-01	FKRP	fukutin related protein	chr19q13.32	227882_at	NM_001039885 /// NM_024301
7.69	7.29	0.41	6.29E-02	3.77E-01	PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	chr16p12-p11	208932_at	NM_002720
5.67	5.24	0.43	6.29E-02	3.77E-01	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	chr22q11.21	217407_x_at	NM_014337 /// NM_148175 /// NM_148176
9.63	9.32	0.31	6.30E-02	3.77E-01	ANXA5	annexin A5	chr4q26-q28|4q28-q32	200782_at	NM_001154
2.85	2.48	0.37	6.30E-02	3.77E-01	---	---	---	241614_at	---
4.16	3.63	0.53	6.30E-02	3.77E-01	NBPF3	neuroblastoma breakpoint family, member 3	chr1p36.12	223638_at	NM_032264
5.20	4.68	0.52	6.31E-02	3.77E-01	MICALL1	MICAL-like 1	chr22q13.1-q13.2	221779_at	NM_033386
5.29	4.88	0.41	6.31E-02	3.77E-01	LRDD	leucine-rich repeats and death domain containing	chr11p15.5	219019_at	NM_018494 /// NM_145886 /// NM_145887
2.17	1.90	0.27	6.31E-02	3.77E-01	---	---	---	234194_at	---
10.31	10.07	0.24	6.32E-02	3.77E-01	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	chrXq24	202298_at	NM_004541
3.59	3.32	0.27	6.32E-02	3.77E-01	LOC100129617	hypothetical protein LOC100129617	chr16q23.2	238086_at	XM_001725256 /// XM_001725301 /// XM_001726846
10.76	10.47	0.29	6.32E-02	3.78E-01	TUBA1C	tubulin, alpha 1c	chr12q12-q14	211750_x_at	NM_032704
2.76	2.43	0.33	6.33E-02	3.78E-01	---	---	---	217166_at	---
5.89	5.46	0.43	6.33E-02	3.78E-01	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	chr16q22.1	40255_at	NM_018380
7.89	7.27	0.62	6.34E-02	3.78E-01	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4	chr17q24-q25	218062_x_at	NM_012121

7.25	6.68	0.57	6.34E-02	3.78E-01	NUDT22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	chr11q13.1	224464_s_at	NM_001128612 /// NM_001128613 /// NM_032344																				
6.78	6.16	0.62	6.35E-02	3.78E-01	TBCC	tubulin folding cofactor C	chr6pter-p12.1	202495_at	NM_003192																				
6.62	6.13	0.50	6.35E-02	3.78E-01	LEPRE1	leucine proline-enriched proteoglycan (leprecan) 1	chr1p34.1	220750_s_at	NM_022356																				
6.51	5.79	0.71	6.35E-02	3.78E-01	B3GNT9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	chr16q22.1	226058_at	NM_033309																				
2.62	2.32	0.31	6.35E-02	3.78E-01	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	chr9q21.31	214688_at	NM_007005																				
5.28	4.66	0.62	6.35E-02	3.78E-01	BRWD2	bromodomain and WD repeat domain containing 2	chr10q26	218090_s_at	NM_018117																				
2.61	2.31	0.31	6.35E-02	3.78E-01	CLEC12A /// CLEC12B	C-type lectin domain family 12, member A /// C-type lectin domain family 12, member B	chr12p13.2	1552398_a_at	NM_001129998 /// NM_138337 /// NM_201623 /// NM_205852																				
6.05	5.62	0.43	6.36E-02	3.79E-01	INTS4	integrator complex subunit 4	chr11q14.1	225169_at	NM_033547																				
2.73	2.39	0.34	6.36E-02	3.79E-01	---	---	---	1562408_at	---																				
5.40	4.62	0.78	6.36E-02	3.79E-01	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	chr10q11.21	226436_at	NM_032023																				
8.31	7.96	0.35	6.36E-02	3.79E-01	PUF60	poly-U binding splicing factor 60KDa	chr8q24.2-qter	209899_s_at	NM_014281 /// NM_078480																				
3.58	3.03	0.55	6.36E-02	3.79E-01	IGSF1	immunoglobulin superfamily, member 1	chrXq25	207695_s_at	NM_001555 /// NM_205833																				
8.39	7.86	0.54	6.37E-02	3.79E-01	SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	chr21q22.3	200740_s_at	NM_006936																				
4.58	4.33	0.24	6.37E-02	3.79E-01	SLC16A11	solute carrier family 16, member 11 (monocarboxylic acid transporter 11)	chr17p13.1	1552761_at	NM_153357																				
9.19	8.77	0.42	6.38E-02	3.79E-01	HAX1	HCLS1 associated protein X-1	chr1q21.3	201145_at	NM_001018837 /// NM_006118																				
5.62	5.03	0.59	6.38E-02	3.79E-01	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	chr2q24	203340_s_at	NM_003705																				
4.92	4.54	0.38	6.38E-02	3.79E-01	NRP2	neuropilin 2	chr2q33.3	210841_s_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279																				
3.45	2.93	0.52	6.38E-02	3.79E-01	ULK2	unc-51-like kinase 2 (C. elegans)	chr17p11.2	204063_s_at	NM_014683																				
9.05	8.67	0.38	6.39E-02	3.79E-01	FAM114A1	family with sequence similarity 114, member A1	chr4p14	213455_at	NM_138389																				
3.68	3.16	0.52	6.39E-02	3.79E-01	HP1BP3	heterochromatin protein 1, binding protein 3	chr1p36.12	1554251_at	NM_016287																				
5.34	4.70	0.63	6.39E-02	3.79E-01	RBM4B	RNA binding motif protein 4B	chr11q13	209497_s_at	NM_031492																				
6.42	5.81	0.61	6.39E-02	3.79E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	217039_x_at	---																				
8.78	8.48	0.30	6.40E-02	3.80E-01	CHCHD8	coiled-coil-helix-coiled-coil-helix domain containing 8	chr11q13.4	220647_s_at	NM_016565																				
4.28	3.94	0.33	6.40E-02	3.80E-01	N4BP1	NEDD4 binding protein 1	chr16q12.1	204601_at	NM_153029																				
3.84	3.55	0.30	6.40E-02	3.80E-01	---	---	---	228216_at	---																				
3.00	2.65	0.35	6.40E-02	3.80E-01	AR	androgen receptor	chrXq11.2-q12	211621_at	NM_000044 /// NM_001011645																				
9.38	9.11	0.27	6.40E-02	3.80E-01	GSTO1	glutathione S-transferase omega 1	chr10q25.1	1557915_s_at	NM_004832																				
8.44	7.76	0.67	6.40E-02	3.80E-01	ACY1	aminoacylase 1	chr3p21.1	202740_at	NM_000666																				
6.04	5.56	0.48	6.40E-02	3.80E-01	SSH3	slingshot homolog 3 (Drosophila)	chr11q13.1	51192_at	NM_017857																				
4.80	4.42	0.38	6.41E-02	3.80E-01	ZKSCAN4	zinc finger with KRAB and SCAN domains 4	chr6p21.33-p21.31	213625_at	NM_019110																				
4.88	4.30	0.58	6.42E-02	3.80E-01	PRICKLE2	prickle homolog 2 (Drosophila)	chr3p14.1	225968_at	NM_198859																				
6.26	5.66	0.61	6.42E-02	3.80E-01	SAP30L	SAP30-like	chr5q33.2	225509_at	NM_001131062 /// NM_001131063 /// NM_024632 /// NR_024084																				
6.91	6.21	0.70	6.43E-02	3.80E-01	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	chr7q36.3	224699_s_at	NM_020728																				
3.68	3.06	0.62	6.43E-02	3.80E-01	ULK2	unc-51-like kinase 2 (C. elegans)	chr17p11.2	204062_s_at	NM_014683																				

7.34	6.76	0.58	6.43E-02	3.80E-01	C1orf2	chromosome 1 open reading frame 2	chr1q21	203550_s_at	NM_006589 /// NM_198264																				
2.54	2.27	0.27	6.44E-02	3.81E-01	WDSOF1	WD repeats and SOF1 domain containing	chr8q22.3	220843_s_at	NM_015420																				
4.85	4.49	0.36	6.44E-02	3.81E-01	GOSR2	golgi SNAP receptor complex member 2	chr17q21	213180_s_at	NM_001012511 /// NM_004287 /// NM_054022																				
9.00	8.62	0.37	6.44E-02	3.81E-01	DCTN3	dynactin 3 (p22)	chr9p13	204246_s_at	NM_007234 /// NM_024348																				
5.84	5.52	0.32	6.44E-02	3.81E-01	LPIN2	lipin 2	chr18p11.31	202460_s_at	NM_014646																				
6.31	5.83	0.47	6.44E-02	3.81E-01	MTERFD1	MTERF domain containing 1	chr8q22.1	219363_s_at	NM_015942																				
5.35	4.32	1.02	6.45E-02	3.81E-01	RPRD1A	Regulation of nuclear pre-mRNA domain containing 1A	chr18q12.2	228566_at	NM_018170																				
5.05	4.55	0.50	6.45E-02	3.81E-01	CNNM2	cyclin M2	chr10q24.32	1554523_a_at	NM_017649 /// NM_199076 /// NM_199077																				
5.65	5.28	0.38	6.45E-02	3.81E-01	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	chr5q33-q34	207829_s_at	NM_001205 /// NM_013978 /// NM_013979 /// NM_013980																				
9.89	9.38	0.51	6.46E-02	3.81E-01	LAPTM4B	lysosomal protein transmembrane 4 beta	chr8q22.1	214039_s_at	NM_018407																				
2.99	2.72	0.27	6.46E-02	3.81E-01	LRRC66	leucine rich repeat containing 66	chr4q12	1568634_a_at	NM_001024611																				
6.68	6.16	0.52	6.46E-02	3.81E-01	MMS19	MMS19 nucleotide excision repair homolog (S. cerevisiae)	chr10q24-q25	202167_s_at	NM_022362																				
2.96	2.74	0.22	6.46E-02	3.81E-01	LAIR2	leukocyte-associated immunoglobulin-like receptor 2	chr19q13.4	207509_s_at	NM_002288 /// NM_021270																				
2.54	2.22	0.32	6.47E-02	3.81E-01	LOC100132760 /// RP11-327P2.4	hypothetical protein LOC100132760 /// hypothetical protein FLJ37307	chr13q14.3	1557465_at	XM_001721162 /// XM_001723292 /// XM_001725783 /// XR_017830 /// XR_017831 /// XR_041498																				
3.47	2.99	0.48	6.47E-02	3.81E-01	C3orf62	chromosome 3 open reading frame 62	chr3p21.31	241817_at	NM_198562																				
7.26	6.59	0.68	6.48E-02	3.81E-01	BANP	BTG3 associated nuclear protein	chr16q24.2-q24.3	228928_x_at	NM_017869 /// NM_079837 /// XM_001718410																				
5.07	4.34	0.73	6.48E-02	3.81E-01	MYO5C	myosin VC	chr15q21	218966_at	NM_018728																				
4.36	2.77	1.59	6.48E-02	3.81E-01	BMPR1B	bone morphogenetic protein receptor, type IB	chr4q22-q24	229975_at	NM_001203																				
5.32	4.29	1.03	6.48E-02	3.81E-01	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	chr12q	219287_at	NM_014505																				

9.92	9.57	0.35	6.49E-02	3.81E-01	SNRPN /// SNURF	small nuclear ribonucleoprotein polypeptide N /// SNRPN upstream reading frame	chr15q11.2 /// chr15q12	201522_x_at	NM_003097 /// NM_005678 /// NM_022804 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 ///																					
2.96	2.52	0.44	6.49E-02	3.81E-01	ZNF789	zinc finger protein 789	chr7q22.1	235231_at	NM_001013258 /// NM_213603																			
8.04	7.65	0.40	6.49E-02	3.82E-01	DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3	chr1q22	219373_at	NM_018973 /// NM_153741																			
3.01	2.31	0.70	6.49E-02	3.82E-01	ELMOD1	ELMO/CED-12 domain containing 1	chr11q22.3	231930_at	NM_001130037 /// NM_018712																			
7.90	7.52	0.38	6.49E-02	3.82E-01	RP11-336K24.9	mitogen-activated protein-binding protein-interacting protein	chr1q22	218291_at	NM_014017																			
2.63	2.35	0.28	6.50E-02	3.82E-01	---	---	---	1563295_at	---																			
7.10	6.66	0.44	6.51E-02	3.82E-01	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	chr10q26.3	203006_at	NM_005539																			
5.69	4.96	0.73	6.52E-02	3.82E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	1557905_s_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392																			
6.23	5.52	0.70	6.52E-02	3.82E-01	TRIP10	thyroid hormone receptor interactor 10	chr19p13.3	202734_at	NM_004240																			
3.77	3.27	0.50	6.52E-02	3.82E-01	CPA4	carboxypeptidase A4	chr7q32	205832_at	NM_016352																			
6.96	6.42	0.54	6.52E-02	3.82E-01	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	chr18q22.3	217752_s_at	NM_018235																			

3.00	2.50	0.50	6.52E-02	3.82E-01	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	chr1p31	211302_s_at	NM_001037339 /// NM_001037340 /// NM_001037341 /// NM_002600
4.05	3.09	0.95	6.52E-02	3.82E-01	SEC31B	SEC31 homolog B (S. cerevisiae)	chr10q24.31	209889_at	NM_015490
5.26	4.50	0.76	6.52E-02	3.82E-01	HEXIM2	hexamthylene bis-acetamide inducible 2	chr17q21.31	238547_at	NM_144608
2.66	2.35	0.31	6.53E-02	3.82E-01	ZBTB26	zinc finger and BTB domain containing 26	chr9q33.2	227162_at	NM_020924
6.60	6.10	0.50	6.53E-02	3.82E-01	TMEM11	transmembrane protein 11	chr17p11.2	203437_at	NM_003876
11.36	10.54	0.82	6.53E-02	3.82E-01	NOV	nephroblastoma overexpressed gene	chr8q24.1	214321_at	NM_002514
3.35	3.08	0.27	6.53E-02	3.82E-01	POU6F1	POU class 6 homeobox 1	chr12q13.13	216330_s_at	NM_002702
8.04	7.51	0.54	6.53E-02	3.82E-01	RBPMS	RNA binding protein with multiple splicing	chr8p12-p11	209487_at	NM_001008710 /// NM_001008711 /// NM_001008712 /// NM_006867
2.65	2.37	0.28	6.53E-02	3.82E-01	ANKRD44	ankyrin repeat domain 44	chr2q33.1	235777_at	NM_153697
7.48	6.58	0.90	6.54E-02	3.82E-01	FAM113B	family with sequence similarity 113, member B	chr12q13.11	228298_at	NM_138371
7.89	7.43	0.46	6.54E-02	3.82E-01	BZW2	basic leucine zipper and W2 domains 2	chr7p21.1	217809_at	NM_014038
6.77	5.95	0.82	6.54E-02	3.82E-01	NR4A1	nuclear receptor subfamily 4, group A, member 1	chr12q13	211143_x_at	NM_002135 /// NM_173157
7.36	6.40	0.96	6.54E-02	3.82E-01	ADORA3	adenosine A3 receptor	chr1p13.2	223660_at	NM_000677 /// NM_001081976 /// NM_020683
9.13	8.09	1.05	6.54E-02	3.82E-01	FN1	fibronectin 1	chr2q34	210495_x_at	NM_002026 /// NM_054034 /// NM_212474 /// NM_212475 /// NM_212476 /// NM_212478 /// NM_212482
5.82	4.98	0.84	6.54E-02	3.82E-01	VEGFC	vascular endothelial growth factor C	chr4q34.1-q34.3	209946_at	NM_005429
2.83	2.52	0.31	6.54E-02	3.82E-01	ACRC	acidic repeat containing	chrXq13.1	238825_at	NM_052957
5.49	4.45	1.04	6.55E-02	3.82E-01	IKZF4	IKAROS family zinc finger 4 (Eos)	chr12q13	226759_at	NM_022465
7.15	6.74	0.40	6.55E-02	3.83E-01	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	chr19q13.2	203149_at	NM_001042724 /// NM_002856
7.23	6.54	0.69	6.56E-02	3.83E-01	FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	chr7p22	201564_s_at	NM_003088
7.96	7.66	0.31	6.56E-02	3.83E-01	CTA-221G9.4 /// LOC100131004	KIAA1671 protein /// hypothetical protein LOC100131004	chr17q24.1 /// chr22q11.23	225525_at	XM_001724436 /// XM_001726153 /// XM_001726855 /// XR_040421 /// XR_040422 /// XR_040423
5.09	3.79	1.30	6.57E-02	3.83E-01	DACH1	dachshund homolog 1 (Drosophila)	chr13q22	205472_s_at	NM_004392 /// NM_080759 /// NM_080760
5.27	4.62	0.66	6.57E-02	3.83E-01	MFHAS1	malignant fibrous histiocytoma amplified sequence 1	chr8p23.1	213457_at	NM_004225
2.90	2.65	0.26	6.57E-02	3.83E-01	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	chr10p13	223685_s_at	NM_003675
8.86	7.72	1.15	6.57E-02	3.83E-01	GATA6	GATA binding protein 6	chr18q11.1-q11.2	210002_at	NM_005257

6.05	4.87	1.19	6.57E-02	3.83E-01	PLAGL1	pleiomorphic adenoma gene-like 1	chr6q24-q25	207002_s_at	NM_001080951 /// NM_001080952 /// NM_001080953 /// NM_001080954 /// NM_001080955 /// NM_001080956 /// NM_002656 /// NM_006718																				
5.10	4.60	0.51	6.58E-02	3.84E-01	ZNF276	zinc finger protein 276	chr16q24.3	213778_x_at	NM_001113525 /// NM_152287																				
2.66	2.46	0.19	6.59E-02	3.84E-01	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	chr19p13.11	222112_at	NM_021235																				
3.82	3.08	0.74	6.59E-02	3.84E-01	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	chr12p13.3	202499_s_at	NM_006931																				
6.86	6.43	0.43	6.59E-02	3.84E-01	TMEM220	transmembrane protein 220	chr17p13.1	229693_at	NM_001004313																				
2.86	2.52	0.34	6.59E-02	3.84E-01	PRO0478	PRO0478 protein	chr17q25.3	220696_at	---																				
5.42	5.01	0.41	6.59E-02	3.84E-01	ARRDC2	arrestin domain containing 2	chr19p13.11	226055_at	NM_001025604 /// NM_015683																				
4.52	3.84	0.68	6.59E-02	3.84E-01	BAIAP2	BAI1-associated protein 2	chr17q25	205294_at	NM_006340 /// NM_017450 /// NM_017451																				
4.60	3.63	0.97	6.60E-02	3.84E-01	C21orf66	chromosome 21 open reading frame 66	chr21q21.3	218515_at	NM_013329 /// NM_016631 /// NM_058191																				
6.31	5.69	0.62	6.60E-02	3.84E-01	BET1L	blocked early in transport 1 homolog (S. cerevisiae)-like	chr11p15.5	223023_at	NM_001098787 /// NM_016526																				
5.33	4.92	0.40	6.60E-02	3.84E-01	LOC100144415 /// RAD9A	hypothetical LOC100144415 /// RAD9 homolog A (S. pombe)	chr11q13.1-q13.2	1562022_s_at	NM_004584																				
12.18	11.92	0.26	6.60E-02	3.84E-01	EEF1G	eukaryotic translation elongation factor 1 gamma	chr11q12.3	200689_x_at	NM_001404																				
4.86	4.19	0.67	6.60E-02	3.84E-01	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	chr10q24.1	209864_at	NM_012083																				
5.40	5.06	0.34	6.60E-02	3.84E-01	EXOC7	exocyst complex component 7	chr17q25.1	212035_s_at	NM_001013839 /// NM_015219																				
2.96	2.63	0.33	6.61E-02	3.84E-01	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	chr12p11	210206_s_at	NM_004399 /// NM_030653 /// NM_152438																				
6.27	5.63	0.64	6.61E-02	3.84E-01	MGC2752	hypothetical LOC65996	chr19q13.43	230528_s_at	XR_039990 /// XR_039991																				
2.40	2.05	0.35	6.61E-02	3.84E-01	ZNF785	zinc finger protein 785	chr16p11.2	1554769_at	NM_152458																				
5.35	4.76	0.59	6.61E-02	3.84E-01	---	---	---	215450_at	---																				
6.66	5.40	1.26	6.62E-02	3.84E-01	RASD1	RAS, dexamethasone-induced 1	chr17p11.2	223467_at	NM_016084																				
7.94	7.51	0.43	6.62E-02	3.84E-01	AP3D1	adaptor-related protein complex 3, delta 1 subunit	chr19p13.3	206592_s_at	NM_001077523 /// NM_003938																				
7.61	7.22	0.39	6.62E-02	3.84E-01	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)	chr12p13	209233_at	NM_006331																				
4.21	3.63	0.58	6.62E-02	3.84E-01	NEK3	NIMA (never in mitosis gene a)-related kinase 3	chr13q14.13	213116_at	NM_002498 /// NM_152720																				
7.01	6.58	0.43	6.63E-02	3.85E-01	DNASE1L1	deoxyribonuclease I-like 1	chrXq28	203912_s_at	NM_001009932 /// NM_001009933 /// NM_001009934 /// NM_006730																				

7.34	6.68	0.66	6.63E-02	3.85E-01	LST1	leukocyte specific transcript 1	chr6p21.3	211582_x_at	NM_007161 /// NM_205837 /// NM_205838 /// NM_205839 /// NM_205840																				
10.11	9.27	0.84	6.64E-02	3.85E-01	DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	chr17q21	200033_at	NM_004396																				
4.49	3.77	0.73	6.64E-02	3.85E-01	MTG1	Mitochondrial GTPase 1 homolog (S. cerevisiae)	chr10q26.3	238333_s_at	NM_138384																				
7.82	7.05	0.77	6.65E-02	3.85E-01	TMEM41A	transmembrane protein 41A	chr3q27.2	225991_at	NM_080652																				
7.33	7.03	0.30	6.65E-02	3.85E-01	NIP30	NEFA-interacting nuclear protein NIP30	chr16q13	222460_s_at	NM_024946																				
2.87	2.64	0.23	6.65E-02	3.85E-01	LOC100131096	hypothetical protein LOC100131096	chr17q25.3	230526_at	XM_001720907 /// XM_001726205 /// XM_001726705																				
3.03	2.58	0.45	6.66E-02	3.85E-01	BHLHB3	basic helix-loop-helix domain containing, class B, 3	chr12p11.23-p12.1	231243_s_at	NM_030762																				
2.94	2.48	0.45	6.66E-02	3.85E-01	CD163	CD163 molecule	chr12p13.3	216233_at	NM_004244 /// NM_203416																				
2.14	1.92	0.23	6.66E-02	3.85E-01	SLFN13	schlafen family member 13	chr17q12	1553423_a_at	NM_144682																				
6.88	4.45	2.43	6.66E-02	3.85E-01	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	chr7q21.1	205765_at	NM_000777																				
2.65	2.19	0.45	6.67E-02	3.85E-01	PFDN6	prefoldin subunit 6	chr6p21.3	222019_at	NM_014260																				
2.32	2.02	0.31	6.67E-02	3.85E-01	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	chr6p21.3	236203_at	NM_002122 /// XM_001722240 /// XM_001723439																				
5.72	5.32	0.40	6.67E-02	3.85E-01	ZNF584	zinc finger protein 584	chr19q13.43	228148_at	NM_173548																				
7.46	7.12	0.34	6.67E-02	3.85E-01	PQLC3	PQ loop repeat containing 3	chr2p25.1	225579_at	NM_152391																				
8.48	7.95	0.53	6.68E-02	3.85E-01	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	chr16p13.3	1554078_s_at	NM_005147																				
6.15	5.64	0.51	6.68E-02	3.86E-01	TEX10	testis expressed 10	chr9q31.1	218104_at	NM_017746																				
7.14	6.56	0.58	6.68E-02	3.86E-01	TRPT1	tRNA phosphotransferase 1	chr11q13.1	223436_s_at	NM_001033678 /// NM_031472																				
9.16	8.42	0.74	6.68E-02	3.86E-01	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	chr10q23-q24	203059_s_at	NM_001015880 /// NM_004670																				
5.27	4.74	0.53	6.68E-02	3.86E-01	SGSM3	small G protein signaling modulator 3	chr22q13.1-q13.2	215519_x_at	NM_015705																				
8.67	8.29	0.38	6.68E-02	3.86E-01	MEA1	male-enhanced antigen 1	chr6p21.3-p21.1	218061_at	NM_014623																				
2.51	2.15	0.35	6.68E-02	3.86E-01	CXCL2	chemokine (C-X-C motif) ligand 2	chr4q21	1569203_at	NM_002089																				
7.27	6.78	0.50	6.68E-02	3.86E-01	RASA1	RAS p21 protein activator (GTPase activating protein) 1	chr5q13.3	202677_at	NM_002890 /// NM_022650																				
2.72	2.34	0.38	6.68E-02	3.86E-01	POLH	Polymerase (DNA directed), eta	chr6p21.1	1557700_at	NM_006502																				
3.71	3.20	0.51	6.69E-02	3.86E-01	---	---	---	243065_at	---																				
2.08	1.85	0.23	6.69E-02	3.86E-01	C8orf45	chromosome 8 open reading frame 45	chr8q13.1	1552359_at	NM_173518																				
2.17	1.92	0.24	6.69E-02	3.86E-01	---	---	---	241040_at	---																				
4.71	4.25	0.45	6.69E-02	3.86E-01	LOC100133352	hypothetical protein LOC100133352	---	230054_at	XM_001722160																				
4.90	4.10	0.80	6.70E-02	3.86E-01	FAM48A	family with sequence similarity 48, member A	chr13q13.3	226330_s_at	NM_001014286 /// NM_017569																				
6.30	5.81	0.49	6.70E-02	3.86E-01	DPH2	DPH2 homolog (S. cerevisiae)	chr1p34	204514_at	NM_001039589 /// NM_001384																				
3.86	3.41	0.45	6.70E-02	3.86E-01	LIMD1	LIM domains containing 1	chr3p21.3	218850_s_at	NM_014240																				
2.82	2.49	0.33	6.71E-02	3.86E-01	HECTD1	HECT domain containing 1	chr14q12	1570251_at	NM_015382																				
6.53	5.72	0.81	6.71E-02	3.86E-01	FLJ22222	hypothetical protein FLJ22222	chr17q25.3	53071_s_at	NM_024648 /// NM_175902																				
3.84	3.48	0.36	6.71E-02	3.86E-01	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	chr2q23.3	226687_at	NM_017892																				
3.76	3.18	0.59	6.71E-02	3.86E-01	FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	chr9q34.3	1559577_at	NM_004108 /// NM_015837																				
6.06	5.52	0.54	6.71E-02	3.86E-01	GPATCH3	G patch domain containing 3	chr1p35.3-p35.1	218895_at	NM_022078																				
2.90	2.50	0.40	6.71E-02	3.86E-01	ANKRD23	Ankyrin repeat domain 23	chr2q11.2	230384_at	NM_144994																				

8.93	7.81	1.12	6.71E-02	3.86E-01	FN1	fibronectin 1	chr2q34	211719_x_at	NM_002026 /// NM_054034 /// NM_212474 /// NM_212475 /// NM_212476 /// NM_212478 /// NM_212482
5.21	4.80	0.40	6.71E-02	3.86E-01	COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	chr16p13.11-p12.3	209745_at	NM_016138
10.51	10.29	0.22	6.71E-02	3.86E-01	HINT1	histidine triad nucleotide binding protein 1	chr5q31.2	207721_x_at	NM_005340
6.74	6.12	0.62	6.72E-02	3.87E-01	MEN1	multiple endocrine neoplasia I	chr11q13	202645_s_at	NM_000244 /// NM_130799 /// NM_130800 /// NM_130801 /// NM_130802 /// NM_130803 /// NM_130804
2.25	1.88	0.37	6.72E-02	3.87E-01	---	---	---	236882_at	---
2.70	2.44	0.26	6.73E-02	3.87E-01	---	---	---	1562933_at	---
5.56	5.08	0.49	6.73E-02	3.87E-01	PEX14	peroxisomal biogenesis factor 14	chr1p36.22	33760_at	NM_004565
4.52	4.24	0.28	6.73E-02	3.87E-01	C10orf109	chromosome 10 open reading frame 109	chr10p15.3	1561127_at	NM_001098830
6.06	5.03	1.03	6.73E-02	3.87E-01	FZD6	frizzled homolog 6 (Drosophila)	chr8q22.3-q23.1	203987_at	NM_003506
3.43	3.08	0.35	6.74E-02	3.87E-01	LOC100134445	hypothetical protein LOC100134445	---	1557034_s_at	XM_001720526
3.20	2.88	0.32	6.74E-02	3.87E-01	SPATC1	spermatogenesis and centriole associated 1	chr8q24.3	241512_at	NM_001134374 /// NM_198572
4.17	3.56	0.62	6.74E-02	3.87E-01	---	---	---	1556121_at	---
7.57	7.01	0.56	6.74E-02	3.87E-01	CORO1B	coronin, actin binding protein, 1B	chr11q13.1	64486_at	NM_001018070 /// NM_020441
2.98	2.36	0.62	6.74E-02	3.87E-01	---	---	---	1561886_a_at	---
12.27	12.06	0.21	6.74E-02	3.87E-01	RPS17	ribosomal protein S17	chr15q	201665_x_at	NM_001021
7.87	7.48	0.40	6.74E-02	3.87E-01	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	chr10q26.3	201849_at	NM_004052
7.13	6.47	0.66	6.74E-02	3.87E-01	DVL1 /// LOC642469	dishevelled, dsh homolog 1 (Drosophila) /// hypothetical LOC642469	chr1p36	203230_at	NM_004421 /// NM_182779 /// XR_042342 /// XR_042429 /// XR_042497
3.73	3.46	0.27	6.75E-02	3.87E-01	ACTR5	ARP5 actin-related protein 5 homolog (yeast)	chr20q11.23	222147_s_at	NM_024855
3.11	2.74	0.37	6.75E-02	3.87E-01	GATA3	GATA binding protein 3	chr10p15	209603_at	NM_001002295 /// NM_002051
3.70	3.29	0.40	6.75E-02	3.87E-01	LRP12	low density lipoprotein-related protein 12	chr8q22.2-q23.1	219631_at	NM_013437
3.23	2.61	0.61	6.75E-02	3.87E-01	TTC18	tetratricopeptide repeat domain 18	chr10q22.2	229170_s_at	NM_145170
9.89	9.46	0.43	6.75E-02	3.87E-01	MGC3205 /// TMEM205	hypothetical protein MGC3205 /// transmembrane protein 205	chr19p13.13 /// chr19p13.2	225003_at	NM_198536
4.08	3.53	0.55	6.75E-02	3.87E-01	FAM84B	family with sequence similarity 84, member B	chr8q24.21	225864_at	NM_174911
4.98	4.54	0.44	6.76E-02	3.87E-01	FANCF	Fanconi anemia, complementation group F	chr11p15	222713_s_at	NM_022725
2.73	2.46	0.26	6.76E-02	3.87E-01	---	---	---	240804_at	---
6.71	6.11	0.60	6.76E-02	3.87E-01	EPOR	erythropoietin receptor	chr19p13.3-p13.2	215054_at	NM_000121
3.09	2.71	0.38	6.77E-02	3.87E-01	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	1563229_at	NR_002612
5.94	5.52	0.41	6.77E-02	3.87E-01	TCEA2	transcription elongation factor A (SII), 2	chr20q13.33	241428_x_at	NM_003195 /// NM_198723
4.81	4.34	0.46	6.78E-02	3.87E-01	MDC1	mediator of DNA damage checkpoint 1	chr6p21.3	203061_s_at	NM_014641

4.75	3.84	0.92	6.78E-02	3.88E-01	AURKA	aurora kinase A	chr20q13.2-q13.3	208079_s_at	NM_003600 /// NM_198433 /// NM_198434 /// NM_198435 /// NM_198436 /// NM_198437																				
5.73	5.28	0.45	6.78E-02	3.88E-01	TBX3	T-box 3	chr12q24.1	222917_s_at	NM_005996 /// NM_016569																				
7.26	6.18	1.07	6.78E-02	3.88E-01	UST	uronyl-2-sulfotransferase	chr6q25.1	205139_s_at	NM_005715																				
3.53	3.07	0.46	6.78E-02	3.88E-01	---	---	---	238485_at	---																				
8.39	8.09	0.30	6.78E-02	3.88E-01	COMMD7	COMM domain containing 7	chr20q11.21	224815_at	NM_001099339 /// NM_053041																				
6.11	5.82	0.29	6.79E-02	3.88E-01	MBD1	methyl-CpG binding domain protein 1	chr18q21	208595_s_at	NM_002384 /// NM_015844 /// NM_015845 /// NM_015846 /// NM_015847																				
6.88	6.53	0.35	6.79E-02	3.88E-01	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	chr22q13.2	225682_s_at	NM_001018050 /// NM_001018052 /// NM_138338																				
6.66	6.32	0.34	6.79E-02	3.88E-01	PPP5C	protein phosphatase 5, catalytic subunit	chr19q13.3	201979_s_at	NM_006247																				
2.48	2.26	0.23	6.79E-02	3.88E-01	---	---	---	221174_at	---																				
10.87	10.41	0.45	6.80E-02	3.88E-01	EEF1B2	eukaryotic translation elongation factor 1 beta 2	chr2q33-q34	200705_s_at	NM_001037663 /// NM_001959 /// NM_021121																				
6.79	6.44	0.35	6.80E-02	3.88E-01	C16orf42	chromosome 16 open reading frame 42	chr16p13.3	213104_at	NM_001001410																				
7.38	6.89	0.50	6.80E-02	3.88E-01	CHMP7	CHMP family, member 7	chr8p21.3	212313_at	NM_152272																				
5.37	4.74	0.63	6.81E-02	3.88E-01	GNAS	GNAS complex locus	chr20q13.3	228173_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259																				
2.24	1.87	0.37	6.81E-02	3.88E-01	LOC100129196	similar to hCG2033298	chr1p35.2	1557557_at	XM_001724260 /// XM_001724594 /// XM_001724756																				

8.90	7.74	1.16	6.81E-02	3.88E-01	FN1	fibronectin 1	chr2q34	212464_s_at	NM_002026 /// NM_054034 /// NM_212474 /// NM_212475 /// NM_212476 /// NM_212478 /// NM_212482																				
2.16	1.92	0.25	6.81E-02	3.88E-01	---	---	---	1557314_at	---																				
3.73	3.17	0.56	6.81E-02	3.88E-01	---	---	---	231233_at	---																				
6.32	5.86	0.46	6.81E-02	3.88E-01	NPM3	nucleophosmin/nucleoplasmin, 3	chr10q24.31	205129_at	NM_006993																				
5.15	4.82	0.33	6.82E-02	3.88E-01	C2orf42	chromosome 2 open reading frame 42	chr2p14	219128_at	NM_017880																				
9.55	9.20	0.36	6.82E-02	3.88E-01	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	chr2q31.1	207508_at	NM_001002258 /// NM_001689																				
2.75	2.29	0.46	6.82E-02	3.88E-01	TUG1	taurine upregulated gene 1	chr22q12.2	228397_at	NR_002323																				
3.64	3.39	0.26	6.82E-02	3.88E-01	DTNA	dystrobrevin, alpha	chr18q12	211493_x_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981																				
2.91	2.56	0.35	6.83E-02	3.88E-01	TPI1	triosephosphate isomerase 1	chr12p13	210050_at	NM_000365																				
7.15	6.85	0.31	6.83E-02	3.88E-01	USE1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	chr19p13.11	219348_at	NM_018467																				
2.72	2.34	0.38	6.83E-02	3.88E-01	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	chr13q32	1554918_a_at	NM_001105515 /// NM_005845																				
5.72	4.52	1.20	6.83E-02	3.88E-01	RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4	chr2q31-q32	205651_x_at	NM_001100397 /// NM_007023																				
2.27	1.96	0.30	6.84E-02	3.88E-01	LOC100131480	similar to hCG2045844	chr2q31.2	237375_at	XM_001722309 /// XM_001722324 /// XM_001725957																				
2.75	2.30	0.45	6.84E-02	3.88E-01	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	chr12p12.1	1557374_at	NM_005691 /// NM_020297 /// NM_020298																				
3.17	2.44	0.73	6.84E-02	3.88E-01	---	---	---	222324_at	---																				
5.98	5.52	0.45	6.84E-02	3.88E-01	SUDS3	suppressor of defective silencing 3 homolog (S. cerevisiae)	chr12q24.23	233841_s_at	NM_022491																				
4.80	4.49	0.31	6.85E-02	3.88E-01	LOC285412 /// TOX4	similar to KIAA0737 protein /// TOX high mobility group box family member 4	chr14q11.2 /// chr4q25	217448_s_at	NM_014828 /// XR_017405 /// XR_019409 /// XR_039448																				
7.22	6.79	0.43	6.86E-02	3.89E-01	GOLGA2	golgi autoantigen, golgin subfamily a, 2	chr9q34.11	225672_at	NM_004486																				
3.57	2.85	0.72	6.87E-02	3.89E-01	F2RL1	coagulation factor II (thrombin) receptor-like 1	chr5q13	206429_at	NM_005242																				
4.10	3.37	0.74	6.87E-02	3.89E-01	EPHA4	EPH receptor A4	chr2q36.1	228948_at	NM_004438																				

7.37	6.62	0.75	6.87E-02	3.89E-01	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	chr16q21-q22.1	224733_at	NM_001048251 /// NM_144601 /// NM_181553 /// NM_181554																			
5.70	5.08	0.62	6.87E-02	3.89E-01	FAM49A	family with sequence similarity 49, member A	chr2p24.3	209683_at	NM_030797																			
8.07	7.61	0.45	6.87E-02	3.89E-01	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	chr19q13.43	203109_at	NM_003969																			
4.43	4.03	0.40	6.87E-02	3.89E-01	MORC2	MORC family CW-type zinc finger 2	chr22q12.2	216863_s_at	NM_014941																			
8.72	8.33	0.39	6.87E-02	3.89E-01	ARL6IP4 /// OGFOD2	ADP-ribosylation-like factor 6 interacting protein 4 /// 2-oxoglutarate and iron-dependent oxygenase domain containing 2	chr12q24.31	218216_x_at	NM_001002251 /// NM_001002252 /// NM_016638 /// NM_018694 /// NM_024623																			
3.12	2.78	0.33	6.88E-02	3.89E-01	ABCA17P	ATP-binding cassette, sub-family A (ABC1), member 17 (pseudogene)	chr16p13.3	231164_at	NR_003574																			
4.70	4.22	0.48	6.88E-02	3.89E-01	CCHCR1	coiled-coil alpha-helical rod protein 1	chr6p21.3	209698_at	NM_001105563 /// NM_001105564 /// NM_019052																			
7.00	6.63	0.37	6.88E-02	3.89E-01	NECAB3	N-terminal EF-hand calcium binding protein 3	chr20q11.22	223954_x_at	NM_031231 /// NM_031232																			
6.82	6.30	0.52	6.88E-02	3.89E-01	CCS	copper chaperone for superoxide dismutase	chr11q13	203522_at	NM_005125																			
5.46	4.98	0.48	6.89E-02	3.89E-01	---	---	---	232515_at	---																			
7.17	5.82	1.35	6.89E-02	3.89E-01	BCAT1	branched chain aminotransferase 1, cytosolic	chr12p12.1	226517_at	NM_005504																			
2.64	2.32	0.33	6.90E-02	3.90E-01	LOC284513	hypothetical protein LOC284513	chr1p36.13	1556597_a_at	---																			
7.35	6.99	0.36	6.90E-02	3.90E-01	GADD45GIP1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	chr19p13.13	212891_s_at	NM_052850																			
2.00	1.80	0.20	6.91E-02	3.90E-01	TPH1	tryptophan hydroxylase 1	chr11p15.3-p14	214601_at	NM_004179																			
3.00	2.66	0.34	6.91E-02	3.90E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	211091_s_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833																			
12.32	12.06	0.26	6.91E-02	3.90E-01	RPS12	ribosomal protein S12	chr6q23.2	213377_x_at	NM_001016																			
6.84	6.52	0.32	6.92E-02	3.90E-01	ALG9	asparagine-linked glycosylation 9 homolog (S. cerevisiae, alpha-1,2-mannosyltransferase)	chr11q23	219374_s_at	NM_001077690 /// NM_001077691 /// NM_001077692 /// NM_024740																			
7.86	6.82	1.05	6.92E-02	3.90E-01	VEGFA	vascular endothelial growth factor A	chr6p12	210512_s_at	NM_001025366 /// NM_001025367 /// NM_001025368 /// NM_001025369 /// NM_001025370 /// NM_001033756 /// NM_003376																			
2.47	2.24	0.22	6.92E-02	3.90E-01	---	---	---	1566462_at	---																			

4.98	4.17	0.81	6.92E-02	3.90E-01	AMIGO3 /// GMPPB	adhesion molecule with Ig-like domain 3 /// GDP-mannose pyrophosphorylase B	chr3p21 /// chr3p21.31	222710_at	NM_013334 /// NM_021971 /// NM_198722																				
3.09	2.58	0.51	6.92E-02	3.90E-01	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	chr3p22	209884_s_at	NM_003615																				
3.20	2.73	0.48	6.92E-02	3.90E-01	GINS1	GINS complex subunit 1 (Psf1 homolog)	chr20p11.21	206102_at	NM_021067																				
6.37	5.93	0.43	6.93E-02	3.90E-01	GAK	cyclin G associated kinase	chr4p16	202281_at	NM_005255																				
1.94	1.76	0.18	6.93E-02	3.90E-01	---	---	---	1560999_a_at	---																				
3.84	3.36	0.48	6.93E-02	3.90E-01	KIAA1704	KIAA1704	chr13q13-q14	229891_x_at	NM_018559																				
3.94	3.63	0.31	6.93E-02	3.90E-01	---	---	---	235159_at	---																				
6.47	6.01	0.47	6.93E-02	3.90E-01	CBX7	chromobox homolog 7	chr22q13.1	212914_at	NM_175709																				
10.19	9.90	0.29	6.94E-02	3.91E-01	EIF3K	eukaryotic translation initiation factor 3, subunit K	chr19q13.2	221494_x_at	NM_013234																				
2.75	2.23	0.52	6.94E-02	3.91E-01	CNTNAP3 /// CNTNAP3B /// LOC643827 /// LOC653355 /// RP11-138L21.1	contactin associated protein-like 3 /// contactin associated protein-like 3B /// similar to cell recognition molecule CASPR3 /// hypothetical LOC653355 /// similar to cell recognition molecule CASPR3	chr9p11.2 /// chr9p13.1 /// chr9p24.3 /// chr9q12	223796_at	NM_033655 /// XM_001128489 /// XM_001714537 /// XM_001720460 /// XM_001720970 /// XM_927067																				
4.56	4.13	0.43	6.96E-02	3.91E-01	FLJ20209	hypothetical LOC57245	chr3p21.31	226171_at	XM_933464 /// XM_944968																				
4.22	3.72	0.50	6.96E-02	3.91E-01	---	---	---	213087_s_at	---																				
7.68	7.28	0.41	6.96E-02	3.91E-01	OTUB1	OTU domain, ubiquitin aldehyde binding 1	chr11q13.1	201245_s_at	NM_017670 /// NR_003089																				
2.76	2.44	0.32	6.97E-02	3.91E-01	ZBTB24	zinc finger and BTB domain containing 24	chr6q21	1554036_at	NM_014797																				
7.02	6.23	0.79	6.97E-02	3.91E-01	LOC283666	Hypothetical LOC283666	chr15q21.3	236266_at	---																				
2.68	2.39	0.28	6.97E-02	3.91E-01	FLJ12547 /// LOC100128612	hypothetical protein FLJ12547 /// hypothetical protein LOC100128612	chr16q24.3	220715_at	XM_001718427 /// XM_001719120 /// XM_001732825																				
5.85	5.29	0.56	6.97E-02	3.91E-01	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	chr12q12-q14	231974_at	NM_003482																				
3.95	3.41	0.54	6.98E-02	3.92E-01	ZNF786	zinc finger protein 786	chr7q36.1	239083_at	NM_152411																				
2.83	2.56	0.27	6.98E-02	3.92E-01	TADA3L	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	chr3p25.3	211221_at	NM_006354 /// NM_133480																				
3.89	3.08	0.81	6.98E-02	3.92E-01	IL1B	interleukin 1, beta	chr2q14	39402_at	NM_000576																				
12.37	11.23	1.14	6.98E-02	3.92E-01	APOE	apolipoprotein E	chr19q13.2	203381_s_at	NM_000041																				
2.44	2.23	0.21	6.99E-02	3.92E-01	KLC4	kinesin light chain 4	chr6p21.1	1553675_at	NM_138343 /// NM_201521 /// NM_201522 /// NM_201523																				
8.49	7.31	1.18	6.99E-02	3.92E-01	MXRA5	matrix-remodelling associated 5	chrXp22.33	209596_at	NM_015419																				
4.15	3.75	0.40	6.99E-02	3.92E-01	C6orf151	chromosome 6 open reading frame 151	chr6p24.3	226263_at	NM_152551																				
3.51	3.21	0.30	7.00E-02	3.92E-01	GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	chr17q25.1	211815_s_at	NM_014001 /// NM_138619																				
3.29	2.78	0.51	7.00E-02	3.92E-01	LYNX1	Ly6/neurotoxin 1	chr8q24.3	244224_x_at	NM_023946 /// NM_177457 /// NM_177458 /// NM_177476 /// NM_177477																				
4.88	4.33	0.55	7.00E-02	3.92E-01	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	chrXp22.2-p22.1	200979_at	NM_000284																				
2.62	2.37	0.25	7.00E-02	3.92E-01	ZSCAN20	zinc finger and SCAN domain containing 20	chr1p34.3	1554790_at	NM_145238																				
2.80	2.49	0.31	7.00E-02	3.92E-01	TTC22	tetratricopeptide repeat domain 22	chr1p32.3	220309_at	NM_001114108 /// NM_017904																				
2.73	2.49	0.24	7.01E-02	3.92E-01	SFMBT2	Scm-like with four mbt domains 2	chr10p14	232938_at	NM_001029880																				

3.63	3.32	0.31	7.01E-02	3.92E-01	ANTXR1	anthrax toxin receptor 1	chr2p13.1	220093_at	NM_018153 /// NM_032208 /// NM_053034																				
3.90	3.14	0.76	7.01E-02	3.92E-01	MYLIP	myosin regulatory light chain interacting protein	chr6p23-p22.3	228097_at	NM_013262																				
6.36	5.70	0.66	7.01E-02	3.92E-01	JMJD2B	jumonji domain containing 2B	chr19p13.3	212495_at	NM_015015																				
6.12	5.48	0.64	7.01E-02	3.92E-01	KIF1B	kinesin family member 1B	chr1p36.2	225878_at	NM_015074 /// NM_183416																				
8.02	7.56	0.46	7.02E-02	3.92E-01	C19orf70	chromosome 19 open reading frame 70	chr19p13.3	225823_at	NM_205767																				
5.37	4.84	0.53	7.02E-02	3.92E-01	C19orf29	chromosome 19 open reading frame 29	chr19p13.3	213815_x_at	NM_001080543 /// NM_021231																				
6.31	5.84	0.47	7.02E-02	3.92E-01	---	---	---	226102_at	---																				
5.05	4.17	0.88	7.03E-02	3.93E-01	LOC100128821 /// ZEB2	hypothetical protein LOC100128821 /// zinc finger E-box binding homeobox 2	chr2q22 /// chr2q22.3	235593_at	NM_014795 /// XM_001723541 /// XM_001723999 /// XM_001724917																				
11.51	11.21	0.30	7.04E-02	3.93E-01	HYPK /// SERF2	Huntingtin interacting protein K /// small EDRK-rich factor 2	chr15q15.3	224625_x_at	NM_001018108 /// NM_016400																				
3.25	2.85	0.40	7.04E-02	3.93E-01	TACR1	tachykinin receptor 1	chr2p13.1	208049_s_at	NM_001058 /// NM_015727																				
3.59	2.18	1.42	7.04E-02	3.93E-01	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	chr3q28	1555996_s_at	NM_001967																				
6.89	6.23	0.66	7.04E-02	3.93E-01	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	chr6p21.31	212747_at	NM_015245																				
5.91	5.41	0.50	7.04E-02	3.93E-01	DICER1	dicer 1, ribonuclease type III	chr14q32.13	212888_at	NM_030621 /// NM_177438																				
2.85	2.30	0.55	7.05E-02	3.93E-01	---	---	---	231697_s_at	---																				
2.20	1.92	0.28	7.05E-02	3.93E-01	SH3TC2	SH3 domain and tetratricopeptide repeats 2	chr5q32	233561_at	NM_024577																				
2.75	2.46	0.29	7.05E-02	3.93E-01	LOC441052	hypothetical gene supported by AF131741	chr4q34.1	232443_at	XR_041938 /// XR_041939 /// XR_041940																				
3.24	2.49	0.75	7.06E-02	3.93E-01	RBBP6	retinoblastoma binding protein 6	chr16p12.2	232044_at	NM_006910 /// NM_018703 /// NM_032626																				
5.56	4.91	0.65	7.06E-02	3.93E-01	GMDS	GDP-mannose 4,6-dehydratase	chr6p25	204875_s_at	NM_001500																				
9.90	9.03	0.87	7.07E-02	3.93E-01	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	chr1q32	1555950_a_at	NM_000574 /// NM_001114752																				
3.70	3.33	0.37	7.07E-02	3.94E-01	TMEM134	transmembrane protein 134	chr11q13.1	233018_at	NM_001078650 /// NM_001078651 /// NM_025124																				
7.47	6.96	0.51	7.07E-02	3.94E-01	KCTD20	potassium channel tetramerisation domain containing 20	chr6p21.31	228299_at	NM_173562																				
6.16	5.79	0.38	7.08E-02	3.94E-01	COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	chr16p13.11-p12.3	209746_s_at	NM_016138																				
4.26	2.88	1.39	7.08E-02	3.94E-01	DCN	Decorin	chr12q21.33	240556_at	NM_001920 /// NM_133503 /// NM_133504 /// NM_133505 /// NM_133506 /// NM_133507																				
6.17	5.38	0.79	7.08E-02	3.94E-01	CAPRIN2	caprin family member 2	chr12p11	218456_at	NM_001002259 /// NM_023925 /// NM_032156																				

4.12	3.76	0.36	7.08E-02	3.94E-01	GGT1 /// GGT2 /// GGT3P /// GGTLC2 /// GGTLC3	gamma-glutamyltransferase 1 /// gamma-glutamyltransferase 2 /// gamma-glutamyltransferase 3 pseudogene /// gamma-glutamyltransferase light chain 2 /// gamma-glutamyltransferase light chain 3	chr22q11.21 /// chr22q11.22 /// chr22q11.23	215603_x_at	NM_001032364 /// NM_001032365 /// NM_005265 /// NM_013430 /// NM_199127 /// NR_003267 /// XM_001128296 /// XM_001128302 /// XM_001128310 /// XM_001129377 /// XM_001129425 /// XR_042175
5.49	5.24	0.25	7.09E-02	3.94E-01	ISY1	ISY1 splicing factor homolog (S. cerevisiae)	chr3q21.3	223429_x_at	NM_020701
7.48	7.17	0.30	7.09E-02	3.94E-01	DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12	chr10q22.1	202867_s_at	NM_001002762 /// NM_017626
4.04	3.70	0.33	7.09E-02	3.94E-01	ATP6V1E2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2	chr2p21	1552286_at	NM_080653
3.27	2.86	0.41	7.09E-02	3.94E-01	CLDN15	claudin 15	chr7q11.22	1552845_at	NM_014343
4.13	3.69	0.45	7.10E-02	3.94E-01	MYBBP1A	MYB binding protein (P160) 1a	chr17p13.3	233803_s_at	NM_001105538 /// NM_014520
6.39	5.68	0.71	7.10E-02	3.94E-01	CNO	cappuccino homolog (mouse)	chr4p16.1	223431_at	NM_018366
7.21	6.55	0.66	7.11E-02	3.94E-01	HDAC3	histone deacetylase 3	chr5q31	216326_s_at	NM_003883
2.99	2.49	0.50	7.11E-02	3.94E-01	KIAA1276	KIAA1276 protein	chr4p16	233823_at	XM_001717325 /// XM_039169 /// XM_940199
7.32	7.09	0.23	7.11E-02	3.94E-01	C20orf43	chromosome 20 open reading frame 43	chr20q13.31	233842_x_at	NM_016407
3.33	2.70	0.63	7.11E-02	3.94E-01	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	chr19p13.3	206907_at	NM_003811
6.38	5.47	0.91	7.11E-02	3.94E-01	JUND	jun D proto-oncogene	chr19p13.2	203751_x_at	NM_005354
2.38	2.11	0.27	7.12E-02	3.94E-01	---	---	---	236875_at	---
7.14	6.81	0.33	7.12E-02	3.94E-01	SIAH1	seven in absentia homolog 1 (Drosophila)	chr16q12	202981_x_at	NM_001006610 /// NM_003031
7.63	7.18	0.44	7.12E-02	3.94E-01	ZNF664	zinc finger protein 664	chr12q24.31	224593_at	NM_152437
3.10	2.42	0.68	7.12E-02	3.94E-01	C1orf104	chromosome 1 open reading frame 104	chr1q22	1552862_at	NM_001039517
2.32	2.01	0.31	7.13E-02	3.94E-01	---	---	---	235629_at	---
5.10	4.43	0.67	7.13E-02	3.94E-01	TMCO6	transmembrane and coiled-coil domains 6	chr5q31.3	221096_s_at	NM_018502
8.11	7.04	1.07	7.14E-02	3.95E-01	IGFBP6	insulin-like growth factor binding protein 6	chr12q13	203851_at	NM_002178
6.59	6.15	0.43	7.14E-02	3.95E-01	PFDN4	prefoldin subunit 4	chr20q13.2	205361_s_at	NM_002623
4.73	4.35	0.38	7.14E-02	3.95E-01	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	chr16p12.1	233458_at	NM_018119
4.18	3.42	0.76	7.14E-02	3.95E-01	FLJ31306	hypothetical protein FLJ31306	chr14q23.1	225724_at	XM_001715627 /// XM_001717968
5.24	4.64	0.60	7.14E-02	3.95E-01	ELF4	E74-like factor 4 (ets domain transcription factor)	chrXq26	31845_at	NM_001127197 /// NM_001421
6.28	5.96	0.32	7.15E-02	3.95E-01	C15orf44	chromosome 15 open reading frame 44	chr15q22.31	221265_s_at	NM_030800
3.18	2.86	0.32	7.15E-02	3.95E-01	LEFTY1	left-right determination factor 1	chr1q42.1	206268_at	NM_020997
4.53	4.01	0.52	7.16E-02	3.95E-01	UBXN11	UBX domain protein 11	chr1p36.11	227716_at	NM_001077262 /// NM_145345 /// NM_183008
5.79	4.99	0.80	7.16E-02	3.95E-01	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	227390_at	NR_002766 /// NR_003530 /// NR_003531
7.65	7.29	0.36	7.16E-02	3.95E-01	JMJD1B	jumonji domain containing 1B	chr5q31	201643_x_at	NM_016604
2.08	1.84	0.24	7.16E-02	3.95E-01	SERAC1	serine active site containing 1	chr6q25.3	1569864_at	NM_032861

3.48	3.18	0.30	7.16E-02	3.95E-01	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	chr22q12.2	210581_x_at	NM_014323 /// NM_032050 /// NM_032051 /// NM_032052
3.76	3.42	0.34	7.16E-02	3.95E-01	---	---	---	1566577_at	---
7.16	6.88	0.29	7.16E-02	3.95E-01	MESDC2	mesoderm development candidate 2	chr15q13	224679_at	NM_015154
4.03	3.46	0.57	7.17E-02	3.95E-01	PLAGL2	pleiomorphic adenoma gene-like 2	chr20q11.21	202925_s_at	NM_002657
7.46	6.75	0.71	7.17E-02	3.95E-01	---	---	---	237186_at	---
5.96	5.65	0.31	7.17E-02	3.95E-01	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	chr19p13.3|19p13.3-p13.2	203093_s_at	NM_006351
5.17	4.53	0.64	7.18E-02	3.96E-01	ABR	active BCR-related gene	chr17p13.3	214671_s_at	NM_001092 /// NM_021962
8.81	7.85	0.96	7.19E-02	3.96E-01	SLC25A37	solute carrier family 25, member 37	chr8p21.2	222528_s_at	NM_016612
6.41	5.02	1.39	7.19E-02	3.96E-01	BHLHB2	basic helix-loop-helix domain containing, class B, 2	chr3p26	201169_s_at	NM_003670
8.30	7.66	0.63	7.19E-02	3.96E-01	FAM36A	family with sequence similarity 36, member A	chr1q44	224820_at	NM_198076
6.14	5.82	0.32	7.20E-02	3.96E-01	TPMT	thiopurine S-methyltransferase	chr6p22.3	203672_x_at	NM_000367
6.79	6.34	0.46	7.21E-02	3.96E-01	KCTD2	potassium channel tetramerisation domain containing 2	chr17q25.1	212564_at	NM_015353
2.62	2.36	0.26	7.21E-02	3.96E-01	LOC731488 /// RGS8	Similar to Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (Fp) (Flavoprotein subunit of complex II) /// Regulator of G-protein signaling 8	chr1q25	234297_at	NM_001102450 /// NM_033345 /// XR_015496
4.75	4.37	0.38	7.21E-02	3.96E-01	NLE1	notchless homolog 1 (Drosophila)	chr17q12	203867_s_at	NM_001014445 /// NM_018096
9.97	9.73	0.24	7.21E-02	3.96E-01	GABARAPL2	GABA(A) receptor-associated protein-like 2	chr16q22.3-q24.1	209046_s_at	NM_007285
8.81	8.28	0.52	7.21E-02	3.96E-01	LIMS1	LIM and senescent cell antigen-like domains 1	chr2q12.3-q13	212687_at	NM_004987
5.00	4.34	0.66	7.22E-02	3.96E-01	PIAS4	protein inhibitor of activated STAT, 4	chr19p13.3	212881_at	NM_015897
4.59	3.98	0.61	7.22E-02	3.96E-01	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	chr12q15	202968_s_at	NM_003583 /// NM_006482
5.24	4.81	0.43	7.23E-02	3.97E-01	ZNF783	zinc finger family member 783	chr7q36.1	78495_at	NM_001004302
4.65	4.13	0.52	7.23E-02	3.97E-01	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	chr18q21.3	206034_at	NM_001031848 /// NM_002640 /// NM_198833
2.80	2.48	0.32	7.23E-02	3.97E-01	ASPHD2	aspartate beta-hydroxylase domain containing 2	chr22q12.1	227014_at	NM_020437
4.71	4.16	0.55	7.24E-02	3.97E-01	RTN1	reticulon 1	chr14q23.1	203485_at	NM_021136 /// NM_206852 /// NM_206857
2.49	2.19	0.30	7.25E-02	3.97E-01	---	---	---	215077_at	---
6.42	5.89	0.53	7.25E-02	3.97E-01	RNF123	ring finger protein 123	chr3p24.3	224186_s_at	NM_022064
4.92	4.26	0.65	7.25E-02	3.97E-01	CRY1	cryptochrome 1 (photolyase-like)	chr12q23-q24.1	209674_at	NM_004075
4.38	4.06	0.32	7.25E-02	3.97E-01	---	---	---	215185_at	---
5.70	5.16	0.54	7.25E-02	3.97E-01	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	chr6q27	224685_at	NM_001040000 /// NM_001040001 /// NM_005936
12.14	11.90	0.24	7.25E-02	3.97E-01	EEF1G	eukaryotic translation elongation factor 1 gamma	chr11q12.3	211345_x_at	NM_001404
3.69	3.30	0.40	7.25E-02	3.97E-01	L3MBTL	l(3)mbt-like (Drosophila)	chr20q13.12	213837_at	NM_015478 /// NM_032107
2.84	2.55	0.30	7.25E-02	3.97E-01	C19orf26	chromosome 19 open reading frame 26	chr19p13.3	215325_x_at	NM_152769
9.80	8.91	0.89	7.26E-02	3.97E-01	TOB1	transducer of ERBB2, 1	chr17q21	202704_at	NM_005749
6.23	5.73	0.50	7.26E-02	3.97E-01	KLHL22	kelch-like 22 (Drosophila)	chr22q11.21	49329_at	NM_032775
7.97	7.62	0.35	7.27E-02	3.97E-01	TMEM179B	transmembrane protein 179B	chr11q12.3	228089_x_at	NM_199337
5.82	5.29	0.53	7.27E-02	3.97E-01	C1orf55	chromosome 1 open reading frame 55	chr1q42.12	244103_at	NM_152608
1.99	1.76	0.23	7.28E-02	3.98E-01	---	---	---	242116_x_at	---
2.52	2.27	0.25	7.29E-02	3.98E-01	---	---	---	1566873_at	---

4.02	3.66	0.36	7.29E-02	3.98E-01	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	chr17q22	210380_s_at	NM_018896 /// NM_198376 /// NM_198377 /// NM_198378 /// NM_198379 /// NM_198380 /// NM_198382 /// NM_198383 /// NM_198384 /// NM_198385 /// NM_198386 /// NM_198387 /// NM_198388 /// NM_198396 /// NM_198397																			
5.84	5.43	0.41	7.30E-02	3.98E-01	MYADM	myeloid-associated differentiation marker	chr19q13.41	224920_x_at	NM_001020818 /// NM_001020819 /// NM_001020820 /// NM_001020821 /// NM_138373																			
2.71	2.42	0.29	7.30E-02	3.98E-01	---	---	---	1561906_at	---																			
7.36	6.94	0.42	7.31E-02	3.99E-01	TSPAN6	tetraspanin 6	chrXq22	209108_at	NM_003270																			
5.19	4.68	0.52	7.31E-02	3.99E-01	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	chr17q21.33	234464_s_at	NM_152463																			
7.31	6.30	1.00	7.31E-02	3.99E-01	CD83	CD83 molecule	chr6p23	204440_at	NM_001040280 /// NM_004233																			
6.28	5.73	0.55	7.31E-02	3.99E-01	TMUB2	transmembrane and ubiquitin-like domain containing 2	chr17q21.31	218419_s_at	NM_001076674 /// NM_024107 /// NM_177441																			
4.93	4.51	0.42	7.31E-02	3.99E-01	ATXN3	ataxin 3	chr14q24.3-q32.2	235240_at	NM_001127696 /// NM_001127697 /// NM_004993 /// NM_030660																			
7.67	7.15	0.52	7.32E-02	3.99E-01	CD53	CD53 molecule	chr1p13	203416_at	NM_000560 /// NM_001040033																			
4.68	3.94	0.74	7.32E-02	3.99E-01	C11orf17 /// NUAK2	chromosome 11 open reading frame 17 /// NUAK family, SNF1-like kinase, 2	chr11p15.3 /// chr1q32.1	220987_s_at	NM_020642 /// NM_030952 /// NM_182901																			
10.07	9.69	0.38	7.33E-02	3.99E-01	PRDX5	peroxiredoxin 5	chr11q13	1560587_s_at	NM_012094 /// NM_181651 /// NM_181652																			
2.54	2.26	0.28	7.35E-02	3.99E-01	---	---	---	217300_at	---																			

7.75	6.42	1.33	7.35E-02	3.99E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	212998_x_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447																				
5.44	4.52	0.92	7.36E-02	4.00E-01	TMEM177	transmembrane protein 177	chr2q14.2	218897_at	NM_001105198 /// NM_001105199 /// NM_030577																				
3.27	2.87	0.40	7.36E-02	4.00E-01	C5orf28	Chromosome 5 open reading frame 28	chr5p12	1557828_a_at	NM_022483																				
2.27	2.05	0.22	7.36E-02	4.00E-01	---	---	---	237644_at	---																				
5.57	5.15	0.42	7.37E-02	4.00E-01	GEMIN8	gem (nuclear organelle) associated protein 8	chrXp22.2	222854_s_at	NM_001042479 /// NM_001042480 /// NM_017856																				
5.03	4.37	0.66	7.37E-02	4.00E-01	NEK4	NIMA (never in mitosis gene a)-related kinase 4	chr3p21.1	204634_at	NM_003157																				
5.90	5.46	0.43	7.37E-02	4.00E-01	ATPAF2	ATP synthase mitochondrial F1 complex assembly factor 2	chr17p11.2	213057_at	NM_145691																				
6.13	5.80	0.32	7.38E-02	4.00E-01	NUP98	nucleoporin 98kDa	chr11p15.5	203195_s_at	NM_005387 /// NM_016320 /// NM_139131 /// NM_139132																				
6.82	6.19	0.63	7.38E-02	4.00E-01	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	chr16q22.1	224904_at	NM_017990																				
5.52	5.06	0.46	7.38E-02	4.00E-01	LARS2	leucyl-tRNA synthetase 2, mitochondrial	chr3p21.3	204016_at	NM_015340																				
7.74	7.29	0.45	7.38E-02	4.00E-01	UNC119B	unc-119 homolog B (C. elegans)	chr12q24.31	202365_at	NM_001080533																				
2.87	2.53	0.34	7.40E-02	4.01E-01	LOC286052	hypothetical protein LOC286052	chr8q24.13	241370_at	---																				

7.38	6.82	0.57	7.40E-02	4.01E-01	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	chr1q42.11	209250_at	NM_003676 /// NM_144780																				
2.46	2.23	0.23	7.40E-02	4.01E-01	---	---	---	1558599_at	---																				
7.54	6.87	0.67	7.40E-02	4.01E-01	EMID1	EMI domain containing 1	chr22q12.2	213779_at	NM_133455																				
2.89	2.57	0.32	7.41E-02	4.01E-01	KLHL23	kelch-like 23 (Drosophila)	chr2q31.1	213610_s_at	NM_144711																				
6.49	6.09	0.40	7.41E-02	4.01E-01	MAP3K3	mitogen-activated protein kinase kinase kinase 3	chr17q23.3	227131_at	NM_002401 /// NM_203351																				
3.69	2.91	0.78	7.41E-02	4.01E-01	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	chr2p13	201450_s_at	NM_022037 /// NM_022173																				
6.20	5.40	0.80	7.42E-02	4.01E-01	ATP10D	ATPase, class V, type 10D	chr4p12	213238_at	NM_020453																				
3.69	3.29	0.40	7.42E-02	4.01E-01	LOC727893 /// PDE4DIP	similar to phosphodiesterase 4D interacting protein (myomegalin) /// phosphodiesterase 4D interacting protein	chr1q12	212390_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359 /// XM_001126245 /// XM_001720581																				
3.97	3.41	0.56	7.42E-02	4.01E-01	MAN2A2	mannosidase, alpha, class 2A, member 2	chr15q26.1	219999_at	NM_006122																				
6.99	6.56	0.43	7.42E-02	4.01E-01	CSNK2A2	casein kinase 2, alpha prime polypeptide	chr16q21	203575_at	NM_001896																				
3.21	2.96	0.25	7.43E-02	4.01E-01	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	chr10q24.1	1559126_at	NM_015179																				
4.90	3.70	1.20	7.43E-02	4.01E-01	NAV3	neuron navigator 3	chr12q14.3	1552658_a_at	NM_014903																				
3.88	3.66	0.23	7.43E-02	4.01E-01	ATP5SL	ATP5S-like	chr19q13.2	230132_at	NM_018035																				
6.72	6.31	0.41	7.43E-02	4.01E-01	ENSA	endosulfine alpha	chr1q21.2	228851_s_at	NM_004436 /// NM_207042 /// NM_207043 /// NM_207044 /// NM_207045 /// NM_207046 /// NM_207047 /// NM_207168																				
6.82	6.51	0.31	7.43E-02	4.01E-01	ACBD6	acyl-Coenzyme A binding domain containing 6	chr1q25.2-q25.3	225317_at	NM_032360																				
7.92	7.53	0.39	7.43E-02	4.01E-01	SNAPIN	SNAP-associated protein	chr1q21.3	223066_at	NM_012437																				
3.61	3.11	0.50	7.44E-02	4.01E-01	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	---	220153_at	NM_020354																				
6.99	6.53	0.46	7.44E-02	4.01E-01	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	chr16p11.2	217370_x_at	NM_004960																				
3.64	2.44	1.20	7.45E-02	4.02E-01	GREB1	GREB1 protein	chr2p25.1	205862_at	NM_014668 /// NM_033090 /// NM_148903																				
6.30	5.82	0.48	7.45E-02	4.02E-01	HEMK1	HemK methyltransferase family member 1	chr3p21.3	218620_s_at	NM_016173																				
5.89	5.57	0.33	7.45E-02	4.02E-01	C20orf7	chromosome 20 open reading frame 7	chr20p12.1	222894_x_at	NM_001039375 /// NM_024120																				
3.01	2.74	0.27	7.46E-02	4.02E-01	FAM117B	family with sequence similarity 117, member B	chr2q33.1	1564868_a_at	NM_173511																				
6.93	6.46	0.47	7.46E-02	4.02E-01	FBXO34	F-box protein 34	chr14q22.3	218539_at	NM_017943 /// NM_152231																				
7.17	6.41	0.76	7.46E-02	4.02E-01	LAPTM4B	lysosomal protein transmembrane 4 beta	chr8q22.1	1554679_a_at	NM_018407																				
3.72	3.50	0.21	7.46E-02	4.02E-01	H2AFB1 /// H2AFB2 /// H2AFB3	H2A histone family, member B1 /// H2A histone family, member B2 /// H2A histone family, member B3	chrXq28	214412_at	NM_001017990 /// NM_001017991 /// NM_080720																				
3.43	2.98	0.45	7.46E-02	4.02E-01	IL27RA	interleukin 27 receptor, alpha	chr19p13.11	222062_at	NM_004843																				
2.38	2.17	0.21	7.46E-02	4.02E-01	ITGB6	integrin, beta 6	chr2q24.2	208084_at	NM_000888																				
4.08	3.76	0.31	7.47E-02	4.02E-01	SFTPB	surfactant protein B	chr2p12-p11.2	214354_x_at	NM_000542 /// NM_198843																				

4.82	4.26	0.56	7.47E-02	4.02E-01	PPP1R3E	protein phosphatase 1, regulatory (inhibitor) subunit 3E	chr14q11.2	227409_at	XR_040048 /// XR_040049 /// XR_040050																			
3.33	2.20	1.13	7.47E-02	4.02E-01	ROBO2	roundabout, axon guidance receptor, homolog 2 (Drosophila)	chr3p12.3	226766_at	NM_001128929 /// NM_002942																			
8.19	7.40	0.79	7.47E-02	4.02E-01	ACSF2	acyl-CoA synthetase family member 2	chr17q21.33	218844_at	NM_025149																			
5.45	4.90	0.55	7.47E-02	4.02E-01	SIN3A	SIN3 homolog A, transcription regulator (yeast)	chr15q24.2	238005_s_at	NM_015477																			
7.28	6.92	0.36	7.47E-02	4.02E-01	CCNY	cyclin Y	chr10p11.21	224651_at	NM_145012 /// NM_181698																			
4.05	3.77	0.28	7.48E-02	4.02E-01	---	---	---	239450_at	---																			
2.98	2.67	0.31	7.48E-02	4.02E-01	WDR91	WD repeat domain 91	chr7q33	222799_at	NM_014149																			
6.41	5.88	0.53	7.48E-02	4.02E-01	RAB7L1	RAB7, member RAS oncogene family-like 1	chr1q32	218699_at	NM_003929																			
6.97	6.53	0.44	7.50E-02	4.02E-01	TMEM103	transmembrane protein 103	chr3p21.31	223277_at	NM_001031703																			
4.66	4.25	0.40	7.50E-02	4.02E-01	CCDC49	coiled-coil domain containing 49	chr17q12	222706_at	NM_017748																			
5.76	5.47	0.29	7.50E-02	4.02E-01	LOC728769	hypothetical protein LOC728769	chr5q14.1	238039_at	XM_001132008																			
4.27	3.75	0.51	7.50E-02	4.02E-01	AVPR1A	arginine vasopressin receptor 1A	chr12q14-q15	206250_x_at	NM_000706																			
5.26	4.09	1.17	7.50E-02	4.02E-01	TNNC1	troponin C type 1 (slow)	chr3p21.3-p14.3	209904_at	NM_003280																			
12.09	11.84	0.25	7.50E-02	4.02E-01	RPL3	ribosomal protein L3	chr22q13	211666_x_at	NM_000967 /// NM_001033853																			
4.04	3.13	0.91	7.51E-02	4.02E-01	NOL12	nucleolar protein 12	chr22q13.1	222057_at	NM_024313																			
11.48	11.05	0.43	7.51E-02	4.02E-01	TMSB10	thymosin beta 10	chr2p11.2	217733_s_at	NM_021103																			
9.04	8.67	0.37	7.51E-02	4.02E-01	TMEM14B	transmembrane protein 14B	chr6p25.1-p23	223133_at	NM_001127711 /// NM_030969																			
5.16	4.45	0.71	7.51E-02	4.02E-01	MARS2	methionyl-tRNA synthetase 2, mitochondrial	chr2q33.1	243529_at	NM_138395																			
6.67	5.84	0.82	7.51E-02	4.02E-01	41523	septin 6	chrXq24	213666_at	NM_015129 /// NM_145799 /// NM_145800 /// NM_145802																			
7.10	6.75	0.35	7.51E-02	4.02E-01	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	chr21q22.3	209042_s_at	NM_003343 /// NM_182688																			
7.07	6.65	0.42	7.53E-02	4.03E-01	DNPEP	aspartyl aminopeptidase	chr2q35	38703_at	NM_012100																			
4.60	4.17	0.43	7.53E-02	4.03E-01	GALE	UDP-galactose-4-epimerase	chr1p36-p35	1557649_at	NM_000403 /// NM_001008216 /// NM_001127621																			
7.79	6.54	1.25	7.54E-02	4.03E-01	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	chr5q23.3	204404_at	NM_001046																			
4.81	4.34	0.46	7.54E-02	4.03E-01	SRPK3	SFRS protein kinase 3	chrXq28	206216_at	NM_014370																			
5.90	5.43	0.47	7.55E-02	4.03E-01	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	chr19q13.2	1554553_s_at	NM_001039671 /// NM_001039672 /// NM_001039673 /// NM_033557																			
4.62	4.24	0.38	7.55E-02	4.03E-01	BET1L	blocked early in transport 1 homolog (S. cerevisiae)-like	chr11p15.5	220470_at	NM_001098787 /// NM_016526																			
6.58	6.29	0.29	7.56E-02	4.04E-01	NUP93	nucleoporin 93kDa	chr16q13	202188_at	NM_014669																			
7.66	7.08	0.58	7.56E-02	4.04E-01	H2AFV	H2A histone family, member V	chr7p13	212205_at	NM_012412 /// NM_138635 /// NM_201436 /// NM_201516 /// NM_201517																			
4.30	3.44	0.86	7.56E-02	4.04E-01	---	---	---	235821_at	---																			
7.55	6.96	0.59	7.57E-02	4.04E-01	MLLT1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	chr19p13.3	224993_at	NM_005934																			
7.76	6.97	0.79	7.57E-02	4.04E-01	RWDD4A	RWD domain containing 4A	chr4q35.1	225574_at	NM_152682																			

8.62	8.28	0.34	7.57E-02	4.04E-01	MRPL40	mitochondrial ribosomal protein L40	chr22q11.21	203152_at	NM_003776
7.30	7.03	0.27	7.59E-02	4.04E-01	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	chr10q26.3	201848_s_at	NM_004052
7.37	6.57	0.80	7.59E-02	4.04E-01	RAI1	retinoic acid induced 1	chr17p11.2	226143_at	NM_030665
5.88	5.53	0.35	7.59E-02	4.04E-01	RGP1	RGP1 retrograde golgi transport homolog (S. cerevisiae)	chr9pter-p22.1	203169_at	NM_001080496
4.12	3.75	0.37	7.59E-02	4.04E-01	ZNF8	zinc finger protein 8	chr19q13.43	214901_at	NM_021089
3.55	2.98	0.57	7.59E-02	4.04E-01	MYO15B	myosin XVB pseudogene	chr17q25.1	219173_at	NR_003587
3.08	2.85	0.22	7.59E-02	4.04E-01	---	---	---	239982_at	---
8.21	7.87	0.34	7.60E-02	4.05E-01	TMEM9	transmembrane protein 9	---	222987_s_at	NM_016456
7.78	6.88	0.90	7.61E-02	4.05E-01	EPS8	epidermal growth factor receptor pathway substrate 8	chr12q13	202609_at	NM_004447
6.40	5.89	0.51	7.61E-02	4.05E-01	ZNF747	zinc finger protein 747	chr16p11.2	206180_x_at	NM_023931
3.98	3.21	0.77	7.61E-02	4.05E-01	ODZ2	odz, odd Oz/ten-m homolog 2 (Drosophila)	chr5q34-q35.1	231867_at	NM_001080428 /// NM_001122679
8.58	8.24	0.35	7.61E-02	4.05E-01	C20orf52	chromosome 20 open reading frame 52	chr20q11.22	224972_at	NM_080748
10.30	10.03	0.26	7.61E-02	4.05E-01	COX4I1	cytochrome c oxidase subunit IV isoform 1	chr16q22-qter	200086_s_at	NM_001861
3.58	3.33	0.25	7.62E-02	4.05E-01	LOC100132923	similar to hCG1993470	chr8p23.1	222194_at	XM_001716286
3.02	2.76	0.25	7.62E-02	4.05E-01	OR1F2P	olfactory receptor, family 1, subfamily F, member 2	chr16p13.3	217308_at	NR_002169
3.41	3.14	0.26	7.63E-02	4.05E-01	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	chr7q36	207623_at	NM_005692 /// NM_007189
5.07	4.57	0.50	7.63E-02	4.05E-01	---	---	---	231086_at	---
4.74	3.69	1.05	7.64E-02	4.05E-01	DOCK10	dedicator of cytokinesis 10	chr2q36.2	219279_at	NM_014689
4.70	3.79	0.91	7.64E-02	4.05E-01	PPT2	palmitoyl-protein thioesterase 2	chr6p21.3	209826_at	NM_005155 /// NM_138717
4.28	3.94	0.34	7.64E-02	4.05E-01	C17orf68	chromosome 17 open reading frame 68	chr17p13.1	219435_at	NM_025099
4.03	3.71	0.31	7.64E-02	4.05E-01	PRR17	proline rich 17	chr20q13.33	233355_at	NM_207349
5.78	5.07	0.71	7.64E-02	4.05E-01	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	chr13q34	206958_s_at	NM_023011 /// NM_080687
4.22	3.44	0.77	7.65E-02	4.05E-01	---	---	---	219367_s_at	---
5.97	5.53	0.44	7.65E-02	4.05E-01	PCGF1	polycomb group ring finger 1	chr2p13.1	210022_at	NM_032673
4.91	4.25	0.66	7.66E-02	4.06E-01	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	chr3q25.32-q25.33	206391_at	NM_002888 /// NM_206963
6.03	5.12	0.92	7.66E-02	4.06E-01	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	chr12q13	203124_s_at	NM_000617
2.79	2.43	0.37	7.67E-02	4.06E-01	DFNB59	deafness, autosomal recessive 59	chr2q31.2	235365_at	NM_001042702
4.45	4.16	0.29	7.67E-02	4.06E-01	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	chr1q42.11	213595_s_at	NM_003607 /// NM_014826
3.73	3.22	0.52	7.67E-02	4.06E-01	LOC282997	Hypothetical protein LOC282997	chr10q25.2	222307_at	XR_041081 /// XR_041082 /// XR_041083
8.38	7.95	0.43	7.67E-02	4.06E-01	GPAA1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	chr8q24.3	215690_x_at	NM_003801
7.91	7.46	0.45	7.68E-02	4.06E-01	C6orf125	chromosome 6 open reading frame 125	chr6p21.31	224448_s_at	NM_032340
5.92	5.56	0.36	7.68E-02	4.06E-01	PA2G4	proliferation-associated 2G4, 38kDa	chr12q13.2	214794_at	NM_006191
5.30	4.89	0.41	7.68E-02	4.06E-01	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene	chr15q11.2	1556739_at	NR_024074 /// XR_017720
3.72	3.01	0.70	7.68E-02	4.06E-01	---	---	---	239178_at	---
2.65	2.12	0.53	7.68E-02	4.06E-01	HOXD3	homeobox D3	chr2q31.1	206601_s_at	NM_006898
5.82	5.37	0.46	7.69E-02	4.06E-01	C16orf5	chromosome 16 open reading frame 5	chr16p13.3	218183_at	NM_013399
7.49	7.00	0.49	7.69E-02	4.06E-01	PPA2	pyrophosphatase (inorganic) 2	chr4q25	1556285_s_at	NM_001034191 /// NM_006903 /// NM_176866 /// NM_176867 /// NM_176869
3.32	2.91	0.41	7.70E-02	4.07E-01	TMEM100	transmembrane protein 100	chr17q22	219230_at	NM_001099640 /// NM_018286
4.88	4.57	0.31	7.70E-02	4.07E-01	ORMDL3	ORM1-like 3 (S. cerevisiae)	chr17q12-q21.1	235136_at	NM_139280
3.23	2.82	0.42	7.70E-02	4.07E-01	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	chr19p13.3	226201_at	NM_032482
4.51	3.66	0.85	7.70E-02	4.07E-01	PGM2	phosphoglucomutase 2	chr4p14	225366_at	NM_018290
7.06	6.58	0.47	7.70E-02	4.07E-01	KIAA2013	KIAA2013	chr1p36.22	224708_at	NM_138346
2.61	2.42	0.20	7.71E-02	4.07E-01	DPCR1	diffuse panbronchiolitis critical region 1	chr6p21.33	241137_at	NM_080870

6.65	6.32	0.33	7.71E-02	4.07E-01	UBIAD1	UbiA prenyltransferase domain containing 1	chr1p36-p34.1	229348_at	NM_013319
3.12	2.82	0.30	7.71E-02	4.07E-01	---	---	---	241864_x_at	---
7.35	7.11	0.24	7.72E-02	4.07E-01	ARL3	ADP-ribosylation factor-like 3	chr10q23.3	202641_at	NM_004311
4.08	3.54	0.54	7.72E-02	4.07E-01	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	chr1q32	201461_s_at	NM_004759 /// NM_032960
6.25	5.70	0.55	7.72E-02	4.07E-01	MUS81	MUS81 endonuclease homolog (S. cerevisiae)	chr11q13	218463_s_at	NM_025128
6.23	5.54	0.69	7.72E-02	4.07E-01	C5AR1	complement component 5a receptor 1	chr19q13.3-q13.4	220088_at	NM_001736
8.31	7.79	0.52	7.72E-02	4.07E-01	GALM	Galactose mutarotase (aldose 1-epimerase)	chr2p22.1	234974_at	NM_138801
5.19	4.81	0.38	7.72E-02	4.07E-01	WDR59	WD repeat domain 59	chr16q23.1	221981_s_at	NM_030581
5.05	4.36	0.69	7.72E-02	4.07E-01	PIAS3	protein inhibitor of activated STAT, 3	chr1q21	203035_s_at	NM_006099
2.82	2.31	0.51	7.73E-02	4.07E-01	BICD1	bicaudal D homolog 1 (Drosophila)	chr12p11.2-p11.1	1554020_at	NM_001003398 /// NM_001714
2.96	2.62	0.34	7.73E-02	4.07E-01	RBMY1E	RNA binding motif protein, Y-linked, family 1, member E	chrYq11.223	207916_at	NM_001006118
7.40	7.00	0.40	7.74E-02	4.07E-01	PEX16	peroxisomal biogenesis factor 16	chr11p11.2	49878_at	NM_004813 /// NM_057174
5.94	5.56	0.38	7.74E-02	4.07E-01	BAD	BCL2-associated agonist of cell death	chr11q13.1	1861_at	NM_004322 /// NM_032989
5.85	5.62	0.23	7.74E-02	4.07E-01	KIAA1217	KIAA1217	chr10p12.2-p12.1	231807_at	NM_001098500 /// NM_001098501 /// NM_019590
6.27	5.78	0.49	7.75E-02	4.07E-01	TMEM101	transmembrane protein 101	chr17q21.31	225004_at	NM_032376
5.01	4.11	0.90	7.75E-02	4.07E-01	PLXNB3	plexin B3	chrXq28	205957_at	NM_005393
7.63	6.79	0.84	7.75E-02	4.07E-01	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	chrXq25	203874_s_at	NM_003069 /// NM_139035
4.84	4.56	0.28	7.76E-02	4.08E-01	PGPEP1	pyroglutamyl-peptidase I	chr19p13.11	1555165_a_at	NM_017712
2.74	2.53	0.21	7.77E-02	4.08E-01	---	---	---	215466_at	---
7.55	7.09	0.47	7.77E-02	4.08E-01	AMHR2	anti-Mullerian hormone receptor, type II	chr12q13	206892_at	NM_020547
7.34	7.12	0.22	7.77E-02	4.08E-01	PFDN1	prefoldin subunit 1	chr5q31	201507_at	NM_002622
6.39	5.97	0.42	7.77E-02	4.08E-01	LCMT2	leucine carboxyl methyltransferase 2	chr15q15.3	204012_s_at	NM_014793
6.44	5.62	0.82	7.78E-02	4.08E-01	CCNG2	cyclin G2	chr4q21.1	211559_s_at	NM_004354
3.80	3.38	0.43	7.79E-02	4.08E-01	KLHDC1	kelch domain containing 1	chr14q22.1	1552733_at	NM_172193
5.90	5.36	0.54	7.79E-02	4.08E-01	C1QTNF1	C1q and tumor necrosis factor related protein 1	chr17q25.3	224197_s_at	NM_030968 /// NM_198593 /// NM_198594
8.08	7.65	0.43	7.79E-02	4.08E-01	GPAA1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	chr8q24.3	201618_x_at	NM_003801
4.41	3.96	0.45	7.79E-02	4.08E-01	AXL	AXL receptor tyrosine kinase	chr19q13.1	202685_s_at	NM_001699 /// NM_021913
2.24	2.02	0.22	7.80E-02	4.08E-01	---	---	---	1555893_at	---
4.65	4.27	0.39	7.80E-02	4.08E-01	AKT2	v-akt murine thymoma viral oncogene homolog 2	chr19q13.1-q13.2	211453_s_at	NM_001626
2.64	2.38	0.26	7.80E-02	4.08E-01	---	---	---	233088_at	---
9.04	8.42	0.62	7.81E-02	4.08E-01	SEPW1	selenoprotein W, 1	chr19q13.3	1555851_s_at	NM_003009
4.19	3.92	0.27	7.81E-02	4.08E-01	MED28	mediator complex subunit 28	chr4p16	224416_s_at	NM_025205
2.81	2.36	0.45	7.81E-02	4.08E-01	KIAA0841	KIAA0841	chr19q13.12	213054_at	NM_015302
4.40	4.00	0.40	7.81E-02	4.08E-01	BRF2	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	chr8p12	218954_s_at	NM_018310
3.19	2.68	0.51	7.82E-02	4.08E-01	CISD2	CDGSH iron sulfur domain 2	chr4q24	226686_at	NM_001008388
9.62	8.71	0.91	7.82E-02	4.08E-01	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	chr1q32	201926_s_at	NM_000574 /// NM_001114752
7.83	7.27	0.56	7.82E-02	4.08E-01	MRPL43	mitochondrial ribosomal protein L43	chr10q24.31	224332_s_at	NM_032112 /// NM_176792 /// NM_176793 /// NM_176794
6.05	5.37	0.68	7.82E-02	4.08E-01	FKBP10	FK506 binding protein 10, 65 kDa	chr17q21.2	219249_s_at	NM_021939
2.23	2.02	0.22	7.82E-02	4.08E-01	KIAA0776	KIAA0776	chr6q16.1	238291_at	NM_015323
6.92	6.61	0.31	7.83E-02	4.09E-01	NEIL2	nei like 2 (E. coli)	chr8p23.1	226585_at	NM_145043
2.63	2.21	0.42	7.83E-02	4.09E-01	C4orf28	chromosome 4 open reading frame 28	chr4p15.31	235554_x_at	NM_001130727 /// NM_145048

2.92	2.73	0.20	7.83E-02	4.09E-01	HERPUD2	HERPUD family member 2	chr7p14.2	1558699_a_at	NM_022373 /// XM_001716505 /// XM_001717741 /// XM_001717961 /// XM_001718593																			
2.26	2.04	0.23	7.83E-02	4.09E-01	ARMC4	armadillo repeat containing 4	chr10p12.1-p11.23	223794_at	NM_018076																			
7.48	7.14	0.34	7.83E-02	4.09E-01	STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	chr11q23.3	202223_at	NM_152713																			
4.62	4.20	0.42	7.84E-02	4.09E-01	SLC9A8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	chr20q13.13	212947_at	NM_015266																			
6.15	5.73	0.42	7.84E-02	4.09E-01	RPA2	replication protein A2, 32kDa	chr1p35	201756_at	NM_002946																			
2.01	1.82	0.19	7.84E-02	4.09E-01	BTG4	B-cell translocation gene 4	chr11q23	1554362_at	NM_017589																			
6.23	5.82	0.41	7.84E-02	4.09E-01	TADA1L	transcriptional adaptor 1 (HFI1 homolog, yeast)-like	chr1q24.1	225455_at	NM_053053																			
4.69	4.26	0.42	7.84E-02	4.09E-01	LOC728568	hypothetical LOC728568	chr12q23.3	226927_at	NR_024026 /// XR_042054 /// XR_042055 /// XR_042056																			
4.40	3.63	0.77	7.84E-02	4.09E-01	RDH10	retinol dehydrogenase 10 (all-trans)	chr8q21.11	227467_at	NM_172037																			
2.59	2.31	0.28	7.84E-02	4.09E-01	TMOD4	tropomodulin 4 (muscle)	chr1q12	223762_at	NM_013353																			
6.93	6.46	0.47	7.85E-02	4.09E-01	---	---	---	225504_at	---																			
6.41	5.91	0.50	7.86E-02	4.09E-01	TSC22D2	TSC22 domain family, member 2	chr3q25.1	204094_s_at	NM_014779																			
6.28	5.79	0.49	7.86E-02	4.09E-01	TBRG4	transforming growth factor beta regulator 4	chr7p14-p13	220789_s_at	NM_004749 /// NM_030900 /// NM_199122																			
3.29	2.84	0.45	7.86E-02	4.09E-01	---	---	---	1569520_at	---																			
3.07	2.75	0.31	7.86E-02	4.09E-01	DPP7	Dipeptidyl-peptidase 7	chr9q34.3	241973_x_at	NM_013379																			
7.75	7.13	0.62	7.87E-02	4.09E-01	HNRNPR	heterogeneous nuclear ribonucleoprotein R	chr1p36.12	208766_s_at	NM_001102397 /// NM_001102398 /// NM_001102399 /// NM_005826																			
7.77	7.25	0.52	7.87E-02	4.09E-01	PSMB4	Proteasome (prosome, macropain) subunit, beta type, 4	chr1q21	228204_at	NM_002796																			
2.48	2.21	0.27	7.87E-02	4.09E-01	C18orf12	chromosome 18 open reading frame 12	chr18q21.1	1553087_at	XR_040897 /// XR_040898 /// XR_040899																			
4.64	4.16	0.47	7.87E-02	4.09E-01	HOOK3	hook homolog 3 (Drosophila)	chr8p11.21	226395_at	NM_032410																			
2.83	2.55	0.29	7.87E-02	4.09E-01	DEFB123	defensin, beta 123	chr20q11.1	229772_at	NM_153324																			
8.64	8.26	0.37	7.87E-02	4.09E-01	PHF11	PHD finger protein 11	chr13q14.3	221816_s_at	NM_001040443 /// NM_001040444																			
9.03	8.80	0.22	7.87E-02	4.09E-01	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	chr1q21.2	211609_x_at	NM_002810																			
8.86	8.26	0.60	7.88E-02	4.09E-01	FLJ10357	hypothetical protein FLJ10357	chr14q11.2	58780_s_at	NM_018071																			
5.63	5.02	0.62	7.88E-02	4.10E-01	CDADC1	cytidine and dCMP deaminase domain containing 1	chr13q14.2	223527_s_at	NM_030911																			
4.96	4.67	0.29	7.88E-02	4.10E-01	MEF2D	myocyte enhancer factor 2D	chr1q12-q23	203004_s_at	NM_005920																			
8.73	7.99	0.74	7.89E-02	4.10E-01	RGN	regucalcin (senescence marker protein-30)	chrXp11.3	210751_s_at	NM_004683 /// NM_152869																			
3.88	3.31	0.57	7.89E-02	4.10E-01	RTTN	rotatin	chr18q22.2	227072_at	NM_173630																			
2.90	2.58	0.32	7.90E-02	4.10E-01	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	chr19p13.11	231926_at	NM_021235																			
7.12	6.60	0.52	7.90E-02	4.10E-01	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	chr7q32	221962_s_at	NM_003344 /// NM_182697																			
6.92	6.49	0.43	7.90E-02	4.10E-01	DCI	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	chr16p13.3	209759_s_at	NM_001919																			
7.78	7.34	0.44	7.90E-02	4.10E-01	MCOLN1	mucolipin 1	chr19p13.3-p13.2	219952_s_at	NM_020533																			
5.79	5.26	0.54	7.91E-02	4.10E-01	LOC387647	patched domain containing 3 pseudogene	chr10p11.23	228786_at	NR_003930																			
10.75	10.48	0.27	7.91E-02	4.10E-01	TUBA1C	tubulin, alpha 1c	chr12q12-q14	209251_x_at	NM_032704																			
6.60	6.19	0.40	7.92E-02	4.10E-01	USP3	ubiquitin specific peptidase 3	chr15q22.3	221654_s_at	NM_006537																			

8.18	7.49	0.68	7.92E-02	4.10E-01	KIAA1522	KIAA1522	chr1p35.1	224746_at	NM_020888
6.80	6.28	0.52	7.92E-02	4.10E-01	MED26	mediator complex subunit 26	chr19p13.11	227538_at	NM_004831
5.48	4.56	0.92	7.92E-02	4.10E-01	RBM3	RNA binding motif (RNP1, RRM) protein 3	chrXp11.2	222026_at	NM_006743
6.61	6.28	0.33	7.92E-02	4.10E-01	AKAP1	A kinase (PRKA) anchor protein 1	chr17q21-q23	201674_s_at	NM_003488
2.27	2.05	0.22	7.92E-02	4.10E-01	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	chr4q31.21	223878_at	NM_001101669 /// NM_003866
2.99	2.72	0.27	7.93E-02	4.10E-01	SESN3	sestrin 3	chr11q21	235684_s_at	NM_144665
2.18	1.96	0.22	7.93E-02	4.11E-01	KRTAP2-2 /// LOC728279	keratin associated protein 2-2 /// hypothetical LOC728279	chr17q12-q21 /// chr17q21.2	234772_s_at	XM_001127057 /// XM_001127069 /// XM_001714719 /// XM_930081
7.57	7.18	0.39	7.93E-02	4.11E-01	MPV17	MpV17 mitochondrial inner membrane protein	chr2p23.3	203466_at	NM_002437
3.30	2.66	0.64	7.93E-02	4.11E-01	NAV3	neuron navigator 3	chr12q14.3	1562234_a_at	NM_014903
2.41	2.12	0.29	7.94E-02	4.11E-01	DPYD	dihydropyrimidine dehydrogenase	chr1p22	1554534_at	NM_000110
4.64	4.27	0.37	7.94E-02	4.11E-01	ZNF77	zinc finger protein 77	chr19p13.3	229000_at	NM_021217
3.87	3.44	0.44	7.94E-02	4.11E-01	LOC100132740 /// LOC100134711 /// STAG3L1 /// STAG3L2 /// STAG3L3	hypothetical protein LOC100132740 /// hypothetical protein LOC100134711 /// stromal antigen 3-like 1 /// stromal antigen 3-like 2 /// stromal antigen 3-like 3	chr7q11.23 /// chr7q11.23-q21.1	223724_s_at	NM_001002840 /// NM_001013739 /// NM_001025202 /// NM_018991 /// XM_001720660 /// XM_001721283 /// XM_001722108
6.10	5.58	0.53	7.94E-02	4.11E-01	LZTR1	leucine-zipper-like transcription regulator 1	chr22q11.21|22q11.1-q11.2	203412_at	NM_006767
6.19	5.87	0.32	7.95E-02	4.11E-01	DRG2	developmentally regulated GTP binding protein 2	chr17p11.2	203267_s_at	NM_001388
4.17	3.05	1.11	7.95E-02	4.11E-01	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	chr8p11.2-p11.1	213006_at	NM_005195
5.65	5.12	0.53	7.96E-02	4.11E-01	PRKD2	protein kinase D2	chr19q13.3	209282_at	NM_001079880 /// NM_001079881 /// NM_001079882 /// NM_016457
3.41	3.04	0.38	7.97E-02	4.11E-01	C22orf15	chromosome 22 open reading frame 15	chr22q11.23	1558334_a_at	NM_182520
6.37	5.86	0.51	7.97E-02	4.11E-01	PPM1F	protein phosphatase 1F (PP2C domain containing)	chr22q11.22	37384_at	NM_014634
3.56	3.19	0.38	7.97E-02	4.11E-01	LOC100144415	hypothetical LOC100144415	---	235990_at	---
5.37	5.09	0.28	7.97E-02	4.11E-01	CYHR1	cysteine/histidine-rich 1	chr8q24.3	213072_at	NM_001129888 /// NM_032687 /// NM_138496
4.16	3.85	0.31	7.98E-02	4.12E-01	---	---	---	1560476_at	---
4.57	3.84	0.73	7.98E-02	4.12E-01	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	chr1p36.12	229163_at	NM_018584
3.01	2.67	0.34	7.98E-02	4.12E-01	LOC646627	phospholipase inhibitor	chr1q44	238143_at	NM_001085474
5.81	5.37	0.44	7.98E-02	4.12E-01	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	chr3q29	235347_at	NM_032773
7.38	7.07	0.32	7.99E-02	4.12E-01	MRPS23	mitochondrial ribosomal protein S23	chr17q22-q23	223156_at	NM_016070
9.88	9.53	0.35	7.99E-02	4.12E-01	HIGD2A	HIG1 domain family, member 2A	chr5q35.2	209329_x_at	NM_138820
7.26	5.28	1.98	7.99E-02	4.12E-01	PSPH	phosphoserine phosphatase	chr7p15.2-p15.1	205048_s_at	NM_004577
4.47	4.12	0.35	8.00E-02	4.12E-01	HAP1	huntingtin-associated protein 1	chr17q21.2-q21.3	211222_s_at	NM_001079870 /// NM_001079871 /// NM_003949 /// NM_177977
4.51	4.16	0.35	8.00E-02	4.12E-01	SRGAP2P1	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 1	chr1p11.2	1568955_at	---
3.42	2.80	0.61	8.00E-02	4.12E-01	---	---	---	228723_at	---
4.34	3.99	0.35	8.00E-02	4.12E-01	---	---	---	1568915_at	---
7.31	6.74	0.57	8.00E-02	4.12E-01	NUDT4 /// NUDT4P1	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	chr12q21 /// chr1q21.1	206302_s_at	NM_019094 /// NM_199040 /// NR_002212

4.91	4.63	0.29	8.00E-02	4.12E-01	WDR68	WD repeat domain 68	chr17q23.3	224730_at	NM_005828
2.94	2.66	0.28	8.01E-02	4.12E-01	---	---	---	238377_s_at	---
4.06	3.25	0.81	8.01E-02	4.12E-01	EFHC1	EF-hand domain (C-terminal) containing 1	chr6p12.3	219833_s_at	NM_018100
5.72	5.11	0.61	8.01E-02	4.12E-01	INO80B /// WBP1	INO80 complex subunit B /// WW domain binding protein 1	chr2p12 /// chr2p13.1	65133_i_at	NM_012477 /// NM_031288
4.34	3.68	0.66	8.01E-02	4.12E-01	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	chr17q23.1-q24.2	206765_at	NM_000891
3.37	3.04	0.33	8.01E-02	4.12E-01	LOC729029	hypothetical protein LOC729029	chr15q15.1	242518_at	XM_001128912 /// XM_001129103 /// XM_001717609
9.31	8.67	0.64	8.02E-02	4.12E-01	KLHDC8B	kelch domain containing 8B	chr3p21.31	225755_at	NM_173546
5.91	5.30	0.61	8.02E-02	4.12E-01	FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	chr7p22	210933_s_at	NM_003088
5.00	4.47	0.53	8.02E-02	4.12E-01	SDCCAG1	serologically defined colon cancer antigen 1	chr14q22	218649_x_at	NM_004713
5.56	4.95	0.61	8.02E-02	4.12E-01	SSBP2	single-stranded DNA binding protein 2	chr5q14.1	203787_at	NM_012446
6.34	6.09	0.25	8.03E-02	4.12E-01	TTC5	tetratricopeptide repeat domain 5	chr14q11.2	226557_at	NM_138376
4.09	3.64	0.45	8.03E-02	4.12E-01	GOPC	golgi associated PDZ and coiled-coil motif containing	chr6q21	225023_at	NM_001017408 /// NM_020399
3.14	2.76	0.37	8.03E-02	4.12E-01	---	---	---	1560023_x_at	---
2.02	1.84	0.18	8.04E-02	4.12E-01	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	chr2q36.1	1555731_a_at	NM_001039569
2.60	2.29	0.31	8.04E-02	4.12E-01	EML5	echinoderm microtubule associated protein like 5	chr14q31.3	1568777_at	NM_183387
5.97	5.67	0.31	8.04E-02	4.12E-01	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	chr17q11.2	208831_x_at	NM_003170
4.59	4.21	0.38	8.05E-02	4.12E-01	---	---	---	1557232_at	---
9.39	9.04	0.35	8.05E-02	4.12E-01	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	chr16q12.2-q13	217168_s_at	NM_001010989 /// NM_001010990 /// NM_014685
7.11	6.74	0.37	8.05E-02	4.12E-01	VPRBP	Vpr (HIV-1) binding protein	chr3p21.2	226481_at	NM_014703
4.23	3.77	0.46	8.05E-02	4.12E-01	RPS19	ribosomal protein S19	chr19q13.2	242451_x_at	NM_001022
6.50	6.11	0.39	8.06E-02	4.12E-01	MADD	MAP-kinase activating death domain	chr11p11.2	210252_s_at	NM_003682 /// NM_130470 /// NM_130471 /// NM_130472 /// NM_130473 /// NM_130474 /// NM_130475 /// NM_130476
6.75	6.23	0.52	8.06E-02	4.12E-01	MED12	mediator complex subunit 12	chrXq13	203506_s_at	NM_005120
7.79	7.12	0.67	8.06E-02	4.13E-01	AHR	aryl hydrocarbon receptor	chr7p15	202820_at	NM_001621
5.91	5.13	0.78	8.06E-02	4.13E-01	TFF3	trefoil factor 3 (intestinal)	chr21q22.3	204623_at	NM_003226
3.88	3.54	0.34	8.07E-02	4.13E-01	ARSD	arylsulfatase D	chrXp22.3	206831_s_at	NM_001669 /// NM_009589
10.70	10.48	0.21	8.07E-02	4.13E-01	HMGN2	high-mobility group nucleosomal binding domain 2	chr1p36.1	208668_x_at	NM_005517
3.27	2.99	0.28	8.07E-02	4.13E-01	LOC731789	similar to amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	chr10p12.1	237236_x_at	XM_001130818 /// XM_001721652 /// XM_001722670
3.43	3.05	0.37	8.07E-02	4.13E-01	PSMB1	Proteasome (prosome, macropain) subunit, beta type, 1	chr6q27	214289_at	NM_002793
7.02	6.69	0.34	8.08E-02	4.13E-01	HCCS	holocytochrome c synthase (cytochrome c heme-lyase)	chrXp22.3	203746_s_at	NM_001122608 /// NM_005333
6.18	5.71	0.48	8.08E-02	4.13E-01	VASH1	vasohibin 1	chr14q24.3	203940_s_at	NM_014909
6.61	6.31	0.29	8.08E-02	4.13E-01	C7orf20	chromosome 7 open reading frame 20	chr7p22.3	224808_s_at	NM_015949
6.55	6.22	0.34	8.08E-02	4.13E-01	UBN1	ubinuclein 1	chr16p13.3	207253_s_at	NM_001079514 /// NM_016936
6.25	5.83	0.43	8.08E-02	4.13E-01	OXSM	3-oxoacyl-ACP synthase, mitochondrial	chr3p24.2	219133_at	NM_017897
5.48	5.00	0.48	8.08E-02	4.13E-01	TTC39C	tetratricopeptide repeat domain 39C	chr18q11.2	230747_s_at	NM_153211
6.93	6.44	0.49	8.09E-02	4.13E-01	CHD1L	chromodomain helicase DNA binding protein 1-like	chr1q12	212539_at	NM_004284
8.70	8.28	0.42	8.09E-02	4.13E-01	TERF2IP	telomeric repeat binding factor 2, interacting protein	chr16q23.1	201174_s_at	NM_018975

6.53	6.04	0.49	8.09E-02	4.13E-01	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	chr12q12-q14	214437_s_at	NM_005412
4.77	3.71	1.06	8.09E-02	4.13E-01	TWIST1	twist homolog 1 (Drosophila)	chr7p21.2	213943_at	NM_000474
6.84	6.13	0.71	8.10E-02	4.13E-01	LONRF1	LON peptidase N-terminal domain and ring finger 1	chr8p23.1	226038_at	NM_152271
3.63	3.09	0.54	8.10E-02	4.13E-01	FKBP1A	FK506 binding protein 1A, 12kDa	chr20p13	210187_at	NM_000801 /// NM_054014
6.27	5.43	0.84	8.10E-02	4.13E-01	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	chr2q37.1	1555962_at	NM_145236
2.24	2.00	0.24	8.11E-02	4.13E-01	LOC100131317 /// POU4F1	similar to hCG1781072 /// POU class 4 homeobox 1	chr13q31.1	206940_s_at	NM_006237 /// XM_001722446
5.32	4.85	0.48	8.11E-02	4.13E-01	STAG3L4	stromal antigen 3-like 4	chr7p11.2-q11.2	222801_s_at	NM_022906
5.71	5.25	0.46	8.12E-02	4.13E-01	NR2C2AP	nuclear receptor 2C2-associated protein	chr19p13.11	226839_at	NM_176880
6.94	6.56	0.38	8.12E-02	4.13E-01	MED16	mediator complex subunit 16	chr19p13.3	221545_x_at	NM_005481
4.97	4.58	0.38	8.12E-02	4.13E-01	ZNF500	zinc finger protein 500	chr16p13.3	41113_at	NM_021646
4.43	4.13	0.30	8.12E-02	4.13E-01	ZNF710	zinc finger protein 710	chr15q26.1	39891_at	NM_198526
5.23	4.46	0.77	8.12E-02	4.13E-01	RAB11FIP3	RAB11 family interacting protein 3 (class II)	chr16p13.3	228613_at	NM_014700
4.15	3.83	0.32	8.13E-02	4.13E-01	---	---	---	214188_at	---
5.98	5.32	0.66	8.13E-02	4.13E-01	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	chr14q24.3-q31	216202_s_at	NM_004863
3.03	2.77	0.25	8.13E-02	4.13E-01	---	---	---	214964_at	---
5.86	5.47	0.39	8.13E-02	4.13E-01	LOC148413	hypothetical LOC148413	chr1p36.33	225920_at	XR_040142 /// XR_040143 /// XR_040144
6.54	6.05	0.49	8.13E-02	4.13E-01	FAM65A	family with sequence similarity 65, member A	chr16q22.1	218029_at	NM_024519
8.24	7.32	0.91	8.13E-02	4.13E-01	PTP4A1	protein tyrosine phosphatase type IVA, member 1	chr6q12	200731_s_at	NM_003463
7.07	6.73	0.34	8.14E-02	4.13E-01	HSF1	heat shock transcription factor 1	chr8q24.3	202344_at	NM_005526
4.83	4.34	0.49	8.14E-02	4.13E-01	CEACAM19	carcinoembryonic antigen-related cell adhesion molecule 19	chr19q13.31	230504_at	NM_001127893 /// NM_020219
12.29	12.10	0.19	8.14E-02	4.13E-01	RPL30	ribosomal protein L30	chr8q22	200062_s_at	NM_000989
2.42	2.19	0.22	8.14E-02	4.13E-01	---	---	---	1570252_at	---
2.85	2.57	0.28	8.14E-02	4.13E-01	---	---	---	1558574_at	---
3.91	3.57	0.34	8.14E-02	4.13E-01	CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	chr20q13.31	32723_at	NM_001033521 /// NM_001033522 /// NM_001324
5.05	4.63	0.42	8.15E-02	4.14E-01	RFC2	replication factor C (activator 1) 2, 40kDa	chr7q11.23	203696_s_at	NM_002914 /// NM_181471
2.29	2.02	0.28	8.15E-02	4.14E-01	RUNDC2B /// RUNDC2C	RUN domain containing 2B /// RUN domain containing 2C	chr16p12.2	1554413_s_at	NM_001012391 /// NR_002939 /// XM_001714307 /// XR_042180
6.28	5.62	0.66	8.15E-02	4.14E-01	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	chr3q25.31	203164_at	NM_004733
2.20	1.93	0.28	8.15E-02	4.14E-01	---	---	---	1570098_at	---
6.11	5.69	0.42	8.16E-02	4.14E-01	ZMYND19	zinc finger, MYND-type containing 19	chr9q34.3	227477_at	NM_138462
3.31	2.78	0.53	8.16E-02	4.14E-01	FLJ22167	hypothetical protein FLJ22167	chr16q23.1	64900_at	NM_001077416 /// NM_001077418 /// NM_001077419
6.04	5.62	0.43	8.16E-02	4.14E-01	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	chr12q13-q15	208735_s_at	NM_005730
5.32	4.69	0.62	8.16E-02	4.14E-01	MAP2K3	mitogen-activated protein kinase kinase 3	chr17q11.2	215498_s_at	NM_002756 /// NM_145109
3.06	2.57	0.49	8.17E-02	4.14E-01	ANKRD23	ankyrin repeat domain 23	chr2q11.2	229052_at	NM_144994
7.94	7.69	0.25	8.17E-02	4.14E-01	C10orf104	chromosome 10 open reading frame 104	chr10q22.1	224665_at	NM_173473
5.95	5.44	0.51	8.17E-02	4.14E-01	POMT2	protein-O-mannosyltransferase 2	chr14q24	225560_at	NM_013382
6.20	5.25	0.95	8.17E-02	4.14E-01	RP5-1022P6.2	hypothetical protein KIAA1434	chr20p12.3	224826_at	NM_019593
3.83	3.26	0.57	8.18E-02	4.14E-01	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	chrXq25-q26	218757_s_at	NM_023010 /// NM_080632
5.15	4.64	0.51	8.18E-02	4.14E-01	F10	coagulation factor X	chr13q34	205620_at	NM_000504
2.65	2.41	0.25	8.18E-02	4.14E-01	DKFZp686L14188	hypothetical gene supported by BX538329	chr8q21.3	231412_at	---

2.78	2.45	0.34	8.18E-02	4.14E-01	LOC644151	similar to calpain 8	chr1q41	229030_at	XM_001715279 /// XM_927359																					
7.98	7.68	0.30	8.19E-02	4.14E-01	SNRPC	small nuclear ribonucleoprotein polypeptide C	chr6p21.31	201342_at	NM_003093																					
5.19	4.38	0.81	8.19E-02	4.14E-01	FHL1	four and a half LIM domains 1	chrXq26	210299_s_at	NM_001449																					
7.31	6.75	0.56	8.19E-02	4.14E-01	FAM158A	family with sequence similarity 158, member A	chr14q11.2	219203_at	NM_016049																					
7.38	6.84	0.55	8.19E-02	4.14E-01	GPR177	G protein-coupled receptor 177	chr1p31.3	228950_s_at	NM_001002292 /// NM_024911																					
7.73	7.29	0.43	8.19E-02	4.14E-01	CIZ1	CDKN1A interacting zinc finger protein 1	chr9q34.1	205516_x_at	NM_001131015 /// NM_001131016 /// NM_001131017 /// NM_001131018 /// NM_012127																					
6.67	6.31	0.37	8.20E-02	4.14E-01	LOC441259 /// LOC730324 /// PMS2L5	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like /// similar to postmeiotic segregation increased 2-like 2 /// postmeiotic segregation increased 2-like 5	chr7q11-q22 /// chr7q11.23	213893_x_at	NM_174930 /// XM_001713820 /// XM_001722095																					
3.58	3.18	0.40	8.20E-02	4.14E-01	BID	BH3 interacting domain death agonist	chr22q11.1	204493_at	NM_001196 /// NM_197966 /// NM_197967																					
4.50	4.13	0.38	8.21E-02	4.15E-01	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	chr5q33-q34	37226_at	NM_001205 /// NM_013978 /// NM_013979 /// NM_013980																					
6.36	5.98	0.38	8.22E-02	4.15E-01	ACVR1	activin A receptor, type I	chr2q23-q24	203935_at	NM_001105 /// NM_001111067																					
2.49	2.24	0.25	8.22E-02	4.15E-01	FLJ42709	hypothetical gene supported by AK124699	chr5q15	1556696_s_at	NR_015369 /// NR_021490 /// NR_021491 /// XM_499008 /// XM_943794																					
3.90	3.54	0.36	8.22E-02	4.15E-01	C17orf51	chromosome 17 open reading frame 51	chr17p11.2	228146_at	NM_001113434 /// XM_001725854 /// XM_378661 /// XM_944416																					
2.36	2.16	0.20	8.22E-02	4.15E-01	HIF3A	hypoxia inducible factor 3, alpha subunit	chr19q13.32	222124_at	NM_022462 /// NM_152794 /// NM_152795																					
3.71	3.47	0.24	8.23E-02	4.15E-01	41520	septin 3	chr22q13.2	223362_s_at	NM_019106 /// NM_145733																					
6.89	6.41	0.48	8.23E-02	4.15E-01	FAM103A1	family with sequence similarity 103, member A1	chr15q25.2	225210_s_at	NM_031452																					
2.46	2.20	0.26	8.23E-02	4.15E-01	RUVBL2	RuvB-like 2 (E. coli)	chr19q13.3	1559945_at	NM_006666																					
2.40	2.10	0.30	8.23E-02	4.15E-01	ANKRD6	ankyrin repeat domain 6	chr6q14.2-q16.1	204672_s_at	NM_014942																					
3.05	2.75	0.31	8.23E-02	4.15E-01	HUWE1	HECT, UBA and WWE domain containing 1	chrXp11.22	236294_at	NM_031407																					
2.57	2.18	0.38	8.24E-02	4.15E-01	---	---	---	241815_at	---																					
12.27	12.04	0.22	8.24E-02	4.15E-01	EEF1G	eukaryotic translation elongation factor 1 gamma	chr11q12.3	211927_x_at	NM_001404																					
7.43	6.69	0.74	8.24E-02	4.15E-01	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	chr20q12	201042_at	NM_004613 /// NM_198951																					

6.80	6.43	0.37	8.25E-02	4.15E-01	KIAA0859	KIAA0859	chr1q24-q25.3	212405_s_at	NM_001007239 /// NM_014955 /// NM_015935																			
3.34	2.93	0.41	8.25E-02	4.15E-01	AFG3L1	AFG3 ATPase family gene 3-like 1 (S. cerevisiae)	chr16q24.3	236250_at	NR_003226 /// NR_003227 /// NR_003228																			
9.66	9.02	0.64	8.25E-02	4.15E-01	MT1E /// MT1H /// MT1M /// MT1P2	metallothionein 1E /// metallothionein 1H /// metallothionein 1M /// metallothionein 1 pseudogene 2	chr16q13 /// chr1q43	216336_x_at	NM_005951 /// NM_175617 /// NM_176870																			
3.94	3.39	0.55	8.26E-02	4.15E-01	RBM19	RNA binding motif protein 19	chr12q24.13-q24.21	206019_at	NM_016196																			
5.60	5.08	0.52	8.26E-02	4.15E-01	CCDC137	coiled-coil domain containing 137	chr17q25.3	225933_at	NM_199287																			
3.63	3.30	0.33	8.26E-02	4.15E-01	---	---	---	240925_at	---																			
2.44	2.18	0.25	8.26E-02	4.15E-01	---	---	---	236633_at	---																			
4.64	4.06	0.58	8.26E-02	4.15E-01	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	chr1p36.1	202819_s_at	NM_003198																			
5.07	4.58	0.49	8.27E-02	4.15E-01	HIG2	hypoxia-inducible protein 2	chr7q32.1	1554452_a_at	NM_001098786 /// NM_013332																			
2.97	2.72	0.26	8.27E-02	4.16E-01	CPNE6	copine VI (neuronal)	chr14q11.2	210408_s_at	NM_006032																			
7.39	7.01	0.38	8.28E-02	4.16E-01	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	chr16q13-q21	214263_x_at	NM_032940																			
3.79	3.06	0.73	8.28E-02	4.16E-01	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	chr18q11.2	216226_at	NM_005640																			
7.38	6.95	0.44	8.29E-02	4.16E-01	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	chr19q13.2-q13.3	203719_at	NM_001983 /// NM_202001																			
5.87	5.33	0.54	8.29E-02	4.16E-01	PCID2	PCI domain containing 2	chr13q34	225149_at	NM_018386 /// XM_001721381 /// XM_001721407 /// XM_001722771																			
3.86	3.40	0.47	8.30E-02	4.16E-01	TRIM5	tripartite motif-containing 5	chr11p15	210705_s_at	NM_033034 /// NM_033092 /// NM_033093																			
9.26	8.17	1.09	8.30E-02	4.16E-01	FN1	fibronectin 1	chr2q34	216442_x_at	NM_002026 /// NM_054034 /// NM_212474 /// NM_212475 /// NM_212476 /// NM_212478 /// NM_212482																			
2.61	2.34	0.27	8.30E-02	4.16E-01	---	---	---	1559313_at	---																			
4.68	4.27	0.40	8.30E-02	4.16E-01	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	chr1p36.2	211282_x_at	NM_001039664 /// NM_003790 /// NM_148965 /// NM_148966 /// NM_148967 /// NM_148970																			
7.65	7.17	0.48	8.31E-02	4.16E-01	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	chr2q33-qter	203979_at	NM_000784																			
2.75	2.52	0.24	8.31E-02	4.16E-01	AURKB	aurora kinase B	chr17p13.1	239219_at	NM_004217																			
4.35	3.85	0.49	8.31E-02	4.16E-01	TOP3B	topoisomerase (DNA) III beta	chr22q11.22	213660_s_at	NM_003935																			
5.64	4.90	0.74	8.31E-02	4.16E-01	NDFIP2	Nedd4 family interacting protein 2	chr13q31.1	224802_at	NM_019080																			

9.59	9.23	0.36	8.31E-02	4.16E-01	NOLA3	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)	chr15q14-q15	217962_at	NM_018648
3.03	2.75	0.28	8.32E-02	4.16E-01	PPFIA4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	chr1q32.1	214978_s_at	NM_015053
7.43	7.03	0.40	8.32E-02	4.16E-01	HYI	hydroxypyruvate isomerase homolog (E. coli)	chr1p34.2	223769_x_at	NM_031207
6.83	6.44	0.39	8.33E-02	4.17E-01	TTC17	tetratricopeptide repeat domain 17	chr11p12-p11.2	224849_at	NM_018259
2.74	2.36	0.38	8.33E-02	4.17E-01	C2orf63	chromosome 2 open reading frame 63	chr2p16.1	228316_at	NM_152385
2.10	1.87	0.23	8.34E-02	4.17E-01	---	---	---	1560705_at	---
7.62	7.11	0.51	8.34E-02	4.17E-01	ACP1	acid phosphatase 1, soluble	chr2p25	201629_s_at	NM_001040649 /// NM_004300 /// NM_007099 /// NR_024080
5.71	5.35	0.36	8.34E-02	4.17E-01	GSDMD	gasdermin D	chr8q24.3	218154_at	NM_024736
4.55	3.89	0.67	8.35E-02	4.17E-01	FAM57A	family with sequence similarity 57, member A	chr17p13.3	218898_at	NM_024792
9.01	8.64	0.37	8.35E-02	4.17E-01	C9orf123	chromosome 9 open reading frame 123	chr9p24.1	224879_at	NM_033428
3.65	2.91	0.74	8.36E-02	4.17E-01	SNAP25	synaptosomal-associated protein, 25kDa	chr20p12-p11.2	202508_s_at	NM_003081 /// NM_130811
8.24	7.77	0.46	8.36E-02	4.17E-01	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	chr14q11.2	200751_s_at	NM_001077442 /// NM_001077443 /// NM_004500 /// NM_031314
2.80	2.44	0.36	8.37E-02	4.17E-01	LOC220930	hypothetical protein LOC220930	chr10p11.23	229090_at	---
5.83	5.23	0.61	8.38E-02	4.18E-01	C16orf58	chromosome 16 open reading frame 58	chr16p11.2	217891_at	NM_022744
7.44	6.98	0.46	8.38E-02	4.18E-01	RNF114	ring finger protein 114	chr20q13.13	211678_s_at	NM_018683
4.22	3.99	0.24	8.38E-02	4.18E-01	ZNF333	zinc finger protein 333	chr19p13	1563783_a_at	NM_032433
6.64	6.26	0.38	8.38E-02	4.18E-01	FOXO1	forkhead box O1	chr13q14.1	202724_s_at	NM_002015
5.84	5.02	0.82	8.38E-02	4.18E-01	INHBB	inhibin, beta B	chr2cen-q13	205258_at	NM_002193
5.78	5.38	0.40	8.39E-02	4.18E-01	PDIA4	protein disulfide isomerase family A, member 4	chr7q35	208658_at	NM_004911
8.53	7.91	0.62	8.40E-02	4.18E-01	MAN1A1	Mannosidase, alpha, class 1A, member 1	chr6q22	221760_at	NM_005907
7.42	6.67	0.75	8.41E-02	4.19E-01	---	---	---	226556_at	---
3.74	3.46	0.28	8.42E-02	4.19E-01	---	---	---	225896_at	---
4.96	4.57	0.38	8.42E-02	4.19E-01	ZNF26	zinc finger protein 26	chr12q24.33	219595_at	NM_019591
8.25	7.85	0.41	8.42E-02	4.19E-01	ATOX1	ATX1 antioxidant protein 1 homolog (yeast)	chr5q32	203454_s_at	NM_004045
6.58	5.98	0.60	8.42E-02	4.19E-01	C11orf17	chromosome 11 open reading frame 17	chr11p15.3	242515_x_at	NM_020642 /// NM_182901
5.82	5.34	0.48	8.42E-02	4.19E-01	ANKZF1	ankyrin repeat and zinc finger domain containing 1	chr2q35	218274_s_at	NM_001042410 /// NM_018089
3.06	2.74	0.32	8.42E-02	4.19E-01	---	---	---	239455_at	---
3.70	3.37	0.33	8.43E-02	4.19E-01	KIAA1772	KIAA1772	chr18q11.1-q11.2	220340_at	XR_040952 /// XR_040953 /// XR_040954
5.22	4.86	0.36	8.43E-02	4.19E-01	TELO2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	chr16p13.3	34260_at	NM_016111
9.03	7.04	1.99	8.44E-02	4.19E-01	CHGB	chromogranin B (secretogranin 1)	chr20pter-p12	204260_at	NM_001819
3.23	2.79	0.45	8.44E-02	4.19E-01	SMC5	structural maintenance of chromosomes 5	chr9q21.11	212927_at	NM_015110
2.79	2.44	0.36	8.44E-02	4.19E-01	VANGL2	vang-like 2 (van gogh, Drosophila)	chr1q22-q23	226029_at	NM_020335
2.80	2.54	0.26	8.45E-02	4.19E-01	PABPC1L	poly(A) binding protein, cytoplasmic 1-like	---	233104_at	NM_001124756 /// XM_001130728 /// XM_001131956 /// XM_001722078
6.92	6.47	0.45	8.45E-02	4.19E-01	POLE4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	chr2p12	1553587_a_at	NM_019896
4.11	3.55	0.56	8.45E-02	4.19E-01	ZNF160	zinc finger protein 160	chr19q13.41	239954_at	NM_001102603 /// NM_033288 /// NM_198893
2.78	2.52	0.26	8.45E-02	4.19E-01	---	---	---	243016_at	---
5.10	4.82	0.28	8.46E-02	4.19E-01	GOSR2	golgi SNAP receptor complex member 2	chr17q21	213144_at	NM_001012511 /// NM_004287 /// NM_054022
4.80	4.20	0.60	8.46E-02	4.19E-01	FAR1	fatty acyl CoA reductase 1	chr11p15.2	224866_at	NM_032228

2.87	2.59	0.27	8.46E-02	4.19E-01	---	---	---	1570138_at	---
3.19	2.55	0.65	8.46E-02	4.19E-01	CYP4V2	cytochrome P450, family 4, subfamily V, polypeptide 2	chr4q35.2	235719_at	NM_207352
7.28	6.71	0.57	8.47E-02	4.19E-01	CALHM2	calcium homeostasis modulator 2	chr10pter-q26.12	221565_s_at	NM_015916
6.17	5.46	0.71	8.47E-02	4.20E-01	KLHL3	kelch-like 3 (Drosophila)	chr5q31	221221_s_at	NM_017415
6.97	6.52	0.45	8.48E-02	4.20E-01	GRB2	growth factor receptor-bound protein 2	chr17q24-q25	215075_s_at	NM_002086 /// NM_203506
6.73	6.22	0.50	8.48E-02	4.20E-01	SOD2	superoxide dismutase 2, mitochondrial	chr6q25.3	215223_s_at	NM_000636 /// NM_001024465 /// NM_001024466
2.42	2.15	0.27	8.48E-02	4.20E-01	C3orf55	chromosome 3 open reading frame 55	chr3q25.32	238969_at	NM_001099777 /// NM_001130001 /// NM_001130002 /// NR_024016
3.02	2.76	0.27	8.48E-02	4.20E-01	---	---	---	231557_at	---
5.36	4.61	0.75	8.48E-02	4.20E-01	ANO8	anoctamin 8	chr19p13.11	1563549_a_at	NM_020959
6.21	5.85	0.35	8.48E-02	4.20E-01	TMEM199	transmembrane protein 199	chr17q11.2	225374_at	NM_152464
3.79	3.20	0.59	8.48E-02	4.20E-01	ITGB8	integrin, beta 8	chr7p15.3	226189_at	NM_002214
5.70	4.85	0.84	8.49E-02	4.20E-01	ACYP1	acylphosphatase 1, erythrocyte (common) type	chr14q24.3	205260_s_at	NM_001107 /// NM_203488
2.48	2.12	0.36	8.49E-02	4.20E-01	---	---	---	230314_at	---
2.63	2.39	0.23	8.49E-02	4.20E-01	TINAG	tubulointerstitial nephritis antigen	chr6p11.2-p12	231154_x_at	NM_014464
6.51	5.92	0.59	8.49E-02	4.20E-01	RABL4	RAB, member of RAS oncogene family-like 4	chr22q13.1	205037_at	NM_006860
5.38	4.86	0.52	8.50E-02	4.20E-01	IL15RA	interleukin 15 receptor, alpha	chr10p15-p14	207375_s_at	NM_002189 /// NM_172200
2.67	2.42	0.26	8.50E-02	4.20E-01	LOC92270	hypothetical protein LOC92270	chr5q14.2	1557523_at	NM_001017971
2.74	2.50	0.24	8.50E-02	4.20E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	1565817_at	NM_006060
5.70	5.39	0.31	8.51E-02	4.20E-01	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	chr11q12.3	203452_at	NM_012200
5.23	4.82	0.41	8.51E-02	4.20E-01	RAB36	RAB36, member RAS oncogene family	chr22q11.22	211471_s_at	NM_004914
9.78	9.12	0.66	8.51E-02	4.20E-01	MT1F	metallothionein 1F	chr16q13	217165_x_at	NM_005949
3.67	3.11	0.56	8.51E-02	4.20E-01	DONSON	downstream neighbor of SON	chr21q22.1	221677_s_at	NM_017613
7.84	7.47	0.38	8.51E-02	4.20E-01	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	chr20q11.2-q13.1	218559_s_at	NM_005461
6.72	6.19	0.53	8.51E-02	4.20E-01	FASTKD5	FAST kinase domains 5	chr20p13	219016_at	NM_021826
6.60	5.91	0.68	8.51E-02	4.20E-01	FHL1	four and a half LIM domains 1	chrXq26	214505_s_at	NM_001449
3.61	3.34	0.27	8.51E-02	4.20E-01	---	---	---	233891_at	---
6.81	6.31	0.50	8.51E-02	4.20E-01	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	chr20cen-q13	224378_x_at	NM_032514 /// NM_181509
5.08	4.49	0.59	8.52E-02	4.20E-01	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	chr18q21	212445_s_at	NM_015277
2.72	2.43	0.29	8.52E-02	4.20E-01	---	---	---	1555973_at	---
5.19	4.46	0.73	8.52E-02	4.20E-01	EPOR	erythropoietin receptor	chr19p13.3-p13.2	37986_at	NM_000121
13.23	12.75	0.48	8.52E-02	4.20E-01	DLK1	delta-like 1 homolog (Drosophila)	chr14q32	209560_s_at	NM_003836
3.21	2.98	0.23	8.53E-02	4.20E-01	LOC149837 /// LOC643406	hypothetical LOC149837 /// hypothetical protein LOC643406	chr20p12.3	229992_at	XM_001723623 /// XM_001725180 /// XM_001725203 /// XR_042108 /// XR_042109 /// XR_042110
5.59	5.12	0.47	8.53E-02	4.20E-01	ABHD2	abhydrolase domain containing 2	chr15q26.1	228490_at	NM_007011 /// NM_152924
4.93	4.59	0.33	8.53E-02	4.20E-01	PPM1F	protein phosphatase 1F (PP2C domain containing)	chr22q11.22	1555470_a_at	NM_014634
6.20	5.65	0.55	8.53E-02	4.20E-01	ZNF746	zinc finger protein 746	chr7q36.1	225848_at	NM_152557
4.26	4.05	0.22	8.54E-02	4.20E-01	PSMC3IP	PSMC3 interacting protein	chr17q12-q21	205956_x_at	NM_013290 /// NM_016556
3.45	3.08	0.37	8.54E-02	4.20E-01	E2F2	E2F transcription factor 2	chr1p36	235582_at	NM_004091
3.74	3.35	0.38	8.54E-02	4.20E-01	---	---	---	231116_at	---

12.00	11.40	0.60	8.54E-02	4.20E-01	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	chr7q36.1	209496_at	NM_002889																			
2.39	2.15	0.23	8.55E-02	4.20E-01	---	---	---	223930_at	---																			
4.70	4.32	0.39	8.55E-02	4.20E-01	PIGM	phosphatidylinositol glycan anchor biosynthesis, class M	chr1q23.2	235532_at	NM_145167																			
5.07	4.78	0.29	8.55E-02	4.20E-01	RNF214	ring finger protein 214	chr11q23.3	227114_at	NM_001077239 /// NM_207343																			
5.94	5.34	0.60	8.55E-02	4.20E-01	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	chr12q24.1	218218_at	NM_018171																			
5.38	4.97	0.42	8.55E-02	4.20E-01	ZMYM3	zinc finger, MYM-type 3	chrXq13.1	1554171_at	NM_005096 /// NM_201599																			
5.62	5.03	0.60	8.56E-02	4.21E-01	S100PBP	S100P binding protein	chr1p35.1	218370_s_at	NM_001017406 /// NM_022753																			
9.32	8.88	0.44	8.57E-02	4.21E-01	TSPYL1	TSPY-like 1	chr6q22-q23	221493_at	NM_003309																			
2.67	2.42	0.25	8.57E-02	4.21E-01	ZNF688	zinc finger protein 688	chr16p11.2	235950_at	NM_001024683 /// NM_145271																			
3.54	2.94	0.60	8.57E-02	4.21E-01	EIF2C4	Eukaryotic translation initiation factor 2C, 4	chr1p34.3	227930_at	NM_017629																			
5.09	4.65	0.44	8.57E-02	4.21E-01	VISA	virus-induced signaling adapter	chr20p13	229741_at	NM_020746																			
8.55	8.05	0.50	8.58E-02	4.21E-01	SGSH	N-sulfoglucosamine sulfohydrolase	chr17q25.3	35626_at	NM_000199																			
3.79	3.25	0.53	8.58E-02	4.21E-01	EP400NL	EP400 N-terminal like	chr12q24.33	229892_at	NR_003290																			
7.30	6.81	0.49	8.58E-02	4.21E-01	FADD	Fas (TNFRSF6)-associated via death domain	chr11q13.3	202535_at	NM_003824																			
7.84	7.50	0.34	8.59E-02	4.21E-01	TRAP1	TNF receptor-associated protein 1	chr16p13.3	201391_at	NM_016292																			
6.23	5.90	0.33	8.59E-02	4.21E-01	ZMAT5	zinc finger, matrin type 5	chr22cen-q12.3	218752_at	NM_001003692 /// NM_019103																			
6.25	5.64	0.61	8.59E-02	4.21E-01	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	chr10q22	207127_s_at	NM_012207 /// NM_021644																			
5.15	4.36	0.79	8.59E-02	4.21E-01	TIFA	TRAF-interacting protein with forkhead-associated domain	chr4q25	226117_at	NM_052864																			
10.45	10.16	0.29	8.60E-02	4.21E-01	LOC728179	similar to LOC100037086 protein	chr6p24.3	234512_x_at	XR_015348 /// XR_015445 /// XR_039369																			
7.07	6.66	0.42	8.60E-02	4.22E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	202249_s_at	NM_015726																			
2.42	2.05	0.37	8.60E-02	4.22E-01	---	---	---	236314_at	---																			
5.43	4.90	0.53	8.61E-02	4.22E-01	WHSC2	Wolf-Hirschhorn syndrome candidate 2	chr4p16.3	203112_s_at	NM_005663																			
5.96	5.55	0.41	8.62E-02	4.23E-01	SDCCAG3	serologically defined colon cancer antigen 3	chr9q34.3	218427_at	NM_001039707 /// NM_001039708 /// NM_006643																			
6.56	6.14	0.42	8.63E-02	4.23E-01	DTX3L	deltex 3-like (Drosophila)	chr3q21.1	225415_at	NM_138287																			
5.39	4.74	0.64	8.64E-02	4.23E-01	SLC25A32	solute carrier family 25, member 32	chr8q22.3	221020_s_at	NM_030780																			
4.80	4.15	0.64	8.64E-02	4.23E-01	NHLRC3	NHL repeat containing 3	chr13q13.3	227040_at	NM_001012754 /// NM_001017370																			
6.71	6.26	0.45	8.66E-02	4.24E-01	HDHD1A	haloacid dehalogenase-like hydrolase domain containing 1A	chrXp22.32	203974_at	NM_012080																			
3.21	2.66	0.54	8.66E-02	4.24E-01	OGFRL1	opioid growth factor receptor-like 1	chr6q13	238469_at	NM_024576																			
3.16	2.91	0.25	8.67E-02	4.24E-01	KIAA1199	KIAA1199	chr15q24	1554685_a_at	NM_018689																			
3.06	2.81	0.25	8.67E-02	4.24E-01	SEC16B	SEC16 homolog B (S. cerevisiae)	chr1q25.2	1564423_a_at	NM_033127																			
8.04	7.55	0.48	8.67E-02	4.24E-01	IFI6	interferon, alpha-inducible protein 6	chr1p35	204415_at	NM_002038 /// NM_022872 /// NM_022873																			
3.73	3.28	0.45	8.68E-02	4.24E-01	---	---	---	228974_at	---																			
2.53	2.25	0.28	8.68E-02	4.24E-01	EXOC6B	exocyst complex component 6B	chr2p13.3-p13.2	215417_at	NM_015189																			
4.99	4.19	0.80	8.69E-02	4.24E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	212014_x_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392																			
2.87	2.57	0.30	8.69E-02	4.24E-01	C16orf46	chromosome 16 open reading frame 46	chr16q23.2	230281_at	NM_001100873 /// NM_152337																			
2.56	2.33	0.23	8.69E-02	4.24E-01	---	---	---	237732_at	---																			

5.88	5.67	0.21	8.70E-02	4.25E-01	ELF2	E74-like factor 2 (ets domain transcription factor)	chr4q28	242735_x_at	NM_006874 /// NM_201999																					
5.64	5.18	0.46	8.70E-02	4.25E-01	RAB11FIP3	RAB11 family interacting protein 3 (class II)	chr16p13.3	203933_at	NM_014700																					
6.00	5.39	0.61	8.71E-02	4.25E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	1557996_at	NR_003655 /// XR_042143 /// XR_042182																					
7.84	7.48	0.36	8.71E-02	4.25E-01	ENSA	endosulfine alpha	chr1q21.2	221486_at	NM_004436 /// NM_207042 /// NM_207043 /// NM_207044 /// NM_207045 /// NM_207046 /// NM_207047 /// NM_207168																					
7.78	7.48	0.29	8.71E-02	4.25E-01	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	chr1p34.3	201585_s_at	NM_005066																					
9.07	8.75	0.32	8.72E-02	4.25E-01	TCF25	transcription factor 25 (basic helix-loop-helix)	chr16q24.3	221495_s_at	NM_014972																					
4.21	3.36	0.85	8.72E-02	4.25E-01	CTH	cystathionase (cystathionine gamma-lyase)	chr1p31.1	206085_s_at	NM_001902 /// NM_153742																					
2.48	2.28	0.20	8.72E-02	4.25E-01	---	---	---	1566984_at	---																					
3.32	2.57	0.75	8.72E-02	4.25E-01	TRSPAP1	tRNA selenocysteine associated protein 1	chr1p35.3	228997_at	NM_017846 /// NR_003109																					
9.81	9.21	0.59	8.72E-02	4.25E-01	MT1H	metallothionein 1H	chr16q13	206461_x_at	NM_005951																					
5.75	5.19	0.56	8.72E-02	4.25E-01	SIN3B	SIN3 homolog B, transcription regulator (yeast)	chr19p13.11	39705_at	NM_015260																					
9.92	9.65	0.27	8.73E-02	4.25E-01	PNRC1	proline-rich nuclear receptor coactivator 1	chr6q15	209034_at	NM_006813																					
3.99	3.66	0.33	8.73E-02	4.25E-01	---	---	---	233729_at	---																					
7.87	7.55	0.32	8.73E-02	4.25E-01	SRP68	signal recognition particle 68kDa	chr17q25.1	224607_s_at	NM_014230																					
5.13	4.54	0.59	8.73E-02	4.25E-01	SHB	Src homology 2 domain containing adaptor protein B	chr9p13.2-p13.1	204657_s_at	NM_003028																					
2.76	2.47	0.29	8.74E-02	4.26E-01	CRYGA	crystallin, gamma A	chr2q33-q35	207587_at	NM_014617																					
7.63	6.47	1.16	8.75E-02	4.26E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	224558_s_at	NR_002819																					
7.77	6.76	1.01	8.75E-02	4.26E-01	RHOB	ras homolog gene family, member B	chr2p24	1553962_s_at	NM_004040																					
3.62	2.95	0.67	8.75E-02	4.26E-01	PLD1	phospholipase D1, phosphatidylcholine-specific	chr3q26	1557126_a_at	NM_001130081 /// NM_002662																					
2.21	2.00	0.21	8.75E-02	4.26E-01	LOC731489	hypothetical protein LOC731489	---	238586_at	XM_001714309																					
6.73	6.26	0.47	8.75E-02	4.26E-01	PHF1	PHD finger protein 1	chr6p21.3	202928_s_at	NM_002636 /// NM_024165																					
5.30	4.91	0.39	8.76E-02	4.26E-01	DTNBP1	dystrobrevin binding protein 1	chr6p22.3	223446_s_at	NM_032122 /// NM_183040 /// NM_183041																					
2.33	2.08	0.25	8.76E-02	4.26E-01	KLHL34	kelch-like 34 (Drosophila)	chrXp22.12	1553873_at	NM_153270																					
3.79	3.41	0.38	8.76E-02	4.26E-01	C8orf42	chromosome 8 open reading frame 42	chr8p23.3	242387_at	NM_175075																					
7.62	7.21	0.41	8.76E-02	4.26E-01	DUS1L	dihydrouridine synthase 1-like (S. cerevisiae)	chr17q25.3	217912_at	NM_022156																					
3.83	3.51	0.32	8.77E-02	4.26E-01	DHX35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	chr20q11.22-q12	218579_s_at	NM_021931																					
3.10	2.85	0.24	8.77E-02	4.26E-01	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	chr8p21	227345_at	NM_003840																					
7.97	7.27	0.70	8.78E-02	4.26E-01	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	chr7q31|14q24.2-q24.3	202842_s_at	NM_012328																					
3.19	2.97	0.22	8.79E-02	4.26E-01	---	---	---	229329_s_at	---																					
2.58	2.36	0.22	8.79E-02	4.27E-01	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)	chr11q22.3	1566514_at	NM_152434																					
8.40	8.04	0.36	8.79E-02	4.27E-01	FAM134C	family with sequence similarity 134, member C	chr17q21.31	212697_at	NM_178126																					
6.02	5.48	0.54	8.80E-02	4.27E-01	RNF123	ring finger protein 123	chr3p24.3	221063_x_at	NM_022064																					
8.94	8.63	0.30	8.80E-02	4.27E-01	SNX17	sorting nexin 17	chr2p23-p22	200991_s_at	NM_014748																					
2.20	1.86	0.34	8.81E-02	4.27E-01	---	---	---	235203_at	---																					
2.07	1.79	0.28	8.81E-02	4.27E-01	SYCP3	synaptonemal complex protein 3	chr12q	1553599_a_at	NM_153694																					

5.00	4.02	0.98	8.81E-02	4.27E-01	LOC100128822	hypothetical protein LOC100128822	chr7q36.1	235174_s_at	XM_001714139 /// XM_001714377 /// XM_001715218																				
7.88	7.27	0.61	8.81E-02	4.27E-01	PREPL	prolyl endopeptidase-like	chr2p21	212215_at	NM_001042385 /// NM_001042386 /// NM_006036																				
9.72	9.03	0.70	8.82E-02	4.27E-01	CCND3	cyclin D3	chr6p21	201700_at	NM_001760																				
2.98	2.67	0.31	8.82E-02	4.27E-01	---	---	---	231038_s_at	---																				
7.93	7.51	0.42	8.83E-02	4.27E-01	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	chr16p13.3	205963_s_at	NM_005147																				
5.81	5.21	0.60	8.83E-02	4.27E-01	HMGB2	high-mobility group box 2	chr4q31	208808_s_at	NM_001130688 /// NM_001130689 /// NM_002129																				
6.56	6.19	0.37	8.83E-02	4.27E-01	FTSJ2	FtsJ homolog 2 (E. coli)	chr7p22	218356_at	NM_013393																				
4.52	3.95	0.57	8.83E-02	4.27E-01	LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	chr1p13.1	205953_at	NM_014813																				
2.92	2.69	0.23	8.84E-02	4.27E-01	LOC153910	hypothetical protein LOC153910	chr6q24.1-q24.2	1561085_at	---																				
2.94	2.66	0.29	8.84E-02	4.27E-01	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3	chr3q26.3-q27	221125_s_at	NM_014407 /// NM_171828 /// NM_171829 /// NM_171830																				
2.35	2.12	0.23	8.85E-02	4.27E-01	---	---	---	238548_at	---																				
6.03	5.67	0.37	8.85E-02	4.28E-01	RPIA	ribose 5-phosphate isomerase A	chr2p11.2	212973_at	NM_144563																				
6.95	6.50	0.45	8.85E-02	4.28E-01	DEDD2	death effector domain containing 2	chr19q13.2	225434_at	NM_133328																				
4.21	3.75	0.46	8.86E-02	4.28E-01	---	---	---	228174_at	---																				
2.48	2.16	0.32	8.87E-02	4.28E-01	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	chr12p11.23-p11.22	1569464_at	NM_003622 /// NM_177444																				
3.39	3.11	0.29	8.88E-02	4.28E-01	SOCS1	suppressor of cytokine signaling 1	chr16p13.13	209999_x_at	NM_003745																				
5.84	5.40	0.45	8.89E-02	4.29E-01	MED4	mediator complex subunit 4	chr13q14.2	217843_s_at	NM_014166																				
3.75	3.40	0.35	8.89E-02	4.29E-01	---	---	---	230998_at	---																				
5.88	5.54	0.33	8.90E-02	4.29E-01	ZMIZ2	zinc finger, MIZ-type containing 2	chr7p13	221924_at	NM_031449 /// NM_174929																				
5.44	5.02	0.42	8.90E-02	4.29E-01	IGHMBP2	immunoglobulin mu binding protein 2	chr11q13.3	31861_at	NM_002180																				
3.32	3.05	0.27	8.91E-02	4.29E-01	PTPN21	protein tyrosine phosphatase, non-receptor type 21	chr14q31.3	1320_at	NM_007039																				
2.92	2.66	0.26	8.91E-02	4.29E-01	MINA	MYC induced nuclear antigen	chr3q11.2	1554774_at	NM_001042533 /// NM_032778 /// NM_153182																				
6.60	6.18	0.42	8.91E-02	4.29E-01	PSMG3	proteasome (prosome, macropain) assembly chaperone 3	chr7p22.3	223363_at	NM_001134340 /// NM_032302																				
3.13	2.86	0.27	8.92E-02	4.29E-01	---	---	---	1562032_at	---																				
6.31	5.78	0.54	8.92E-02	4.29E-01	STX3	syntaxin 3	chr11q12.1	209238_at	NM_004177																				
5.12	4.59	0.53	8.93E-02	4.29E-01	---	---	---	1556123_a_at	---																				
6.81	6.05	0.76	8.93E-02	4.30E-01	ADM	adrenomedullin	chr11p15.4	202912_at	NM_001124																				
7.12	6.69	0.43	8.93E-02	4.30E-01	ZNF410	zinc finger protein 410	chr14q24.3	202010_s_at	NM_021188																				
3.69	3.25	0.44	8.94E-02	4.30E-01	PPM1B	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	chr2p21	213225_at	NM_001033556 /// NM_001033557 /// NM_002706 /// NM_177968 /// NM_177969																				
6.20	5.74	0.45	8.94E-02	4.30E-01	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	chr3q25.31	203165_s_at	NM_004733																				
8.53	8.23	0.30	8.94E-02	4.30E-01	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	chr9p21.1	203613_s_at	NM_002493 /// NM_182739																				
7.05	6.46	0.59	8.95E-02	4.30E-01	BTG3	BTG family, member 3	chr21q21.1-q21.2	213134_x_at	NM_001130914 /// NM_006806																				

4.01	3.43	0.58	8.96E-02	4.30E-01	LOC652968 /// TBC1D10A	hypothetical protein LOC652968 /// TBC1 domain family, member 10A	chr22q12 /// chr22q12.1-qter	226613_at	NM_001037666 /// NM_031937																				
7.06	6.12	0.94	8.96E-02	4.30E-01	MERTK	c-mer proto-oncogene tyrosine kinase	chr2q14.1	211913_s_at	NM_006343																				
2.09	1.86	0.23	8.97E-02	4.30E-01	TBX22	T-box 22	chrXq21.1	224017_at	NM_001109878 /// NM_001109879 /// NM_016954																				
7.68	7.25	0.42	8.99E-02	4.30E-01	MED12	mediator complex subunit 12	chrXq13	211342_x_at	NM_005120																				
9.31	8.46	0.85	8.99E-02	4.30E-01	FAM166B	family with sequence similarity 166, member B	chr9p13.3	229941_at	NM_001099951																				
3.16	2.83	0.33	8.99E-02	4.30E-01	---	---	---	216040_x_at	---																				
3.80	3.18	0.62	8.99E-02	4.30E-01	HIC2	hypermethylated in cancer 2	chr22q11.21	212966_at	NM_015094																				
7.19	6.76	0.43	8.99E-02	4.30E-01	POLD4	polymerase (DNA-directed), delta 4	chr11q13	202996_at	NM_021173																				
4.69	4.27	0.42	9.00E-02	4.31E-01	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	chr12q12-q14	214095_at	NM_005412																				
7.77	7.25	0.52	9.00E-02	4.31E-01	ZNF362	zinc finger protein 362	chr1p35.1	226820_at	NM_152493																				
2.66	2.30	0.36	9.00E-02	4.31E-01	---	---	---	1558600_a_at	---																				
6.18	5.79	0.39	9.00E-02	4.31E-01	KCTD6	potassium channel tetramerisation domain containing 6	chr3p14.3	238077_at	NM_001128214 /// NM_153331																				
2.88	2.57	0.31	9.00E-02	4.31E-01	COMMD2	COMM domain containing 2	chr3q25.1	223491_at	NM_016094																				
5.90	5.57	0.32	9.00E-02	4.31E-01	POMT1	protein-O-mannosyltransferase 1	chr9q34.1	218476_at	NM_001077365 /// NM_001077366 /// NM_007171																				
6.01	5.12	0.90	9.01E-02	4.31E-01	LIMCH1	LIM and calponin homology domains 1	chr4p13	212325_at	NM_001112717 /// NM_001112718 /// NM_001112719 /// NM_001112720 /// NM_014988																				
4.56	3.94	0.62	9.01E-02	4.31E-01	CISD3	CDGSH iron sulfur domain 3	chr17q12	230727_at	XM_001714917 /// XM_001716624 /// XM_001718346																				
6.82	6.51	0.31	9.01E-02	4.31E-01	COG4	component of oligomeric golgi complex 4	chr16q22.1	212189_s_at	NM_015386																				
3.89	3.40	0.48	9.01E-02	4.31E-01	ACOT8	Acyl-CoA thioesterase 8	chr20q13.12	236514_at	NM_005469 /// NM_183386																				
2.51	2.29	0.22	9.03E-02	4.31E-01	---	---	---	221275_s_at	---																				
2.61	2.41	0.20	9.04E-02	4.31E-01	C7orf64	chromosome 7 open reading frame 64	chr7q21.2	221594_at	NM_032120																				
2.82	2.40	0.42	9.04E-02	4.32E-01	---	---	---	237571_at	---																				
7.98	7.67	0.31	9.05E-02	4.32E-01	TRAPPC3	trafficking protein particle complex 3	chr1p34.3	203511_s_at	NM_014408																				
3.62	3.19	0.43	9.05E-02	4.32E-01	LOC791120	hypothetical LOC791120	chr7q36.1	213367_at	NR_015357 /// XR_039872 /// XR_039873 /// XR_039874 /// XR_039875																				
4.52	4.09	0.44	9.05E-02	4.32E-01	FAM135A	family with sequence similarity 135, member A	chr6q12-q13	223497_at	NM_001105531 /// NM_020819																				
2.93	2.47	0.47	9.05E-02	4.32E-01	C6orf12	HLA complex group 8	chr6p21.33	215985_at	XR_041144 /// XR_041145																				
6.69	6.34	0.35	9.06E-02	4.32E-01	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	chr17q22	242553_at	NM_003786																				
6.86	6.02	0.85	9.06E-02	4.32E-01	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	chr1p36.13-p36.12	207826_s_at	NM_002167																				
3.29	2.82	0.47	9.07E-02	4.32E-01	---	---	---	244044_at	---																				
6.92	6.58	0.34	9.07E-02	4.32E-01	FAM100B	family with sequence similarity 100, member B	chr17q25.1	224785_at	NM_182565																				
4.67	4.15	0.52	9.08E-02	4.32E-01	DUT	deoxyuridine triphosphatase	chr15q15-q21.1	208955_at	NM_001025248 /// NM_001025249 /// NM_001948																				
5.93	5.56	0.38	9.08E-02	4.32E-01	TCTN2	tectonic family member 2	chr12q24.31	206438_x_at	NM_024809																				

8.21	7.71	0.50	9.08E-02	4.32E-01	C14orf2	chromosome 14 open reading frame 2	chr14q32.33	202279_at	NM_001127393 /// NM_004894																				
6.80	6.44	0.36	9.08E-02	4.32E-01	BCL2L2	BCL2-like 2	chr14q11.2-q12	209311_at	NM_004050																				
7.69	7.31	0.38	9.08E-02	4.32E-01	C19orf62	chromosome 19 open reading frame 62	chr19p13.11	221711_s_at	NM_001033549 /// NM_014173																				
4.61	3.98	0.64	9.09E-02	4.32E-01	RGS16	regulator of G-protein signaling 16	chr1q25-q31	209325_s_at	NM_002928																				
2.57	2.30	0.27	9.09E-02	4.32E-01	ZNF311	zinc finger protein 311	chr6p22.1	236551_at	NM_001010877																				
6.18	5.60	0.58	9.09E-02	4.32E-01	EXOSC10	exosome component 10	chr1p36.22	207541_s_at	NM_001001998 /// NM_002685																				
3.65	3.29	0.36	9.09E-02	4.32E-01	---	---	---	221963_x_at	---																				
3.16	2.81	0.34	9.10E-02	4.32E-01	ZAN	zonadhesin	chr7q22	224268_x_at	NM_003386 /// NM_173059																				
2.16	1.96	0.20	9.10E-02	4.32E-01	---	---	---	1559865_at	---																				
3.07	2.67	0.39	9.10E-02	4.32E-01	MESDC2	mesoderm development candidate 2	chr15q13	238679_at	NM_015154																				
7.81	7.54	0.27	9.10E-02	4.32E-01	RABL5	RAB, member RAS oncogene family-like 5	chr7q22.1	222742_s_at	NM_001130820 /// NM_001130821 /// NM_001130822 /// NM_022777																				
3.83	3.42	0.40	9.11E-02	4.32E-01	LOC286434	hypothetical protein LOC286434	chrXp22.33	1556102_x_at	XM_001717193																				
3.38	2.77	0.61	9.11E-02	4.33E-01	C19orf36	chromosome 19 open reading frame 36	chr19p13.3	215734_at	NM_001031735 /// NM_001039846																				
8.88	8.31	0.57	9.11E-02	4.33E-01	MT1G	metallothionein 1G	chr16q13	204745_x_at	NM_005950																				
6.60	5.83	0.78	9.12E-02	4.33E-01	PRTFDC1	phosphoribosyl transferase domain containing 1	chr10p12.1	222803_at	NM_020200																				
4.30	3.64	0.66	9.12E-02	4.33E-01	ZDBF2	zinc finger, DBF-type containing 2	chr2q33.3	228749_at	NM_020923																				
6.21	5.85	0.37	9.12E-02	4.33E-01	---	---	---	216547_at	---																				
12.30	12.10	0.20	9.13E-02	4.33E-01	RPL13	ribosomal protein L13	chr16q24.3|17p11.2	208929_x_at	NM_000977 /// NM_033251																				
2.43	2.18	0.25	9.13E-02	4.33E-01	---	---	---	239973_at	---																				
5.62	5.29	0.33	9.13E-02	4.33E-01	RBM33	RNA binding motif protein 33	chr7q36.3	226732_at	NM_001008408 /// NM_053043																				
5.95	5.66	0.29	9.13E-02	4.33E-01	BCAS3	breast carcinoma amplified sequence 3	chr17q23	220488_s_at	NM_001099432 /// NM_017679																				
6.56	5.68	0.88	9.14E-02	4.33E-01	TRIM68	tripartite motif-containing 68	chr11p15.4	219405_at	NM_018073																				
4.15	3.47	0.68	9.14E-02	4.33E-01	THSD1 /// THSD1P	thrombospondin, type I, domain containing 1 /// thrombospondin, type I, domain containing 1 pseudogene	chr13q14.3	219477_s_at	NM_018676 /// NM_199263 /// NR_002816																				
2.43	2.13	0.30	9.14E-02	4.33E-01	RPAIN	RPA interacting protein	chr17p13.2	1556088_at	NM_001033002																				
2.69	2.49	0.20	9.14E-02	4.33E-01	---	---	---	AFFX-r2-Bs-thr-3_s_at	---																				
3.44	3.07	0.37	9.14E-02	4.33E-01	POP1	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)	chr8q22.1	213449_at	NM_015029																				
7.08	5.94	1.14	9.14E-02	4.33E-01	TMEM108	transmembrane protein 108	chr3q21	223524_s_at	NM_023943																				
6.24	5.87	0.37	9.15E-02	4.33E-01	CSNK1E	casein kinase 1, epsilon	chr22q13.1	202332_at	NM_001894 /// NM_152221																				
5.07	4.67	0.40	9.15E-02	4.33E-01	tcag7.1228	hypothetical protein FLJ25778	chr7q34	225444_at	NM_173569																				
7.75	7.39	0.36	9.16E-02	4.33E-01	OAZ2	ornithine decarboxylase antizyme 2	chr15q22.31	201365_at	NM_002537																				
6.74	6.28	0.46	9.16E-02	4.33E-01	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	chr20cen-q13	227219_x_at	NM_032514 /// NM_181509																				
7.27	6.78	0.48	9.16E-02	4.33E-01	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	chr17q21	209852_x_at	NM_005789 /// NM_176863																				
5.46	4.91	0.55	9.16E-02	4.33E-01	VKORC1L1	vitamin K epoxide reductase complex, subunit 1-like 1	chr7q11.21	224881_at	NM_173517																				
6.22	5.78	0.44	9.16E-02	4.33E-01	ADCK2	aarF domain containing kinase 2	chr7q32-q34	44120_at	NM_052853																				
6.97	6.60	0.36	9.16E-02	4.33E-01	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	chrXp22.2-p22.1	1555864_s_at	NM_000284																				
3.60	2.49	1.10	9.17E-02	4.34E-01	LOC284702	hypothetical protein LOC284702	chr1q44	225786_at	---																				

2.98	2.69	0.29	9.18E-02	4.34E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	215311_at	NM_001007156 /// NM_001012338 /// NM_002530																				
10.62	10.20	0.42	9.18E-02	4.34E-01	CRTAP	cartilage associated protein	chr3p22.3	1555889_a_at	NM_006371																				
3.86	3.36	0.50	9.20E-02	4.34E-01	FBXO28	F-box protein 28	chr1q42.11	1555970_at	NM_015176																				
2.17	1.96	0.21	9.20E-02	4.34E-01	C3orf55	chromosome 3 open reading frame 55	chr3q25.32	1558552_s_at	NM_001099777 /// NM_001130001 /// NM_001130002 /// NR_024016																				
2.21	2.01	0.19	9.20E-02	4.34E-01	---	---	---	1558968_at	---																				
4.34	3.85	0.49	9.21E-02	4.34E-01	PRRT3	proline-rich transmembrane protein 3	chr3p25.3	1556308_at	NM_207351																				
5.28	4.76	0.52	9.21E-02	4.34E-01	ZNF71	zinc finger protein 71	chr19q13.4	226514_at	NM_021216																				
6.79	6.31	0.48	9.21E-02	4.34E-01	TMEM42	transmembrane protein 42	chr3p21.31	226361_at	NM_144638																				
6.03	5.53	0.50	9.22E-02	4.34E-01	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	chr3p21.31	230871_at	NM_014966 /// NM_138615																				
4.70	4.21	0.49	9.22E-02	4.34E-01	ADAT3	adenosine deaminase, tRNA-specific 3, TAD3 homolog (S. cerevisiae)	chr19p13.3	230634_x_at	NM_138422																				
3.85	3.50	0.34	9.22E-02	4.34E-01	---	---	---	230343_at	---																				
7.41	6.70	0.70	9.22E-02	4.34E-01	DDR1	discoidin domain receptor tyrosine kinase 1	chr6p21.3	208779_x_at	NM_001954 /// NM_013993 /// NM_013994																				
11.71	11.50	0.21	9.22E-02	4.34E-01	RPL13	ribosomal protein L13	chr16q24.3|17p11.2	214351_x_at	NM_000977 /// NM_033251																				
2.45	2.26	0.20	9.23E-02	4.35E-01	---	---	---	1561092_at	---																				
4.18	3.75	0.42	9.23E-02	4.35E-01	COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	chr10q24	221550_at	NM_004376 /// NM_078470																				
7.68	7.35	0.33	9.24E-02	4.35E-01	C17orf49 /// RNASEK	chromosome 17 open reading frame 49 /// ribonuclease, RNase K	chr17p13.1	224574_at	NM_001004333 /// NM_174893																				
4.89	4.51	0.37	9.24E-02	4.35E-01	---	---	---	1570185_at	---																				
2.55	2.14	0.40	9.24E-02	4.35E-01	HOOK3	hook homolog 3 (Drosophila)	chr8p11.21	235114_x_at	NM_032410																				
6.83	6.55	0.28	9.24E-02	4.35E-01	TOX4	TOX high mobility group box family member 4	chr14q11.2	201684_s_at	NM_014828																				
6.91	6.46	0.46	9.24E-02	4.35E-01	POP7	processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae)	chr7q22	209482_at	NM_005837																				
5.32	4.96	0.36	9.25E-02	4.35E-01	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2	chr15q11-q12	209870_s_at	NM_001130414 /// NM_005503																				
2.90	2.63	0.28	9.25E-02	4.35E-01	---	---	---	240748_at	---																				
8.38	7.89	0.49	9.25E-02	4.35E-01	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	chr2q14.1	213102_at	NM_005721																				
6.23	5.92	0.32	9.26E-02	4.35E-01	KIAA0415	KIAA0415	chr7p22.2	209913_x_at	NM_014855																				
4.04	3.81	0.23	9.26E-02	4.35E-01	SFTPB	surfactant protein B	chr2p12-p11.2	213936_x_at	NM_000542 /// NM_198843																				
5.44	4.63	0.81	9.26E-02	4.35E-01	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	chr6p21	201188_s_at	NM_002224																				
6.63	6.19	0.43	9.26E-02	4.35E-01	PNPO	pyridoxamine 5'-phosphate oxidase	chr17q21.32	218511_s_at	NM_018129																				
10.39	10.05	0.34	9.26E-02	4.35E-01	MGST3	microsomal glutathione S-transferase 3	chr1q23	201403_s_at	NM_004528																				
2.52	2.16	0.36	9.27E-02	4.35E-01	DOCK7	dedicator of cytokinesis 7	chr1p31.3	237470_at	NM_033407																				
2.81	2.52	0.29	9.28E-02	4.35E-01	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	chr4q13.3	239562_at	NM_001004346																				
5.32	4.99	0.33	9.28E-02	4.35E-01	ZCCHC10	zinc finger, CCHC domain containing 10	chr5q31.1	1559399_s_at	NM_017665																				
5.94	4.82	1.12	9.29E-02	4.36E-01	CAB39L	calcium binding protein 39-like	chr13q14.2-q14.3	225914_s_at	NM_001079670 /// NM_030925																				
4.91	4.59	0.32	9.29E-02	4.36E-01	DEDD	death effector domain containing	chr1q23.3	211255_x_at	NM_001039711 /// NM_001039712 /// NM_032998																				
2.29	2.05	0.23	9.29E-02	4.36E-01	---	---	---	1561324_at	---																				
7.04	6.52	0.52	9.29E-02	4.36E-01	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	chr2q35-q36	204091_at	NM_002601																				
3.80	3.45	0.34	9.31E-02	4.36E-01	C18orf19	chromosome 18 open reading frame 19	chr18p11.21	235022_at	NM_001098801 /// NM_152352																				
7.24	6.94	0.30	9.31E-02	4.36E-01	MARS	methionyl-tRNA synthetase	chr12q13.2	201475_x_at	NM_004990																				
4.22	3.82	0.40	9.32E-02	4.36E-01	MYOZ3	myozenin 3	chr5q33.1	1562004_x_at	NM_001122853 /// NM_133371																				

8.38	7.91	0.47	9.32E-02	4.36E-01	F8A1 /// F8A2 /// F8A3	coagulation factor VIII-associated (intronic transcript) 1 /// coagulation factor VIII-associated (intronic transcript) 2 /// coagulation factor VIII-associated (intronic transcript) 3	chrXq28	203274_at	NM_001007523 /// NM_001007524 /// NM_012151																				
5.57	5.24	0.34	9.32E-02	4.36E-01	TMC6	transmembrane channel-like 6	chr17q25.3	204328_at	NM_001127198 /// NM_007267																				
4.95	4.57	0.38	9.32E-02	4.36E-01	C19orf28	chromosome 19 open reading frame 28	chr19p13.3	220178_at	NM_001042680 /// NM_021731 /// NM_174983																				
4.99	4.45	0.55	9.33E-02	4.36E-01	SPON1	spondin 1, extracellular matrix protein	chr11p15.2	213994_s_at	NM_006108																				
9.02	8.15	0.87	9.34E-02	4.36E-01	---	---	---	230130_at	---																				
3.54	2.70	0.84	9.34E-02	4.36E-01	---	---	---	230577_at	---																				
2.35	2.15	0.20	9.34E-02	4.36E-01	---	---	---	237927_at	---																				
8.53	8.10	0.43	9.35E-02	4.36E-01	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	chr1p35.1-p36.23	202139_at	NM_003689																				
3.24	2.87	0.36	9.35E-02	4.37E-01	---	---	---	229087_s_at	---																				
5.30	4.32	0.98	9.35E-02	4.37E-01	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	chr3q25.32-q25.33	206392_s_at	NM_002888 /// NM_206963																				
2.96	2.66	0.30	9.36E-02	4.37E-01	---	---	---	231022_at	---																				
5.63	4.98	0.65	9.36E-02	4.37E-01	PHF2	PHD finger protein 2	chr9q22.31	212726_at	NM_005392																				
6.66	6.37	0.28	9.36E-02	4.37E-01	NOL14	nucleolar protein 14	chr4p16.3	214661_s_at	NM_003703																				
5.72	5.40	0.33	9.36E-02	4.37E-01	ABI2	abl interactor 2	chr2q33	207268_x_at	NM_005759																				
10.94	10.60	0.35	9.36E-02	4.37E-01	GPX1	glutathione peroxidase 1	chr3p21.3	200736_s_at	NM_000581 /// NM_201397																				
7.35	6.66	0.69	9.36E-02	4.37E-01	C9orf82	chromosome 9 open reading frame 82	chr9p21.2	219276_x_at	NM_024828																				
4.15	3.84	0.31	9.37E-02	4.37E-01	C10orf54	chromosome 10 open reading frame 54	chr10q22.1	225372_at	NM_022153																				
9.85	9.41	0.44	9.38E-02	4.37E-01	SAT2	spermidine/spermine N1-acetyltransferase family member 2	chr17p13.1	225272_at	NM_133491																				
4.21	3.71	0.51	9.38E-02	4.37E-01	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	chr20q13.3-qter	235694_at	NM_006602																				
6.24	5.48	0.77	9.39E-02	4.37E-01	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	chr2q37.1	1555963_x_at	NM_145236																				
5.57	5.26	0.31	9.39E-02	4.37E-01	RNF40	ring finger protein 40	chr16p11.2-p11.1	239801_at	NM_014771																				
6.10	5.48	0.62	9.40E-02	4.37E-01	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	chr21q22.3|21q22.2	201329_s_at	NM_005239																				
6.39	5.81	0.58	9.40E-02	4.37E-01	EXOSC6	exosome component 6	chr16q22.1	1558044_s_at	NM_058219																				
9.35	8.94	0.41	9.41E-02	4.37E-01	CIB1	calcium and integrin binding 1 (calmyrin)	chr15q25.3-q26	201953_at	NM_006384																				
8.39	8.05	0.34	9.41E-02	4.37E-01	SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	chr1p36.33	223051_at	NM_014188																				
3.53	3.32	0.21	9.41E-02	4.37E-01	OTUB2	OTU domain, ubiquitin aldehyde binding 2	chr14q32.13	1555682_at	NM_023112																				
12.66	12.44	0.21	9.42E-02	4.38E-01	RPS10	ribosomal protein S10	chr6p21.31	211542_x_at	NM_001014																				
2.59	2.34	0.25	9.44E-02	4.38E-01	NXPH2	neurexophilin 2	chr2q22.1	232334_at	NM_007226																				
6.96	6.46	0.49	9.45E-02	4.38E-01	CANT1	calcium activated nucleotidase 1	chr17q25.3	221732_at	NM_138793																				
4.75	4.36	0.39	9.46E-02	4.39E-01	CAPN1	calpain 1, (mu/I) large subunit	chr11q13	232012_at	NM_005186																				
5.92	5.28	0.64	9.46E-02	4.39E-01	ASNS	asparagine synthetase	chr7q21.3	205047_s_at	NM_001673 /// NM_133436 /// NM_183356																				
4.66	3.71	0.95	9.46E-02	4.39E-01	RDH10	retinol dehydrogenase 10 (all-trans)	chr8q21.11	226021_at	NM_172037																				
4.86	4.46	0.40	9.47E-02	4.39E-01	MRPS25	mitochondrial ribosomal protein S25	chr3p25	224015_s_at	NM_022497																				
6.65	6.24	0.41	9.47E-02	4.39E-01	FLJ35776	hypothetical LOC649446	chr18p11.31	238432_at	NM_001039796 /// NR_024101																				
6.66	6.28	0.38	9.47E-02	4.39E-01	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	chr3p22.1	225460_at	NM_004206 /// NM_032970																				
6.30	5.79	0.50	9.47E-02	4.39E-01	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	chr10q22.2	213088_s_at	NM_015190																				
8.79	8.35	0.44	9.48E-02	4.39E-01	ARMCX6 /// LOC653354	armadillo repeat containing, X-linked 6 /// hypothetical LOC653354	chrXq21.33-q22.3 /// chrXq22.1	214749_s_at	NM_001009584 /// NM_019007 /// XM_001713898 /// XM_001717012 /// XM_001717888																				
2.46	2.27	0.20	9.48E-02	4.39E-01	---	---	---	1566044_at	---																				
4.82	3.98	0.85	9.48E-02	4.39E-01	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	chr11q22.3	235713_at	NM_138775																				

5.51	5.12	0.39	9.48E-02	4.39E-01	CIZ1	CDKN1A interacting zinc finger protein 1	chr9q34.1	211358_s_at	NM_001131015 /// NM_001131016 /// NM_001131017 /// NM_001131018 /// NM_012127
5.86	5.05	0.81	9.48E-02	4.39E-01	CDR2L	cerebellar degeneration-related protein 2-like	chr17q25.1	213230_at	NM_014603
8.89	8.59	0.30	9.49E-02	4.39E-01	SEC61G	Sec61 gamma subunit	chr7p11.2	203484_at	NM_001012456 /// NM_014302
4.21	3.84	0.36	9.49E-02	4.39E-01	LSDP5	Lipid storage droplet protein 5	chr19p13.3	1560456_at	NM_001013706
6.76	6.32	0.45	9.49E-02	4.39E-01	TFPT	TCF3 (E2A) fusion partner (in childhood Leukemia)	chr19q13	218996_at	NM_013342
5.97	5.52	0.45	9.50E-02	4.39E-01	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	chr19p13.3	202356_s_at	NM_002096
2.96	2.63	0.33	9.50E-02	4.39E-01	FAM76B	family with sequence similarity 76, member B	chr11q21	232048_at	NM_144664
7.67	6.57	1.10	9.50E-02	4.39E-01	PLAGL1	pleiomorphic adenoma gene-like 1	chr6q24-q25	209318_x_at	NM_001080951 /// NM_001080952 /// NM_001080953 /// NM_001080954 /// NM_001080955 /// NM_001080956 /// NM_002656 /// NM_006718
2.65	2.25	0.40	9.50E-02	4.39E-01	THAP2	THAP domain containing, apoptosis associated protein 2	chr12q21.1	230380_at	NM_031435
4.56	4.08	0.48	9.51E-02	4.39E-01	TXN	Thioredoxin	chr9q31	216609_at	NM_003329
3.40	2.85	0.55	9.52E-02	4.40E-01	TTLL11	tubulin tyrosine ligase-like family, member 11	chr9q33.2	231157_at	NM_194252
7.02	6.64	0.37	9.52E-02	4.40E-01	RPP40	ribonuclease P/MRP 40kDa subunit	chr6p25.1	213427_at	NM_006638
6.15	5.75	0.40	9.52E-02	4.40E-01	TMEM201	transmembrane protein 201	chr1p36.22	227617_at	NM_001010866 /// NM_001130924
5.68	5.37	0.32	9.54E-02	4.40E-01	TFDP1	transcription factor Dp-1	chr13q34	204147_s_at	NM_007111
5.63	5.19	0.44	9.54E-02	4.40E-01	PLK3	polo-like kinase 3 (Drosophila)	chr1p34.1	215462_at	NM_004073
2.12	1.92	0.20	9.54E-02	4.40E-01	---	---	---	1554723_x_at	---
6.19	5.91	0.27	9.54E-02	4.40E-01	CCDC90A	coiled-coil domain containing 90A	chr6p24.3-p23	220094_s_at	NM_001031713
6.90	6.47	0.43	9.54E-02	4.40E-01	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	chr1q42.11	207431_s_at	NM_003676 /// NM_144780
2.34	2.11	0.24	9.54E-02	4.40E-01	SLC22A2	solute carrier family 22 (organic cation transporter), member 2	chr6q26	207429_at	NM_003058
3.56	2.99	0.57	9.54E-02	4.40E-01	HOXC9	homeobox C9	chr12q13.3	231936_at	NM_006897
7.47	6.94	0.53	9.54E-02	4.40E-01	TNFSF12 /// TNFSF12-TNFSF13 /// TNFSF13	tumor necrosis factor (ligand) superfamily, member 12 /// TNFSF12-TNFSF13 /// tumor necrosis factor (ligand) superfamily, member 13	chr17p13 /// chr17p13.1	209500_x_at	NM_003808 /// NM_003809 /// NM_172087 /// NM_172088 /// NM_172089
3.97	3.37	0.60	9.55E-02	4.40E-01	SCARA3	scavenger receptor class A, member 3	chr8p21	223842_s_at	NM_016240 /// NM_182826
3.63	3.14	0.49	9.55E-02	4.40E-01	MGC12916	hypothetical protein MGC12916	chr17p11.2	224507_s_at	---
4.36	3.86	0.50	9.56E-02	4.40E-01	CECR6	cat eye syndrome chromosome region, candidate 6	---	224393_s_at	NM_031890
5.89	5.49	0.40	9.57E-02	4.41E-01	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	chr1q32.1	227649_s_at	NM_001042758 /// NM_015326
6.25	5.84	0.42	9.57E-02	4.41E-01	ZSCAN21	zinc finger and SCAN domain containing 21	chr7q22.1	223424_s_at	NM_145914
5.85	5.25	0.60	9.57E-02	4.41E-01	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	chr12p13.3	202497_x_at	NM_006931
5.29	4.82	0.46	9.57E-02	4.41E-01	PPP2R5D	protein phosphatase 2, regulatory subunit B', delta isoform	chr6p21.1	211159_s_at	NM_006245 /// NM_180976 /// NM_180977

4.33	4.09	0.24	9.58E-02	4.41E-01	KY	kyphoscoliosis peptidase	chr3q22.2	1564254_at	NM_178554
2.90	2.37	0.53	9.58E-02	4.41E-01	TAS2R14	taste receptor, type 2, member 14	chr12p13	235762_at	NM_023922
2.96	2.69	0.27	9.58E-02	4.41E-01	---	---	---	227857_at	---
2.36	2.12	0.24	9.59E-02	4.41E-01	---	---	---	1559966_a_at	---
3.55	3.27	0.28	9.59E-02	4.41E-01	RNF130	Ring finger protein 130	chr5q35.3	236292_at	NM_018434
5.83	4.97	0.86	9.60E-02	4.41E-01	C1orf53	chromosome 1 open reading frame 53	chr1q31.3	1558508_a_at	NM_001024594
2.90	2.63	0.27	9.60E-02	4.41E-01	LOC339978	hypothetical protein LOC339978	chr4q12	1562540_at	---
2.72	2.43	0.29	9.61E-02	4.41E-01	CSHL1	chorionic somatomammotropin hormone-like 1	chr17q24.2	207285_x_at	NM_001318 /// NM_022579 /// NM_022580 /// NM_022581
7.13	6.51	0.62	9.61E-02	4.41E-01	OTUD1	OTU domain containing 1	chr10p12.2	226140_s_at	XR_040063 /// XR_040064 /// XR_040065
2.43	2.20	0.23	9.61E-02	4.41E-01	---	---	---	1568791_s_at	---
12.99	12.81	0.18	9.61E-02	4.41E-01	RPL3	ribosomal protein L3	chr22q13	201217_x_at	NM_000967 /// NM_001033853
2.17	1.95	0.22	9.62E-02	4.41E-01	COL4A6	collagen, type IV, alpha 6	chrXq22	213992_at	NM_001847 /// NM_033641
3.02	2.82	0.21	9.62E-02	4.41E-01	---	---	---	1569996_at	---
7.59	7.26	0.32	9.62E-02	4.41E-01	ARHGAP17	Rho GTPase activating protein 17	chr16p12.1	218076_s_at	NM_001006634 /// NM_018054
7.70	7.18	0.51	9.62E-02	4.41E-01	PNPLA4	patatin-like phospholipase domain containing 4	chrXp22.3	209739_s_at	NM_004650
4.30	3.93	0.37	9.62E-02	4.41E-01	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	chr13q14	205135_s_at	NM_012345
7.26	6.95	0.31	9.62E-02	4.41E-01	PSMD13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	chr11p15.5	201232_s_at	NM_002817 /// NM_175932
5.90	5.53	0.37	9.62E-02	4.41E-01	SLC30A5	solute carrier family 30 (zinc transporter), member 5	chr5q12.1	220181_x_at	NM_022902 /// NM_024055
7.13	5.56	1.57	9.62E-02	4.41E-01	CCNL1	cyclin L1	chr3q25.32	1555411_a_at	NM_020307
6.11	5.69	0.42	9.63E-02	4.41E-01	---	---	---	226624_at	---
6.06	5.69	0.37	9.63E-02	4.41E-01	PAIP1	poly(A) binding protein interacting protein 1	chr5p12	208051_s_at	NM_006451 /// NM_182789 /// NM_183323
4.43	3.90	0.53	9.63E-02	4.41E-01	SR140	U2-associated SR140 protein	chr3q23	212060_at	NM_001080415
6.27	5.79	0.49	9.63E-02	4.41E-01	D2HGDH /// LOC100133930 /// LOC257054	D-2-hydroxyglutarate dehydrogenase /// similar to D-2-hydroxyglutarate dehydrogenase, mitochondrial /// similar to D-2-hydroxyglutarate dehydrogenase	chr2q37.3	228738_at	NM_152783 /// XM_001716439 /// XM_001720547
6.60	5.81	0.79	9.64E-02	4.41E-01	IKZF4	IKAROS family zinc finger 4 (Eos)	chr12q13	226761_at	NM_022465
4.69	4.05	0.64	9.64E-02	4.42E-01	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	chr12q12-q14	227528_s_at	NM_003482
2.81	2.33	0.47	9.65E-02	4.42E-01	---	---	---	1557740_a_at	---
2.53	2.26	0.27	9.66E-02	4.42E-01	---	---	---	236256_at	---
2.33	2.01	0.31	9.66E-02	4.42E-01	HERC4	hect domain and RLD 4	chr10q21.3	232026_at	NM_015601 /// NM_022079
7.19	6.70	0.49	9.66E-02	4.42E-01	SLC12A7	solute carrier family 12 (potassium/chloride transporters), member 7	chr5p15	218066_at	NM_006598
7.26	6.78	0.47	9.66E-02	4.42E-01	ORMDL1	ORM1-like 1 (S. cerevisiae)	chr2q32	223187_s_at	NM_001128150 /// NM_016467
4.12	3.85	0.27	9.67E-02	4.42E-01	ZFHX2	zinc finger homeobox 2	chr14q11.2	231946_at	XM_001714980 /// XM_001720095 /// XM_001722719
3.87	3.60	0.27	9.67E-02	4.42E-01	SFI1	Sfi1 homolog, spindle assembly associated (yeast)	chr22q12.2	214402_s_at	NM_001007467 /// NM_014775

4.57	4.20	0.37	9.67E-02	4.42E-01	TAF1C	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	chr16q24	203937_s_at	NM_005679 /// NM_139353
7.21	6.88	0.33	9.67E-02	4.42E-01	METT10D	methyltransferase 10 domain containing	chr17p13.3	226744_at	NM_024086
2.53	2.22	0.30	9.67E-02	4.42E-01	---	---	---	1557624_at	---
2.51	2.28	0.23	9.68E-02	4.42E-01	---	---	---	1561052_s_at	---
2.49	2.26	0.23	9.68E-02	4.42E-01	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	chr16p13.11	1555347_at	NM_015027
5.45	4.95	0.50	9.69E-02	4.42E-01	PARVB	parvin, beta	chr22q13.2-q13.33	37965_at	NM_001003828 /// NM_013327
6.39	5.92	0.47	9.70E-02	4.43E-01	ZFAND2A	zinc finger, AN1-type domain 2A	chr7p22.3	226650_at	NM_182491
5.15	4.51	0.64	9.70E-02	4.43E-01	TTC14	tetratricopeptide repeat domain 14	chr3q26.33	225180_at	NM_001042601 /// NM_133462
5.78	5.30	0.48	9.71E-02	4.43E-01	GNG2	guanine nucleotide binding protein (G protein), gamma 2	chr14q21	224964_s_at	NM_053064
5.65	4.90	0.75	9.71E-02	4.43E-01	LARP6	La ribonucleoprotein domain family, member 6	chr15q23	218651_s_at	NM_018357 /// NM_197958
5.44	4.62	0.83	9.71E-02	4.43E-01	ZNF747	zinc finger protein 747	chr16p11.2	228856_at	NM_023931
5.39	4.79	0.59	9.71E-02	4.43E-01	DEFB124	defensin, beta 124	chr20q11.1	1568377_x_at	NM_001037500
7.01	6.55	0.46	9.71E-02	4.43E-01	ATP13A1	ATPase type 13A1	chr19p13.11	218052_s_at	NM_020410
8.85	8.50	0.35	9.72E-02	4.43E-01	TXNDC14	thioredoxin domain containing 14	chr11cen-q22.3	201175_at	NM_015959
5.82	5.46	0.35	9.72E-02	4.43E-01	FEN1	flap structure-specific endonuclease 1	chr11q12	204767_s_at	NM_004111
7.54	6.95	0.59	9.72E-02	4.43E-01	ACOT1 /// ACOT2	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2	chr14q24.3	202982_s_at	NM_001037161 /// NM_006821
2.37	2.20	0.18	9.72E-02	4.43E-01	OR52K3P	olfactory receptor, family 52, subfamily K, member 3 pseudogene	chr11p15.4	232829_at	---
5.81	5.45	0.36	9.73E-02	4.43E-01	PPP1R10	protein phosphatase 1, regulatory (inhibitor) subunit 10	chr6p21.3	201702_s_at	NM_002714
9.45	9.17	0.28	9.74E-02	4.43E-01	NME1 /// NME2	non-metastatic cells 1, protein (NM23A) expressed in /// non-metastatic cells 2, protein (NM23B) expressed in	chr17q21.3	201577_at	NM_000269 /// NM_001018137 /// NM_001018138 /// NM_001018139 /// NM_002512 /// NM_198175
2.27	2.02	0.25	9.74E-02	4.44E-01	RASGEF1B	RasGEF domain family, member 1B	chr4q21.21-q21.22	1553785_at	NM_152545
4.96	4.68	0.29	9.74E-02	4.44E-01	C10orf78	chromosome 10 open reading frame 78	chr10q25.1	236027_at	NM_001002759 /// NM_145247
5.70	5.17	0.53	9.75E-02	4.44E-01	ZNF496	zinc finger protein 496	chr1q44	225335_at	NM_032752
3.85	3.48	0.37	9.76E-02	4.44E-01	C1orf107	chromosome 1 open reading frame 107	chr1q32.2	214193_s_at	NM_014388
4.84	4.30	0.55	9.76E-02	4.44E-01	GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	chr17q25.1	209411_s_at	NM_014001 /// NM_138619
3.70	3.39	0.30	9.76E-02	4.44E-01	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	chr14q24-q31	206851_at	NM_002935
7.55	7.16	0.40	9.77E-02	4.44E-01	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	chr11q12.2	203103_s_at	NM_014502
7.04	6.63	0.41	9.77E-02	4.44E-01	NOTCH2	Notch homolog 2 (Drosophila)	chr1p13-p11	210756_s_at	NM_024408
2.71	2.27	0.45	9.77E-02	4.44E-01	SOX7	SRY (sex determining region Y)-box 7	chr8p22	224013_s_at	NM_031439
6.54	6.28	0.26	9.77E-02	4.44E-01	NADSYN1	NAD synthetase 1	chr11q13.4	218840_s_at	NM_018161
5.30	5.01	0.29	9.78E-02	4.44E-01	GOLGA8A /// GOLGA8B	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B	chr15q11.2 /// chr15q14	213650_at	NM_001023567 /// NM_181077 /// XM_001714558
5.22	4.90	0.32	9.78E-02	4.44E-01	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	chr16p12.3	227514_at	NM_001034841
6.53	6.18	0.35	9.79E-02	4.44E-01	WDFY2	WD repeat and FYVE domain containing 2	chr13q14.3	227490_at	NM_052950
6.54	6.04	0.50	9.80E-02	4.45E-01	C7orf49	chromosome 7 open reading frame 49	chr7q33	220949_s_at	NM_024033
7.22	6.87	0.36	9.81E-02	4.45E-01	MRPS16	mitochondrial ribosomal protein S16	chr10q22.1	222499_at	NM_016065
5.52	5.19	0.32	9.81E-02	4.45E-01	---	---	---	224429_x_at	---
5.93	5.54	0.39	9.81E-02	4.45E-01	STAMBP	STAM binding protein	chr2p13.1	202811_at	NM_006463 /// NM_201647 /// NM_213622
5.22	4.84	0.38	9.84E-02	4.46E-01	---	---	---	244555_at	---
7.86	7.32	0.54	9.84E-02	4.46E-01	C2orf24	chromosome 2 open reading frame 24	chr2q35	200070_at	NM_015680

3.41	2.95	0.46	9.85E-02	4.46E-01	THADA	thyroid adenoma associated	chr2p21	1558306_at	NM_001083953 /// NM_022065
5.54	4.91	0.63	9.85E-02	4.46E-01	FAM107A	family with sequence similarity 107, member A	chr3p21.1	209074_s_at	NM_001076778 /// NM_007177
5.27	4.46	0.80	9.85E-02	4.46E-01	IGFBP3	insulin-like growth factor binding protein 3	chr7p13-p12	212143_s_at	NM_000598 /// NM_001013398
6.31	5.87	0.44	9.85E-02	4.46E-01	SLC39A13	solute carrier family 39 (zinc transporter), member 13	chr11p11.2	225277_at	NM_001128225 /// NM_152264
2.18	2.00	0.19	9.86E-02	4.46E-01	CALR3	calreticulin 3	chr19p13.11	1552421_a_at	NM_145046
3.22	3.01	0.21	9.87E-02	4.46E-01	LOC91431	prematurely terminated mRNA decay factor-like	chr4q25	1565935_at	NM_001099776
4.16	3.82	0.34	9.87E-02	4.46E-01	---	---	---	1556445_at	---
2.35	2.13	0.23	9.87E-02	4.46E-01	C20orf29	Chromosome 20 open reading frame 29	chr20p13	1559252_a_at	NM_018347
5.16	4.75	0.41	9.88E-02	4.46E-01	---	---	---	228664_at	---
2.66	2.43	0.24	9.88E-02	4.46E-01	LOC284080	hypothetical protein LOC284080	chr17q21.33	1557607_at	---
7.87	7.47	0.40	9.88E-02	4.46E-01	MDM4	Mdm4 p53 binding protein homolog (mouse)	chr1q32	236814_at	NM_002393
6.51	6.16	0.35	9.89E-02	4.46E-01	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	chr2q32-q34	202500_at	NM_001039550 /// NM_006736
5.34	4.52	0.83	9.89E-02	4.46E-01	MGP	matrix Gla protein	chr12p13.1-p12.3	238481_at	NM_000900
6.50	6.24	0.26	9.90E-02	4.46E-01	JMJD2A	jumonji domain containing 2A	chr1p34.1	203205_at	NM_014663
5.10	4.86	0.24	9.91E-02	4.47E-01	---	---	---	1565627_a_at	---
5.13	4.47	0.66	9.92E-02	4.47E-01	TNRP	TMF regulated nuclear protein	chr1p36.11	227862_at	NM_001013642
10.51	10.25	0.25	9.92E-02	4.47E-01	PPIB	peptidylprolyl isomerase B (cyclophilin B)	chr15q21-q22	200968_s_at	NM_000942
2.82	2.62	0.21	9.92E-02	4.47E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	1555301_a_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891
7.92	7.57	0.36	9.92E-02	4.47E-01	WDR1	WD repeat domain 1	chr4p16.1	200611_s_at	NM_005112 /// NM_017491
2.70	2.52	0.18	9.92E-02	4.47E-01	---	---	---	236111_at	---
2.51	2.25	0.26	9.92E-02	4.47E-01	LOC751071 /// SNORA57	hypothetical protein LOC751071 /// small nucleolar RNA, H/ACA box 57	chr11q12.2 /// chr11q12.3	238680_at	NM_001043229 /// NR_004390
3.94	3.37	0.57	9.93E-02	4.47E-01	C15orf40	chromosome 15 open reading frame 40	chr15q25.2	1552310_at	NM_144597
6.56	6.01	0.55	9.93E-02	4.47E-01	FOSL2	FOS-like antigen 2	chr2p23.3	218881_s_at	NM_005253
4.53	4.13	0.40	9.94E-02	4.47E-01	LOC100133835 /// LOC100133836 /// SMN1 /// SMN2	hypothetical protein LOC100133835 /// hypothetical protein LOC100133836 /// survival of motor neuron 1, telomeric /// survival of motor neuron 2, centromeric	chr5q13	203852_s_at	NM_000344 /// NM_017411 /// NM_022874 /// NM_022875 /// NM_022876 /// NM_022877 /// XM_001713608 /// XM_001713714 /// XM_001713731 /// XM_001713732 /// XM_001713733 /// XM_001713734 /// XM_001720319
3.31	2.98	0.33	9.94E-02	4.47E-01	---	---	---	237043_at	---
4.91	4.39	0.52	9.94E-02	4.47E-01	---	---	---	242239_at	---
5.69	5.24	0.45	9.94E-02	4.47E-01	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	chr7q22.1	205196_s_at	NM_001283 /// NM_057089

7.74	7.26	0.48	9.94E-02	4.47E-01	SSR1	signal sequence receptor, alpha	chr6p24.3	225435_at	NM_003144
4.68	3.79	0.88	9.95E-02	4.47E-01	PLD5	phospholipase D family, member 5	chr1q43	1563933_a_at	NM_152666
7.38	6.94	0.44	9.95E-02	4.47E-01	RANGAP1	Ran GTPase activating protein 1	chr22q13	212127_at	NM_002883
2.61	2.36	0.26	9.95E-02	4.47E-01	CLEC2D	C-type lectin domain family 2, member D	chr12p13	233500_x_at	NM_001004419 /// NM_013269
5.74	5.38	0.36	9.95E-02	4.47E-01	PEX7	peroxisomal biogenesis factor 7	chr6q23.3	211033_s_at	NM_000288
7.54	7.04	0.51	9.95E-02	4.47E-01	DALRD3 /// LOC100133719	DALR anticodon binding domain containing 3 /// similar to DALR anticodon binding domain containing 3	chr3p21.31	221934_s_at	NM_001009996 /// NM_018114 /// XM_001714835
4.97	4.36	0.61	9.96E-02	4.47E-01	PID1	phosphotyrosine interaction domain containing 1	chr2q36.3	237867_s_at	NM_001100818 /// NM_017933
8.17	7.79	0.38	9.96E-02	4.47E-01	HNRNPM	heterogeneous nuclear ribonucleoprotein M	chr19p13.3-p13.2	200072_s_at	NM_005968 /// NM_031203
3.76	3.39	0.38	9.97E-02	4.48E-01	LSDP5	lipid storage droplet protein 5	chr19p13.3	1568666_at	NM_001013706
3.02	2.75	0.28	9.97E-02	4.48E-01	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	chr16p11.2	1554240_a_at	NM_001114380 /// NM_002209
11.48	11.27	0.22	9.97E-02	4.48E-01	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	chr19p13.1-p12	221700_s_at	NM_001033930 /// NM_003333
8.44	7.75	0.69	9.98E-02	4.48E-01	LAPTM5	lysosomal multispanning membrane protein 5	chr1p34	201720_s_at	NM_006762
2.96	2.44	0.52	9.98E-02	4.48E-01	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	chr15q21.1	226492_at	NM_020858 /// NM_024966 /// NM_153616 /// NM_153617 /// NM_153618 /// NM_153619
3.73	3.27	0.46	9.99E-02	4.48E-01	---	---	---	244114_x_at	---
3.78	3.39	0.39	9.99E-02	4.48E-01	TG	thyroglobulin	chr8q24	203673_at	NM_003235
8.14	7.88	0.26	1.00E-01	4.49E-01	IAH1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	chr2p25.1	225908_at	NM_001039613
9.11	8.85	0.26	1.00E-01	4.49E-01	NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	chr1q23	201966_at	NM_004550
2.83	2.36	0.47	1.00E-01	4.49E-01	DKFZP434I0714	hypothetical protein DKFZP434I0714	chr4q31.23	231954_at	XM_001715987 /// XM_929673 /// XM_938519
6.89	6.43	0.46	1.00E-01	4.49E-01	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	chr9q34	233173_x_at	NM_001122823 /// NM_012087
2.79	2.53	0.27	1.00E-01	4.49E-01	C20orf196	chromosome 20 open reading frame 196	chr20p12.3	243508_at	NM_152504
10.02	9.49	0.53	1.00E-01	4.49E-01	MRPL33	mitochondrial ribosomal protein L33	chr2p21	203781_at	NM_004891 /// NM_145330
3.87	3.47	0.40	1.00E-01	4.49E-01	MCC	mutated in colorectal cancers	chr5q21	226225_at	NM_001085377 /// NM_002387
7.30	7.04	0.26	1.00E-01	4.49E-01	RNF115	ring finger protein 115	chr1q21.1	212742_at	NM_014455
3.29	2.73	0.56	1.00E-01	4.49E-01	FRG1 /// FRG1B /// LOC100134091 /// LOC642236	FSHD region gene 1 /// FSHD region gene 1 family, member B /// hypothetical protein LOC100134091 /// similar to FRG1 protein (FSHD region gene 1 protein)	chr20q11.1 /// chr4q35 /// chr9q12	235535_x_at	NM_004477 /// NR_003579 /// XM_001721785 /// XM_001721786 /// XR_041084 /// XR_041085 /// XR_041086 /// XR_041087

7.77	7.23	0.54	1.01E-01	4.49E-01	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	chrXq26.3	209539_at	NM_004840
4.95	4.53	0.42	1.01E-01	4.49E-01	SAMD1	sterile alpha motif domain containing 1	chr19p13.12	225650_at	NM_138352
8.20	7.94	0.26	1.01E-01	4.49E-01	LOC401152	HCV F-transactivated protein 1	chr4q26	224602_at	NM_001001701
2.70	2.45	0.25	1.01E-01	4.49E-01	CA5B	carbonic anhydrase VB, mitochondrial	chrXp21.1	214082_at	NM_007220
2.66	2.38	0.29	1.01E-01	4.49E-01	FAM154A	family with sequence similarity 154, member A	chr9p22.1	231570_at	NM_153707
5.97	5.47	0.50	1.01E-01	4.50E-01	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	chr10q21-q22	209817_at	NM_021132
6.53	6.02	0.51	1.01E-01	4.50E-01	B4GALT3	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3	chr1q21-q23	210243_s_at	NM_003779
3.80	3.58	0.22	1.01E-01	4.50E-01	LOC339807	hypothetical protein LOC339807	chr2p14	1562776_at	---
4.73	4.19	0.54	1.01E-01	4.50E-01	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	chr14q11.2	216604_s_at	NM_012244 /// NM_182728
3.28	2.89	0.39	1.01E-01	4.50E-01	---	---	---	238684_at	---
2.16	1.95	0.21	1.01E-01	4.50E-01	---	---	---	237996_at	---
6.42	5.91	0.51	1.01E-01	4.50E-01	ACIN1	apoptotic chromatin condensation inducer 1	chr14q11.2	201715_s_at	NM_014977
2.62	2.27	0.35	1.01E-01	4.50E-01	NIPSNAP3B	nipsnap homolog 3B (C. elegans)	chr9q31.1	223764_x_at	NM_018376
6.13	5.73	0.39	1.01E-01	4.51E-01	FAM177A1	family with sequence similarity 177, member A1	chr14q13.2	227029_at	NM_001079519 /// NM_173607
8.55	8.19	0.36	1.01E-01	4.51E-01	AES	amino-terminal enhancer of split	chr19p13.3	217729_s_at	NM_001130 /// NM_198969 /// NM_198970
4.62	4.12	0.50	1.01E-01	4.51E-01	BCL6	B-cell CLL/lymphoma 6	chr3q27	228758_at	NM_001130845 /// NM_001134738 /// NM_001706 /// NM_138931
6.46	5.91	0.55	1.01E-01	4.51E-01	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	chr4q21	207827_x_at	NM_000345 /// NM_007308
5.00	4.57	0.43	1.01E-01	4.51E-01	---	---	---	227682_at	---
5.21	4.73	0.48	1.01E-01	4.51E-01	HBEGF	heparin-binding EGF-like growth factor	chr5q23	38037_at	NM_001945
6.31	5.57	0.75	1.01E-01	4.51E-01	BTG3	BTG family, member 3	chr21q21.1-q21.2	205548_s_at	NM_001130914 /// NM_006806
3.46	3.01	0.45	1.01E-01	4.51E-01	EID2B	EP300 interacting inhibitor of differentiation 2B	chr19q13.2	242470_at	NM_152361
6.60	6.31	0.30	1.01E-01	4.51E-01	XPC	xeroderma pigmentosum, complementation group C	chr3p25	209375_at	NM_004628
4.68	4.29	0.40	1.01E-01	4.51E-01	RNF24	ring finger protein 24	chr20p13-p12.1	210706_s_at	NM_001134337 /// NM_001134338 /// NM_007219
5.16	4.49	0.68	1.01E-01	4.51E-01	AMACR /// C1QTNF3	alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein 3	chr5p13	209424_s_at	NM_014324 /// NM_030945 /// NM_181435 /// NM_203382
7.46	7.05	0.41	1.01E-01	4.51E-01	CSNK1G2	casein kinase 1, gamma 2	chr19p13.3	202573_at	NM_001319
7.69	7.24	0.45	1.01E-01	4.51E-01	RNPEP	arginyl aminopeptidase (aminopeptidase B)	chr1q32	208270_s_at	NM_020216
4.77	4.47	0.31	1.01E-01	4.51E-01	C14orf180	chromosome 14 open reading frame 180	chr14q32.33	1558420_at	NM_001008404
3.61	3.19	0.41	1.02E-01	4.51E-01	---	---	---	228700_at	---
3.74	3.37	0.38	1.02E-01	4.51E-01	GIGYF2	GRB10 interacting GYF protein 2	chr2q37.1	237052_x_at	NM_001103146 /// NM_001103147 /// NM_001103148 /// NM_015575
2.68	2.33	0.35	1.02E-01	4.52E-01	EPB41L5	erythrocyte membrane protein band 4.1 like 5	chr2q14.2	229292_at	NM_020909
6.93	6.33	0.60	1.02E-01	4.52E-01	TMEM134	transmembrane protein 134	chr11q13.1	218531_at	NM_001078650 /// NM_001078651 /// NM_025124
2.54	2.31	0.23	1.02E-01	4.52E-01	---	---	---	239347_at	---
4.08	3.65	0.43	1.02E-01	4.52E-01	CCDC93	coiled-coil domain containing 93	chr2q14.1	219774_at	NM_019044

6.85	6.51	0.33	1.02E-01	4.52E-01	ITSN1	intersectin 1 (SH3 domain protein)	chr21q22.1-q22.2	209297_at	NM_001001132 /// NM_003024																				
6.84	5.72	1.11	1.02E-01	4.52E-01	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	chr6p21	201189_s_at	NM_002224																				
8.08	7.79	0.29	1.02E-01	4.52E-01	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)	chr9p13.2	228053_s_at	NM_001001790 /// NM_001134484 /// NM_001134485																				
2.84	2.05	0.79	1.02E-01	4.52E-01	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	chr5q35.3	213472_at	NM_005520																				
6.97	6.53	0.44	1.02E-01	4.52E-01	LOC283951	hypothetical protein LOC283951	chr16p13.3	225749_at	NM_001010878																				
5.86	5.39	0.47	1.02E-01	4.52E-01	HHLA3	HERV-H LTR-associating 3	chr1p31.1	220387_s_at	NM_001031693 /// NM_001036645 /// NM_001036646 /// NM_007071																				
4.70	4.09	0.61	1.02E-01	4.52E-01	RCOR3	REST corepressor 3	chr1q32.2-q32.3	218344_s_at	NM_018254																				
2.97	2.62	0.35	1.02E-01	4.52E-01	---	---	---	1556784_at	---																				
3.09	2.60	0.49	1.02E-01	4.52E-01	QSER1	glutamine and serine rich 1	chr11p13	244563_at	NM_001076786																				
4.57	3.80	0.76	1.02E-01	4.52E-01	PHF12	PHD finger protein 12	chr17q11.2	231815_at	NM_001033561 /// NM_020889																				
6.25	4.91	1.34	1.02E-01	4.52E-01	GBP3	guanylate binding protein 3	chr1p22.2	223434_at	NM_018284																				
4.13	3.39	0.74	1.02E-01	4.52E-01	NAPSB	napsin B aspartic peptidase pseudogene	chr19q13.33	228056_s_at	NR_002798																				
6.62	5.90	0.72	1.02E-01	4.52E-01	USP35	ubiquitin specific peptidase 35	chr11q14.1	229198_at	NM_020798																				
6.05	5.45	0.60	1.02E-01	4.52E-01	CANT1	calcium activated nucleotidase 1	chr17q25.3	46323_at	NM_138793																				
2.57	2.29	0.28	1.02E-01	4.52E-01	---	---	---	1558919_a_at	---																				
6.86	6.32	0.55	1.02E-01	4.52E-01	DAXX	death-domain associated protein	chr6p21.3	201763_s_at	NM_001350																				
3.71	3.52	0.19	1.02E-01	4.52E-01	MME	membrane metallo-endopeptidase	chr3q25.1-q25.2	203435_s_at	NM_000902 /// NM_007287 /// NM_007288 /// NM_007289																				
4.33	3.97	0.36	1.03E-01	4.52E-01	FCF1 /// MAPK1IP1L	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae) /// mitogen-activated protein kinase 1 interacting protein 1-like	chr14q22.3 /// chr14q24.3	212499_s_at	NM_015962 /// NM_144578																				
8.23	7.96	0.26	1.03E-01	4.52E-01	PDCD6	programmed cell death 6	chr5p15.33	203415_at	NM_013232 /// XM_001714855 /// XM_001720072 /// XM_001723249																				
3.33	2.92	0.41	1.03E-01	4.52E-01	NIPSNAP3B	nipsnap homolog 3B (C. elegans)	chr9q31.1	221104_s_at	NM_018376																				
3.01	2.72	0.29	1.03E-01	4.52E-01	TXLNA	taxilin alpha	chr1p35.1	1561358_at	NM_175852																				
4.96	4.42	0.54	1.03E-01	4.52E-01	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	chr17q22-q23	201208_s_at	NM_021137																				
3.68	3.37	0.31	1.03E-01	4.52E-01	CXCR5	chemokine (C-X-C motif) receptor 5	chr11q23.3	216734_s_at	NM_001716 /// NM_032966																				
8.70	8.38	0.32	1.03E-01	4.52E-01	TFG	TRK-fused gene	chr3q12.2	217839_at	NM_001007565 /// NM_006070																				
5.11	4.19	0.92	1.03E-01	4.52E-01	CLK4	CDC-like kinase 4	chr5q35	210346_s_at	NM_020666																				
6.33	5.69	0.63	1.03E-01	4.53E-01	INTS5	integrator complex subunit 5	chr11q12.3	53968_at	NM_030628																				
3.04	2.73	0.31	1.03E-01	4.53E-01	---	---	---	1558605_at	---																				
3.82	3.60	0.22	1.03E-01	4.53E-01	C4orf29	chromosome 4 open reading frame 29	chr4q28.2	236240_at	NM_001039717																				
2.05	1.86	0.19	1.03E-01	4.53E-01	---	---	---	237566_at	---																				
5.66	5.36	0.30	1.03E-01	4.53E-01	ANKLE2	ankyrin repeat and LEM domain containing 2	chr12q24.33	212200_at	NM_015114																				
2.47	2.15	0.32	1.03E-01	4.53E-01	---	---	---	243729_at	---																				
4.79	4.46	0.33	1.03E-01	4.53E-01	KCTD5	potassium channel tetramerisation domain containing 5	chr16p13.3	222645_s_at	NM_018992																				
6.89	6.26	0.63	1.03E-01	4.53E-01	---	---	---	227092_at	---																				
2.59	2.33	0.26	1.03E-01	4.53E-01	LRP2BP	LRP2 binding protein	chr4q35.1	207797_s_at	NM_018409																				
4.33	3.92	0.41	1.03E-01	4.53E-01	---	---	---	244647_at	---																				
4.10	3.83	0.26	1.03E-01	4.53E-01	KDSR	3-ketodihydrosphingosine reductase	chr18q21.3	229850_at	NM_002035																				
2.16	1.97	0.19	1.03E-01	4.53E-01	---	---	---	234783_at	---																				
6.61	5.78	0.83	1.03E-01	4.53E-01	ZNF521	zinc finger protein 521	chr18q11.2	226677_at	NM_015461																				

3.12	2.79	0.34	1.03E-01	4.53E-01	RBM14	RNA binding motif protein 14	chr11q13.1	1555639_a_at	NM_006328
7.02	6.56	0.46	1.03E-01	4.53E-01	BCL7C	B-cell CLL/lymphoma 7C	chr16p11	219072_at	NM_004765
2.85	2.66	0.19	1.03E-01	4.53E-01	LOC100129592	Hypothetical protein LOC100129592	chr2q32.2	228803_at	XM_001723349 /// XM_001723373 /// XM_001726308
6.32	5.62	0.70	1.03E-01	4.53E-01	---	---	---	244677_at	---
6.82	6.42	0.40	1.03E-01	4.54E-01	---	---	---	221877_at	---
4.14	3.71	0.43	1.03E-01	4.54E-01	---	---	---	215252_at	---
9.91	9.61	0.30	1.03E-01	4.54E-01	FUT5 /// NDUFA11	fucosyltransferase 5 (alpha (1,3) fucosyltransferase) /// NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	chr19p13.3	225304_s_at	NM_002034 /// NM_175614
4.86	4.62	0.24	1.03E-01	4.54E-01	C22orf29	chromosome 22 open reading frame 29	chr22q11.21	219560_at	NM_024627
7.03	6.71	0.33	1.03E-01	4.54E-01	VRK3	vaccinia related kinase 3	chr19q13	218022_at	NM_001025778 /// NM_016440
3.59	3.09	0.51	1.03E-01	4.54E-01	DIO2	deiodinase, iodothyronine, type II	chr14q24.2-q24.3	203700_s_at	NM_000793 /// NM_001007023 /// NM_013989
5.55	4.97	0.58	1.03E-01	4.54E-01	LMNB2	lamin B2	chr19p13.3	216952_s_at	NM_032737
3.81	3.56	0.25	1.03E-01	4.54E-01	---	---	---	228430_at	---
6.33	5.97	0.36	1.04E-01	4.54E-01	MTG1	mitochondrial GTPase 1 homolog (S. cerevisiae)	chr10q26.3	212767_at	NM_138384
6.41	5.94	0.47	1.04E-01	4.54E-01	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	chr20p11.2-p11.22	201704_at	NM_001114089 /// NM_001247
3.59	3.25	0.34	1.04E-01	4.54E-01	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)	chr17q25.3	240084_at	NM_005189 /// NM_032647
3.83	3.42	0.41	1.04E-01	4.54E-01	SIRPA	signal-regulatory protein alpha	chr20p13	217024_x_at	NM_001040022 /// NM_001040023 /// NM_080792
4.16	3.91	0.24	1.04E-01	4.54E-01	---	---	---	217052_x_at	---
6.17	5.40	0.76	1.04E-01	4.55E-01	GPRASP1	G protein-coupled receptor associated sorting protein 1	chrXq22.1	204793_at	NM_001099410 /// NM_001099411 /// NM_014710
2.31	2.07	0.24	1.04E-01	4.55E-01	---	---	---	1562976_at	---
3.18	2.88	0.30	1.04E-01	4.55E-01	---	---	---	242786_at	---
5.32	4.92	0.40	1.04E-01	4.55E-01	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	chr5q33-q34	204930_s_at	NM_001205 /// NM_013978 /// NM_013979 /// NM_013980
3.65	3.21	0.44	1.04E-01	4.55E-01	WDR35	WD repeat domain 35	chr2p24.1	226890_at	NM_001006657 /// NM_020779
5.64	5.06	0.58	1.04E-01	4.55E-01	LOC153546	hypothetical protein LOC153546	chr5p13.3	236124_at	---
6.96	6.40	0.56	1.04E-01	4.55E-01	NAP1L5	nucleosome assembly protein 1-like 5	chr4q22.1|4q21-q22	228063_s_at	NM_153757
6.89	6.62	0.26	1.04E-01	4.55E-01	TK2	thymidine kinase 2, mitochondrial	chr16q22-q23.1	204276_at	NM_004614
4.37	3.92	0.45	1.04E-01	4.55E-01	PRRT1	proline-rich transmembrane protein 1	chr6p21.32	229890_at	NM_030651
2.54	2.15	0.40	1.04E-01	4.55E-01	UTS2	urotensin 2	chr1p36	220784_s_at	NM_006786 /// NM_021995
7.79	7.45	0.34	1.04E-01	4.55E-01	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	chr19q13.2-q13.3	203720_s_at	NM_001983 /// NM_202001
2.76	2.49	0.27	1.04E-01	4.55E-01	ANKRD44	ankyrin repeat domain 44	chr2q33.1	235778_s_at	NM_153697
4.39	4.03	0.36	1.04E-01	4.55E-01	ZBTB46	zinc finger and BTB domain containing 46	chr20q13.33	227329_at	NM_025224
3.60	3.26	0.34	1.04E-01	4.55E-01	---	---	---	1558906_a_at	---

8.28	7.86	0.42	1.04E-01	4.55E-01	COASY	Coenzyme A synthase	chr17q12-q21	201913_s_at	NM_001042529 /// NM_001042530 /// NM_001042531 /// NM_001042532 /// NM_025233																			
3.43	3.12	0.32	1.04E-01	4.55E-01	AK7	adenylate kinase 7	chr14q32.2	1569700_s_at	NM_152327																			
6.15	5.82	0.34	1.04E-01	4.55E-01	PAIP1	poly(A) binding protein interacting protein 1	chr5p12	209064_x_at	NM_006451 /// NM_182789 /// NM_183323																			
6.04	5.35	0.69	1.04E-01	4.55E-01	ULK3	unc-51-like kinase 3 (C. elegans)	chr15q24.1	225067_at	NM_001099436																			
12.34	12.15	0.18	1.04E-01	4.55E-01	RPS17	ribosomal protein S17	chr15q	211487_x_at	NM_001021																			
7.13	6.75	0.38	1.04E-01	4.56E-01	MIF4GD	MIF4G domain containing	chr17q25.1	223411_at	NM_020679																			
2.04	1.86	0.18	1.04E-01	4.56E-01	---	---	---	1557463_at	---																			
8.00	7.56	0.43	1.04E-01	4.56E-01	CIAPIN1	cytokine induced apoptosis inhibitor 1	chr16q13-q21	208968_s_at	NM_020313																			
4.94	4.60	0.34	1.05E-01	4.56E-01	APOM	apolipoprotein M	chr6p21.33	205682_x_at	NM_019101																			
6.84	6.21	0.63	1.05E-01	4.56E-01	KIF16B	kinesin family member 16B	chr20p11.23	219570_at	NM_024704																			
3.35	2.87	0.48	1.05E-01	4.56E-01	LOC100127983	hypothetical protein LOC100127983	chr8q21.3	228107_at	XM_001722508 /// XM_001722530 /// XM_001722571																			
6.59	5.75	0.83	1.05E-01	4.56E-01	HOXC4 /// HOXC6	homeobox C4 /// homeobox C6	chr12q13.3	206858_s_at	NM_004503 /// NM_014620 /// NM_153633 /// NM_153693																			
7.18	6.99	0.19	1.05E-01	4.56E-01	MBTPS1	membrane-bound transcription factor peptidase, site 1	chr16|16q24	217543_s_at	NM_003791																			
2.32	2.11	0.21	1.05E-01	4.56E-01	REV1	REV1 homolog (S. cerevisiae)	chr2q11.1-q11.2	243592_at	NM_001037872 /// NM_016316																			
3.69	3.26	0.42	1.05E-01	4.56E-01	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	chr9p13.3	207453_s_at	NM_012266																			
3.85	3.44	0.41	1.05E-01	4.56E-01	L3MBTL4	l(3)mbt-like 4 (Drosophila)	chr18p11.31	228557_at	NM_173464																			
5.97	5.64	0.34	1.05E-01	4.56E-01	C16orf58	chromosome 16 open reading frame 58	chr16p11.2	222190_s_at	NM_022744																			
7.30	6.94	0.36	1.05E-01	4.56E-01	RHOT2	ras homolog gene family, member T2	chr16p13.3	65770_at	NM_138769																			
3.82	3.51	0.32	1.05E-01	4.56E-01	NARG2	NMDA receptor regulated 2	chr15q22.2	228960_at	NM_001018089 /// NM_024611																			
7.14	6.55	0.59	1.05E-01	4.56E-01	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	chr11q23.2-q24.2	203509_at	NM_003105																			
3.36	2.92	0.44	1.05E-01	4.56E-01	---	---	---	228843_at	---																			
3.78	3.43	0.35	1.05E-01	4.56E-01	DALRD3	DALR anticodon binding domain containing 3	chr3p21.31	218808_at	NM_001009996 /// NM_018114																			
2.78	2.46	0.31	1.05E-01	4.56E-01	C9orf79	chromosome 9 open reading frame 79	chr9q22.1	1563868_a_at	NM_178828																			
2.03	1.86	0.17	1.05E-01	4.56E-01	---	---	---	241291_at	---																			
6.91	6.51	0.41	1.05E-01	4.57E-01	TOR3A	torsin family 3, member A	chr1q25.2	218459_at	NM_022371																			
7.57	6.58	0.99	1.05E-01	4.57E-01	---	---	---	229641_at	---																			

									NM_000982 /// NM_001011538 /// XM_001128906 /// XM_001132984 /// XM_001133535 /// XM_001717133 /// XM_001718175 /// XM_001720625 /// XM_001721328 /// XM_001722740 /// XM_001722741 /// XM_001722742 /// XM_001723025 /// XM_001724792 /// XM_001724793 /// XM_001726144 /// XM_001726209 /// XM_001732837 /// XM_001732839 /// XM_001732851 /// XM_929340 /// XR_015134 /// XR_015894 /// XR_015915 /// XR_016005 /// XR_016010 /// XR_016036 /// XR_016115 /// XR_016770 /// XR_017157 /// XR_017589 /// XR_017625 /// XR_018513																			
					LOC100129141 /// LOC100131672 /// LOC100133273 /// LOC100133773 /// LOC387753 /// LOC389156 /// LOC402176 /// LOC440575 /// LOC442160 /// LOC641293 /// LOC642738 /// LOC645157 /// LOC645174 /// LOC646279 /// LOC650059 /// LOC653079 /// LOC653665 /// LOC653737 /// LOC727821 /// LOC728782 /// LOC729208 /// LOC729402 /// LOC729484 ///	similar to ribosomal protein L21 /// similar to mCG9390 /// similar to hCG2016451 /// hypothetical LOC100133773 /// similar to 60S ribosomal protein L21 /// similar to 60S ribosomal protein L21 /// similar to ribosomal protein L21 /// similar to ribosomal protein L21 /// ribosomal protein L21 pseudogene /// similar to hCG2016451 /// similar to mCG9390 /// hypothetical LOC645174 /// similar to hCG2028654 /// similar to ribosomal protein L21 /// hypothetical LOC653079 /// similar to mCG4465 /// hypothetical LOC653737 /// similar to mCG9390 /// similar to ribosomal protein L21 /// hypothetical LOC729208 /// hypothetical LOC729402 /// hypothetical LOC729484 ///	chr10p11.23 /// chr10q26.12 /// chr11p15.4 /// chr12q14.3 /// chr12q21.2 /// chr13q12.2 /// chr14q23.3 /// chr15q22.1 /// chr16p13.2 /// chr1p36.12 /// chr1q32.1 /// chr2p15 /// chr3q24 /// chr4p14 /// chr4p15.31 /// chr4q12 /// chr6p22.3 /// chr6p24.3 /// chr6q25.3 /// chr8p12 /// chr9q22.31 /// chr9q31.3 ///																						
2.77	2.53	0.24	1.05E-01	4.57E-01	RPL21		chrXq13.3	216479_at																				
3.41	2.84	0.57	1.05E-01	4.57E-01	---	---	---	229939_at	---																			
6.48	6.17	0.31	1.05E-01	4.57E-01	CYTH2	cytohesin 2	chr19q13.3	209158_s_at	NM_004228 /// NM_017457																			
3.87	3.03	0.84	1.05E-01	4.57E-01	---	---	---	228812_at	---																			
3.77	2.75	1.02	1.05E-01	4.57E-01	CEL	carboxyl ester lipase (bile salt-stimulated lipase)	chr9q34.3	1553970_s_at	NM_001807																			
3.60	2.77	0.83	1.05E-01	4.57E-01	SDPR	serum deprivation response (phosphatidylserine binding protein)	chr2q32-q33	222717_at	NM_004657																			
2.29	2.07	0.22	1.05E-01	4.57E-01	MMP10	matrix metallopeptidase 10 (stromelysin 2)	chr11q22.3	205680_at	NM_002425																			
7.41	6.66	0.75	1.05E-01	4.57E-01	LIMCH1	LIM and calponin homology domains 1	chr4p13	212327_at	NM_001112717 /// NM_001112718 /// NM_001112719 /// NM_001112720 /// NM_014988																			
2.30	1.91	0.40	1.05E-01	4.57E-01	LOC643827	similar to cell recognition molecule CASPR3	chr9q12	244065_at	XM_001714537																			
3.40	3.16	0.24	1.05E-01	4.57E-01	---	---	---	1556422_at	---																			
5.65	5.27	0.37	1.05E-01	4.57E-01	RBMX2	RNA binding motif protein, X-linked 2	chrXq25	204097_s_at	NM_016024																			
6.14	5.71	0.43	1.05E-01	4.57E-01	GEMIN4	gem (nuclear organelle) associated protein 4	chr17p13	205527_s_at	NM_015721																			
3.69	3.38	0.32	1.05E-01	4.57E-01	AR	androgen receptor	chrXq11.2-q12	211110_s_at	NM_000044 /// NM_001011645																			

2.51	2.27	0.24	1.05E-01	4.57E-01	---	---	---	240327_at	---
2.54	2.31	0.23	1.05E-01	4.57E-01	---	---	---	216498_at	---
5.43	5.03	0.39	1.05E-01	4.57E-01	NBPF10 /// NBPF11	neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11	chr1q21.1	242191_at	NM_001039703 /// NM_183372 /// XM_001722184
2.31	2.07	0.24	1.06E-01	4.57E-01	C7orf45	chromosome 7 open reading frame 45	chr7q32.2	1553330_at	NM_145268
5.01	4.41	0.61	1.06E-01	4.57E-01	C2orf60	chromosome 2 open reading frame 60	chr2q33.1	235181_at	NM_001039693 /// NR_004862
2.76	2.53	0.23	1.06E-01	4.57E-01	GAS1	growth arrest-specific 1	chr9q21.3-q22	204456_s_at	NM_002048
4.35	3.90	0.45	1.06E-01	4.57E-01	SOCS1	suppressor of cytokine signaling 1	chr16p13.13	210001_s_at	NM_003745
2.58	2.29	0.29	1.06E-01	4.57E-01	---	---	---	235464_at	---
3.80	3.49	0.31	1.06E-01	4.57E-01	VILL	villin-like	chr3p21.3	209950_s_at	NM_015873
7.07	6.67	0.40	1.06E-01	4.57E-01	SEDLP /// TRAPPC2 /// ZNF547	spondyloepiphyseal dysplasia, late, pseudogene /// trafficking protein particle complex 2 /// zinc finger protein 547	chr19q13.4 /// chr19q13.43 /// chrXp22	209751_s_at	NM_001011658 /// NM_001128835 /// NM_014563 /// NM_173631 /// NR_002166
6.92	6.53	0.38	1.06E-01	4.57E-01	ZFHX3	zinc finger homeobox 3	chr16q22.3-q23.1	226137_at	NM_006885
2.36	2.08	0.28	1.06E-01	4.57E-01	---	---	---	230048_at	---
6.62	6.22	0.40	1.06E-01	4.58E-01	WDR23	WD repeat domain 23	chr14q12	201886_at	NM_025230 /// NM_181357
3.86	3.64	0.22	1.06E-01	4.58E-01	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17p13.3	229653_at	NM_001128159 /// NM_018289
5.92	5.50	0.41	1.06E-01	4.58E-01	TOLLIP	toll interacting protein	chr11p15.5	217930_s_at	NM_019009
5.05	4.71	0.34	1.06E-01	4.58E-01	C15orf17	chromosome 15 open reading frame 17	chr15q24.1	224798_s_at	NM_020447
7.75	7.22	0.53	1.06E-01	4.58E-01	BCAT2	branched chain aminotransferase 2, mitochondrial	chr19q13	203576_at	NM_001190
4.46	3.84	0.62	1.06E-01	4.58E-01	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	chr5q22.2	228256_s_at	NM_022140
5.65	5.28	0.37	1.06E-01	4.58E-01	EIF2C2	eukaryotic translation initiation factor 2C, 2	chr8q24	225827_at	NM_012154
4.28	3.70	0.58	1.06E-01	4.58E-01	RHOF	Ras homolog gene family, member F (in filopodia)	chr12q24.31	219154_at	NM_019034
2.96	2.69	0.27	1.06E-01	4.58E-01	LEAP2	liver expressed antimicrobial peptide 2	chr5q31.1	1552362_a_at	NM_052971
7.17	6.73	0.43	1.06E-01	4.58E-01	STAT5B	signal transducer and activator of transcription 5B	chr17q11.2	212549_at	NM_012448
5.10	4.63	0.47	1.06E-01	4.58E-01	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	chr14q11.2	227110_at	NM_001077442 /// NM_001077443 /// NM_004500 /// NM_031314
2.48	2.20	0.28	1.06E-01	4.58E-01	LOC100129592	Hypothetical protein LOC100129592	chr2q32.2	236609_at	XM_001723349 /// XM_001723373 /// XM_001726308
3.14	2.71	0.43	1.06E-01	4.58E-01	AASS	aminoadipate-semialdehyde synthase	chr7q31.3	210852_s_at	NM_005763
4.28	3.47	0.81	1.07E-01	4.58E-01	---	---	---	1556602_at	---
7.59	7.11	0.48	1.07E-01	4.58E-01	C10orf72	chromosome 10 open reading frame 72	chr10q11.22	213381_at	NM_001031746 /// NM_144984
2.13	1.88	0.25	1.07E-01	4.59E-01	ANKAR	ankyrin and armadillo repeat containing	chr2q32.2	1552438_a_at	NM_144708
3.32	2.94	0.39	1.07E-01	4.59E-01	LOC401431	hypothetical gene LOC401431	chr7q36.1	229094_at	XR_040272 /// XR_040273 /// XR_040274 /// XR_040275
3.98	3.58	0.40	1.07E-01	4.59E-01	---	---	---	1564069_at	---
7.19	6.77	0.42	1.07E-01	4.59E-01	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal	chr11p15.4-p15.1	209420_s_at	NM_000543 /// NM_001007593

8.96	8.62	0.34	1.07E-01	4.59E-01	RHOC	ras homolog gene family, member C	chr1p13.1	200885_at	NM_001042678 /// NM_001042679 /// NM_175744																				
4.90	4.37	0.53	1.07E-01	4.59E-01	U2AF1L4	U2 small nuclear RNA auxiliary factor 1-like 4	chr19q13.12	226700_at	NM_001040425 /// NM_144987																				
5.42	5.06	0.36	1.07E-01	4.60E-01	POMGNT1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	chr1p34.1	233638_s_at	NM_017739																				
3.96	3.38	0.58	1.07E-01	4.60E-01	LYSMD4	LysM, putative peptidoglycan-binding, domain containing 4	chr15q26.3	228954_at	NM_152449																				
4.72	4.28	0.45	1.07E-01	4.60E-01	POLDIP3	polymerase (DNA-directed), delta interacting protein 3	chr22q13.2	215357_s_at	NM_032311 /// NM_178136																				
4.47	4.05	0.43	1.07E-01	4.60E-01	ADAM19	ADAM metallopeptidase domain 19 (meltrin beta)	chr5q32-q33	209765_at	NM_023038 /// NM_033274																				
4.93	4.67	0.26	1.07E-01	4.60E-01	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	chr17p13.3	221987_s_at	NM_018128																				
2.79	2.42	0.37	1.07E-01	4.60E-01	C8orf59	chromosome 8 open reading frame 59	chr8q21.2	1555241_at	NM_001099670 /// NM_001099671 /// NM_001099672 /// NM_001099673																				
6.41	5.67	0.75	1.07E-01	4.60E-01	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	chr5q14.3	209662_at	NM_004365																				
9.84	9.49	0.35	1.07E-01	4.60E-01	CLTA	clathrin, light chain (Lca)	chr9p13	216295_s_at	NM_001076677 /// NM_001833 /// NM_007096																				
2.47	2.12	0.36	1.07E-01	4.60E-01	FBXO5	F-box protein 5	chr6q25-q26	218875_s_at	NM_012177																				
8.81	8.41	0.39	1.07E-01	4.60E-01	GANAB	glucosidase, alpha; neutral AB	chr11q12.3	211934_x_at	NM_198334 /// NM_198335																				
5.28	4.79	0.49	1.07E-01	4.60E-01	RCSD1	RCSD domain containing 1	chr1q22-q24	225763_at	NM_052862																				
3.70	2.96	0.74	1.07E-01	4.60E-01	---	---	---	237189_at	---																				
6.84	6.41	0.43	1.07E-01	4.60E-01	SDF2L1	stromal cell-derived factor 2-like 1	chr22q11.21	218681_s_at	NM_022044																				
4.90	4.66	0.23	1.07E-01	4.60E-01	IPPK	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	chr9q21.33-q22.31	222823_at	NM_022755																				
2.69	2.43	0.26	1.07E-01	4.60E-01	LOC286059	hypothetical protein LOC286059	chr8p21.2	234141_s_at	---																				
4.40	3.74	0.66	1.07E-01	4.60E-01	ZNF641	zinc finger protein 641	chr12q13.11	235179_at	NM_152320																				
5.60	4.68	0.92	1.07E-01	4.60E-01	CXorf40A	chromosome X open reading frame 40A	chrXq28	228809_at	NM_178124																				
2.87	2.58	0.29	1.07E-01	4.60E-01	---	---	---	237830_at	---																				
5.01	4.38	0.64	1.07E-01	4.60E-01	ZNF83	zinc finger protein 83	chr19q13.3	221645_s_at	NM_001105549 /// NM_001105550 /// NM_001105551 /// NM_001105552 /// NM_001105553 /// NM_001105554 /// NM_018300 /// NR_003936																				
6.02	5.45	0.57	1.07E-01	4.60E-01	FBXO28	F-box protein 28	chr1q42.11	202272_s_at	NM_015176																				
3.49	2.95	0.53	1.07E-01	4.61E-01	ATF3	activating transcription factor 3	chr1q32.3	1554420_at	NM_001030287 /// NM_001040619 /// NM_001674 /// NM_004024																				
8.21	7.49	0.72	1.07E-01	4.61E-01	STT3B	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	chr3p23	224700_at	NM_178862																				
7.77	7.42	0.36	1.08E-01	4.61E-01	PEF1	penta-EF-hand domain containing 1	chr1p34	217923_at	NM_012392																				
2.52	2.30	0.22	1.08E-01	4.61E-01	HMCN2	hemicentin 2	chr9q34.11	1563532_at	XM_001715154 /// XM_001726942																				

6.54	6.22	0.32	1.08E-01	4.61E-01	TMEM199	transmembrane protein 199	chr17q11.2	225375_at	NM_152464
5.46	5.11	0.34	1.08E-01	4.61E-01	RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	chr2p11.2	212479_s_at	NM_022780
2.60	2.25	0.35	1.08E-01	4.61E-01	PGAP1	post-GPI attachment to proteins 1	chr2q33.1	239725_at	NM_024989
7.99	7.63	0.36	1.08E-01	4.61E-01	FSTL3	follistatin-like 3 (secreted glycoprotein)	chr19p13	203592_s_at	NM_005860
6.89	6.39	0.50	1.08E-01	4.61E-01	FAM3C	family with sequence similarity 3, member C	chr7q31	201889_at	NM_001040020 /// NM_014888
5.81	5.25	0.56	1.08E-01	4.61E-01	ARMCX5	armadillo repeat containing, X-linked 5	chrXq22.1-q22.3	219335_at	NM_022838
3.32	2.18	1.14	1.08E-01	4.61E-01	C9orf135	chromosome 9 open reading frame 135	chr9q21.11	243610_at	NM_001010940
3.38	3.09	0.29	1.08E-01	4.61E-01	MYH7B	myosin, heavy chain 7B, cardiac muscle, beta	chr20q11.22	233949_s_at	NM_020884
3.78	3.29	0.49	1.08E-01	4.61E-01	C1QTNF4	C1q and tumor necrosis factor related protein 4	chr11q11	223708_at	NM_031909
3.80	3.54	0.27	1.08E-01	4.61E-01	MRGPRX4	MAS-related GPR, member X4	chr11p15.1	1553504_at	NM_054032
3.38	3.18	0.20	1.08E-01	4.61E-01	---	---	---	1560049_at	---
3.73	3.40	0.33	1.08E-01	4.62E-01	MID1	midline 1 (Opitz/BBB syndrome)	chrXp22	210694_s_at	NM_000381 /// NM_001098624 /// NM_033290
7.00	6.65	0.36	1.08E-01	4.62E-01	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	chr14q21	211061_s_at	NM_002408
5.90	5.46	0.44	1.08E-01	4.62E-01	KIFC2	kinesin family member C2	chr8q24.3	226792_s_at	NM_145754
6.18	5.73	0.46	1.08E-01	4.62E-01	RABGGTA	Rab geranylgeranyltransferase, alpha subunit	chr14q11.2	203573_s_at	NM_004581 /// NM_182836
4.98	4.71	0.27	1.08E-01	4.62E-01	NEO1	neogenin homolog 1 (chicken)	chr15q22.3-q23	204321_at	NM_002499
4.43	4.02	0.40	1.08E-01	4.62E-01	CCDC111	coiled-coil domain containing 111	chr4q35.1	227157_at	NM_152683
3.76	3.46	0.29	1.08E-01	4.62E-01	41530	Septin 13	chr7p13	1569974_x_at	XM_001126402 /// XM_001133108 /// XM_001717249 /// XM_001718865
6.25	5.91	0.34	1.08E-01	4.62E-01	ZNF408	zinc finger protein 408	chr11p11.2	219224_x_at	NM_024741
5.02	4.54	0.49	1.08E-01	4.62E-01	RELB	v-rel reticuloendotheliosis viral oncogene homolog B	chr19q13.32	205205_at	NM_006509
2.86	2.26	0.61	1.08E-01	4.62E-01	---	---	---	227745_at	---
5.26	4.65	0.61	1.08E-01	4.62E-01	C10orf137	chromosome 10 open reading frame 137	chr10q26.13-q26.2	213410_at	NM_015608
6.10	5.65	0.45	1.08E-01	4.62E-01	KIAA0329	KIAA0329	chr14q32.31	204308_s_at	NM_014844
8.84	8.45	0.39	1.08E-01	4.62E-01	BRI3	brain protein I3	chr7q21.3	223376_s_at	NM_015379
5.00	4.81	0.19	1.09E-01	4.63E-01	PEX5	peroxisomal biogenesis factor 5	chr12p13.31	215481_s_at	NM_000319 /// NM_001131023 /// NM_001131024 /// NM_001131025 /// NM_001131026
7.14	6.88	0.26	1.09E-01	4.63E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	202548_s_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735
5.93	5.45	0.48	1.09E-01	4.63E-01	ZNF395	zinc finger protein 395	chr8p21.1	223216_x_at	NM_018660
2.91	2.59	0.33	1.09E-01	4.63E-01	SLC22A11	solute carrier family 22 (organic anion/urate transporter), member 11	chr11q13.1	220100_at	NM_018484
7.19	6.50	0.69	1.09E-01	4.63E-01	ZBTB16	zinc finger and BTB domain containing 16	chr11q23.1	205883_at	NM_001018011 /// NM_006006
6.91	5.76	1.15	1.09E-01	4.63E-01	GLDN	gliomedin	chr15q21.2	230360_at	NM_181789
6.18	4.18	2.01	1.09E-01	4.63E-01	NR4A3	nuclear receptor subfamily 4, group A, member 3	chr9q22	207978_s_at	NM_006981 /// NM_173198 /// NM_173199 /// NM_173200

4.86	4.19	0.68	1.09E-01	4.64E-01	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	chr2q31-q33|2q31.1	213677_s_at	NM_000534 /// NM_001128143 /// NM_001128144																			
3.78	3.52	0.26	1.09E-01	4.64E-01	NCR2	Natural cytotoxicity triggering receptor 2	chr6p21.1	221074_at	NM_004828																			
4.16	3.71	0.45	1.09E-01	4.64E-01	MANSC1	MANSC domain containing 1	chr12p13.2	220945_x_at	NM_018050																			
7.52	7.21	0.31	1.09E-01	4.64E-01	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	chr20q11.2-q13.1	222670_s_at	NM_005461																			
2.18	1.95	0.23	1.09E-01	4.64E-01	ALG5	Asparagine-linked glycosylation 5 homolog (S. cerevisiae, dolichyl-phosphate beta-glucosyltransferase)	chr13q13.3	1560733_at	NM_013338																			
3.04	2.79	0.26	1.09E-01	4.64E-01	---	---	---	230899_at	---																			
2.60	2.22	0.38	1.09E-01	4.64E-01	PHC3	polyhomeotic homolog 3 (Drosophila)	chr3q26.2	238693_at	NM_024947																			
3.60	3.28	0.32	1.09E-01	4.64E-01	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	chr7p22.3	206750_at	NM_002360																			
8.71	8.51	0.20	1.09E-01	4.64E-01	ATPIF1	ATPase inhibitory factor 1	---	218671_s_at	NM_016311 /// NM_178190 /// NM_178191																			
6.56	6.31	0.25	1.09E-01	4.64E-01	RNMTL1	RNA methyltransferase like 1	chr17p13.3	218993_at	NM_018146																			
9.07	8.64	0.43	1.09E-01	4.64E-01	TMEM9	transmembrane protein 9	---	222988_s_at	NM_016456																			
5.07	4.72	0.35	1.10E-01	4.65E-01	LOC100131058 /// LOC100133666 /// LOC440104	similar to PP10764 /// hypothetical protein LOC100133666 /// similar to RIKEN cDNA 1110012D08	chr12q13.2	227106_at	XM_001716571 /// XM_001719370 /// XM_001721986 /// XM_001721988 /// XM_001721989 /// XM_001721993 /// XM_001722083 /// XM_001725885 /// XM_927712																			
6.19	5.64	0.56	1.10E-01	4.65E-01	ASXL1	additional sex combs like 1 (Drosophila)	chr20q11.1	242438_at	NM_015338																			
8.88	8.02	0.87	1.10E-01	4.65E-01	IER2	immediate early response 2	chr19p13.13	202081_at	NM_004907																			
7.19	6.62	0.57	1.10E-01	4.65E-01	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	chr9q21.31	204872_at	NM_007005																			
3.48	3.15	0.33	1.10E-01	4.65E-01	LSM11	LSM11, U7 small nuclear RNA associated	chr5q33.3	241599_at	NM_173491																			
8.61	7.84	0.77	1.10E-01	4.65E-01	PEG10	paternally expressed 10	chr7q21	212092_at	NM_001040152 /// NM_015068																			
3.72	3.47	0.25	1.10E-01	4.65E-01	ZNF490	zinc finger protein 490	chr19p13.2	231988_x_at	NM_020714																			
2.34	2.12	0.22	1.10E-01	4.65E-01	KIAA1609	KIAA1609	chr16q24.1	65438_at	NM_020947																			
5.69	5.30	0.40	1.10E-01	4.65E-01	---	---	---	226040_at	---																			
5.65	5.23	0.41	1.10E-01	4.65E-01	MYO19	myosin XIX	chr17q12	225947_at	NM_001033580 /// NM_025109																			
3.10	2.81	0.29	1.10E-01	4.65E-01	PRDX3	peroxiredoxin 3	chr10q25-q26	209766_at	NM_006793 /// NM_014098																			
4.27	3.97	0.30	1.10E-01	4.65E-01	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene	chr7q11-q22	215412_x_at	NR_003614 /// XR_042144 /// XR_042161 /// XR_042167																			
4.69	4.41	0.28	1.10E-01	4.65E-01	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	chr1q25	223405_at	NM_030769																			
7.53	7.13	0.40	1.10E-01	4.65E-01	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	chrXp11.23	203342_at	NM_005834																			
2.51	2.25	0.26	1.10E-01	4.65E-01	C9orf135	chromosome 9 open reading frame 135	chr9q21.11	236519_at	NM_001010940																			
3.00	2.60	0.40	1.10E-01	4.65E-01	ACPP	acid phosphatase, prostate	chr3q21-q23	204393_s_at	NM_001099 /// NM_001134194																			

5.17	4.94	0.23	1.10E-01	4.65E-01	TRIO	triple functional domain (PTPRF interacting)	chr5p15.2	209013_x_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929																			
3.98	3.30	0.69	1.10E-01	4.65E-01	MSRB3	methionine sulfoxide reductase B3	chr12q14.3	225790_at	NM_001031679 /// NM_198080																			
4.96	4.64	0.32	1.10E-01	4.65E-01	NUDT16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	chr3q22.1	235054_at	NM_152395																			
8.16	7.31	0.85	1.10E-01	4.65E-01	MAOB	monoamine oxidase B	chrXp11.23	204041_at	NM_000898																			
2.81	2.44	0.37	1.10E-01	4.65E-01	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	chr5p15	204675_at	NM_001047																			
8.35	7.82	0.53	1.10E-01	4.65E-01	SFRS6	splicing factor, arginine/serine-rich 6	chr20q12-q13.1	208804_s_at	NM_006275																			
5.28	5.00	0.28	1.10E-01	4.66E-01	CASP7	caspase 7, apoptosis-related cysteine peptidase	chr10q25	207181_s_at	NM_001227 /// NM_033338 /// NM_033339 /// NM_033340																			
2.93	2.51	0.41	1.10E-01	4.66E-01	C19orf55	chromosome 19 open reading frame 55	chr19q13.12	1553162_x_at	NM_001039887																			
5.61	5.32	0.29	1.10E-01	4.66E-01	GOLGA1	golgi autoantigen, golgin subfamily a, 1	chr9q33.3	203383_s_at	NM_002077																			
8.51	8.02	0.50	1.10E-01	4.66E-01	GLA	galactosidase, alpha	chrXq22	214430_at	NM_000169																			
4.67	3.99	0.67	1.10E-01	4.66E-01	C9orf82	chromosome 9 open reading frame 82	chr9p21.2	231995_at	NM_024828																			
8.25	7.91	0.35	1.10E-01	4.66E-01	NIPSNAP1	nipsnap homolog 1 (C. elegans)	chr22q12.2	201709_s_at	NM_003634																			
2.66	2.35	0.31	1.11E-01	4.66E-01	DTYMK /// LOC727761	deoxythymidylate kinase (thymidylate kinase) /// similar to Deoxythymidylate kinase (thymidylate kinase)	chr2q37.3	1565694_at	NM_012145 /// XM_001126163 /// XM_001126184 /// XM_001126211																			
3.18	2.98	0.19	1.11E-01	4.66E-01	FAM120AOS	Family with sequence similarity 120A opposite strand	chr9q22.31	239391_at	NM_198841																			
5.28	4.88	0.40	1.11E-01	4.66E-01	DGCR14	DiGeorge syndrome critical region gene 14	chr22q11.21|22q11.2	204383_at	NM_022719																			
3.16	2.83	0.33	1.11E-01	4.66E-01	TTLL11	tubulin tyrosine ligase-like family, member 11	chr9q33.2	242545_at	NM_194252																			
3.22	2.73	0.49	1.11E-01	4.66E-01	---	---	---	241048_at	---																			
5.07	4.64	0.43	1.11E-01	4.66E-01	TAZ	tafazzin	chrXq28	37278_at	NM_000116 /// NM_181311 /// NM_181312 /// NM_181313 /// NR_024048																			
2.26	2.04	0.22	1.11E-01	4.66E-01	---	---	---	241875_at	---																			
3.38	3.00	0.38	1.11E-01	4.66E-01	---	---	---	240333_at	---																			
8.09	7.68	0.41	1.11E-01	4.66E-01	ACAA1	acetyl-Coenzyme A acyltransferase 1	chr3p23-p22	214274_s_at	NM_001130410 /// NM_001607 /// NR_024024																			
2.68	2.26	0.41	1.11E-01	4.66E-01	C2orf37	chromosome 2 open reading frame 37	chr2q31.1	220172_at	NM_025000																			
5.64	5.21	0.44	1.11E-01	4.66E-01	TBXAS1	thromboxane A synthase 1 (platelet)	chr7q34-q35	208130_s_at	NM_001061 /// NM_001130966 /// NM_030984																			
6.12	5.76	0.36	1.11E-01	4.66E-01	ADAT3	adenosine deaminase, tRNA-specific 3, TAD3 homolog (S. cerevisiae)	chr19p13.3	1553968_a_at	NM_138422																			

3.89	3.55	0.34	1.11E-01	4.66E-01	FGFR1	fibroblast growth factor receptor 1	chr8p11.2-p11.1	222164_at	NM_015850 /// NM_023105 /// NM_023106 /// NM_023107 /// NM_023108 /// NM_023110 /// NM_023111																				
4.17	2.87	1.30	1.11E-01	4.66E-01	LOC645722	hypothetical LOC645722	chr17q23.2	1555216_a_at	XM_944447																				
6.78	6.33	0.46	1.11E-01	4.66E-01	C6orf66	chromosome 6 open reading frame 66	chr6q16.1	219006_at	NM_014165																				
2.51	2.23	0.28	1.11E-01	4.66E-01	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	chr19q13.2	206755_at	NM_000767																				
3.19	2.63	0.57	1.11E-01	4.66E-01	PHF20L1	PHD finger protein 20-like 1	chr8q24.22	231967_at	NM_016018 /// NM_032205 /// NM_198513																				
2.31	2.13	0.19	1.11E-01	4.66E-01	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	chr2q31-q33|2q31.1	1554743_x_at	NM_000534 /// NM_001128143 /// NM_001128144																				
7.68	7.32	0.36	1.11E-01	4.66E-01	SLC41A3	solute carrier family 41, member 3	chr3q21.2	224931_at	NM_001008485 /// NM_001008486 /// NM_001008487 /// NM_017836																				
3.06	2.42	0.65	1.11E-01	4.66E-01	PEX13	peroxisomal biogenesis factor 13	chr2p14-p16	1558164_s_at	NM_002618																				
6.04	5.63	0.41	1.11E-01	4.66E-01	SETD4	SET domain containing 4	chr21q22.13	213989_x_at	NM_001007259 /// NM_017438																				
3.56	3.15	0.42	1.11E-01	4.66E-01	HIST1H2AB /// HIST1H2AE	histone cluster 1, H2ab /// histone cluster 1, H2ae	chr6p21.3 /// chr6p22.2-p21.1	214469_at	NM_003513 /// NM_021052																				
7.83	7.47	0.36	1.11E-01	4.67E-01	ADD1	adducin 1 (alpha)	chr4p16.3	208030_s_at	NM_001119 /// NM_014189 /// NM_014190 /// NM_176801																				
7.45	6.99	0.46	1.11E-01	4.67E-01	ARFGAP2	ADP-ribosylation factor GTPase activating protein 2	chr11p11.2-p11.12	211975_at	NM_032389																				
5.61	5.01	0.59	1.11E-01	4.67E-01	C21orf119	chromosome 21 open reading frame 119	chr21q22.11	227424_x_at	XR_040263 /// XR_040264 /// XR_040265																				
6.99	6.66	0.33	1.11E-01	4.67E-01	ZFYVE20	zinc finger, FYVE domain containing 20	chr3p24.3	226581_at	NM_022340																				
3.67	2.95	0.72	1.11E-01	4.67E-01	---	---	---	1558686_at	---																				
2.81	2.56	0.25	1.11E-01	4.67E-01	ZNF101	zinc finger protein 101	chr19p13.11	1552634_a_at	NM_033204																				
2.39	2.15	0.24	1.11E-01	4.67E-01	---	---	---	1562825_at	---																				
2.77	2.42	0.35	1.11E-01	4.67E-01	NPFF	neuropeptide FF-amide peptide precursor	chr12q13.13	214184_at	NM_003717																				
5.58	5.27	0.31	1.11E-01	4.67E-01	CROCC	ciliary rootlet coiled-coil, rootletin	chr1pter-p36.11	206274_s_at	NM_014675																				
6.53	6.29	0.24	1.11E-01	4.67E-01	---	---	---	224645_at	---																				
2.49	2.17	0.32	1.12E-01	4.67E-01	LOC100131683	hypothetical protein LOC100131683	chr4q35.1	240289_at	XM_001720263 /// XM_001723828 /// XM_001723858																				
6.83	6.47	0.36	1.12E-01	4.67E-01	MLX	MAX-like protein X	chr17q21.1	217909_s_at	NM_170607 /// NM_198204 /// NM_198205																				
5.78	5.15	0.63	1.12E-01	4.67E-01	DFNB31	deafness, autosomal recessive 31	chr9q32-q34	47553_at	NM_001083885 /// NM_015404																				
5.01	4.34	0.67	1.12E-01	4.67E-01	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	chrXp22.12	201016_at	NM_001412																				

7.49	6.79	0.70	1.12E-01	4.67E-01	NR1D1 /// THRA	nuclear receptor subfamily 1, group D, member 1 /// thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	chr17q11.2	31637_s_at	NM_003250 /// NM_021724 /// NM_199334																				
6.73	6.38	0.34	1.12E-01	4.67E-01	KIAA0319L	KIAA0319-like	chr1p34.2	222468_at	NM_024874 /// NM_182686																				
5.80	4.61	1.19	1.12E-01	4.67E-01	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	chr1q23.3	209681_at	NM_006996																				
4.43	4.13	0.30	1.12E-01	4.67E-01	C14orf102	chromosome 14 open reading frame 102	chr14q32.11	227575_s_at	NM_017970 /// NM_199043																				
3.31	3.06	0.25	1.12E-01	4.67E-01	LCE1E	late cornified envelope 1E	chr1q21.3	1559226_x_at	NM_178353																				
7.41	6.87	0.54	1.12E-01	4.68E-01	MARCKS	myristoylated alanine-rich protein kinase C substrate	chr6q22.2	201669_s_at	NM_002356																				
7.44	6.87	0.56	1.12E-01	4.68E-01	DMAP1	DNA methyltransferase 1 associated protein 1	chr1p34	224163_s_at	NM_001034023 /// NM_001034024 /// NM_019100																				
5.12	4.79	0.34	1.12E-01	4.68E-01	C10orf30	chromosome 10 open reading frame 30	chr10p13	227341_at	NM_001100912 /// NM_152751																				
4.21	3.56	0.65	1.12E-01	4.68E-01	C4orf28	chromosome 4 open reading frame 28	chr4p15.31	235260_s_at	NM_001130727 /// NM_145048																				
2.51	2.12	0.39	1.12E-01	4.68E-01	---	---	---	228464_at	---																				
7.73	7.33	0.39	1.12E-01	4.68E-01	MBD3	methyl-CpG binding domain protein 3	chr19p13.3	41160_at	NM_003926																				
11.91	11.44	0.47	1.12E-01	4.68E-01	LOC644191 /// LOC728937 /// RPS26	similar to hCG15685 /// similar to 40S ribosomal protein S26 /// ribosomal protein S26	chr12q13 /// chr17q21.31 /// chr4q26	217753_s_at	NM_001029 /// NM_001093731 /// XM_001722150 /// XM_001724376 /// XM_001724435 /// XM_001725335 /// XM_930072																				
7.35	7.10	0.25	1.12E-01	4.68E-01	MFN2	mitofusin 2	chr1p36.22	201155_s_at	NM_001127660 /// NM_014874																				
2.41	2.25	0.16	1.12E-01	4.68E-01	LOC151760	hypothetical LOC151760	chr3q13.13	1564838_a_at	XR_041820 /// XR_041821 /// XR_041822																				
3.76	3.23	0.53	1.12E-01	4.68E-01	CBX4	chromobox homolog 4 (Pc class homolog, Drosophila)	chr17q25.3	206724_at	NM_003655																				
2.64	2.38	0.26	1.12E-01	4.68E-01	---	---	---	231099_at	---																				
4.69	4.17	0.52	1.12E-01	4.68E-01	CALML4	calmodulin-like 4	chr15q23	64408_s_at	NM_001031733 /// NM_033429																				
5.34	4.80	0.54	1.12E-01	4.68E-01	UNKL	unkempt homolog (Drosophila)-like	chr16p13.3	229908_s_at	NM_001037125 /// NM_023076																				
10.97	10.54	0.43	1.12E-01	4.68E-01	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	chr10q23-q24	203060_s_at	NM_001015880 /// NM_004670																				
8.50	8.29	0.21	1.12E-01	4.68E-01	TMEM85	transmembrane protein 85	chr15q14	223857_x_at	NM_016454																				
3.22	2.74	0.47	1.12E-01	4.68E-01	TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	chr1q42.13	1554415_at	NM_001025247 /// NM_014409																				
6.20	5.44	0.76	1.12E-01	4.68E-01	SPATA13	spermatogenesis associated 13	chr13q12.12	225564_at	NM_153023																				
3.35	3.01	0.34	1.13E-01	4.68E-01	HSF2BP	heat shock transcription factor 2 binding protein	chr21q22.3	207020_at	NM_007031																				
2.69	2.39	0.30	1.13E-01	4.68E-01	HIST1H3H	histone cluster 1, H3h	chr6p22-p21.3	206110_at	NM_003536																				
8.57	8.12	0.45	1.13E-01	4.69E-01	IFNGR1	interferon gamma receptor 1	chr6q23.3	202727_s_at	NM_000416																				
3.88	3.27	0.60	1.13E-01	4.69E-01	---	---	---	1559600_at	---																				
8.17	7.94	0.23	1.13E-01	4.69E-01	SNF8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	chr17q21.32	218391_at	NM_007241																				
8.96	8.19	0.77	1.13E-01	4.69E-01	FDX1	ferredoxin 1	chr11q22	239161_at	NM_004109																				
5.36	4.81	0.55	1.13E-01	4.69E-01	ZNF319	zinc finger protein 319	chr16q13	228460_at	NM_020807																				
6.03	5.48	0.55	1.13E-01	4.69E-01	CUEDC1	CUE domain containing 1	chr17q23.2	219468_s_at	NM_017949																				

4.66	4.29	0.37	1.13E-01	4.69E-01	BCL2L11	BCL2-like 11 (apoptosis facilitator)	chr2q13	1558143_a_at	NM_006538 /// NM_138621 /// NM_207002																				
4.83	4.56	0.28	1.13E-01	4.69E-01	LOC554175	hypothetical LOC554175	chr15q23	1570055_at	XR_016015 /// XR_040089 /// XR_040090																				
5.49	4.99	0.50	1.13E-01	4.69E-01	MAPK7	mitogen-activated protein kinase 7	chr17p11.2	35617_at	NM_002749 /// NM_139032 /// NM_139033 /// NM_139034																				
8.06	7.69	0.37	1.13E-01	4.69E-01	C3AR1	complement component 3a receptor 1	chr12p13.31	209906_at	NM_004054																				
7.74	7.32	0.42	1.13E-01	4.69E-01	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	chr10q26	209974_s_at	NM_001007793 /// NM_004725																				
10.15	9.91	0.24	1.13E-01	4.69E-01	PRICKLE4 /// TOMM6	prickle homolog 4 (Drosophila) /// translocase of outer mitochondrial membrane 6 homolog (yeast)	chr6p21.31	218233_s_at	NM_001134493 /// NM_013397																				
4.19	3.73	0.47	1.13E-01	4.69E-01	SETDB2	SET domain, bifurcated 2	chr13q14	235338_s_at	NM_031915																				
4.31	4.03	0.27	1.13E-01	4.69E-01	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	chr1q22-q24	210256_s_at	NM_003557																				
5.30	4.90	0.40	1.13E-01	4.69E-01	TMEM39A	transmembrane protein 39A	chr3q13.33	218615_s_at	NM_018266																				
2.76	2.44	0.32	1.13E-01	4.69E-01	RFFL	ring finger and FYVE-like domain containing 1	chr17q12	1552651_a_at	NM_001017368 /// NM_057178																				
5.31	4.97	0.33	1.13E-01	4.69E-01	STX5	syntaxin 5	chr11q12.3	203330_s_at	NM_003164																				
5.42	5.03	0.39	1.13E-01	4.69E-01	LDLRAP1	low density lipoprotein receptor adaptor protein 1	chr1p36-p35	57082_at	NM_015627																				
2.74	2.48	0.26	1.13E-01	4.69E-01	---	---	---	216936_at	---																				
8.87	8.50	0.37	1.13E-01	4.69E-01	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)	chr19p13.13	221506_s_at	NM_013433																				
2.81	2.55	0.26	1.13E-01	4.69E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	222208_s_at	NR_003655 /// XR_042143 /// XR_042182																				
8.21	7.80	0.41	1.13E-01	4.69E-01	EXOSC7	exosome component 7	chr3p21.31	212627_s_at	NM_015004 /// NR_023353																				
3.65	3.34	0.31	1.13E-01	4.69E-01	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	chr2p13.1	228660_x_at	NM_004263																				
2.50	2.15	0.35	1.13E-01	4.69E-01	ARSJ	arylsulfatase family, member J	chr4q26	219973_at	NM_024590																				
12.90	12.71	0.19	1.13E-01	4.69E-01	---	---	---	221798_x_at	---																				
4.97	4.29	0.68	1.13E-01	4.69E-01	C9orf91	chromosome 9 open reading frame 91	chr9q32	221865_at	NM_153045																				
2.50	2.26	0.25	1.13E-01	4.69E-01	EVI5L	Ecotropic viral integration site 5-like	chr19p13.2	242534_at	NM_145245																				
5.84	5.47	0.37	1.13E-01	4.70E-01	SHPK	sedoheptulokinase	chr17p13	219713_at	NM_013276																				
2.59	2.11	0.48	1.13E-01	4.70E-01	PGAP1	post-GPI attachment to proteins 1	chr2q33.1	213469_at	NM_024989																				
4.66	4.20	0.45	1.13E-01	4.70E-01	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	chr11p15.1	229594_at	NM_194285																				
6.23	5.63	0.61	1.14E-01	4.70E-01	FAM36A /// HOXA7	family with sequence similarity 36, member A /// homeobox A7	chr1q44 /// chr7p15-p14	206848_at	NM_006896 /// NM_198076																				
4.62	4.05	0.56	1.14E-01	4.70E-01	---	---	---	226854_at	---																				
3.05	2.78	0.27	1.14E-01	4.70E-01	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	chr3p24.2	207044_at	NM_000461 /// NM_001128176 /// NM_001128177																				
10.66	10.30	0.36	1.14E-01	4.70E-01	NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	chr14q32.12	206790_s_at	NM_004545																				
2.62	2.43	0.19	1.14E-01	4.70E-01	GLI4	GLI-Kruppel family member GLI4	chr8q24.3	238364_x_at	NM_138465																				
6.19	5.42	0.77	1.14E-01	4.70E-01	SNX21	sorting nexin family member 21	chr20q13.12	1553960_at	NM_001042632 /// NM_001042633 /// NM_033421 /// NM_152897																				
5.61	4.72	0.89	1.14E-01	4.70E-01	EHMT1	euchromatic histone-lysine N-methyltransferase 1	chr9q34.3	225461_at	NM_024757																				
3.58	2.89	0.69	1.14E-01	4.70E-01	FAM80B	family with sequence similarity 80, member B	chr12p13.31	229344_x_at	NM_020734																				
2.45	2.15	0.30	1.14E-01	4.70E-01	LRRC4C	leucine rich repeat containing 4C	chr11p12	241585_at	NM_020929																				
3.74	3.42	0.32	1.14E-01	4.70E-01	---	---	---	238580_at	---																				

3.90	3.56	0.34	1.14E-01	4.71E-01	---	---	---	238640_at	---
3.01	2.65	0.37	1.14E-01	4.71E-01	---	---	---	243405_at	---
3.81	3.43	0.38	1.14E-01	4.71E-01	PTPN3	protein tyrosine phosphatase, non-receptor type 3	chr9q31	203997_at	NM_002829
6.65	6.34	0.31	1.14E-01	4.71E-01	SNX1	sorting nexin 1	chr15q22.31	214531_s_at	NM_003099 /// NM_148955 /// NM_152826
4.73	4.34	0.39	1.14E-01	4.71E-01	---	---	---	229728_at	---
5.99	5.37	0.62	1.14E-01	4.71E-01	ZNF689	zinc finger protein 689	chr16p11.2	227445_at	NM_138447
3.35	3.06	0.29	1.14E-01	4.71E-01	C11orf70	chromosome 11 open reading frame 70	chr11q22.1	241198_s_at	NM_032930
2.63	2.39	0.24	1.14E-01	4.71E-01	C13orf15	Chromosome 13 open reading frame 15	chr13q14.11	228193_s_at	NM_014059
7.49	7.21	0.27	1.14E-01	4.71E-01	MGC12966	hypothetical protein LOC84792	chr7p22.1	224452_s_at	NM_001037163
4.76	4.41	0.35	1.14E-01	4.71E-01	SLC30A3	solute carrier family 30 (zinc transporter), member 3	chr2p23.3	207035_at	NM_003459
3.16	2.91	0.26	1.14E-01	4.71E-01	---	---	---	1555853_at	---
3.76	3.47	0.29	1.14E-01	4.71E-01	---	---	---	1570281_at	---
7.38	6.97	0.41	1.14E-01	4.71E-01	PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	chr1q21	206138_s_at	NM_002651
5.29	4.85	0.44	1.14E-01	4.71E-01	CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	chr20q13.31	202190_at	NM_001033521 /// NM_001033522 /// NM_001324
6.09	5.69	0.39	1.14E-01	4.71E-01	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	chr7q36	209247_s_at	NM_005692 /// NM_007189
4.34	3.72	0.62	1.14E-01	4.71E-01	---	---	---	231055_at	---
2.71	2.53	0.18	1.14E-01	4.71E-01	---	---	---	1559889_at	---
7.81	7.54	0.27	1.14E-01	4.71E-01	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	chr22q13.2-q13.31	201076_at	NM_001003796 /// NM_005008
3.34	2.97	0.37	1.14E-01	4.71E-01	PARL	presenilin associated, rhomboid-like	chr3q27.1	228881_at	NM_001037639 /// NM_018622
2.65	2.42	0.23	1.15E-01	4.71E-01	NOC2L	nucleolar complex associated 2 homolog (S. cerevisiae)	chr1p36.33	1559139_at	NM_015658
3.16	2.85	0.30	1.15E-01	4.71E-01	---	---	---	241597_at	---
5.52	5.15	0.37	1.15E-01	4.72E-01	PRMT6	protein arginine methyltransferase 6	chr1p13.3	223275_at	NM_018137
5.58	4.87	0.71	1.15E-01	4.72E-01	MTUS1	Mitochondrial tumor suppressor 1	chr8p22	239576_at	NM_001001924 /// NM_001001925 /// NM_001001931 /// NM_020749
4.34	4.05	0.29	1.15E-01	4.72E-01	LOC441108	Hypothetical gene supported by AK128882	chr5q31.1	1560128_x_at	NM_001013717
4.76	4.17	0.59	1.15E-01	4.72E-01	ZWINT	ZW10 interactor	chr10q21-q22	204026_s_at	NM_001005413 /// NM_007057 /// NM_032997
7.89	7.59	0.30	1.15E-01	4.72E-01	AK2	adenylate kinase 2	chr1p34	208967_s_at	NM_001625 /// NM_013411
4.02	3.63	0.39	1.15E-01	4.72E-01	KIAA0226	KIAA0226	chr3q29	212735_at	NM_014687
6.20	5.62	0.58	1.15E-01	4.72E-01	TTYH3	tweety homolog 3 (Drosophila)	chr7p22	224674_at	NM_025250
5.10	4.77	0.33	1.15E-01	4.72E-01	RPS28	ribosomal protein S28	chr19p13.2	208902_s_at	NM_001031
3.66	3.18	0.48	1.15E-01	4.72E-01	---	---	---	1558250_s_at	---
5.22	4.80	0.42	1.15E-01	4.72E-01	PLA2G12A	Phospholipase A2, group XIIA	chr4q25	228084_at	NM_030821
3.15	2.97	0.18	1.15E-01	4.72E-01	---	---	---	244365_at	---
5.52	5.22	0.29	1.15E-01	4.72E-01	ZNF407	zinc finger protein 407	chr18q23	227768_at	NM_017757
7.00	6.34	0.66	1.15E-01	4.72E-01	NR0B2	nuclear receptor subfamily 0, group B, member 2	chr1p36.1	206410_at	NM_021969
2.72	2.48	0.25	1.15E-01	4.72E-01	---	---	---	235162_at	---
7.76	7.49	0.27	1.15E-01	4.72E-01	HYAL2	hyaluronoglucosaminidase 2	chr3p21.3	206855_s_at	NM_003773 /// NM_033158
3.72	3.41	0.32	1.15E-01	4.72E-01	MAPK8	mitogen-activated protein kinase 8	chr10q11.22	229664_at	NM_002750 /// NM_139046 /// NM_139047 /// NM_139049
5.82	5.34	0.48	1.15E-01	4.72E-01	TAF2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	chr8q24.12	209523_at	NM_003184
3.05	2.83	0.22	1.15E-01	4.72E-01	---	---	---	238829_at	---

6.98	6.78	0.20	1.15E-01	4.72E-01	DDX19A /// DDX19B	DEAD (Asp-Glu-Ala-As) box polypeptide 19A /// DEAD (Asp-Glu-Ala-As) box polypeptide 19B	chr16q22.1	202576_s_at	NM_001014449 /// NM_001014451 /// NM_007242 /// NM_018332																				
8.58	8.18	0.39	1.15E-01	4.72E-01	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	chr12q13-q15	203445_s_at	NM_005730																				
5.37	4.97	0.40	1.15E-01	4.72E-01	SF3A1	splicing factor 3a, subunit 1, 120kDa	chr22q12.2	201357_s_at	NM_001005409 /// NM_005877																				
4.55	4.09	0.46	1.16E-01	4.73E-01	FUT11	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	chr10q22.2	238551_at	NM_173540																				
5.37	4.92	0.45	1.16E-01	4.73E-01	TRABD	TraB domain containing	chr22q13.33	225360_at	NM_025204																				
2.57	2.38	0.19	1.16E-01	4.73E-01	WDFY4	WDFY family member 4	chr10q11.22	1553863_at	NM_020945 /// XM_001124973 /// XM_001124974 /// XM_001714299 /// XM_001719015																				
3.58	3.20	0.38	1.16E-01	4.73E-01	PHF20L1	PHD finger protein 20-like 1	chr8q24.22	1554472_a_at	NM_016018 /// NM_032205 /// NM_198513																				
2.31	2.12	0.19	1.16E-01	4.73E-01	MKL2	MKL/myocardin-like 2	chr16p13.12	1558778_s_at	NM_014048																				
11.88	11.69	0.19	1.16E-01	4.73E-01	LOC642741	similar to ribosomal protein L3	chr6q21	215963_x_at	XR_016455 /// XR_019077 /// XR_039514																				
5.04	4.39	0.64	1.16E-01	4.73E-01	CREBZF	CREB/ATF bZIP transcription factor	chr11q14	213584_s_at	NM_001039618																				
3.77	3.47	0.30	1.16E-01	4.73E-01	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	221480_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370																				
3.31	2.85	0.46	1.16E-01	4.73E-01	CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	chr1p34-p12	210096_at	NM_000779 /// NM_001099772																				
7.87	7.59	0.28	1.16E-01	4.73E-01	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	chr1p36.1-p35	202675_at	NM_003000																				
2.66	2.45	0.21	1.16E-01	4.73E-01	---	---	---	1564143_at	---																				
4.32	4.09	0.23	1.16E-01	4.73E-01	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	216506_x_at	NM_001009569 /// NM_004641																				
3.18	2.92	0.26	1.16E-01	4.73E-01	OASL	2'-5'-oligoadenylate synthetase-like	chr12q24.2	205660_at	NM_003733 /// NM_198213																				
6.49	6.08	0.41	1.16E-01	4.73E-01	PRELID1	PRELI domain containing 1	chr5q35.3	224232_s_at	NM_013237																				
2.79	2.53	0.26	1.16E-01	4.73E-01	GLRA2	glycine receptor, alpha 2	chrXp22.1-p21.3	207462_at	NM_001118885 /// NM_001118886 /// NM_002063																				
3.08	2.79	0.28	1.16E-01	4.73E-01	AGBL5	ATP/GTP binding protein-like 5	chr2p23.3	238889_at	NM_001035507 /// NM_021831																				

2.95	2.48	0.47	1.16E-01	4.73E-01	PTPN20A /// PTPN20B	protein tyrosine phosphatase, non-receptor type 20A /// protein tyrosine phosphatase, non-receptor type 20B	chr10q11.22	215172_at	NM_001042357 /// NM_001042358 /// NM_001042359 /// NM_001042360 /// NM_001042361 /// NM_001042362 /// NM_001042363 /// NM_001042364 /// NM_001042365 /// NM_001042387 /// NM_001042389 /// NM_001042390 /// NM_001042391 /// NM_001042392 /// NM_001042393 /// NM_001042394 /// NM_001042395 /// NM_001042396 /// NM_001042397 /// NM_015605																			
6.42	6.08	0.34	1.16E-01	4.73E-01	CAMTA1	Calmodulin binding transcription activator 1	chr1p36.31-p36.23	227328_at	NM_015215																				
7.92	7.47	0.45	1.16E-01	4.74E-01	STK35	serine/threonine kinase 35	chr20p13	225649_s_at	NM_080836																				
8.77	8.49	0.28	1.16E-01	4.74E-01	PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	chr17p13.3	200000_s_at	NM_006445																				
2.24	2.04	0.20	1.16E-01	4.74E-01	---	---	---	244856_at	---																				
4.47	4.20	0.28	1.16E-01	4.74E-01	MMP16	matrix metallopeptidase 16 (membrane-inserted)	chr8q21	207013_s_at	NM_005941 /// NM_022564																				
3.09	2.45	0.65	1.16E-01	4.74E-01	MYSM1	myb-like, SWIRM and MPN domains 1	chr1p32.1	225760_at	NM_001085487																				
2.20	2.02	0.19	1.16E-01	4.74E-01	FLJ25694 /// KRTAP21-1 /// LOC100128202	hypothetical protein FLJ25694 /// keratin associated protein 21-1 /// hypothetical protein LOC100128202	chr13q21.31 /// chr21q22.1	241953_at	NM_181619 /// XM_001716986 /// XM_001721733 /// XM_001723719																				
7.15	6.91	0.25	1.17E-01	4.74E-01	C21orf59	chromosome 21 open reading frame 59	chr21q22.1	218123_at	NM_021254																				
2.77	2.36	0.41	1.17E-01	4.74E-01	---	---	---	1562263_at	---																				
12.46	12.29	0.17	1.17E-01	4.74E-01	RPL13	ribosomal protein L13	chr16q24.3|17p11.2	212734_x_at	NM_000977 /// NM_033251																				
7.19	6.92	0.26	1.17E-01	4.74E-01	NUB1	negative regulator of ubiquitin-like proteins 1	chr7q36	222512_at	NM_016118																				
7.36	6.91	0.45	1.17E-01	4.74E-01	PTPRE	protein tyrosine phosphatase, receptor type, E	chr10q26	221840_at	NM_006504 /// NM_130435																				
6.78	6.18	0.61	1.17E-01	4.74E-01	RGS10	regulator of G-protein signaling 10	chr10q25	204319_s_at	NM_001005339 /// NM_002925																				
3.71	3.30	0.41	1.17E-01	4.74E-01	PTPN14	protein tyrosine phosphatase, non-receptor type 14	chr1q32.2	205503_at	NM_005401																				
4.37	3.87	0.50	1.17E-01	4.74E-01	TFEB	transcription factor EB	chr6p21	50221_at	NM_007162																				
5.23	4.62	0.62	1.17E-01	4.74E-01	THBS1	thrombospondin 1	chr15q15	201110_s_at	NM_003246																				
3.10	2.81	0.29	1.17E-01	4.74E-01	---	---	---	231314_at	---																				
6.15	5.84	0.31	1.17E-01	4.75E-01	SOX13	SRY (sex determining region Y)-box 13	chr1q32	209736_at	NM_005686																				

2.89	2.57	0.32	1.17E-01	4.75E-01	KIAA1217	KIAA1217	chr10p12.2-p12.1	1554438_at	NM_001098500 /// NM_001098501 /// NM_019590																				
6.67	6.33	0.34	1.17E-01	4.75E-01	ORMDL3	ORM1-like 3 (S. cerevisiae)	chr17q12-q21.1	223259_at	NM_139280																				
3.09	2.85	0.24	1.17E-01	4.75E-01	SP3	Sp3 transcription factor	chr2q31	229217_at	NM_001017371 /// NM_003111																				
5.85	5.35	0.51	1.17E-01	4.75E-01	NCOA1	nuclear receptor coactivator 1	chr2p23	209105_at	NM_003743 /// NM_147223 /// NM_147233																				
10.24	9.99	0.25	1.17E-01	4.75E-01	PRDX6	peroxiredoxin 6	chr1q25.1	200844_s_at	NM_004905																				
2.27	2.07	0.20	1.17E-01	4.75E-01	---	---	---	239678_at	---																				
7.02	6.64	0.38	1.17E-01	4.75E-01	DKC1	dyskeratosis congenita 1, dyskerin	chrXq28	201479_at	NM_001363																				
4.36	4.15	0.22	1.17E-01	4.75E-01	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	chr14q24.3	1569536_at	NM_017791																				
3.34	2.98	0.36	1.17E-01	4.75E-01	---	---	---	216730_at	---																				
2.27	2.10	0.17	1.17E-01	4.75E-01	LRRC51	leucine rich repeat containing 51	chr11q13.4	1568882_at	NM_145309																				
6.29	6.00	0.29	1.17E-01	4.75E-01	FTSJ1	FtsJ homolog 1 (E. coli)	chrXp11.23	213937_s_at	NM_012280 /// NM_177434 /// NM_177439																				
5.37	4.83	0.53	1.17E-01	4.75E-01	PPAT	phosphoribosyl pyrophosphate amidotransferase	chr4q12	209434_s_at	NM_002703																				
2.29	2.05	0.23	1.17E-01	4.75E-01	NUP62	Interleukin 4 induced 1	chr19q13.33	236505_at	NM_012346 /// NM_016553 /// NM_153718 /// NM_153719																				
4.52	4.02	0.50	1.17E-01	4.75E-01	LOC284023	hypothetical protein LOC284023	chr17p13.1	238096_at	XM_001715822 /// XM_001717540 /// XM_941810																				
7.05	6.71	0.34	1.17E-01	4.75E-01	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	chr5q35.3	215994_x_at	NM_015043 /// NM_198868																				
5.78	5.25	0.53	1.17E-01	4.75E-01	FLCN	folliculin	chr17p11.2	1552664_at	NM_144606 /// NM_144997																				
6.45	6.08	0.37	1.17E-01	4.75E-01	WDR23	WD repeat domain 23	chr14q12	216389_s_at	NM_025230 /// NM_181357																				
2.50	2.18	0.33	1.18E-01	4.75E-01	GREB1	GREB1 protein	chr2p25.1	210562_at	NM_014668 /// NM_033090 /// NM_148903																				
2.06	1.86	0.19	1.18E-01	4.75E-01	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	chr1q23.3	223381_at	NM_031423 /// NM_145697																				
5.51	5.08	0.44	1.18E-01	4.75E-01	FLJ22795 /// LOC727751 /// LOC727849	hypothetical protein FLJ22795 /// similar to cis-Golgi matrix protein GM130 /// similar to cis-Golgi matrix protein GM130	chr15q25.2	223327_x_at	XM_001713899 /// XR_040862 /// XR_041987																				
5.33	4.92	0.41	1.18E-01	4.75E-01	---	---	---	232130_at	---																				
3.78	3.52	0.26	1.18E-01	4.75E-01	CDKL3	cyclin-dependent kinase-like 3	chr5q31	1561190_at	NM_001113575 /// NM_016508																				
8.63	8.29	0.34	1.18E-01	4.75E-01	BAT3	HLA-B associated transcript 3	chr6p21.3	201255_x_at	NM_001098534 /// NM_004639 /// NM_080702 /// NM_080703																				
5.11	4.67	0.44	1.18E-01	4.75E-01	EPSTI1	epithelial stromal interaction 1 (breast)	chr13q13.3	227609_at	NM_001002264 /// NM_033255																				
5.52	4.76	0.75	1.18E-01	4.75E-01	COL4A4	collagen, type IV, alpha 4	chr2q35-q37	229779_at	NM_000092																				

4.58	4.32	0.26	1.18E-01	4.75E-01	MOV10	Mov10, Moloney leukemia virus 10, homolog (mouse)	chr1p13.2	233917_s_at	NM_001130079 /// NM_020963
2.65	2.33	0.31	1.18E-01	4.75E-01	---	---	---	1562012_at	---
6.24	5.71	0.53	1.18E-01	4.75E-01	SGSH	N-sulfoglucosamine sulfohydrolase	chr17q25.3	204293_at	NM_000199
6.44	5.90	0.54	1.18E-01	4.76E-01	LST1	leukocyte specific transcript 1	chr6p21.3	215633_x_at	NM_007161 /// NM_205837 /// NM_205838 /// NM_205839 /// NM_205840
7.87	7.41	0.45	1.18E-01	4.76E-01	LEPROTL1	leptin receptor overlapping transcript-like 1	chr8p21.2-p21.1	202595_s_at	NM_001128208 /// NM_015344
3.94	3.59	0.35	1.18E-01	4.76E-01	MYO15B	myosin XVB pseudogene	chr17q25.1	59375_at	NR_003587
12.73	12.55	0.18	1.18E-01	4.76E-01	RPL3	ribosomal protein L3	chr22q13	211073_x_at	NM_000967 /// NM_001033853
9.02	8.65	0.37	1.18E-01	4.76E-01	MRPL23	mitochondrial ribosomal protein L23	chr11p15.5-p15.4	213897_s_at	NM_021134
8.46	8.15	0.31	1.18E-01	4.76E-01	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	chr17q21.32	208972_s_at	NM_001002027 /// NM_005175
8.54	7.98	0.55	1.18E-01	4.76E-01	LOC255783	hypothetical protein LOC255783	chr19q13.32	227325_at	NR_002797
2.16	1.95	0.21	1.18E-01	4.76E-01	---	---	---	1557861_at	---
4.86	4.41	0.45	1.18E-01	4.76E-01	ATP9B	ATPase, class II, type 9B	chr18q23	214934_at	NM_198531
7.95	7.16	0.80	1.18E-01	4.76E-01	PSAT1	phosphoserine aminotransferase 1	chr9q21.2	220892_s_at	NM_021154 /// NM_058179
6.62	6.31	0.31	1.18E-01	4.76E-01	IQSEC1	IQ motif and Sec7 domain 1	chr3p25.1	203907_s_at	NM_001134382 /// NM_014869
7.53	7.22	0.31	1.18E-01	4.76E-01	TRADD	TNFRSF1A-associated via death domain	chr16q22	205641_s_at	NM_003789
2.24	1.99	0.25	1.18E-01	4.76E-01	BTBD8	BTB (POZ) domain containing 8	chr1p22.1	1569693_at	NM_183242
2.23	1.97	0.25	1.18E-01	4.76E-01	---	---	---	237963_x_at	---
6.53	6.19	0.34	1.18E-01	4.76E-01	FAM3A	family with sequence similarity 3, member A	chrXq28	38043_at	NM_021806
2.35	2.15	0.20	1.18E-01	4.76E-01	---	---	---	230953_at	---
7.12	6.66	0.46	1.18E-01	4.76E-01	ENDOG	endonuclease G	chr9q34.1	204824_at	NM_004435
5.98	5.55	0.43	1.18E-01	4.76E-01	RAB7A	RAB7A, member RAS oncogene family	chr3q21.3	211960_s_at	NM_004637
5.27	4.84	0.43	1.18E-01	4.76E-01	PTPRV	Chromosome 9 open reading frame 44	chr9q22.31	235776_x_at	NR_015444 /// XM_001715492 /// XM_001716174 /// XM_001717683
5.94	5.49	0.45	1.18E-01	4.76E-01	C11orf24	chromosome 11 open reading frame 24	chr11q13	52164_at	NM_022338
2.35	2.05	0.30	1.18E-01	4.76E-01	KIAA1377	KIAA1377	chr11q22.1	236325_at	NM_020802
8.38	7.97	0.41	1.18E-01	4.77E-01	BLCAP	bladder cancer associated protein	chr20q11.2-q12	201032_at	NM_006698
6.38	5.90	0.48	1.18E-01	4.77E-01	MYEF2	myelin expression factor 2	chr15q21.1	232676_x_at	NM_016132
2.22	2.03	0.19	1.19E-01	4.77E-01	BDNFOS	BDNF opposite strand (non-protein coding)	chr11p14.1	1567361_at	NR_002832
2.43	2.09	0.34	1.19E-01	4.77E-01	STAMBPL1	STAM binding protein-like 1	chr10q23.31	220803_at	NM_020799
6.33	6.05	0.28	1.19E-01	4.77E-01	FBXL11	F-box and leucine-rich repeat protein 11	chr11q13.1	208989_s_at	NM_012308
8.44	8.06	0.38	1.19E-01	4.77E-01	MRPL34	mitochondrial ribosomal protein L34	chr19p13.1	221692_s_at	NM_023937
8.01	7.55	0.46	1.19E-01	4.77E-01	CRTC3	CREB regulated transcription coactivator 3	chr15q26.1	218648_at	NM_001042574 /// NM_022769
7.28	6.89	0.39	1.19E-01	4.77E-01	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	chr13q34	218153_at	NM_024537
3.37	3.00	0.37	1.19E-01	4.77E-01	LOC388795	similar to hCG2019498	chr20q11.21	239729_at	XM_001720320 /// XM_371397 /// XM_936526
6.30	5.88	0.43	1.19E-01	4.77E-01	VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)	chr15q14-q15	223346_at	NM_020857
4.24	3.61	0.63	1.19E-01	4.77E-01	IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble	chr2q33.3	242001_at	NM_005896
4.28	4.03	0.26	1.19E-01	4.77E-01	TRIO	triple functional domain (PTPRF interacting)	chr5p15.2	208178_x_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929

2.76	2.41	0.36	1.19E-01	4.77E-01	LIG4	ligase IV, DNA, ATP-dependent	chr13q33-q34	227766_at	NM_001098268 /// NM_002312 /// NM_206937
3.02	2.62	0.39	1.19E-01	4.77E-01	SIRT4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	chr12q	220047_at	NM_012240
7.82	7.35	0.47	1.19E-01	4.77E-01	PHF10	PHD finger protein 10	chr6q27	219126_at	NM_018288 /// NM_133325
9.03	8.75	0.29	1.19E-01	4.77E-01	LOC649299 /// RPL36A	similar to mCG7611 /// ribosomal protein L36a	chr19p12 /// chrXq22.1	217256_x_at	NM_021029 /// XM_001128478 /// XM_001714884 /// XM_001719759
6.48	6.15	0.32	1.19E-01	4.77E-01	LOC90110	hypothetical protein LOC90110	chr17q21.2	226842_at	---
6.34	6.03	0.30	1.19E-01	4.77E-01	PGCP	plasma glutamate carboxypeptidase	chr8q22.2	208454_s_at	NM_016134
7.84	7.46	0.37	1.19E-01	4.77E-01	SNX5	sorting nexin 5	chr20p11	217792_at	NM_014426 /// NM_152227
5.33	4.41	0.92	1.19E-01	4.77E-01	HOXB3	homeobox B3	chr17q21.3	228904_at	NM_002146
5.54	5.07	0.47	1.19E-01	4.77E-01	UBTF	upstream binding transcription factor, RNA polymerase I	chr17q21.3	1558215_s_at	NM_001076683 /// NM_001076684 /// NM_014233
6.97	6.77	0.20	1.19E-01	4.77E-01	SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	chr19q13	201480_s_at	NM_001111020 /// NM_001130824 /// NM_001130825 /// NM_003169
3.95	3.59	0.37	1.19E-01	4.78E-01	C9orf66	chromosome 9 open reading frame 66	chr9p24.3	1552755_at	NM_152569
6.35	5.72	0.62	1.19E-01	4.78E-01	NR5A1	nuclear receptor subfamily 5, group A, member 1	chr9q33	210333_at	NM_004959
8.41	7.93	0.48	1.19E-01	4.78E-01	HIST3H2A	histone cluster 3, H2a	chr1q42.13	221582_at	NM_033445
6.77	6.45	0.31	1.19E-01	4.78E-01	XPO6	exportin 6	chr16p11.2	214784_x_at	NM_015171
5.39	4.74	0.65	1.19E-01	4.78E-01	ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	---	228255_at	NM_001044385 /// NM_152388
7.09	6.85	0.24	1.19E-01	4.78E-01	NOLA2	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs)	chr5q35.3	216583_x_at	NM_001034833 /// NM_017838
2.05	1.86	0.19	1.19E-01	4.78E-01	RBM46	RNA binding motif protein 46	chr4q32.1	242516_x_at	NM_144979
2.70	2.48	0.22	1.19E-01	4.78E-01	---	---	---	1560661_x_at	---
6.79	6.23	0.56	1.19E-01	4.78E-01	LST1	leukocyte specific transcript 1	chr6p21.3	214574_x_at	NM_007161 /// NM_205837 /// NM_205838 /// NM_205839 /// NM_205840
3.64	3.20	0.43	1.19E-01	4.78E-01	---	---	---	235102_x_at	---
3.27	2.71	0.56	1.19E-01	4.78E-01	FGFR1OP2	FGFR1 oncogene partner 2	chr12p11.23	236808_at	NM_015633
7.99	7.75	0.24	1.19E-01	4.78E-01	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	chr13q31.2-q32.3	208854_s_at	NM_001032296 /// NM_003576
7.56	6.77	0.79	1.19E-01	4.78E-01	MOXD1	monooxygenase, DBH-like 1	chr6q23.1-q23.3	1554474_a_at	NM_015529
2.76	2.59	0.17	1.19E-01	4.78E-01	C17orf51	chromosome 17 open reading frame 51	chr17p11.2	238166_s_at	NM_001113434 /// XM_001725854 /// XM_378661 /// XM_944416
4.43	3.82	0.60	1.19E-01	4.78E-01	TRIM73	tripartite motif-containing 73	chr7q11.23	1554250_s_at	NM_198924
2.58	2.33	0.25	1.19E-01	4.78E-01	LOC100131998	Hypothetical protein LOC100131998	chr16p12.1	238413_at	XM_001725049
2.79	2.59	0.21	1.19E-01	4.78E-01	CDH8	cadherin 8, type 2	chr16q22.1	210518_at	NM_001796
2.59	2.34	0.25	1.19E-01	4.78E-01	RPL35A	ribosomal protein L35a	chr3q29-qter	215249_at	NM_000996
8.85	8.44	0.41	1.19E-01	4.78E-01	MSRB2	methionine sulfoxide reductase B2	chr10p12	218773_s_at	NM_012228

8.38	7.91	0.47	1.19E-01	4.78E-01	PTS	6-pyruvoyltetrahydropterin synthase	chr11q22.3-q23.3	209694_at	NM_000317																			
4.78	4.43	0.35	1.19E-01	4.78E-01	ACTL6A	actin-like 6A	chr3q26.33	202666_s_at	NM_004301 /// NM_177989 /// NM_178042																			
7.88	7.60	0.28	1.19E-01	4.78E-01	FAM168B	family with sequence similarity 168, member B	chr2q21.1	212017_at	NM_001009993																			
7.05	6.70	0.35	1.19E-01	4.78E-01	KIAA1267	KIAA1267	chr17q21.31	225117_at	NM_015443																			
10.54	10.13	0.42	1.19E-01	4.78E-01	ASS1	argininosuccinate synthetase 1	chr9q34.1	207076_s_at	NM_000050 /// NM_054012																			
12.27	12.09	0.18	1.20E-01	4.78E-01	RPS17	ribosomal protein S17	chr15q	212578_x_at	NM_001021																			
5.02	4.63	0.39	1.20E-01	4.78E-01	RAD1	RAD1 homolog (S. pombe)	chr5p13.2	235253_at	NM_002853 /// NM_133377																			
5.47	4.97	0.50	1.20E-01	4.78E-01	MIF4GD	MIF4G domain containing	chr17q25.1	231727_s_at	NM_020679																			
6.85	6.07	0.78	1.20E-01	4.78E-01	ASTN1	astrotactin 1	chr1q25.2	213197_at	NM_004319 /// NM_207108																			
3.82	3.44	0.38	1.20E-01	4.78E-01	---	---	---	226964_at	---																			
2.74	2.47	0.27	1.20E-01	4.78E-01	CROCCL2	ciliary rootlet coiled-coil, rootletin-like 2	chr1p36.13	219139_s_at	NR_023386 /// XM_001129099 /// XM_001130544 /// XM_001714120																			
8.23	7.83	0.40	1.20E-01	4.78E-01	PMPCA	peptidase (mitochondrial processing) alpha	chr9q34.3	212088_at	NM_015160																			
7.75	7.37	0.38	1.20E-01	4.78E-01	SHISA5	shisa homolog 5 (Xenopus laevis)	chr3p21.31	222986_s_at	NM_016479																			
6.35	5.99	0.36	1.20E-01	4.78E-01	LOC100129250	similar to hCG1811779	chr9p21.1	221979_at	XM_001722063 /// XM_001723459 /// XM_001725563																			
3.48	3.24	0.23	1.20E-01	4.79E-01	PCSK7	Proprotein convertase subtilisin/kexin type 7	chr11q23-q24	232521_at	NM_004716																			
5.48	4.67	0.81	1.20E-01	4.79E-01	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	chr6q23	202643_s_at	NM_006290																			
6.35	6.08	0.27	1.20E-01	4.79E-01	MPZL1	myelin protein zero-like 1	chr1q24.2	201875_s_at	NM_003953 /// NM_024569																			
7.76	7.44	0.32	1.20E-01	4.79E-01	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	chr1pter-q24	202297_s_at	NM_007033																			
2.81	2.56	0.25	1.20E-01	4.79E-01	---	---	---	244815_at	---																			
3.80	3.61	0.20	1.20E-01	4.79E-01	FOXN4	forkhead box N4	chr12q24.11	1562695_at	NM_213596																			
7.11	6.59	0.52	1.20E-01	4.79E-01	EHMT2	euchromatic histone-lysine N-methyltransferase 2	chr6p21.31	202326_at	NM_006709 /// NM_025256																			
7.63	7.32	0.30	1.20E-01	4.80E-01	TCTN3	tectonic family member 3	chr10q23.33	212121_at	NM_015631																			
2.76	2.49	0.27	1.21E-01	4.80E-01	KCNK13	potassium channel, subfamily K, member 13	chr14q31-q32	221325_at	NM_022054																			
6.32	5.69	0.64	1.21E-01	4.80E-01	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	chr21q22.12	212944_at	NM_006933																			
7.41	6.86	0.55	1.21E-01	4.80E-01	GLUL	glutamate-ammonia ligase (glutamine synthetase)	chr1q31	200648_s_at	NM_001033044 /// NM_001033056 /// NM_002065																			
2.35	2.14	0.21	1.21E-01	4.80E-01	ARF1	ADP-ribosylation factor 1	chr1q42	1565650_at	NM_001024226 /// NM_001024227 /// NM_001024228 /// NM_001658																			
2.61	2.42	0.19	1.21E-01	4.80E-01	MAG	malignancy-associated gene	chr19q13.1	217102_at	---																			
2.64	2.41	0.23	1.21E-01	4.80E-01	---	---	---	242636_at	---																			
3.56	3.25	0.31	1.21E-01	4.80E-01	FLT4	fms-related tyrosine kinase 4	chr5q35.3	229902_at	NM_002020 /// NM_182925																			
4.93	4.55	0.38	1.21E-01	4.80E-01	ASB1	ankyrin repeat and SOCS box-containing 1	chr2q37	212818_s_at	NM_001040445																			
5.14	4.74	0.39	1.21E-01	4.80E-01	SNAPC4	small nuclear RNA activating complex, polypeptide 4, 190kDa	chr9q34.3	215926_x_at	NM_003086																			

7.84	7.51	0.32	1.21E-01	4.80E-01	SLC41A3	solute carrier family 41, member 3	chr3q21.2	219175_s_at	NM_001008485 /// NM_001008486 /// NM_001008487 /// NM_017836																			
3.77	3.16	0.60	1.21E-01	4.80E-01	SCYL1BP1	SCY1-like 1 binding protein 1	chr1q24.2	226337_at	NM_152281																			
7.82	6.95	0.86	1.21E-01	4.80E-01	HIST1H4J	histone cluster 1, H4j	chr6p22-p21.3	214463_x_at	NM_021968																			
4.99	4.59	0.40	1.21E-01	4.80E-01	NDE1	NudE nuclear distribution gene E homolog 1 (A. nidulans)	chr16p13.11	227249_at	NM_017668																			
2.73	2.50	0.23	1.21E-01	4.80E-01	---	---	---	231206_at	---																			
3.71	3.16	0.55	1.21E-01	4.80E-01	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	chr2p16.1	219497_s_at	NM_018014 /// NM_022893 /// NM_138559																			
5.86	5.33	0.53	1.21E-01	4.80E-01	PITPNM1	phosphatidylinositol transfer protein, membrane-associated 1	chr11q13	203826_s_at	NM_001130848 /// NM_004910																			
4.00	3.53	0.47	1.21E-01	4.80E-01	ZNF641	zinc finger protein 641	chr12q13.11	1554958_at	NM_152320																			
6.37	5.91	0.46	1.21E-01	4.81E-01	SFXN5	sideroflexin 5	---	226373_at	NM_144579																			
2.95	2.68	0.27	1.21E-01	4.81E-01	OR52D1	olfactory receptor, family 52, subfamily D, member 1	chr11p15.4	234617_at	NM_001005163																			
2.87	2.61	0.26	1.21E-01	4.81E-01	ABLIM2	Actin binding LIM protein family, member 2	chr4p16-p15	1567623_at	NM_001130083 /// NM_001130084 /// NM_001130085 /// NM_001130086 /// NM_001130087 /// NM_001130088 /// NM_032432																			
4.90	4.65	0.25	1.21E-01	4.81E-01	ZKSCAN2	zinc finger with KRAB and SCAN domains 2	chr16p12.1	232019_at	NM_001012981																			
8.58	8.21	0.38	1.21E-01	4.81E-01	MESDC2	mesoderm development candidate 2	chr15q13	224675_at	NM_015154																			
6.48	6.12	0.36	1.21E-01	4.81E-01	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	chr2q35-q36	216883_x_at	NM_002601																			
2.37	2.12	0.24	1.21E-01	4.81E-01	NHLRC2	NHL repeat containing 2	chr10q25.3	235356_at	NM_198514																			
8.77	8.33	0.43	1.21E-01	4.81E-01	GLRX	glutaredoxin (thioltransferase)	chr5q14	209276_s_at	NM_001118890 /// NM_002064																			
6.38	5.98	0.40	1.22E-01	4.81E-01	---	---	---	213074_at	---																			
9.85	9.55	0.30	1.22E-01	4.81E-01	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	chr17q12	201400_at	NM_002795																			
4.33	3.89	0.44	1.22E-01	4.81E-01	NEDD1	neural precursor cell expressed, developmentally down-regulated 1	chr12q23.1	234984_at	NM_152905																			
5.29	4.85	0.44	1.22E-01	4.81E-01	CLNS1A	Chloride channel, nucleotide-sensitive, 1A	chr11q13.5-q14	242492_at	NM_001293																			
5.12	4.76	0.37	1.22E-01	4.81E-01	MYO1D	myosin ID	chr17q11-q12	212338_at	NM_015194																			
6.52	5.83	0.69	1.22E-01	4.81E-01	SS18	synovial sarcoma translocation, chromosome 18	chr18q11.2	202817_s_at	NM_001007559 /// NM_005637																			
6.77	6.32	0.45	1.22E-01	4.81E-01	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	chr17q21.33	201474_s_at	NM_002204 /// NM_005501																			
7.71	7.41	0.30	1.22E-01	4.81E-01	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	chrXp22.2-p22.1	200980_s_at	NM_000284																			
2.56	2.32	0.24	1.22E-01	4.81E-01	SLC44A5	solute carrier family 44, member 5	chr1p31.1	1552779_a_at	NM_001130058 /// NM_152697																			
3.30	3.10	0.21	1.22E-01	4.81E-01	PRKCE	protein kinase C, epsilon	chr2p21	206248_at	NM_005400																			
5.50	5.00	0.49	1.22E-01	4.81E-01	TRIM14	tripartite motif-containing 14	chr9q22.33	203148_s_at	NM_014788 /// NM_033219 /// NM_033220 /// NM_033221																			
9.75	9.32	0.43	1.22E-01	4.81E-01	BST2	bone marrow stromal cell antigen 2	chr19p13.2	201641_at	NM_004335																			
7.66	7.27	0.39	1.22E-01	4.81E-01	SNAP23	synaptosomal-associated protein, 23kDa	chr15q15.1	209130_at	NM_003825 /// NM_130798																			
2.89	2.65	0.24	1.22E-01	4.81E-01	LOC196913	hypothetical protein LOC196913	chr14q22.1	1564785_at	NM_001014830																			

8.82	8.40	0.42	1.22E-01	4.81E-01	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	chr1q24	201243_s_at	NM_001001787 /// NM_001677
2.40	2.21	0.19	1.22E-01	4.81E-01	MYH4	myosin, heavy chain 4, skeletal muscle	chr17p13.1	208148_at	NM_017533
2.89	2.61	0.28	1.22E-01	4.81E-01	---	---	---	236086_at	---
7.49	7.22	0.26	1.22E-01	4.81E-01	MKRN1	makorin ring finger protein 1	chr7q34	201285_at	NM_013446
7.06	6.85	0.21	1.22E-01	4.81E-01	C1orf31	chromosome 1 open reading frame 31	chr1q42.2	225638_at	NM_001012985
6.63	6.38	0.25	1.22E-01	4.81E-01	FAM136A	family with sequence similarity 136, member A	chr2p14	215947_s_at	NM_032822
7.55	7.31	0.24	1.22E-01	4.81E-01	PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	chr2p23.3	200913_at	NM_002707 /// NM_177983
6.60	6.11	0.49	1.22E-01	4.81E-01	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	chr16q22.1	238554_at	NM_030579
11.70	10.94	0.76	1.22E-01	4.81E-01	NOV	nephroblastoma overexpressed gene	chr8q24.1	204501_at	NM_002514
8.79	8.49	0.30	1.22E-01	4.81E-01	GYG1	glycogenin 1	chr3q24-q25.1	211275_s_at	NM_004130
6.32	5.92	0.40	1.22E-01	4.81E-01	COBRA1	cofactor of BRCA1	chr9q34	202757_at	NM_015456
3.26	2.71	0.55	1.22E-01	4.81E-01	CNOT3	CCR4-NOT transcription complex, subunit 3	chr19q13.4	229143_at	NM_014516
4.68	4.36	0.32	1.22E-01	4.81E-01	CXYorf2	chromosome X and Y open reading frame 2	chrXp22.33; Yp11.3	1552873_s_at	XR_040863 /// XR_040864
6.64	6.21	0.42	1.22E-01	4.81E-01	POMGNT1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	chr1p34.1	217944_at	NM_017739
7.30	6.95	0.36	1.22E-01	4.82E-01	SYPL1	synaptophysin-like 1	chr7q22.2	201260_s_at	NM_006754 /// NM_182715
11.42	10.72	0.70	1.22E-01	4.82E-01	RHOB	ras homolog gene family, member B	chr2p24	212099_at	NM_004040
4.04	3.04	0.99	1.22E-01	4.82E-01	CRHBP	corticotropin releasing hormone binding protein	chr5q11.2-q13.3	205984_at	NM_001882
6.11	5.70	0.41	1.23E-01	4.82E-01	---	---	---	239128_at	---
7.58	7.04	0.53	1.23E-01	4.82E-01	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	chr6p25	212268_at	NM_030666
10.11	9.84	0.28	1.23E-01	4.82E-01	EIF3G	eukaryotic translation initiation factor 3, subunit G	chr19p13.2	208887_at	NM_003755
2.84	2.55	0.29	1.23E-01	4.82E-01	---	---	---	240421_x_at	---
2.78	2.52	0.27	1.23E-01	4.82E-01	PRKCB	Protein kinase C, beta	chr16p11.2	230437_s_at	NM_002738 /// NM_212535
4.32	3.98	0.34	1.23E-01	4.82E-01	TPCN1	two pore segment channel 1	chr12q24.13	1557185_at	NM_017901
9.14	8.86	0.28	1.23E-01	4.82E-01	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	chr17q25	200656_s_at	NM_000918
3.46	3.11	0.35	1.23E-01	4.82E-01	TSC2	tuberous sclerosis 2	chr16p13.3	215624_at	NM_000548 /// NM_001077183 /// NM_001114382
2.50	2.32	0.18	1.23E-01	4.82E-01	---	---	---	243535_at	---
3.57	3.35	0.23	1.23E-01	4.82E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	233781_s_at	NM_018151
8.34	7.99	0.34	1.23E-01	4.82E-01	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	chr12q12-q14	214096_s_at	NM_005412
6.36	6.04	0.32	1.23E-01	4.82E-01	C19orf12	chromosome 19 open reading frame 12	chr19q12	225863_s_at	NM_001031726 /// NM_031448
7.07	6.81	0.26	1.23E-01	4.82E-01	NUDT3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	chr6p21.2	221579_s_at	NM_006703
3.96	3.51	0.45	1.23E-01	4.82E-01	PRC1	protein regulator of cytokinesis 1	chr15q26.1	218009_s_at	NM_003981 /// NM_199413 /// NM_199414
2.87	2.58	0.29	1.23E-01	4.82E-01	---	---	---	227452_at	---
4.27	3.73	0.53	1.23E-01	4.82E-01	GNAS	GNAS complex locus	chr20q13.3	214157_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259
6.48	6.14	0.34	1.23E-01	4.82E-01	PEX26	peroxisomal biogenesis factor 26	chr22q11.21	219180_s_at	NM_001127649 /// NM_017929
4.96	4.74	0.21	1.23E-01	4.82E-01	---	---	---	228110_x_at	---

4.51	3.85	0.66	1.23E-01	4.82E-01	SOD2	superoxide dismutase 2, mitochondrial	chr6q25.3	216841_s_at	NM_000636 /// NM_001024465 /// NM_001024466
2.12	1.86	0.26	1.23E-01	4.82E-01	CHD2	Chromodomain helicase DNA binding protein 2	chr15q26	226830_x_at	NM_001042572 /// NM_001271
2.23	2.02	0.21	1.23E-01	4.82E-01	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	chr2q33.3	1555113_at	NM_057177 /// NM_152526 /// NM_205863
7.39	6.94	0.45	1.23E-01	4.82E-01	CDK5	cyclin-dependent kinase 5	chr7q36	204247_s_at	NM_004935
10.78	10.60	0.18	1.23E-01	4.82E-01	CCDC72	coiled-coil domain containing 72	chr3p21.31	221791_s_at	NM_015933
6.93	6.55	0.38	1.23E-01	4.82E-01	CPSF4	cleavage and polyadenylation specific factor 4, 30kDa	chr7q22.1	206688_s_at	NM_001081559 /// NM_006693
7.70	7.41	0.29	1.23E-01	4.82E-01	ODC1	ornithine decarboxylase 1	chr2p25	200790_at	NM_002539
4.50	3.64	0.86	1.23E-01	4.83E-01	SPATA13	Spermatogenesis associated 13	chr13q12.12	1556601_a_at	NM_153023
8.11	7.65	0.46	1.23E-01	4.83E-01	TMEM138	transmembrane protein 138	chr11q12.2	223113_at	NM_016464
3.07	2.83	0.24	1.24E-01	4.83E-01	H2AFJ	H2A histone family, member J	chr12p12	228213_at	NM_177925
7.75	6.04	1.71	1.24E-01	4.83E-01	NR4A3	nuclear receptor subfamily 4, group A, member 3	chr9q22	209959_at	NM_006981 /// NM_173198 /// NM_173199 /// NM_173200
8.57	8.29	0.28	1.24E-01	4.83E-01	CD47	CD47 molecule	chr3q13.1-q13.2	211075_s_at	NM_001025079 /// NM_001777 /// NM_198793
5.14	4.70	0.44	1.24E-01	4.83E-01	CBLN4	cerebellin 4 precursor	chr20q13.13-q13.33	234024_at	NM_080617
5.91	5.41	0.51	1.24E-01	4.83E-01	STAT5A	signal transducer and activator of transcription 5A	chr17q11.2	203010_at	NM_003152
7.05	6.61	0.44	1.24E-01	4.83E-01	MAPRE2	Microtubule-associated protein, RP/EB family, member 2	chr18q12.1	213489_at	NM_014268
6.87	6.57	0.30	1.24E-01	4.83E-01	EXOC3	exocyst complex component 3	chr5p15.33	212630_at	NM_007277
7.09	6.74	0.36	1.24E-01	4.83E-01	FAHD1	fumarylacetoacetate hydrolase domain containing 1	chr16p13.3	227960_s_at	NM_001018104 /// NM_031208
4.65	4.25	0.40	1.24E-01	4.84E-01	ZNF500	zinc finger protein 500	chr16p13.3	213639_s_at	NM_021646
4.38	3.89	0.49	1.24E-01	4.84E-01	IL20RA	interleukin 20 receptor, alpha	chr6q22.33-q23.1	219115_s_at	NM_014432
7.21	6.64	0.58	1.24E-01	4.84E-01	KCTD3	potassium channel tetramerisation domain containing 3	chr1q41	217894_at	NM_016121
2.77	2.56	0.20	1.24E-01	4.84E-01	LOC120376	Hypothetical protein LOC120376	chr11q23.1	242469_at	XM_001718669 /// XM_071712 /// XM_943506
5.44	4.50	0.95	1.24E-01	4.84E-01	PDE8B	phosphodiesterase 8B	chr5q14.1	213228_at	NM_001029851 /// NM_001029852 /// NM_001029853 /// NM_001029854 /// NM_003719
3.65	3.23	0.42	1.24E-01	4.84E-01	AKT2	V-akt murine thymoma viral oncogene homolog 2	chr19q13.1-q13.2	1560689_s_at	NM_001626
5.99	5.72	0.27	1.24E-01	4.84E-01	---	---	---	225750_at	---
5.02	4.77	0.25	1.24E-01	4.84E-01	---	---	---	1554597_at	---
8.27	7.97	0.29	1.24E-01	4.84E-01	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	chr16p12.3	227792_at	NM_001034841
2.60	2.41	0.20	1.24E-01	4.84E-01	ALS2CR10	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 10	chr2q33	1556924_at	---
6.23	5.87	0.36	1.24E-01	4.84E-01	LOC100131178 /// PQLC1	hypothetical protein LOC100131178 /// PQ loop repeat containing 1	chr18q23	218208_at	NM_025078 /// XM_001718060 /// XM_001721775 /// XM_001721798
2.07	1.91	0.16	1.24E-01	4.84E-01	---	---	---	1561053_at	---

9.61	9.32	0.29	1.24E-01	4.84E-01	POLR2J	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa	chr7q22.1	212782_x_at	NM_006234																				
5.79	5.41	0.38	1.24E-01	4.84E-01	ZFAND2B	zinc finger, AN1-type domain 2B	chr2q35	226168_at	NM_138802																				
4.99	4.79	0.19	1.24E-01	4.84E-01	SSH3	slingshot homolog 3 (Drosophila)	chr11q13.1	219919_s_at	NM_017857																				
2.12	1.92	0.20	1.24E-01	4.84E-01	ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	chr22q13.1	1559072_a_at	NM_052906																				
3.37	2.99	0.37	1.24E-01	4.84E-01	C21orf66	chromosome 21 open reading frame 66	chr21q21.3	221158_at	NM_013329 /// NM_016631 /// NM_058191																				
3.76	3.37	0.39	1.25E-01	4.85E-01	C18orf1	chromosome 18 open reading frame 1	chr18p11.2	209574_s_at	NM_001003674 /// NM_001003675 /// NM_004338 /// NM_181481 /// NM_181482 /// NM_181483																				
6.83	6.09	0.74	1.25E-01	4.85E-01	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	chr15q21.1	216733_s_at	NM_001482																				
6.30	5.90	0.39	1.25E-01	4.85E-01	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	chr7q22	90610_at	NM_002319																				
5.71	5.49	0.22	1.25E-01	4.85E-01	C1orf69	chromosome 1 open reading frame 69	chr1q42.13	231983_at	NM_001010867																				
3.46	3.09	0.37	1.25E-01	4.85E-01	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	chr17p12-p11.2	213889_at	NM_004278																				
6.40	6.12	0.28	1.25E-01	4.85E-01	NAP1L4	nucleosome assembly protein 1-like 4	chr11p15.5	1560339_s_at	NM_005969																				
7.50	6.75	0.75	1.25E-01	4.85E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	212063_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392																				
2.69	2.38	0.31	1.25E-01	4.85E-01	PABPC1L	poly(A) binding protein, cytoplasmic 1-like	---	231838_at	NM_001124756 /// XM_001130728 /// XM_001131956 /// XM_001722078																				
3.51	2.87	0.63	1.25E-01	4.85E-01	ADAMTSL1	ADAMTS-like 1	chr9p22.2-p22.1	1552457_a_at	NM_001040272 /// NM_052866																				
2.50	2.30	0.21	1.25E-01	4.85E-01	FAM122C	family with sequence similarity 122C	chrXq26.3	1552323_s_at	NM_138819																				
6.37	5.82	0.55	1.25E-01	4.85E-01	ENSA	endosulfine alpha	chr1q21.2	221487_s_at	NM_004436 /// NM_207042 /// NM_207043 /// NM_207044 /// NM_207045 /// NM_207046 /// NM_207047 /// NM_207168																				
5.85	5.54	0.31	1.25E-01	4.86E-01	HDAC8	histone deacetylase 8	chrXq13	223909_s_at	NM_018486																				
2.40	2.20	0.20	1.25E-01	4.86E-01	---	---	---	243384_at	---																				
6.93	6.48	0.45	1.25E-01	4.86E-01	NR2F1	Nuclear receptor subfamily 2, group F, member 1	chr5q14	209505_at	NM_005654																				
6.92	6.50	0.42	1.25E-01	4.86E-01	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1	chr3q21	229164_s_at	NM_032548 /// NM_172027 /// NM_172028																				
2.23	2.00	0.23	1.25E-01	4.86E-01	GLCCI1	Glucocorticoid induced transcript 1	chr7p21.3	1560315_at	NM_138426																				

2.81	2.63	0.18	1.25E-01	4.86E-01	ITGA9	integrin, alpha 9	chr3p21.3	1555335_at	NM_002207																				
6.46	5.94	0.52	1.25E-01	4.86E-01	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	chr12q13.12	224872_at	NM_173602																				
2.89	2.64	0.25	1.25E-01	4.86E-01	LOC284998	hypothetical protein LOC284998	chr2q12.1	239879_at	XM_001719992 /// XM_498907 /// XM_944715																				
2.59	2.37	0.22	1.25E-01	4.86E-01	GAL	galanin prepropeptide	chr11q13.2	214240_at	NM_015973																				
8.27	8.02	0.26	1.25E-01	4.86E-01	HAGH	hydroxyacylglutathione hydrolase	chr16p13.3	205012_s_at	NM_001040427 /// NM_005326																				
5.72	5.45	0.27	1.25E-01	4.86E-01	MYBBP1A	MYB binding protein (P160) 1a	chr17p13.3	219098_at	NM_001105538 /// NM_014520																				
5.01	4.64	0.37	1.25E-01	4.86E-01	TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	chr6p21.31	209358_at	NM_005643																				
5.94	5.49	0.45	1.26E-01	4.86E-01	SF4	splicing factor 4	chr19p13.11	215004_s_at	NM_172231																				
3.52	3.19	0.32	1.26E-01	4.86E-01	AIFM3	apoptosis-inducing factor, mitochondrion-associated, 3	chr22q11.21	244084_at	NM_001018060 /// NM_144704																				
7.23	6.35	0.88	1.26E-01	4.87E-01	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	chr6p21.3	211656_x_at	NM_002123 /// XM_001722253 /// XM_001723447																				
3.82	3.40	0.42	1.26E-01	4.87E-01	LOC100128309	hypothetical protein LOC100128309	chr10q23.2	232300_at	XM_001716892 /// XM_001717579																				
4.85	4.57	0.29	1.26E-01	4.87E-01	IDS	iduronate 2-sulfatase	chrXq28	217432_s_at	NM_000202 /// NM_006123																				
6.44	5.96	0.48	1.26E-01	4.87E-01	CDK9	cyclin-dependent kinase 9	chr9q34.1	203198_at	NM_001261																				
4.98	4.52	0.45	1.26E-01	4.87E-01	BCOR	BCL6 co-repressor	chrXp21.2-p11.4	223915_at	NM_001123383 /// NM_001123384 /// NM_001123385 /// NM_001130139 /// NM_017745 /// NM_020926																				
2.30	2.12	0.18	1.26E-01	4.87E-01	---	---	---	231506_at	---																				
3.81	3.50	0.31	1.26E-01	4.87E-01	WDR4	WD repeat domain 4	chr21q22.3	226882_x_at	NM_018669 /// NM_033661																				
7.92	7.16	0.76	1.26E-01	4.87E-01	KLF6	Kruppel-like factor 6	chr10p15	1555832_s_at	NM_001300																				
3.38	3.20	0.17	1.26E-01	4.87E-01	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	chr10q	217500_at	NM_001033925 /// NM_003252																				
3.04	2.71	0.32	1.26E-01	4.87E-01	LOC728054	hypothetical LOC728054	chr16q24.3	234664_at	XM_001718812 /// XM_001718858																				
4.48	4.12	0.37	1.26E-01	4.87E-01	STAG3L1	stromal antigen 3-like 1	chr7q11.23-q21.1	221191_at	NM_001002840 /// NM_018991 /// XM_001720660																				
7.30	6.96	0.34	1.26E-01	4.87E-01	FLII	flightless I homolog (Drosophila)	chr17p11.2	222065_s_at	NM_002018																				
3.86	3.63	0.24	1.26E-01	4.87E-01	SPINT1	Serine peptidase inhibitor, Kunitz type 1	chr15q15.1	235546_at	NM_001032367 /// NM_003710 /// NM_181642																				
3.01	2.68	0.33	1.26E-01	4.87E-01	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	chr20q11.2	220668_s_at	NM_006892 /// NM_175848 /// NM_175849 /// NM_175850																				

6.39	5.99	0.39	1.26E-01	4.87E-01	SH2B3	SH2B adaptor protein 3	chr12q24	203320_at	NM_005475
4.98	4.65	0.33	1.26E-01	4.87E-01	SLC35D2	solute carrier family 35, member D2	chr9q22.32	213083_at	NM_007001
2.94	2.65	0.29	1.26E-01	4.87E-01	FBXO41	F-box protein 41	chr2p13.2	221945_at	NM_001080410
6.84	6.33	0.50	1.26E-01	4.87E-01	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	chr5q33.1	225007_at	NM_005754 /// NM_198395
2.59	2.37	0.21	1.26E-01	4.87E-01	CNTF /// ZFP91 /// ZFP91-CNTF	ciliary neurotrophic factor /// zinc finger protein 91 homolog (mouse) /// ZFP91-CNTF	chr11q12 /// chr11q12.2	208597_at	NM_000614 /// NM_053023 /// NM_170768 /// NR_024091
3.20	2.81	0.39	1.26E-01	4.87E-01	NRL	neural retina leucine zipper	chr14q11.1-q11.2	206596_s_at	NM_006177
6.64	6.20	0.44	1.26E-01	4.87E-01	DFNB31	deafness, autosomal recessive 31	chr9q32-q34	221887_s_at	NM_001083885 /// NM_015404
5.12	4.63	0.49	1.26E-01	4.87E-01	TMEM38A	transmembrane protein 38A	chr19p13.11	222896_at	NM_024074
6.66	6.36	0.31	1.26E-01	4.87E-01	MAST2	microtubule associated serine/threonine kinase 2	chr1p34.1	215903_s_at	NM_015112
2.90	2.65	0.25	1.27E-01	4.87E-01	NKAIN4	Na+/K+ transporting ATPase interacting 4	chr20q13.33	228018_at	NM_152864
4.57	4.28	0.30	1.27E-01	4.87E-01	---	---	---	1568616_a_at	---
3.94	3.59	0.35	1.27E-01	4.87E-01	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	chr6p24-p22.3	204512_at	NM_002114
4.94	4.56	0.38	1.27E-01	4.87E-01	ZNF765	zinc finger protein 765	chr19q13.41	1558943_x_at	NM_001040185
3.37	3.13	0.24	1.27E-01	4.88E-01	TRIM10	tripartite motif-containing 10	chr6p21.3	56748_at	NM_006778 /// NM_052828
3.81	3.55	0.25	1.27E-01	4.88E-01	LOC100133039	hypothetical protein LOC100133039	chr3p25.2	1560141_at	XM_001720775
4.69	4.37	0.32	1.27E-01	4.88E-01	C2orf49	chromosome 2 open reading frame 49	chr2q12.2	219662_at	NM_024093
2.58	2.36	0.21	1.27E-01	4.88E-01	---	---	---	1557513_a_at	---
2.68	2.48	0.21	1.27E-01	4.88E-01	HHIPL2	HHIP-like 2	chr1q41	220283_at	NM_024746
4.97	4.47	0.49	1.27E-01	4.88E-01	TRIT1	tRNA isopentenyltransferase 1	chr1p35.3-p34.1	218617_at	NM_017646
7.69	7.24	0.45	1.27E-01	4.88E-01	LOC730052 /// RNPEP /// TMEM189 /// TMEM189-UBE2V1 /// UBE2V1	similar to ubiquitin-conjugating enzyme E2 /// arginyl aminopeptidase (aminopeptidase B) /// transmembrane protein 189 /// TMEM189-UBE2V1 /// ubiquitin-conjugating enzyme E2 variant 1	chr1q32 /// chr20q13.2 /// chr3q26.31	201003_x_at	NM_001032288 /// NM_003349 /// NM_020216 /// NM_021988 /// NM_022442 /// NM_199129 /// NM_199144 /// NM_199203 /// XR_016022 /// XR_016054 /// XR_038933
5.69	5.27	0.42	1.27E-01	4.88E-01	CENPB	centromere protein B, 80kDa	chr20p13	212437_at	NM_001810
3.26	2.90	0.36	1.27E-01	4.88E-01	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	chr19p13.1	216234_s_at	NM_002730 /// NM_207518
1.97	1.80	0.17	1.27E-01	4.88E-01	---	---	---	1566445_at	---
3.24	2.97	0.27	1.27E-01	4.88E-01	LOC100130519	Putative transmembrane protein ENSP00000342162	chr19p13.11	1559687_at	XM_001718752 /// XM_001719696
7.68	7.25	0.43	1.27E-01	4.88E-01	GOLGB1	golgin B1, golgi integral membrane protein	chr3q13	201057_s_at	NM_004487
4.51	4.12	0.39	1.27E-01	4.88E-01	KLF9	Kruppel-like factor 9	chr9q13	230636_s_at	NM_001206
4.71	4.37	0.34	1.27E-01	4.88E-01	DGCR8	DiGeorge syndrome critical region gene 8	chr22q11.2	91617_at	NM_022720
6.98	6.47	0.52	1.27E-01	4.88E-01	PTGFRN	prostaglandin F2 receptor negative regulator	chr1p13.1	224950_at	NM_020440
2.25	2.05	0.20	1.27E-01	4.88E-01	---	---	---	1563139_at	---
2.19	1.98	0.21	1.27E-01	4.88E-01	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	chr15q11-q12	241834_at	NR_023915
7.34	7.01	0.33	1.27E-01	4.88E-01	MRPL45	mitochondrial ribosomal protein L45	chr17q21.2	224479_s_at	NM_032351
2.47	2.22	0.24	1.27E-01	4.88E-01	HIST1H1T	histone cluster 1, H1t	chr6p21.3	1553568_a_at	NM_005323
2.56	2.18	0.38	1.27E-01	4.88E-01	MARS	methionyl-tRNA synthetase	chr12q13.2	213672_at	NM_004990
2.56	2.38	0.17	1.27E-01	4.88E-01	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	chr1p13-p12	240110_at	NM_005518
6.28	5.83	0.45	1.27E-01	4.89E-01	FGFR1OP2	FGFR1 oncogene partner 2	chr12p11.23	223262_s_at	NM_015633

3.60	3.29	0.32	1.27E-01	4.89E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	224065_at	NM_001113239 /// NM_022740																				
6.35	5.49	0.85	1.27E-01	4.89E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	204489_s_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392																				
3.07	2.76	0.32	1.27E-01	4.89E-01	EIF3K	eukaryotic translation initiation factor 3, subunit K	chr19q13.2	236605_at	NM_013234																				
6.09	5.59	0.50	1.27E-01	4.89E-01	PPARD	peroxisome proliferator-activated receptor delta	chr6p21.2-p21.1	37152_at	NM_006238																				
6.50	6.16	0.34	1.27E-01	4.89E-01	ISOC2	isochorismatase domain containing 2	chr19q13.42	218893_at	NM_024710																				
2.36	2.06	0.31	1.27E-01	4.89E-01	LOC647070	hypothetical LOC647070	chr1q25.3	215468_at	XR_041237 /// XR_041238 /// XR_041239																				
4.84	4.48	0.36	1.27E-01	4.89E-01	FARP2	FERM, RhoGEF and pleckstrin domain protein 2	chr2q37.3	204511_at	NM_014808																				
4.93	4.42	0.51	1.28E-01	4.89E-01	ZNF592	zinc finger protein 592	chr15q25.3	204473_s_at	NM_014630																				
6.82	6.46	0.35	1.28E-01	4.89E-01	C18orf55	chromosome 18 open reading frame 55	chr18q22.3	223180_s_at	NM_014177																				
5.96	5.55	0.41	1.28E-01	4.89E-01	SYNGR1	synaptogyrin 1	chr22q13.1	204287_at	NM_004711 /// NM_145731 /// NM_145738																				
5.44	4.97	0.47	1.28E-01	4.89E-01	ARHGAP30	Rho GTPase activating protein 30	chr1q23.3	226219_at	NM_001025598 /// NM_181720																				
7.28	6.83	0.45	1.28E-01	4.89E-01	GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	chr22q13.31	218114_at	NM_001001560 /// NM_001001561 /// NM_013365																				
5.64	5.22	0.42	1.28E-01	4.89E-01	PHYHD1	phytanoyl-CoA dioxygenase domain containing 1	chr9q34.11	226846_at	NM_001100876 /// NM_001100877 /// NM_174933																				
4.79	4.54	0.25	1.28E-01	4.89E-01	RBMX2	RNA binding motif protein, X-linked 2	chrXq25	204098_at	NM_016024																				
7.28	6.86	0.42	1.28E-01	4.89E-01	ANKRD9	ankyrin repeat domain 9	chr14q32.31	230972_at	NM_152326																				
8.42	7.86	0.56	1.28E-01	4.89E-01	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	chr4q13-q21	209067_s_at	NM_031372 /// NR_003249																				
2.53	2.32	0.20	1.28E-01	4.89E-01	CRYBA4	crystallin, beta A4	chr22q11.2-q13.1|22q12.1	206843_at	NM_001886																				
5.87	5.42	0.44	1.28E-01	4.89E-01	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	chr22q12	204153_s_at	NM_002405																				
5.18	4.82	0.36	1.28E-01	4.89E-01	ABHD8	abhydrolase domain containing 8	chr19p13.11	219101_x_at	NM_024527																				
8.47	7.98	0.49	1.28E-01	4.89E-01	SERP1	stress-associated endoplasmic reticulum protein 1	chr3q25.1	200969_at	NM_014445																				
2.84	2.56	0.28	1.28E-01	4.89E-01	C11orf45	chromosome 11 open reading frame 45	chr11q24.3	1553787_at	NM_145013																				
6.69	6.28	0.41	1.28E-01	4.89E-01	BBS1 /// DPP3	Bardet-Biedl syndrome 1 /// dipeptidyl-peptidase 3	chr11q12-q13.1 /// chr11q13.1	232510_s_at	NM_005700 /// NM_024649 /// NM_130443																				
8.47	8.13	0.34	1.28E-01	4.89E-01	HEXA	hexosaminidase A (alpha polypeptide)	chr15q23-q24	201765_s_at	NM_000520																				
2.43	2.25	0.17	1.28E-01	4.89E-01	---	---	---	217531_at	---																				
11.68	10.70	0.98	1.28E-01	4.89E-01	APOE	apolipoprotein E	chr19q13.2	203382_s_at	NM_000041																				
2.34	2.05	0.29	1.28E-01	4.89E-01	DST	dystonin	chr6p12.1	204455_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380																				
5.74	5.33	0.41	1.28E-01	4.89E-01	TNIP2	TNFAIP3 interacting protein 2	chr4p16.3	48531_at	NM_024309																				

2.32	2.12	0.20	1.28E-01	4.89E-01	LOC100130423 /// SUGT1L1	similar to SGT1, suppressor of G2 allele of SKP1 like 1 (S. cerevisiae) /// SGT1, suppressor of G2 allele of SKP1 like 1 (S. cerevisiae)	chr13q14.11	1554143_a_at	NR_003365 /// XM_001718775 /// XM_001721699 /// XM_001725074																			
5.09	4.86	0.23	1.28E-01	4.89E-01	ILF3	interleukin enhancer binding factor 3, 90kDa	chr19p13.2	208930_s_at	NM_004516 /// NM_012218 /// NM_153464																			
6.66	6.26	0.40	1.28E-01	4.89E-01	BAX	BCL2-associated X protein	chr19q13.3-q13.4	208478_s_at	NM_004324 /// NM_138761 /// NM_138763 /// NM_138764 /// NM_138765																			
9.92	9.56	0.36	1.28E-01	4.89E-01	CTSB	cathepsin B	chr8p22	200839_s_at	NM_001908 /// NM_147780 /// NM_147781 /// NM_147782 /// NM_147783																			
2.78	2.50	0.29	1.28E-01	4.89E-01	ART1	ADP-ribosyltransferase 1	chr11p15	1570480_s_at	NM_004314																			
5.46	5.05	0.42	1.28E-01	4.89E-01	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	chr22q13.31-q13.33	227910_at	NM_022098																			
2.65	2.40	0.24	1.28E-01	4.89E-01	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	chr1p36.1-p35	214166_at	NM_003000																			
3.96	3.63	0.33	1.28E-01	4.89E-01	CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	chr1p21	204029_at	NM_001408																			
2.61	2.29	0.31	1.28E-01	4.89E-01	PPARD	peroxisome proliferator-activated receptor delta	chr6p21.2-p21.1	242218_at	NM_006238																			
9.09	7.47	1.63	1.28E-01	4.89E-01	GSTT1	glutathione S-transferase theta 1	chr22q11.23	203815_at	NM_000853																			
2.40	2.16	0.24	1.28E-01	4.89E-01	OR5P2	olfactory receptor, family 5, subfamily P, member 2	chr11p15.4	1552991_at	NM_153444																			
6.16	5.61	0.55	1.29E-01	4.90E-01	FAM134A	family with sequence similarity 134, member A	chr2q35	221983_at	NM_024293																			
4.76	4.16	0.60	1.29E-01	4.90E-01	C6orf136	chromosome 6 open reading frame 136	chr6p21.33	227455_at	NM_001109938 /// NM_145029																			
8.34	8.13	0.21	1.29E-01	4.90E-01	CAMLG	calcium modulating ligand	chr5q23	203538_at	NM_001745																			
7.69	7.38	0.31	1.29E-01	4.90E-01	CLPP	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	chr19p13.3	202799_at	NM_006012																			
2.38	2.17	0.20	1.29E-01	4.90E-01	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B	chr12q23.1	240292_x_at	NM_020140 /// NM_152788 /// NM_181670																			
5.63	5.33	0.29	1.29E-01	4.90E-01	MEMO1	mediator of cell motility 1	chr2p22-p21	1555522_s_at	NM_015955																			
2.79	2.57	0.22	1.29E-01	4.90E-01	---	---	---	233935_at	---																			
5.43	4.90	0.53	1.29E-01	4.90E-01	MED30	mediator complex subunit 30	chr8q24.11	227787_s_at	NM_080651																			
4.76	4.04	0.72	1.29E-01	4.90E-01	---	---	---	1558105_a_at	---																			
1.92	1.76	0.16	1.29E-01	4.90E-01	ZNF750	zinc finger protein 750	chr17q25.3	219995_s_at	NM_024702																			
3.06	2.32	0.74	1.29E-01	4.90E-01	---	---	---	229787_s_at	---																			
8.72	8.20	0.52	1.29E-01	4.90E-01	41521	septin 4	chr17q22-q23	210657_s_at	NM_004574 /// NM_080415 /// NM_080416																			
5.60	4.91	0.69	1.29E-01	4.90E-01	ZNF836	zinc finger protein 836	chr19q13.33	1569077_x_at	NM_001102657																			

6.00	5.29	0.70	1.29E-01	4.90E-01	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	chr14q32.1	211429_s_at	NM_000295 /// NM_001002235 /// NM_001002236 /// NM_001127700 /// NM_001127701 /// NM_001127702 /// NM_001127703 /// NM_001127704 /// NM_001127705 /// NM_001127706 /// NM_001127707																				
2.14	1.94	0.20	1.29E-01	4.90E-01	---	---	---	1569486_at	---																				
5.57	4.95	0.62	1.29E-01	4.90E-01	LOC399959	hypothetical gene supported by BX647608	chr11q24.1	225381_at	---																				
5.30	4.78	0.52	1.29E-01	4.90E-01	MIS12	MIS12, MIND kinetochore complex component, homolog (yeast)	chr17p13.2	221559_s_at	NM_024039																				
5.00	4.54	0.46	1.29E-01	4.90E-01	---	---	---	234954_at	---																				
2.10	1.89	0.21	1.29E-01	4.90E-01	DOPEY1	dopey family member 1	chr6q15	213267_at	NM_015018																				
6.08	5.79	0.30	1.29E-01	4.90E-01	C9orf156	chromosome 9 open reading frame 156	chr9q22.33	222195_s_at	NM_016481																				
6.73	5.97	0.76	1.29E-01	4.91E-01	COTL1	coactosin-like 1 (Dictyostelium)	chr16q24.1	224583_at	NM_021149																				
3.51	3.27	0.24	1.29E-01	4.91E-01	---	---	---	236336_at	---																				
4.57	4.16	0.41	1.29E-01	4.91E-01	---	---	---	223409_at	---																				
6.96	6.37	0.59	1.29E-01	4.91E-01	EID1	EP300 interacting inhibitor of differentiation 1	chr15q21.1-q21.2	211698_at	NM_014335																				
2.54	2.33	0.20	1.29E-01	4.91E-01	CACNA1E	Calcium channel, voltage-dependent, R type, alpha 1E subunit	chr1q25-q31	240650_at	NM_000721																				
6.00	5.76	0.24	1.30E-01	4.91E-01	PRPSAP2	phosphoribosyl pyrophosphate synthetase-associated protein 2	chr17p11.2-p12	203537_at	NM_002767																				
3.92	3.42	0.50	1.30E-01	4.91E-01	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	chr10q24	215134_at	NM_018425																				
3.39	2.97	0.42	1.30E-01	4.91E-01	RUNX2	runt-related transcription factor 2	chr6p21	232231_at	NM_001015051 /// NM_001024630 /// NM_004348																				
3.26	2.98	0.28	1.30E-01	4.91E-01	NBEAL2	neurobeachin-like 2	chr3p21.31	1556017_at	NM_015175																				
6.38	5.98	0.39	1.30E-01	4.91E-01	GTPBP6	GTP binding protein 6 (putative)	chrXp22.33; Yp11.32	203314_at	NM_012227																				
5.65	5.16	0.49	1.30E-01	4.91E-01	CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9q34.3	212711_at	NM_015447																				
7.75	7.43	0.32	1.30E-01	4.91E-01	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	chr19p13.3	217854_s_at	NM_002695																				
4.91	4.49	0.42	1.30E-01	4.91E-01	LOC116236	hypothetical protein LOC116236	chr17q11.2	226796_at	NM_198147																				
10.85	10.55	0.30	1.30E-01	4.91E-01	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	chr12q24.1	209075_s_at	NM_014301 /// NM_213595																				
6.37	6.06	0.31	1.30E-01	4.91E-01	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	chr22q13.2	211754_s_at	NM_006358																				
4.09	3.75	0.34	1.30E-01	4.91E-01	FLJ35220	hypothetical protein FLJ35220	chr17q25.3	238401_at	NM_173627																				
3.63	3.33	0.30	1.30E-01	4.91E-01	HCG22	HLA complex group 22	chr6p21.33	1560767_at	NR_003948																				
3.89	3.52	0.36	1.30E-01	4.91E-01	SLC25A45	solute carrier family 25, member 45	chr11q13.1	236436_at	NM_001077241 /// NM_182556																				
5.35	4.90	0.45	1.30E-01	4.91E-01	SLC22A5	solute carrier family 22 (organic cation/carnitine transporter), member 5	chr5q31	205074_at	NM_003060																				
6.40	6.09	0.31	1.30E-01	4.91E-01	ARSD	arylsulfatase D	chrXp22.3	230131_x_at	NM_001669 /// NM_009589																				
2.33	2.14	0.20	1.30E-01	4.91E-01	RGS5	Regulator of G-protein signaling 5	chr1q23.1	230678_at	NM_003617																				
3.40	3.09	0.31	1.30E-01	4.91E-01	HOXB5	homeobox B5	chr17q21.3	205600_x_at	NM_002147																				
4.87	4.59	0.28	1.30E-01	4.91E-01	RND1	Rho family GTPase 1	chr12q12-q13	210056_at	NM_014470																				
3.08	2.25	0.83	1.30E-01	4.91E-01	NEFL	neurofilament, light polypeptide 68kDa	chr8p21	221805_at	NM_006158																				
7.61	7.33	0.28	1.30E-01	4.91E-01	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	chr16q13-q21	208996_s_at	NM_032940																				
6.00	5.16	0.84	1.30E-01	4.91E-01	TMEM163	transmembrane protein 163	chr2q21.3	223503_at	NM_030923																				
3.65	3.21	0.45	1.30E-01	4.91E-01	LOC387647	patched domain containing 3 pseudogene	chr10p11.23	230737_s_at	NR_003930																				
9.62	8.85	0.78	1.30E-01	4.91E-01	PTP4A1	protein tyrosine phosphatase type IVA, member 1	chr6q12	200732_s_at	NM_003463																				

4.80	4.36	0.45	1.30E-01	4.91E-01	LOC100129461	Hypothetical protein LOC100129461	chr6p25.1	1556555_at	XM_001719437 /// XM_001724530 /// XM_001725016																			
5.48	5.17	0.31	1.30E-01	4.91E-01	PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)	chr11q13	213384_x_at	NM_000932																			
3.60	3.25	0.36	1.30E-01	4.91E-01	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	chrXp11.23	218619_s_at	NM_003173																			
5.39	5.08	0.31	1.30E-01	4.91E-01	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	chr11q24	211304_x_at	NM_000890																			
2.92	2.64	0.28	1.30E-01	4.91E-01	---	---	---	217659_at	---																			
4.04	3.85	0.19	1.30E-01	4.91E-01	KIAA1731	KIAA1731	chr11q21	229878_at	NM_033395																			
7.93	7.54	0.38	1.30E-01	4.91E-01	SUMF2	sulfatase modifying factor 2	chr7q11.1	225002_s_at	NM_001042468 /// NM_001042469 /// NM_001042470 /// NM_001130069 /// NM_001130070 /// NM_015411																			
2.64	2.35	0.29	1.30E-01	4.91E-01	NSUN7	NOL1/NOP2/Sun domain family, member 7	chr4p14	238983_at	NM_024677																			
3.86	3.64	0.22	1.31E-01	4.92E-01	CCDC123	coiled-coil domain containing 123	chr19q13.11	1553732_s_at	NM_032816																			
2.69	2.38	0.31	1.31E-01	4.92E-01	PLD1	phospholipase D1, phosphatidylcholine-specific	chr3q26	215724_at	NM_001130081 /// NM_002662																			
6.07	5.70	0.36	1.31E-01	4.92E-01	THOC2	THO complex 2	chrXq25-q26.3	226626_at	NM_001081550 /// NM_020449																			
7.27	6.84	0.43	1.31E-01	4.92E-01	SFRS11	splicing factor, arginine/serine-rich 11	chr1p31	200686_s_at	NM_004768																			
3.53	3.28	0.24	1.31E-01	4.92E-01	LOC81691	exonuclease NEF-sp	chr16p12.2	208107_s_at	NM_030941																			
7.43	7.11	0.32	1.31E-01	4.92E-01	ZNF652	Zinc finger protein 652	chr17q21.32	225266_at	NM_014897																			
7.70	7.45	0.25	1.31E-01	4.92E-01	SNX1	sorting nexin 1	chr15q22.31	201716_at	NM_003099 /// NM_148955 /// NM_152826																			
5.58	5.06	0.52	1.31E-01	4.93E-01	PPM1M	protein phosphatase 1M (PP2C domain containing)	chr3p21.1	226074_at	NM_001122870 /// NM_144641																			
6.50	5.91	0.59	1.31E-01	4.93E-01	MOSPD1	motile sperm domain containing 1	chrXq26.3	218853_s_at	NM_019556																			
7.49	7.15	0.34	1.31E-01	4.93E-01	LOC729926	similar to rCG45476	chr19p12	234875_at	XR_015934 /// XR_016046 /// XR_038426																			
2.87	2.61	0.27	1.31E-01	4.93E-01	---	---	---	1564155_x_at	---																			
4.96	4.51	0.45	1.31E-01	4.93E-01	PEX10	peroxisomal biogenesis factor 10	chr1p36.32	206351_s_at	NM_002617 /// NM_153818																			
7.83	7.33	0.50	1.31E-01	4.93E-01	CTBP1	C-terminal binding protein 1	chr4p16	213980_s_at	NM_001012614 /// NM_001328																			
8.03	7.01	1.02	1.31E-01	4.93E-01	CLDN1	claudin 1	chr3q28-q29	222549_at	NM_021101																			
2.74	2.47	0.27	1.31E-01	4.93E-01	TSNARE1	t-SNARE domain containing 1	chr8q24.3	1552799_at	NM_145003																			
7.95	7.75	0.20	1.31E-01	4.93E-01	LCMT1	leucine carboxyl methyltransferase 1	chr16p12.3-p12.1	221515_s_at	NM_001032391 /// NM_016309																			
6.36	6.01	0.36	1.31E-01	4.93E-01	GAB2	GRB2-associated binding protein 2	chr11q14.1	203853_s_at	NM_012296 /// NM_080491																			
5.65	5.29	0.36	1.31E-01	4.93E-01	RUNDC1	RUN domain containing 1	chr17q21.31	226298_at	NM_173079																			
2.64	2.30	0.34	1.31E-01	4.93E-01	NDP	Norrie disease (pseudoglioma)	chrXp11.4	206022_at	NM_000266																			
2.96	2.78	0.19	1.31E-01	4.93E-01	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	chr14q21-q22	205909_at	NM_002692																			
3.20	2.83	0.37	1.31E-01	4.93E-01	USP37	ubiquitin specific peptidase 37	chr2q35	226730_s_at	NM_020935																			
3.21	2.86	0.35	1.31E-01	4.93E-01	---	---	---	226900_at	---																			
6.78	6.24	0.54	1.31E-01	4.93E-01	SNHG7	small nucleolar RNA host gene 7 (non-protein coding)	chr9q34.3	229050_s_at	NR_003672																			
7.11	6.65	0.46	1.31E-01	4.93E-01	KLF10	Kruppel-like factor 10	chr8q22.2	202393_s_at	NM_001032282 /// NM_005655																			
4.07	3.77	0.30	1.32E-01	4.93E-01	---	---	---	238758_at	---																			
4.57	4.37	0.20	1.32E-01	4.93E-01	UNC45A	unc-45 homolog A (C. elegans)	chr15q26.1	207499_x_at	NM_001039675 /// NM_018671																			
6.71	6.52	0.19	1.32E-01	4.94E-01	SNF1LK2	SNF1-like kinase 2	chr11q23.1	213221_s_at	NM_015191																			

4.38	3.65	0.73	1.32E-01	4.94E-01	C2orf49	chromosome 2 open reading frame 49	chr2q12.2	226951_at	NM_024093																			
7.02	6.66	0.35	1.32E-01	4.94E-01	LGALS9	lectin, galactoside-binding, soluble, 9	chr17q11.1	203236_s_at	NM_002308 /// NM_009587 /// NR_024043																			
8.96	8.59	0.37	1.32E-01	4.94E-01	BTF3	basic transcription factor 3	chr5q13.2	214800_x_at	NM_001037637 /// NM_001207																			
6.51	6.04	0.48	1.32E-01	4.94E-01	ATF1	activating transcription factor 1	chr12q13	222103_at	NM_005171																			
8.09	7.84	0.25	1.32E-01	4.94E-01	PQBP1	polyglutamine binding protein 1	chrXp11.23	207769_s_at	NM_001032381 /// NM_001032382 /// NM_001032383 /// NM_001032384 /// NM_005710																			
2.38	2.19	0.19	1.32E-01	4.94E-01	C5orf51	chromosome 5 open reading frame 51	chr5p13.1	238809_at	NM_175921																			
8.34	8.08	0.25	1.32E-01	4.94E-01	NGRN	neugrin, neurite outgrowth associated	chr15q26.1	224281_s_at	NM_001033088 /// NM_016645																			
3.15	2.83	0.32	1.32E-01	4.94E-01	---	---	---	1556138_a_at	---																			
6.12	5.64	0.48	1.32E-01	4.94E-01	B9D1	B9 protein domain 1	chr17p11.2	210534_s_at	NM_015681																			
7.64	7.41	0.23	1.32E-01	4.94E-01	FAM44B	family with sequence similarity 44, member B	chr5q35.2	225030_at	NM_138369																			
5.04	4.73	0.31	1.32E-01	4.94E-01	BGLAP /// PMF1	bone gamma-carboxyglutamate (gla) protein /// polyamine-modulated factor 1	chr1q12 /// chr1q25-q31	206956_at	NM_007221 /// NM_199173																			
2.55	2.18	0.37	1.32E-01	4.94E-01	TC2N	tandem C2 domains, nuclear	chr14q32.12	234970_at	NM_001128595 /// NM_001128596 /// NM_152332																			
2.35	2.17	0.18	1.32E-01	4.94E-01	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2	chr3q26.1-q26.2	207636_at	NM_006217																			
2.21	2.05	0.16	1.32E-01	4.94E-01	---	---	---	240894_at	---																			
6.36	6.01	0.34	1.32E-01	4.94E-01	EIF4ENIF1	eukaryotic translation initiation factor 4E nuclear import factor 1	chr22q11.2	218626_at	NM_019843																			
6.92	6.49	0.44	1.32E-01	4.94E-01	MYADM	myeloid-associated differentiation marker	chr19q13.41	225673_at	NM_001020818 /// NM_001020819 /// NM_001020820 /// NM_001020821 /// NM_138373																			
5.55	5.14	0.41	1.32E-01	4.94E-01	ZCCHC11	zinc finger, CCHC domain containing 11	chr1p32.3	212704_at	NM_001009881 /// NM_001009882 /// NM_015269																			
8.01	7.68	0.32	1.32E-01	4.94E-01	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	chr1q23.3	215088_s_at	NM_001035511 /// NM_001035512 /// NM_001035513 /// NM_003001																			
10.90	10.66	0.24	1.32E-01	4.94E-01	HYPK /// SERF2	Huntingtin interacting protein K /// small EDRK-rich factor 2	chr15q15.3	217756_x_at	NM_001018108 /// NM_016400																			
6.49	6.14	0.34	1.32E-01	4.94E-01	ZGPAT	zinc finger, CCCH-type with G patch domain	chr20q13.3	57539_at	NM_001083113 /// NM_032527 /// NM_181485																			
3.72	3.40	0.32	1.32E-01	4.94E-01	LOC729839	hypothetical LOC729839	chr17q12	236692_at	XR_016021 /// XR_016053 /// XR_037215																			
2.56	2.36	0.21	1.32E-01	4.94E-01	---	---	---	231362_at	---																			

3.83	3.59	0.24	1.33E-01	4.95E-01	MOBKL2C	MOB1, Mps One Binder kinase activator-like 2C (yeast)	chr1p33	243052_at	NM_145279 /// NM_201403																				
2.11	1.95	0.16	1.33E-01	4.95E-01	---	---	---	244785_at	---																				
5.94	5.17	0.77	1.33E-01	4.95E-01	MED17	mediator complex subunit 17	chr11q14	221517_s_at	NM_004268																				
7.69	7.36	0.33	1.33E-01	4.95E-01	JAM3 /// LOC100133502	junctional adhesion molecule 3 /// hypothetical protein LOC100133502	chr11q25	212813_at	NM_032801 /// XM_001726649																				
4.24	3.73	0.51	1.33E-01	4.95E-01	MITD1	MIT, microtubule interacting and transport, domain containing 1	chr2q11.2	226329_s_at	NM_138798																				
2.34	2.12	0.22	1.33E-01	4.95E-01	KLHL6	kelch-like 6 (Drosophila)	---	1560396_at	NM_130446																				
1.91	1.76	0.15	1.33E-01	4.95E-01	---	---	---	242090_x_at	---																				
2.18	1.98	0.21	1.33E-01	4.95E-01	NBPF8	neuroblastoma breakpoint family, member 8	chr1q21.1	237917_at	XM_001717802 /// XM_001726946																				
2.17	1.92	0.25	1.33E-01	4.95E-01	---	---	---	1561511_at	---																				
7.29	6.83	0.47	1.33E-01	4.95E-01	ASB13	ankyrin repeat and SOCS box-containing 13	chr10p15.1	218862_at	NM_024701																				
3.88	3.14	0.73	1.33E-01	4.95E-01	PDE8B	phosphodiesterase 8B	chr5q14.1	1554789_a_at	NM_001029851 /// NM_001029852 /// NM_001029853 /// NM_001029854 /// NM_003719																				
7.49	7.25	0.24	1.33E-01	4.95E-01	BUD31	BUD31 homolog (S. cerevisiae)	chr7q22.1	205690_s_at	NM_003910																				
5.45	4.63	0.82	1.33E-01	4.95E-01	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	chr11p15	210971_s_at	NM_001030272 /// NM_001030273 /// NM_001178																				
3.28	2.96	0.32	1.33E-01	4.95E-01	LOC400713	zinc finger-like	chr19q13.33	235913_at	XR_039381 /// XR_039390 /// XR_039621																				
4.88	4.46	0.42	1.33E-01	4.95E-01	---	---	---	1557300_s_at	---																				
6.27	5.72	0.56	1.33E-01	4.95E-01	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	chr10q22	210110_x_at	NM_012207 /// NM_021644																				
5.73	5.29	0.44	1.33E-01	4.95E-01	CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9q34.3	212712_at	NM_015447																				
3.20	2.95	0.25	1.33E-01	4.96E-01	---	---	---	1570221_at	---																				
3.73	3.47	0.27	1.33E-01	4.96E-01	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	chr14q12	210277_at	NM_001128126 /// NM_007077																				
5.49	5.06	0.43	1.33E-01	4.96E-01	C14orf167	chromosome 14 open reading frame 167	chr14q11.2-q21.3	227446_s_at	NR_023921 /// NR_023922 /// NR_023923 /// NR_023924																				
8.79	8.49	0.31	1.33E-01	4.96E-01	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	chr14q11.2	200014_s_at	NM_001077442 /// NM_001077443 /// NM_004500 /// NM_031314																				
6.77	6.40	0.37	1.33E-01	4.96E-01	MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)	chr22q13.31	213132_s_at	NM_014507 /// NM_173467																				
8.02	7.64	0.38	1.33E-01	4.96E-01	TXNDC15	thioredoxin domain containing 15	chr5q31.1	220495_s_at	NM_024715																				
5.92	5.52	0.41	1.33E-01	4.96E-01	WHSC2	Wolf-Hirschhorn syndrome candidate 2	chr4p16.3	34225_at	NM_005663																				
4.00	3.80	0.20	1.33E-01	4.96E-01	CCDC57	coiled-coil domain containing 57	chr17q25.3	214818_at	NM_198082																				
2.26	2.04	0.22	1.34E-01	4.96E-01	---	---	---	215601_at	---																				
5.67	5.36	0.31	1.34E-01	4.96E-01	C12orf47	chromosome 12 open reading frame 47	chr12q24.12	1553987_at	NR_015404 /// XR_017874 /// XR_017973																				
3.63	3.11	0.52	1.34E-01	4.96E-01	USP49	ubiquitin specific peptidase 49	chr6p21	229351_at	NM_018561																				
7.31	6.59	0.72	1.34E-01	4.96E-01	GLIPR1	GLI pathogenesis-related 1	chr12q21.2	204222_s_at	NM_006851																				

2.72	2.29	0.43	1.34E-01	4.96E-01	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	chr2p16.1	222270_at	NM_001122964 /// NM_020463
6.45	5.93	0.52	1.34E-01	4.96E-01	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	chr14q22.3	225643_at	NM_144578
5.15	4.55	0.60	1.34E-01	4.96E-01	TMEM194A	transmembrane protein 194A	chr12q13.3	212621_at	NM_001130963 /// NM_015257
3.62	3.35	0.27	1.34E-01	4.97E-01	WDR27	WD repeat domain 27	chr6q27	228326_at	NM_182552
5.53	4.92	0.61	1.34E-01	4.97E-01	GPX8	glutathione peroxidase 8	chr5q11.2	227628_at	NM_001008397
2.37	2.06	0.31	1.34E-01	4.97E-01	ABHD13	abhydrolase domain containing 13	chr13q33.3	235348_at	NM_032859
2.97	2.55	0.42	1.34E-01	4.97E-01	CA4	carbonic anhydrase IV	chr17q23	206209_s_at	NM_000717
4.22	3.76	0.46	1.34E-01	4.97E-01	HEXA	Hexosaminidase A (alpha polypeptide)	chr15q23-q24	215155_at	NM_000520
7.60	7.29	0.31	1.34E-01	4.97E-01	AIP	aryl hydrocarbon receptor interacting protein	chr11q13.3	201782_s_at	NM_003977
6.72	6.16	0.56	1.34E-01	4.97E-01	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	chr10q22	210588_x_at	NM_012207 /// NM_021644
9.29	9.07	0.22	1.34E-01	4.97E-01	EDF1	endothelial differentiation-related factor 1	chr9q34.3	209059_s_at	NM_003792 /// NM_153200
6.85	6.50	0.35	1.34E-01	4.97E-01	C11orf17	chromosome 11 open reading frame 17	chr11p15.3	219953_s_at	NM_020642 /// NM_182901
2.36	2.15	0.21	1.34E-01	4.97E-01	HIST1H3D	histone cluster 1, H3d	chr6p21.3	214472_at	NM_003530
7.02	6.71	0.31	1.34E-01	4.97E-01	FEM1A	fem-1 homolog a (C. elegans)	chr19p13.3	223175_s_at	NM_018708
5.36	5.01	0.35	1.34E-01	4.97E-01	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	chr10q24.1	216913_s_at	NM_015179
3.63	3.31	0.32	1.34E-01	4.97E-01	ABBA-1	actin-bundling protein with BAIAP2 homology	chr16q22.1	1555894_s_at	NM_138383
5.38	4.60	0.78	1.34E-01	4.97E-01	NOPE	neighbor of Punc E11	chr15q22.31	227870_at	NM_020962
9.39	9.05	0.34	1.34E-01	4.98E-01	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	chr19q13.3	1555575_a_at	NM_006801
3.78	3.23	0.55	1.34E-01	4.98E-01	ZNF567	zinc finger protein 567	chr19q13.12	235648_at	NM_152603
6.56	6.18	0.37	1.34E-01	4.98E-01	MPHOSPH8	M-phase phosphoprotein 8	chr13q12.11	227026_at	NM_017520
6.25	5.74	0.51	1.34E-01	4.98E-01	GAS7	growth arrest-specific 7	chr17p13.1	202192_s_at	NM_001130831 /// NM_003644 /// NM_201432 /// NM_201433
4.52	4.28	0.24	1.35E-01	4.98E-01	---	---	---	215557_at	---
4.02	3.72	0.30	1.35E-01	4.98E-01	SLC8A3	solute carrier family 8 (sodium/calcium exchanger), member 3	chr14q24.1	1568859_a_at	NM_001130417 /// NM_033262 /// NM_058240 /// NM_182932 /// NM_182936 /// NM_183002
4.37	3.84	0.53	1.35E-01	4.98E-01	ICK	intestinal cell (MAK-like) kinase	chr6p12.3-p11.2	204569_at	NM_014920 /// NM_016513
7.64	7.24	0.40	1.35E-01	4.98E-01	IL13RA1	interleukin 13 receptor, alpha 1	chrXq24	201887_at	NM_001560
2.18	2.01	0.16	1.35E-01	4.98E-01	---	---	---	237814_at	---
6.63	6.31	0.31	1.35E-01	4.98E-01	FLII	flightless I homolog (Drosophila)	chr17p11.2	212025_s_at	NM_002018
5.02	4.63	0.39	1.35E-01	4.98E-01	PHLPPL	PH domain and leucine rich repeat protein phosphatase-like	chr16q22.3	213407_at	NM_015020
2.25	2.03	0.22	1.35E-01	4.98E-01	---	---	---	1556166_x_at	---
3.12	2.90	0.22	1.35E-01	4.98E-01	TEP1	telomerase-associated protein 1	chr14q11.2	205727_at	NM_007110
3.64	2.42	1.22	1.35E-01	4.98E-01	7A5	putative binding protein 7a5	chr7p15.3	1566764_at	NM_182762
5.71	4.50	1.22	1.35E-01	4.98E-01	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	chr6p21.3	213831_at	NM_002122 /// XM_001722240 /// XM_001723439
7.18	6.81	0.37	1.35E-01	4.98E-01	CTDSP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	chr2q35	217844_at	NM_021198 /// NM_182642
2.28	2.08	0.20	1.35E-01	4.98E-01	IQSEC3 /// LOC100134209 /// LOC731035	IQ motif and Sec7 domain 3 /// similar to IQ motif and Sec7 domain-containing protein 3 /// similar to IQ motif and Sec7 domain 3	chr12p13.33	242694_at	NM_015232 /// XM_001126365 /// XM_001720539
5.85	5.48	0.37	1.35E-01	4.98E-01	ZNF576	zinc finger protein 576	chr19q13.31	219088_s_at	NM_024327

5.86	5.43	0.42	1.35E-01	4.99E-01	FAM152B	family with sequence similarity 152, member B	chr22q13.2	212527_at	NM_015704
4.32	3.45	0.87	1.35E-01	4.99E-01	PGM2L1	phosphoglucomutase 2-like 1	chr11q13.4	229553_at	NM_173582
2.13	1.93	0.20	1.35E-01	4.99E-01	---	---	---	1556492_a_at	---
2.17	1.98	0.19	1.35E-01	4.99E-01	SAMD5	sterile alpha motif domain containing 5	chr6q24.3	1569433_at	NM_001030060
6.77	6.31	0.46	1.35E-01	4.99E-01	DGCR2	DiGeorge syndrome critical region gene 2	chr22q11.21	214198_s_at	NM_005137
2.46	2.22	0.25	1.35E-01	4.99E-01	ZNF587	zinc finger protein 587	chr19q13.43	231820_x_at	NM_032828
4.54	4.14	0.41	1.35E-01	4.99E-01	LOC253842 /// NR6A1	hypothetical protein LOC253842 /// nuclear receptor subfamily 6, group A, member 1	chr9q33-q34.1 /// chr9q34.11	228894_at	NM_001489 /// NM_033334
2.52	2.28	0.24	1.35E-01	4.99E-01	---	---	---	1566623_at	---
5.91	5.37	0.54	1.35E-01	4.99E-01	GIMAP6	GTPase, IMAP family member 6	---	229367_s_at	NM_001007224 /// NM_024711 /// NR_024115
2.30	2.11	0.18	1.35E-01	4.99E-01	RABEPK	Rab9 effector protein with kelch motifs	chr9q33.3	1558021_at	NM_005833
6.21	5.86	0.35	1.35E-01	4.99E-01	BCL7B	B-cell CLL/lymphoma 7B	chr7q11.23	202518_at	NM_001707
2.23	2.02	0.21	1.35E-01	4.99E-01	LOC100132051	Hypothetical protein LOC100132051	chr8p21.1	1557791_at	XM_001723429 /// XM_001723755 /// XM_001724287
2.50	2.29	0.21	1.36E-01	4.99E-01	METTL6	Methyltransferase like 6	chr3p24.3	232102_at	NM_152396
2.96	2.67	0.29	1.36E-01	4.99E-01	PCNX	pecanex homolog (Drosophila)	chr14q24.2	238792_at	NM_014982
4.92	4.39	0.53	1.36E-01	4.99E-01	SUDS3	suppressor of defective silencing 3 homolog (S. cerevisiae)	chr12q24.23	224974_at	NM_022491
4.14	3.77	0.38	1.36E-01	4.99E-01	LOC257152	hypothetical protein LOC257152	chr8q22.3	215302_at	---
2.55	2.36	0.18	1.36E-01	4.99E-01	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	chr10q21-q24	207818_s_at	NM_000872 /// NM_019859 /// NM_019860
3.65	3.18	0.47	1.36E-01	4.99E-01	RABL4	RAB, member of RAS oncogene family-like 4	chr22q13.1	213784_at	NM_006860
4.71	4.36	0.35	1.36E-01	4.99E-01	SIAH1	seven in absentia homolog 1 (Drosophila)	chr16q12	202980_s_at	NM_001006610 /// NM_003031
7.89	6.61	1.28	1.36E-01	4.99E-01	HLA-DQA1 /// HLA-DQA2	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2	chr6p21.3	212671_s_at	NM_002122 /// NM_020056 /// XM_001722240 /// XM_001723439
6.14	5.72	0.41	1.36E-01	4.99E-01	---	---	---	234983_at	---
5.05	4.71	0.34	1.36E-01	4.99E-01	FAM165B	family with sequence similarity 165, member B	chr21q22.12	1554430_at	NM_058182
8.71	8.11	0.60	1.36E-01	4.99E-01	PDGFC	platelet derived growth factor C	chr4q32	218718_at	NM_016205
5.57	5.30	0.27	1.36E-01	4.99E-01	C19orf61	chromosome 19 open reading frame 61	chr19q13.31	223188_at	NM_019108
4.41	4.13	0.28	1.36E-01	4.99E-01	---	---	---	1556242_a_at	---
9.44	8.79	0.65	1.36E-01	4.99E-01	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	chr6p21.3	211991_s_at	NM_033554
6.06	5.55	0.51	1.36E-01	4.99E-01	FRAG1	FGF receptor activating protein 1	chr11p15.5	41858_at	NM_014489
4.25	3.94	0.31	1.36E-01	4.99E-01	---	---	---	216650_at	---
3.15	2.89	0.26	1.36E-01	4.99E-01	---	---	---	1567591_at	---
2.47	2.27	0.20	1.36E-01	4.99E-01	---	---	---	238403_at	---
2.39	2.05	0.34	1.36E-01	4.99E-01	N4BP2L2	NEDD4 binding protein 2-like 2	chr13q13.1	235547_at	NM_014887 /// NM_033111
8.01	7.66	0.35	1.36E-01	4.99E-01	ALKBH5	alkB, alkylation repair homolog 5 (E. coli)	chr17p11.2	234302_s_at	NM_017758
3.74	3.39	0.36	1.36E-01	5.00E-01	SERHL /// SERHL2	serine hydrolase-like /// serine hydrolase-like 2	chr22q13 /// chr22q13.2-q13.31	217284_x_at	NM_014509 /// NM_170694 /// XM_001719595
9.43	9.14	0.29	1.36E-01	5.00E-01	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	chr2p21	201256_at	NM_004718
7.03	6.45	0.58	1.37E-01	5.00E-01	ASCC1	activating signal cointegrator 1 complex subunit 1	chr10pter-q25.3	1554627_a_at	NM_015947
8.20	7.93	0.27	1.37E-01	5.00E-01	HP1BP3	heterochromatin protein 1, binding protein 3	chr1p36.12	224592_x_at	NM_016287
3.54	3.17	0.37	1.37E-01	5.00E-01	ENO3	enolase 3 (beta, muscle)	chr17pter-p11	204483_at	NM_001976 /// NM_053013
2.59	2.37	0.22	1.37E-01	5.00E-01	FGF20	fibroblast growth factor 20	chr8p22-p21.3	220394_at	NM_019851
3.37	3.07	0.29	1.37E-01	5.00E-01	TTLL3	tubulin tyrosine ligase-like family, member 3	chr3p25.3	1555474_at	NM_001025930 /// NM_015644
7.24	6.93	0.32	1.37E-01	5.00E-01	RPA3	replication protein A3, 14kDa	chr7p22	209507_at	NM_002947

5.81	5.28	0.52	1.37E-01	5.00E-01	C4orf32	chromosome 4 open reading frame 32	chr4q25	227856_at	NM_152400
2.25	2.05	0.19	1.37E-01	5.00E-01	---	---	---	1559695_a_at	---
2.65	2.45	0.21	1.37E-01	5.00E-01	BAG4	BCL2-associated athanogene 4	chr8p12	219624_at	NM_004874
6.93	6.50	0.43	1.37E-01	5.00E-01	RNF40	ring finger protein 40	chr16p11.2-p11.1	206845_s_at	NM_014771
3.24	2.95	0.29	1.37E-01	5.01E-01	TREM1	triggering receptor expressed on myeloid cells 1	chr6p21.1	219434_at	NM_018643
7.64	7.31	0.33	1.37E-01	5.01E-01	ZFP36L2	zinc finger protein 36, C3H type-like 2	chr2p22.3-p21	201369_s_at	NM_006887
3.21	2.43	0.78	1.37E-01	5.01E-01	FGFR1OP2	FGFR1 oncogene partner 2	chr12p11.23	243619_at	NM_015633
3.20	2.87	0.33	1.37E-01	5.01E-01	SCARF1	scavenger receptor class F, member 1	chr17p13.3	1555021_a_at	NM_003693 /// NM_145349 /// NM_145350 /// NM_145351 /// NM_145352
3.47	2.98	0.49	1.37E-01	5.01E-01	FBXO41	F-box protein 41	chr2p13.2	44040_at	NM_001080410
6.11	5.59	0.51	1.37E-01	5.01E-01	HIP1R	huntingtin interacting protein 1 related	chr12q24	209558_s_at	NM_003959
6.54	6.05	0.49	1.37E-01	5.01E-01	LOC286167	hypothetical LOC286167	chr8q24.22	225033_at	---
4.50	4.15	0.35	1.37E-01	5.01E-01	TSPAN18	tetraspanin 18	chr11p11.2	228819_at	NM_001031730 /// NM_130783
7.56	7.25	0.31	1.37E-01	5.01E-01	MPDU1	mannose-P-dolichol utilization defect 1	chr17p13.1-p12	209208_at	NM_004870
3.48	3.22	0.26	1.37E-01	5.01E-01	RP11-216L13.5	MSFL2541	chr9q34.3	1569532_a_at	NM_203347
5.48	5.03	0.46	1.37E-01	5.01E-01	TRAM2	translocation associated membrane protein 2	chr6p21.1-p12	202369_s_at	NM_012288
3.91	3.45	0.46	1.37E-01	5.02E-01	VHL	von Hippel-Lindau tumor suppressor	chr3p26-p25	1559227_s_at	NM_000551 /// NM_198156
2.91	2.69	0.22	1.37E-01	5.02E-01	---	---	---	236170_x_at	---
4.82	4.40	0.42	1.38E-01	5.02E-01	IRF9 /// RNF31	interferon regulatory factor 9 /// ring finger protein 31	chr14q11.2	220788_s_at	NM_006084 /// NM_017999
2.47	2.25	0.21	1.38E-01	5.02E-01	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	chr10p11.23	243265_at	NM_000818 /// NM_001134366
8.00	7.69	0.31	1.38E-01	5.02E-01	GTF2A2	general transcription factor IIA, 2, 12kDa	chr15q22.2	202678_at	NM_004492
2.64	2.34	0.30	1.38E-01	5.02E-01	---	---	---	235236_at	---
6.17	5.72	0.45	1.38E-01	5.02E-01	RY1	putative nucleic acid binding protein RY-1	chr2p14	212438_at	NM_006857
9.74	9.12	0.62	1.38E-01	5.02E-01	TBX3	T-box 3	chr12q24.1	219682_s_at	NM_005996 /// NM_016569
8.15	7.83	0.32	1.38E-01	5.02E-01	MRPL37	mitochondrial ribosomal protein L37	chr1p32.1	222993_at	NM_016491
8.35	7.69	0.66	1.38E-01	5.02E-01	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	chr10q11.1	209687_at	NM_000609 /// NM_001033886 /// NM_199168
6.54	6.07	0.46	1.38E-01	5.02E-01	ACBD4	acyl-Coenzyme A binding domain containing 4	chr17q21.31	219413_at	NM_024722
3.86	3.61	0.25	1.38E-01	5.02E-01	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	chr22q13.31-q13.33	228820_at	NM_022098
5.72	5.37	0.35	1.38E-01	5.02E-01	CALR	calreticulin	chr19p13.3-p13.2	200935_at	NM_004343
6.18	5.77	0.41	1.38E-01	5.02E-01	PARP2	poly (ADP-ribose) polymerase 2	chr14q11.2-q12	214086_s_at	NM_001042618 /// NM_005484
5.72	5.03	0.69	1.38E-01	5.02E-01	---	---	---	232338_at	---
2.91	2.54	0.36	1.38E-01	5.02E-01	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	chr13q12.11-q12.3	227812_at	NM_018647 /// NM_148957
2.36	2.17	0.19	1.38E-01	5.02E-01	---	---	---	240695_at	---
5.90	5.44	0.46	1.38E-01	5.02E-01	TRMT12	tRNA methyltransferase 12 homolog (S. cerevisiae)	chr8q24.13	219299_at	NM_017956
3.00	2.73	0.27	1.38E-01	5.02E-01	IL9R /// LOC729486	interleukin 9 receptor /// similar to hCG1790853	chr16p13.3 /// chrXq28 and Yq12	208164_s_at	NM_002186 /// NM_176786 /// NR_024033 /// XR_042290 /// XR_042385 /// XR_042402
4.34	4.06	0.28	1.38E-01	5.02E-01	SLC7A6OS	solute carrier family 7, member 6 opposite strand	chr16q22.1	232057_at	NM_032178
7.77	7.47	0.30	1.38E-01	5.02E-01	RUVBL2	RuvB-like 2 (E. coli)	chr19q13.3	1559946_s_at	NM_006666
6.17	5.73	0.44	1.38E-01	5.02E-01	HMHA1	histocompatibility (minor) HA-1	chr19p13.3	212873_at	NM_012292

3.54	3.18	0.36	1.38E-01	5.02E-01	LRDD	leucine-rich repeats and death domain containing	chr11p15.5	221640_s_at	NM_018494 /// NM_145886 /// NM_145887																				
8.10	7.79	0.31	1.38E-01	5.02E-01	SNRPF	small nuclear ribonucleoprotein polypeptide F	chr12q22	203832_at	NM_003095																				
2.52	2.33	0.20	1.38E-01	5.03E-01	---	---	---	241521_at	---																				
5.56	5.22	0.34	1.38E-01	5.03E-01	---	---	---	229558_at	---																				
2.06	1.88	0.19	1.38E-01	5.03E-01	---	---	---	1561463_at	---																				
6.09	5.75	0.34	1.38E-01	5.03E-01	ARID1B /// LOC729446	AT rich interactive domain 1B (SWI1-like) /// hypothetical LOC729446	chr6q25.1	225181_at	NM_017519 /// NM_020732 /// NM_175863 /// XM_001133842																				
4.34	3.81	0.53	1.38E-01	5.03E-01	MIB1	mindbomb homolog 1 (Drosophila)	chr18q11.2	224725_at	NM_020774																				
5.23	4.49	0.75	1.38E-01	5.03E-01	ANO4	anoctamin 4	chr12q23.1-q23.2	229749_at	NM_178826																				
7.62	7.13	0.49	1.38E-01	5.03E-01	CRLS1	cardiolipin synthase 1	chr20p13-p12.3	225324_at	NM_001127458 /// NM_019095																				
3.46	2.81	0.65	1.38E-01	5.03E-01	---	---	---	236307_at	---																				
3.21	2.81	0.40	1.39E-01	5.03E-01	MCTP2	multiple C2 domains, transmembrane 2	chr15q26.2	220603_s_at	NM_018349																				
6.04	5.64	0.40	1.39E-01	5.03E-01	NOL7	nucleolar protein 7, 27kDa	chr6p23	213838_at	NM_016167																				
7.64	7.28	0.36	1.39E-01	5.03E-01	SP1	Sp1 transcription factor	chr12q13.1	224754_at	NM_138473																				
6.86	6.41	0.45	1.39E-01	5.03E-01	SLC25A29	solute carrier family 25, member 29	chr14q32.2	225305_at	NM_001039355																				
4.11	3.54	0.57	1.39E-01	5.04E-01	THUMPD2	THUMP domain containing 2	chr2p22.1|2p22-p21	219248_at	NM_025264																				
2.65	2.33	0.32	1.39E-01	5.04E-01	---	---	---	230315_at	---																				
6.27	5.93	0.34	1.39E-01	5.04E-01	LUC7L2	LUC7-like 2 (S. cerevisiae)	chr7q34	220099_s_at	NM_016019																				
2.17	2.01	0.16	1.39E-01	5.04E-01	C11orf41	chromosome 11 open reading frame 41	chr11p13	214772_at	NM_012194																				
6.37	6.11	0.26	1.39E-01	5.04E-01	VPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)	chr20p13-p12	203459_s_at	NM_022575 /// NM_080413 /// NM_080414																				
4.57	4.33	0.25	1.39E-01	5.04E-01	LPCAT3	Lysophosphatidylcholine acyltransferase 3	chr12p13	213615_at	NM_005768																				
4.68	4.43	0.25	1.39E-01	5.04E-01	PVR	poliovirus receptor	chr19q13.2	32699_s_at	NM_006505																				

5.65	4.92	0.73	1.39E-01	5.04E-01	SNRPN	Small nuclear ribonucleoprotein polypeptide N	chr15q11.2	228370_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																					
4.68	4.46	0.22	1.39E-01	5.04E-01	SPTAN1	Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	chr9q33-q34	241150_at	NM_001130438 /// NM_003127																			
4.13	3.61	0.53	1.39E-01	5.04E-01	RGS16	regulator of G-protein signaling 16	chr1q25-q31	209324_s_at	NM_002928																			
2.82	2.60	0.22	1.39E-01	5.04E-01	---	---	---	1566040_at	---																			
5.79	4.78	1.00	1.39E-01	5.04E-01	RORA	RAR-related orphan receptor A	chr15q21-q22	210479_s_at	NM_002943 /// NM_134260 /// NM_134261 /// NM_134262																			
4.39	4.16	0.22	1.39E-01	5.04E-01	VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)	chr15q14-q15	1552276_a_at	NM_020857																			
3.82	3.41	0.41	1.39E-01	5.04E-01	DEFB106A /// DEFB106B	defensin, beta 106A /// defensin, beta 106B	chr8p23.1	1552411_at	NM_001040704 /// NM_152251																			
6.02	5.55	0.47	1.39E-01	5.04E-01	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	chr2p24.3-p11.2	222056_s_at	NM_016044																			
2.94	2.59	0.35	1.39E-01	5.04E-01	SLMO1	slowmo homolog 1 (Drosophila)	chr18p11.21	206273_at	NM_006553																			
6.51	5.47	1.04	1.39E-01	5.04E-01	SPP1	secreted phosphoprotein 1	chr4q21-q25	209875_s_at	NM_000582 /// NM_001040058 /// NM_001040060																			
3.34	2.99	0.35	1.39E-01	5.04E-01	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	chr12q24.31	1552924_a_at	NM_020845																			
5.71	5.40	0.31	1.39E-01	5.04E-01	ZNF576	zinc finger protein 576	chr19q13.31	219089_s_at	NM_024327																			

4.96	4.63	0.33	1.39E-01	5.04E-01	LRP4	low density lipoprotein receptor-related protein 4	chr11p11.2-p12	212850_s_at	NM_002334
6.90	5.89	1.00	1.39E-01	5.04E-01	APCDD1	adenomatosis polyposis coli down-regulated 1	chr18p11.22	225016_at	NM_153000
7.30	6.71	0.60	1.40E-01	5.05E-01	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	chr21q22.3	1555349_a_at	NM_000211 /// NM_001127491
7.38	7.09	0.29	1.40E-01	5.05E-01	TSR2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	chrXp11.22	213079_at	NM_058163
6.25	6.01	0.24	1.40E-01	5.05E-01	RAD51C	RAD51 homolog C (S. cerevisiae)	chr17q22-q23	206066_s_at	NM_002876 /// NM_058216
4.50	4.30	0.20	1.40E-01	5.05E-01	41530	Septin 13	chr7p13	1569973_at	XM_001126402 /// XM_001133108 /// XM_001717249 /// XM_001718865
8.05	7.32	0.74	1.40E-01	5.05E-01	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	chr20q13.1-q13.2	221484_at	NM_004776
4.28	4.03	0.25	1.40E-01	5.05E-01	HPS4	Hermansky-Pudlak syndrome 4	chr22cen-q12.3	54037_at	NM_022081 /// NM_152841
7.71	7.01	0.70	1.40E-01	5.05E-01	FERMT1	fermitin family homolog 1 (Drosophila)	chr20p12.3	218796_at	NM_017671
5.55	5.31	0.24	1.40E-01	5.05E-01	WDR60	WD repeat domain 60	chr7q36.3	219251_s_at	NM_018051
4.00	3.71	0.29	1.40E-01	5.05E-01	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17p13.3	235882_at	NM_001128159 /// NM_018289
4.61	4.34	0.28	1.40E-01	5.05E-01	KIAA1543	KIAA1543	chr19p13.3-p13.2	226494_at	NM_001080429 /// NM_020902
5.01	4.26	0.75	1.40E-01	5.05E-01	THBD	thrombomodulin	chr20p11.2	203887_s_at	NM_000361
6.70	6.42	0.28	1.40E-01	5.05E-01	FAM82A2	family with sequence similarity 82, member A2	chr15q15.1	218126_at	NM_018145
6.10	5.75	0.35	1.40E-01	5.05E-01	---	---	---	241897_at	---
6.67	6.33	0.34	1.40E-01	5.05E-01	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	chr20p13	201053_s_at	NM_006814 /// NM_178578
7.18	6.91	0.27	1.40E-01	5.05E-01	MRPL10	mitochondrial ribosomal protein L10	chr17q21.32	224671_at	NM_145255 /// NM_148887
2.42	1.97	0.44	1.40E-01	5.05E-01	CDC23	cell division cycle 23 homolog (S. cerevisiae)	chr5q31	223651_x_at	NM_004661
2.89	2.30	0.58	1.40E-01	5.05E-01	MBD4	methyl-CpG binding domain protein 4	chr3q21-q22	214048_at	NM_003925
3.66	3.06	0.60	1.40E-01	5.05E-01	RGS7	regulator of G-protein signaling 7	chr1q43|1q23.1	1554500_a_at	NM_002924
3.40	3.03	0.37	1.40E-01	5.05E-01	---	---	---	242932_at	---
10.26	9.92	0.34	1.40E-01	5.05E-01	TMEM14B /// TMEM14C	transmembrane protein 14B /// transmembrane protein 14C	chr6p24.2 /// chr6p25.1-p23	223105_s_at	NM_001127711 /// NM_016462 /// NM_030969
2.35	2.12	0.23	1.40E-01	5.05E-01	PHKA2	phosphorylase kinase, alpha 2 (liver)	chrXp22.2-p22.1	1560358_at	NM_000292
5.42	5.12	0.30	1.40E-01	5.05E-01	C15orf41	chromosome 15 open reading frame 41	chr15q14	224486_s_at	NM_001130010 /// NM_032499
7.41	7.06	0.35	1.40E-01	5.05E-01	KCTD2	potassium channel tetramerisation domain containing 2	chr17q25.1	34858_at	NM_015353
7.37	6.98	0.39	1.40E-01	5.06E-01	SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	chr3q21.3	222385_x_at	NM_013336
4.54	4.29	0.25	1.40E-01	5.06E-01	PHLDB1	pleckstrin homology-like domain, family B, member 1	chr11q23.3	216019_x_at	NM_015157
6.95	6.53	0.41	1.40E-01	5.06E-01	CALCOCO1	calcium binding and coiled-coil domain 1	chr12q13.13	209002_s_at	NM_020898
8.09	7.79	0.30	1.41E-01	5.06E-01	CTSL1	cathepsin L1	chr9q21-q22	202087_s_at	NM_001912 /// NM_145918
3.07	2.82	0.25	1.41E-01	5.06E-01	---	---	---	230642_at	---
6.73	6.21	0.53	1.41E-01	5.06E-01	INSR	insulin receptor	chr19p13.3-p13.2	226216_at	NM_000208 /// NM_001079817
2.14	1.95	0.19	1.41E-01	5.06E-01	SAMD12	sterile alpha motif domain containing 12	chr8q24.12	1562637_at	NM_001101676 /// NM_207506
5.84	5.47	0.37	1.41E-01	5.06E-01	LINS1	lines homolog 1 (Drosophila)	chr15q26.3	228348_at	NM_001040614 /// NM_001040615 /// NM_001040616 /// NM_018148
2.74	2.49	0.26	1.41E-01	5.06E-01	---	---	---	234612_at	---

4.16	3.90	0.26	1.41E-01	5.06E-01	ZMYND8	Zinc finger, MYND-type containing 8	chr20q13.12	243814_at	NM_012408 /// NM_183047 /// NM_183048																				
2.45	2.21	0.24	1.41E-01	5.06E-01	---	---	---	231051_at	---																				
3.11	2.80	0.31	1.41E-01	5.06E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC643332 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// similar to Nonsecretory ribonuclease precursor (Ribonuclease US) (Eosinophil-derived neurotoxin) (RNase Upl-2) (Ribonuclease 2) (RNase 2) /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q11.2 /// chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	216667_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447 /// XR_016287 /// XR_041734 /// XR_041735																				
4.46	4.22	0.25	1.41E-01	5.06E-01	DERL1	Der1-like domain family, member 1	chr8q24.13	225488_at	NM_001134671 /// NM_024295																				
4.21	3.91	0.29	1.41E-01	5.06E-01	---	---	---	1562449_s_at	---																				
2.23	2.04	0.19	1.41E-01	5.06E-01	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	chr5q11	234967_at	NM_002184 /// NM_175767																				
7.91	6.99	0.93	1.41E-01	5.06E-01	KIAA1576	KIAA1576 protein	chr16q23.1	226415_at	NM_020927																				
3.28	3.07	0.21	1.41E-01	5.07E-01	RAPGEFL1	Rap guanine nucleotide exchange factor (GEF)-like 1	chr17q21.1-q21.2	218657_at	NM_016339																				
2.35	2.18	0.18	1.41E-01	5.07E-01	PPARA	Peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	237142_at	NM_001001928 /// NM_005036																				
6.22	5.82	0.40	1.41E-01	5.07E-01	RMND5B	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	chr5q35.3	218262_at	NM_022762																				
2.27	2.06	0.21	1.41E-01	5.07E-01	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	chr18q21.32	204286_s_at	NM_021127																				
3.77	3.57	0.19	1.41E-01	5.07E-01	---	---	---	235679_at	---																				

7.91	7.48	0.44	1.41E-01	5.07E-01	PRNP	prion protein	chr20p13	201300_s_at	NM_000311 /// NM_001080121 /// NM_001080122 /// NM_001080123 /// NM_183079																			
5.79	5.51	0.28	1.41E-01	5.07E-01	CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1	chr2q33.2	219565_at	NM_177538																			
2.27	2.10	0.17	1.41E-01	5.07E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	215289_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447																			
4.01	2.81	1.20	1.41E-01	5.07E-01	RGS1	regulator of G-protein signaling 1	chr1q31	202988_s_at	NM_002922																			
4.64	4.31	0.34	1.42E-01	5.07E-01	MEGF6	multiple EGF-like-domains 6	chr1p36.3	213942_at	NM_001409																			
4.32	3.85	0.47	1.42E-01	5.07E-01	BCR /// FLJ42953 /// LOC100133163 /// LOC644165 /// LOC728468	breakpoint cluster region /// breakpoint cluster region pseudogene /// similar to breakpoint cluster region /// similar to breakpoint cluster region /// hypothetical LOC728468	chr22q11.21 /// chr22q11.23 /// chr22q11|22q11.23	226602_s_at	NM_004327 /// NM_021574 /// XM_001129467 /// XM_001721519 /// XM_001722808 /// XM_001726385 /// XM_933701																			
7.20	6.90	0.30	1.42E-01	5.07E-01	SP1	Sp1 transcription factor	chr12q13.1	224760_at	NM_138473																			

7.03	6.64	0.39	1.42E-01	5.07E-01	C10orf33	chromosome 10 open reading frame 33	chr10q24.2	228384_s_at	NM_032709 /// XM_001714371 /// XM_001725107 /// XM_001725403																				
5.52	5.25	0.27	1.42E-01	5.07E-01	PREP	prolyl endopeptidase	chr6q22	37950_at	NM_002726																				
2.66	2.31	0.36	1.42E-01	5.07E-01	PANK2	Pantothenate kinase 2	chr20p13	238856_s_at	NM_024960 /// NM_153638 /// NM_153640																				
5.00	4.72	0.29	1.42E-01	5.07E-01	C9orf30 /// TMEFF1	chromosome 9 open reading frame 30 /// transmembrane protein with EGF-like and two follistatin-like domains 1	chr9q31 /// chr9q31.1	1552277_a_at	NM_003692 /// NM_080655																				
6.74	6.38	0.36	1.42E-01	5.07E-01	ZNF76	zinc finger protein 76 (expressed in testis)	chr6p21.3-p21.2	207494_s_at	NM_003427																				
3.52	3.08	0.44	1.42E-01	5.07E-01	TRIOBP	TRIO and F-actin binding protein	chr22q13.1	1552334_at	NM_001039141 /// NM_007032 /// NM_138632																				
2.85	2.19	0.66	1.42E-01	5.07E-01	CCNE2	cyclin E2	chr8q22.1	211814_s_at	NM_057749																				
4.47	3.76	0.71	1.42E-01	5.07E-01	---	---	---	236045_x_at	---																				
2.03	1.86	0.16	1.42E-01	5.07E-01	---	---	---	241441_at	---																				
4.87	4.51	0.35	1.42E-01	5.07E-01	THAP5	THAP domain containing 5	chr7q31.1	227636_at	NM_001130475 /// NM_182529																				
10.23	10.01	0.21	1.42E-01	5.08E-01	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	chr11q23.3	207573_x_at	NM_006476																				
6.62	5.85	0.76	1.42E-01	5.08E-01	HLF	hepatic leukemia factor	chr17q22	204754_at	NM_002126																				
2.72	2.47	0.25	1.42E-01	5.08E-01	MBD3L1	methyl-CpG binding domain protein 3-like 1	chr19p13.2	1552459_a_at	NM_145208																				
2.27	2.06	0.21	1.42E-01	5.08E-01	DENND1B	DENN/MADD domain containing 1B	chr1q31.3	1552835_at	NM_019049 /// NM_144977																				
6.77	6.43	0.34	1.42E-01	5.08E-01	SCML2	sex comb on midleg-like 2 (Drosophila)	chrXp22	206147_x_at	NM_006089																				
7.26	6.66	0.60	1.42E-01	5.08E-01	FAM21C /// FAM21D	family with sequence similarity 21, member C /// family with sequence similarity 21, member D	chr10q11.1 /// chr10q11.23	211068_x_at	NM_015262 /// XM_370557																				
6.53	6.10	0.44	1.42E-01	5.08E-01	LOC100128443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	chr5q12.3	225613_at	NM_015183 /// NM_198828 /// XM_001720470 /// XM_001720479 /// XM_001722488																				
2.19	2.00	0.19	1.42E-01	5.08E-01	---	---	---	240835_at	---																				
5.57	5.02	0.55	1.42E-01	5.08E-01	EMP2	epithelial membrane protein 2	chr16p13.2	225078_at	NM_001424																				
3.33	3.06	0.27	1.42E-01	5.08E-01	CXYorf2	chromosome X and Y open reading frame 2	chrXp22.33; Yp11.3	207288_at	XR_040863 /// XR_040864																				
3.33	2.70	0.63	1.43E-01	5.09E-01	---	---	---	240405_at	---																				
4.13	3.67	0.46	1.43E-01	5.09E-01	NIT1	nitrilase 1	chr1q21-q22	241395_at	NM_005600																				
5.67	5.04	0.63	1.43E-01	5.09E-01	NPY6R	Neuropeptide Y receptor Y6 (pseudogene)	chr5q31	236860_at	NR_002713																				
6.82	6.52	0.29	1.43E-01	5.09E-01	JARID1B	jumonji, AT rich interactive domain 1B	chr1q32.1	201549_x_at	NM_006618																				
3.23	2.91	0.32	1.43E-01	5.09E-01	C20orf112	chromosome 20 open reading frame 112	chr20q11.1-q11.23	230955_s_at	NM_080616																				
2.91	2.67	0.25	1.43E-01	5.09E-01	DRD5	dopamine receptor D5	chr4p16.1	208486_at	NM_000798																				
2.84	2.61	0.23	1.43E-01	5.09E-01	---	---	---	244051_at	---																				
6.86	6.42	0.44	1.43E-01	5.09E-01	ADNP2	ADNP homeobox 2	chr18q23	203322_at	NM_014913																				
3.57	3.19	0.38	1.43E-01	5.09E-01	FLJ22795 /// LOC727751 /// LOC727849	hypothetical protein FLJ22795 /// similar to cis-Golgi matrix protein GM130 /// similar to cis-Golgi matrix protein GM130	chr15q25.2	223326_s_at	XM_001713899 /// XR_040862 /// XR_041987																				
4.37	3.70	0.66	1.43E-01	5.09E-01	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	chr11p13-p12	225491_at	NM_004171																				
5.70	5.30	0.40	1.43E-01	5.09E-01	KIAA0649	KIAA0649	chr9q34.3	203955_at	NM_014811																				
5.54	5.08	0.46	1.43E-01	5.10E-01	FAM48A	family with sequence similarity 48, member A	chr13q13.3	221774_x_at	NM_001014286 /// NM_017569																				
5.60	5.21	0.39	1.43E-01	5.10E-01	AARS2	alanyl-tRNA synthetase 2, mitochondrial (putative)	chr6p21.1	231845_at	NM_020745																				

2.88	2.65	0.23	1.43E-01	5.10E-01	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	chr20q12-q13.1	230686_s_at	NM_001011554 /// NM_022829																				
5.40	5.00	0.40	1.43E-01	5.10E-01	SSH3	slingshot homolog 3 (Drosophila)	chr11q13.1	219241_x_at	NM_017857																				
5.07	4.64	0.44	1.43E-01	5.10E-01	---	---	---	222368_at	---																				
2.21	1.96	0.24	1.43E-01	5.10E-01	---	---	---	244887_at	---																				
5.80	5.34	0.46	1.43E-01	5.10E-01	LIN37	lin-37 homolog (C. elegans)	chr19q13.1	213526_s_at	NM_019104																				
5.55	5.10	0.45	1.43E-01	5.10E-01	FLJ36070	likely ortholog of MEF2-activating SAP transcriptional regulator	chr19q13.33	1557091_at	NM_001130915 /// NM_182574																				
5.32	4.74	0.58	1.43E-01	5.10E-01	BAIAP2L1 /// LOC100128461	BAI1-associated protein 2-like 1 /// hypothetical protein LOC100128461	chr7q21.3	227372_s_at	NM_018842 /// XM_001722656 /// XM_001724217 /// XM_001724858																				
2.59	2.31	0.29	1.43E-01	5.10E-01	CCDC127	Coiled-coil domain containing 127	chr5p15.33	1560354_at	NM_145265																				
6.92	6.71	0.22	1.43E-01	5.10E-01	CYB5D2	cytochrome b5 domain containing 2	chr17p13.2	225804_at	NM_144611 /// NR_023346 /// NR_023347																				
2.17	1.95	0.22	1.43E-01	5.10E-01	---	---	---	1570261_at	---																				
4.12	3.89	0.23	1.43E-01	5.10E-01	POLDIP3	Polymerase (DNA-directed), delta interacting protein 3	chr22q13.2	243411_at	NM_032311 /// NM_178136																				
2.96	2.51	0.44	1.44E-01	5.10E-01	CLK4	CDC-like kinase 4	chr5q35	228751_at	NM_020666																				
5.84	5.59	0.25	1.44E-01	5.10E-01	MAPK9	Mitogen-activated protein kinase 9	chr5q35	225781_at	NM_002752 /// NM_139068 /// NM_139069 /// NM_139070																				
2.63	2.31	0.32	1.44E-01	5.10E-01	---	---	---	1569713_at	---																				
2.62	2.45	0.17	1.44E-01	5.10E-01	---	---	---	243321_at	---																				
3.56	3.32	0.24	1.44E-01	5.10E-01	C9orf41	chromosome 9 open reading frame 41	chr9q21.13	228324_at	NM_152420																				
2.13	1.95	0.18	1.44E-01	5.10E-01	hCG_2025798	hCG2025798	chr4q34.3	1556099_at	XM_001127776 /// XM_001132623 /// XM_001723394																				
6.87	6.43	0.44	1.44E-01	5.10E-01	FOXK1	forkhead box K1	chr7p22.1	226715_at	NM_001037165																				
7.13	6.86	0.26	1.44E-01	5.11E-01	PARP1	poly (ADP-ribose) polymerase 1	chr1q41-q42	208644_at	NM_001618																				
8.99	8.60	0.39	1.44E-01	5.11E-01	CD81	CD81 molecule	chr11p15.5	200675_at	NM_004356																				
6.45	5.99	0.46	1.44E-01	5.11E-01	PKP4	plakophilin 4	chr2q23-q31	201928_at	NM_001005476 /// NM_003628																				
3.95	3.44	0.51	1.44E-01	5.11E-01	LRFN5	leucine rich repeat and fibronectin type III domain containing 5	chr14q21.2	230644_at	NM_152447																				
3.54	3.17	0.37	1.44E-01	5.11E-01	WRNIP1	Werner helicase interacting protein 1	chr6p25.2	230847_at	NM_020135 /// NM_130395																				
3.17	2.91	0.27	1.44E-01	5.11E-01	RBM12B	RNA binding motif protein 12B	chr8q22.1	238122_at	NM_203390																				
11.96	11.79	0.17	1.44E-01	5.11E-01	PPIA	peptidylprolyl isomerase A (cyclophilin A)	chr7p13	211978_x_at	NM_021130																				
5.72	5.30	0.42	1.44E-01	5.11E-01	KIAA1545	KIAA1545 protein	chr12q24.33	225703_at	XM_001716046 /// XM_495939 /// XM_936428																				
3.56	3.35	0.21	1.44E-01	5.11E-01	RHBDL2	rhomboid, veinlet-like 2 (Drosophila)	chr1p34.3	1554895_a_at	NM_017821																				
5.22	4.71	0.52	1.44E-01	5.11E-01	---	---	---	230416_at	---																				

2.93	2.68	0.25	1.44E-01	5.11E-01	WHSC1	Wolf-Hirschhorn syndrome candidate 1	chr4p16.3	209052_s_at	NM_001042424 /// NM_007331 /// NM_133330 /// NM_133331 /// NM_133334 /// NM_133335																				
8.33	8.04	0.29	1.44E-01	5.11E-01	C10orf26	chromosome 10 open reading frame 26	chr10q24.32	202808_at	NM_001083913 /// NM_017787																				
4.50	4.28	0.22	1.44E-01	5.11E-01	LOC149478	Hypothetical protein LOC149478	chr1p34.1	238102_s_at	XM_001725220 /// XM_001725874 /// XM_001726015																				
5.44	4.95	0.49	1.44E-01	5.11E-01	CCDC131	coiled-coil domain containing 131	chr12q21.1	213065_at	NM_144982																				
2.24	2.05	0.19	1.44E-01	5.11E-01	---	---	---	1566899_at	---																				
2.72	2.26	0.46	1.44E-01	5.11E-01	MDM1	Mdm1 nuclear protein homolog (mouse)	chr12q15	213761_at	NM_017440 /// NM_020128																				
3.31	3.08	0.23	1.44E-01	5.11E-01	LIMK1	LIM domain kinase 1	chr7q11.23	208372_s_at	NM_002314																				
5.46	4.64	0.82	1.44E-01	5.11E-01	ZC3H12C	zinc finger CCCH-type containing 12C	chr11q22.3	231899_at	NM_033390																				
3.46	3.22	0.24	1.44E-01	5.11E-01	SGSM2	small G protein signaling modulator 2	chr17p13.3	217538_at	NM_001098509 /// NM_014853																				
2.94	2.76	0.18	1.44E-01	5.11E-01	---	---	---	222174_at	---																				
2.65	2.42	0.23	1.44E-01	5.11E-01	EFR3B	EFR3 homolog B (S. cerevisiae)	chr2p23.3	215334_at	NM_014971 /// XM_001717587 /// XM_039733 /// XM_940464																				
6.46	6.03	0.43	1.44E-01	5.11E-01	MGC5370	hypothetical protein MGC5370	chr12q14.3	229711_s_at	---																				
4.71	4.37	0.34	1.44E-01	5.11E-01	---	---	---	241968_at	---																				
2.17	2.00	0.17	1.44E-01	5.11E-01	---	---	---	237122_at	---																				
4.15	3.77	0.38	1.44E-01	5.11E-01	POLM	polymerase (DNA directed), mu	chr7p13	222238_s_at	NM_013284																				
3.59	3.01	0.58	1.44E-01	5.11E-01	---	---	---	235901_at	---																				
2.68	2.41	0.26	1.44E-01	5.11E-01	---	---	---	236978_at	---																				
3.32	3.06	0.27	1.44E-01	5.11E-01	RET	ret proto-oncogene	chr10q11.2	215771_x_at	NM_020630 /// NM_020975																				
5.98	5.60	0.38	1.44E-01	5.11E-01	KIAA0194	KIAA0194 protein	chr5q33.1	34221_at	XM_001714730 /// XM_001717202 /// XM_001717459																				
5.88	5.42	0.46	1.44E-01	5.11E-01	---	---	---	227200_at	---																				
7.79	7.47	0.31	1.44E-01	5.11E-01	C18orf10	chromosome 18 open reading frame 10	chr18q12.2	212055_at	NM_015476																				
5.27	4.98	0.29	1.44E-01	5.11E-01	MYOZ3	myozenin 3	chr5q33.1	1562002_at	NM_001122853 /// NM_133371																				
3.15	2.87	0.28	1.45E-01	5.11E-01	LENEP	lens epithelial protein	chr1q22	221115_s_at	NM_018655																				
2.10	1.92	0.18	1.45E-01	5.11E-01	RBM46	RNA binding motif protein 46	chr4q32.1	244351_at	NM_144979																				
2.80	2.56	0.24	1.45E-01	5.11E-01	TFE3	transcription factor binding to IGHM enhancer 3	chrXp11.22	1565347_s_at	NM_006521																				
5.40	4.61	0.79	1.45E-01	5.11E-01	GRIA3	glutamate receptor, ionotrophic, AMPA 3	chrXq25-q26	1569290_s_at	NM_000828 /// NM_007325																				
4.19	3.97	0.22	1.45E-01	5.11E-01	---	---	---	243210_at	---																				
2.90	2.68	0.22	1.45E-01	5.11E-01	KIR2DL5A	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A	chr19p13.3	211410_x_at	NM_020535																				
2.90	2.60	0.30	1.45E-01	5.11E-01	LOC100133019	similar to hCG1983765	chr16p11.2	1559125_at	XM_001715216 /// XM_001725599																				
2.87	2.62	0.25	1.45E-01	5.11E-01	RPL13	Ribosomal protein L13	chr16q24.3|17p11.2	1565759_at	NM_000977 /// NM_033251																				
7.42	6.78	0.63	1.45E-01	5.11E-01	PLAT	plasminogen activator, tissue	chr8p12	201860_s_at	NM_000930 /// NM_033011																				

4.98	4.78	0.20	1.45E-01	5.11E-01	ZNF843	zinc finger protein 843	chr16p11.2	1564362_x_at	XM_001720820 /// XM_290712 /// XM_937979																				
3.86	3.39	0.46	1.45E-01	5.11E-01	---	---	---	228869_at	---																				
2.33	2.06	0.27	1.45E-01	5.11E-01	C16orf54 /// hCG_1644884	chromosome 16 open reading frame 54 /// similar to chromosome 16 open reading frame 54	chr16p11.2	1559584_a_at	NM_175900 /// XM_001128758																				
2.59	1.96	0.64	1.45E-01	5.12E-01	ARL5B	ADP-ribosylation factor-like 5B	chr10p12.33	242727_at	NM_178815																				
3.33	3.15	0.18	1.45E-01	5.12E-01	CTSE	cathepsin E	chr1q31	205927_s_at	NM_001910 /// NM_148964																				
2.23	2.04	0.18	1.45E-01	5.12E-01	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	chr3q13.11	208348_s_at	NM_170662																				
3.55	3.26	0.29	1.45E-01	5.12E-01	STAMBP	STAM binding protein	chr2p13.1	227515_at	NM_006463 /// NM_201647 /// NM_213622																				
7.83	7.51	0.32	1.45E-01	5.12E-01	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	chr17p13.1	201557_at	NM_014232																				
3.06	2.56	0.50	1.45E-01	5.12E-01	CLEC7A	C-type lectin domain family 7, member A	chr12p13.2	1555756_a_at	NM_022570 /// NM_197947 /// NM_197948 /// NM_197949 /// NM_197950 /// NM_197954																				
5.08	4.62	0.46	1.45E-01	5.12E-01	PRO2852	hypothetical protein PRO2852	---	223797_at	---																				
4.05	3.10	0.96	1.45E-01	5.12E-01	CEL	carboxyl ester lipase (bile salt-stimulated lipase)	chr9q34.3	205910_s_at	NM_001807																				
7.39	6.94	0.45	1.45E-01	5.12E-01	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	chr22q11.21	210010_s_at	NM_005984																				
2.99	2.80	0.19	1.45E-01	5.12E-01	WDR1	WD repeat domain 1	chr4p16.1	210936_at	NM_005112 /// NM_017491																				
5.47	4.80	0.67	1.45E-01	5.12E-01	SLC2A14 /// SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 14 /// solute carrier family 2 (facilitated glucose transporter), member 3	chr12p13.3 /// chr12p13.31	216236_s_at	NM_006931 /// NM_153449																				
2.91	2.69	0.22	1.45E-01	5.12E-01	C3orf52	chromosome 3 open reading frame 52	chr3q13.2	219474_at	NM_024616																				
6.84	6.55	0.29	1.45E-01	5.12E-01	DUSP22	dual specificity phosphatase 22	chr6p25.3	218845_at	NM_020185																				
7.63	7.42	0.22	1.45E-01	5.12E-01	PDAP1	PDGFA associated protein 1	chr7q22.1	202290_at	NM_014891																				
3.08	2.68	0.40	1.46E-01	5.12E-01	RPGR	retinitis pigmentosa GTPase regulator	chrXp11.4	207624_s_at	NM_000328 /// NM_001034853																				
3.21	2.95	0.26	1.46E-01	5.12E-01	C15orf57	chromosome 15 open reading frame 57	chr15q15.1	1558648_at	NM_001080791 /// NM_001080792 /// NM_052849																				
2.68	2.41	0.27	1.46E-01	5.12E-01	PCBP3	Poly(rC) binding protein 3	chr21q22.3	233998_x_at	NM_001130141 /// NM_020528																				
6.79	6.58	0.21	1.46E-01	5.12E-01	NOLA1	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	chr4q25	219110_at	NM_018983 /// NM_032993																				
8.63	8.36	0.27	1.46E-01	5.12E-01	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	chr1p21	220948_s_at	NM_000701 /// NM_001001586																				
3.08	2.87	0.21	1.46E-01	5.13E-01	FAM160B2	family with sequence similarity 160, member B2	chr8p21.3	222929_at	NM_022749																				
3.52	3.17	0.35	1.46E-01	5.13E-01	FBXL8	F-box and leucine-rich repeat protein 8	chr16q22.1	220080_at	NM_018378																				
4.02	3.79	0.23	1.46E-01	5.13E-01	UBAP2L	ubiquitin associated protein 2-like	chr1q21.3	214695_at	NM_001127320 /// NM_014847																				
7.30	6.93	0.36	1.46E-01	5.13E-01	TUSC2	tumor suppressor candidate 2	chr3p21.3	203272_s_at	NM_007275																				
2.51	2.24	0.28	1.46E-01	5.13E-01	KIAA1324	KIAA1324	chr1p13.3	221874_at	NM_020775																				
2.02	1.87	0.15	1.46E-01	5.13E-01	OR5K1	olfactory receptor, family 5, subfamily K, member 1	chr3q11.2	1567287_at	NM_001004736																				

3.34	3.04	0.30	1.46E-01	5.13E-01	SPAST	spastin	chr2p24-p21	209748_at	NM_014946 /// NM_199436																				
7.11	6.09	1.02	1.46E-01	5.13E-01	NOSTRIN	nitric oxide synthase trafficker	chr2q24.3	226992_at	NM_001039724 /// NM_052946																				
4.68	4.10	0.58	1.46E-01	5.13E-01	---	---	---	239258_at	---																				
8.92	8.63	0.29	1.46E-01	5.13E-01	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	chr17q25	1564494_s_at	NM_000918																				
3.00	2.77	0.23	1.46E-01	5.13E-01	---	---	---	238208_at	---																				
4.08	3.66	0.42	1.46E-01	5.13E-01	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	chr5q33.1-qter	205269_at	NM_005565																				
2.90	2.57	0.34	1.46E-01	5.13E-01	---	---	---	237329_at	---																				
3.33	3.05	0.28	1.47E-01	5.13E-01	---	---	---	233422_at	---																				
6.96	5.66	1.29	1.47E-01	5.13E-01	HOPX	HOP homeobox	chr4q11-q12	211597_s_at	NM_032495 /// NM_139211 /// NM_139212																				
3.97	3.62	0.35	1.47E-01	5.13E-01	KIAA0467	KIAA0467	chr1p34.2	203900_at	NM_015284																				
4.55	4.38	0.17	1.47E-01	5.13E-01	---	---	---	244285_at	---																				
6.20	5.73	0.47	1.47E-01	5.13E-01	SLC44A2	solute carrier family 44, member 2	chr19p13.1	224609_at	NM_020428																				
6.26	5.85	0.41	1.47E-01	5.14E-01	ASXL1	additional sex combs like 1 (Drosophila)	chr20q11.1	242439_s_at	NM_015338																				
4.48	4.03	0.45	1.47E-01	5.14E-01	LOC100128223 /// TARDBP	hypothetical protein LOC100128223 /// TAR DNA binding protein	chr1p36.22	221264_s_at	NM_007375 /// XM_001713887 /// XM_001720151 /// XM_001721043																				
3.65	3.29	0.36	1.47E-01	5.14E-01	EFCAB2	EF-hand calcium binding domain 2	chr1q44	211200_s_at	NM_032328																				
3.01	2.54	0.47	1.47E-01	5.14E-01	TSC22D1	TSC22 domain family, member 1	chr13q14	235315_at	NM_006022 /// NM_183422																				
2.54	2.34	0.20	1.47E-01	5.14E-01	C15orf48	chromosome 15 open reading frame 48	chr15q21.1	223484_at	NM_032413 /// NM_197955																				
4.59	3.91	0.68	1.47E-01	5.14E-01	FAM60A	family with sequence similarity 60, member A	chr12p11	223038_s_at	NM_021238																				
2.55	2.24	0.31	1.47E-01	5.14E-01	LOC284242	hypothetical protein LOC284242	chr18q12.1	1560250_s_at	---																				
5.71	5.30	0.41	1.47E-01	5.14E-01	RP5-1077B9.4	invasion inhibitory protein 45	chr1p36.22	48659_at	NM_021933																				
2.45	2.28	0.18	1.47E-01	5.14E-01	---	---	---	230766_at	---																				
2.63	2.42	0.21	1.47E-01	5.14E-01	LOC647109	similar to hCG2021878	chr3q26.1	240371_at	XM_001716977 /// XM_930126 /// XM_941431																				
3.20	2.99	0.21	1.47E-01	5.14E-01	---	---	---	239361_at	---																				
2.54	2.36	0.19	1.47E-01	5.14E-01	POU3F2	POU class 3 homeobox 2	chr6q16	242455_at	NM_005604																				
12.14	11.95	0.19	1.47E-01	5.14E-01	RPL13	ribosomal protein L13	chr16q24.3|17p11.2	212191_x_at	NM_000977 /// NM_033251																				
7.23	7.00	0.22	1.47E-01	5.14E-01	MRPS27	mitochondrial ribosomal protein S27	chr5q13.2	212145_at	NM_015084																				
5.09	4.80	0.30	1.47E-01	5.14E-01	KLHL24	kelch-like 24 (Drosophila)	chr3q27.1	226158_at	NM_017644																				
4.79	4.61	0.19	1.47E-01	5.14E-01	PHF19	PHD finger protein 19	chr9q33.2	227211_at	NM_001009936 /// NM_015651																				
3.63	3.35	0.28	1.47E-01	5.15E-01	UBE3B	ubiquitin protein ligase E3B	chr12q24.11	212404_s_at	NM_130466 /// NM_183415																				
4.85	4.64	0.22	1.47E-01	5.15E-01	ZNF527	zinc finger protein 527	chr19q13.1	244861_at	NM_032453																				
2.66	2.40	0.26	1.47E-01	5.15E-01	EXOSC10	exosome component 10	chr1p36.22	1559031_at	NM_001001998 /// NM_002685																				
2.51	2.33	0.18	1.47E-01	5.15E-01	CNTN1	contactin 1	chr12q11-q12	1554784_at	NM_001843 /// NM_175038																				
7.89	7.56	0.33	1.47E-01	5.15E-01	TBC1D14	TBC1 domain family, member 14	chr4p16.1	224622_at	NM_001113361 /// NM_001113363 /// NM_020773																				
7.07	6.72	0.35	1.47E-01	5.15E-01	AP1M1	adaptor-related protein complex 1, mu 1 subunit	chr19p13.12	223025_s_at	NM_001130524 /// NM_032493																				
2.69	2.42	0.27	1.48E-01	5.15E-01	TIGD7	Tigger transposable element derived 7	chr16p13.3	232089_at	NM_033208																				

3.48	3.20	0.29	1.48E-01	5.15E-01	DNAH6 /// DNHL1 /// LOC200383	dynein, axonemal, heavy chain 6 /// dynein heavy chain-like 1 /// similar to Dynein heavy chain at 16F	chr2p11.2	1561616_a_at	NM_001370 /// NM_173645
6.38	6.01	0.37	1.48E-01	5.15E-01	C20orf11	chromosome 20 open reading frame 11	chr20q13.33	225376_at	NM_017896
4.30	3.86	0.44	1.48E-01	5.15E-01	---	---	---	1568983_a_at	---
3.26	2.97	0.29	1.48E-01	5.15E-01	MGC12916	hypothetical protein MGC12916	chr17p11.2	224508_at	---
5.41	4.96	0.45	1.48E-01	5.15E-01	CASP3	caspase 3, apoptosis-related cysteine peptidase	chr4q34	202763_at	NM_004346 /// NM_032991
4.86	4.49	0.38	1.48E-01	5.15E-01	TMEM19	transmembrane protein 19	chr12q21.1	226860_at	NM_018279
4.82	4.50	0.32	1.48E-01	5.15E-01	---	---	---	226203_at	---
4.80	4.43	0.37	1.48E-01	5.15E-01	AK2	adenylate kinase 2	chr1p34	212174_at	NM_001625 /// NM_013411
5.20	4.64	0.55	1.48E-01	5.15E-01	AASDH	aminoadipate-semialdehyde dehydrogenase	chr4q12	228041_at	NM_181806
4.62	3.49	1.13	1.48E-01	5.15E-01	ELL2	elongation factor, RNA polymerase II, 2	chr5q15	226099_at	NM_012081
7.52	7.25	0.27	1.48E-01	5.15E-01	PBXIP1	Pre-B-cell leukemia homeobox interacting protein 1	chr1q21.3	214176_s_at	NM_020524
3.11	2.83	0.28	1.48E-01	5.15E-01	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)	chr17q25.3	226473_at	NM_005189 /// NM_032647
7.12	6.61	0.51	1.48E-01	5.15E-01	WDR34	WD repeat domain 34	chr9q34.11	224715_at	NM_052844
6.61	6.17	0.44	1.48E-01	5.15E-01	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	chr9q31-q33	209161_at	NM_004697
3.49	3.25	0.25	1.48E-01	5.15E-01	CD19	CD19 molecule	chr16p11.2	206398_s_at	NM_001770
3.30	2.97	0.33	1.48E-01	5.15E-01	---	---	---	217606_at	---
8.79	8.55	0.24	1.48E-01	5.15E-01	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	chr17q21.3	214179_s_at	NM_003204
12.59	12.43	0.16	1.48E-01	5.15E-01	RPL3	ribosomal protein L3	chr22q13	212039_x_at	NM_000967 /// NM_001033853
2.48	2.21	0.27	1.48E-01	5.15E-01	---	---	---	1568846_at	---
8.07	7.78	0.29	1.48E-01	5.15E-01	TRAPPC4	trafficking protein particle complex 4	chr11q23.3	217958_at	NM_016146
6.81	6.31	0.50	1.48E-01	5.15E-01	AMD1	adenosylmethionine decarboxylase 1	chr6q21-q22	201197_at	NM_001033059 /// NM_001634
3.47	3.26	0.22	1.48E-01	5.15E-01	RP1-21O18.1	Kazrin	chr1p36.21	238641_at	NM_001017999 /// NM_001018000 /// NM_001018001 /// NM_015209 /// NM_201628
2.56	2.36	0.20	1.48E-01	5.15E-01	---	---	---	229157_at	---
3.61	3.39	0.22	1.48E-01	5.15E-01	KEL	Kell blood group, metallo-endopeptidase	chr7q33	206077_at	NM_000420
2.26	2.04	0.22	1.48E-01	5.15E-01	---	---	---	217012_at	---
4.86	4.52	0.34	1.48E-01	5.15E-01	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	214190_x_at	NM_015044
3.82	3.62	0.19	1.48E-01	5.15E-01	C10orf33	Chromosome 10 open reading frame 33	chr10q24.2	232942_at	NM_032709 /// XM_001714371 /// XM_001725107 /// XM_001725403
2.29	2.08	0.21	1.48E-01	5.15E-01	---	---	---	228925_at	---
5.58	5.37	0.21	1.48E-01	5.15E-01	LINGO3	leucine rich repeat and Ig domain containing 3	chr19p13.3	1560439_at	NM_001101391
3.11	2.91	0.20	1.48E-01	5.15E-01	---	---	---	238294_at	---
5.47	4.99	0.47	1.48E-01	5.15E-01	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2	chr12p13.31	223580_at	NM_032641
6.90	6.50	0.40	1.48E-01	5.15E-01	SFXN3	sideroflexin 3	chr10q24.31	220974_x_at	NM_030971
6.15	5.37	0.79	1.48E-01	5.15E-01	GLIPR1	GLI pathogenesis-related 1	chr12q21.2	226136_at	NM_006851
4.28	3.96	0.32	1.48E-01	5.15E-01	LOC100132352	Similar to hCG1989297	chr9q12	232140_at	XM_001720717 /// XM_001720724
7.31	7.03	0.28	1.48E-01	5.15E-01	FBXO25	F-box protein 25	chr8p23.3|tdb9938	225591_at	NM_012173 /// NM_183420 /// NM_183421
5.19	4.77	0.43	1.48E-01	5.15E-01	---	---	---	230383_x_at	---
5.36	4.99	0.37	1.48E-01	5.15E-01	RNF181	Ring finger protein 181	chr2p11.2	229932_at	NM_016494
1.97	1.83	0.15	1.48E-01	5.15E-01	---	---	---	1564813_at	---

4.52	4.33	0.20	1.48E-01	5.15E-01	CTNND1	catenin (cadherin-associated protein), delta 1	chr11q11	1557944_s_at	NM_001085458 /// NM_001085459 /// NM_001085460 /// NM_001085461 /// NM_001085462 /// NM_001085463 /// NM_001085464 /// NM_001085465 /// NM_001085466 /// NM_001085467 /// NM_001085468 /// NM_001085469 /// NM_001331																			
8.49	8.04	0.44	1.48E-01	5.15E-01	LAPTM4B	lysosomal protein transmembrane 4 beta	chr8q22.1	208767_s_at	NM_018407																				
7.50	7.07	0.43	1.49E-01	5.15E-01	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	chr4q12	201013_s_at	NM_001079524 /// NM_001079525 /// NM_006452																				
3.63	3.41	0.22	1.49E-01	5.15E-01	NHLRC2	NHL repeat containing 2	chr10q25.3	219353_at	NM_198514																				
2.87	2.56	0.31	1.49E-01	5.15E-01	---	---	---	238031_at	---																				
6.68	6.42	0.26	1.49E-01	5.15E-01	TOR1B	torsin family 1, member B (torsin B)	chr9q34	209593_s_at	NM_014506																				
3.24	3.05	0.19	1.49E-01	5.15E-01	---	---	---	239530_at	---																				
6.30	5.86	0.44	1.49E-01	5.15E-01	TTC8	tetratricopeptide repeat domain 8	chr14q31.3	226120_at	NM_144596 /// NM_198309 /// NM_198310																				
2.49	2.25	0.24	1.49E-01	5.15E-01	KLF8	Kruppel-like factor 8	chrXp11.21	219930_at	NM_007250																				
5.98	5.50	0.48	1.49E-01	5.15E-01	C11orf71	chromosome 11 open reading frame 71	chr11q14.2-q14.3	218789_s_at	NM_019021																				
2.79	2.62	0.17	1.49E-01	5.15E-01	FAM138A /// FAM138B /// FAM138F	family with sequence similarity 138, member A /// family with sequence similarity 138, member B /// family with sequence similarity 138, member F	chr19p13.3 /// chr1p36.33 /// chr2q14.1	1555822_at	XM_925817 /// XM_930492 /// XM_930652 /// XM_935059																				
4.97	4.42	0.55	1.49E-01	5.16E-01	FAM119B	family with sequence similarity 119, member B	chr12q14.1	213861_s_at	NM_015433 /// NM_206914																				
2.74	2.50	0.24	1.49E-01	5.16E-01	EYA1	eyes absent homolog 1 (Drosophila)	chr8q13.3	214608_s_at	NM_000503 /// NM_172058 /// NM_172059 /// NM_172060																				
6.66	6.37	0.29	1.49E-01	5.16E-01	UBTF	upstream binding transcription factor, RNA polymerase I	chr17q21.3	202692_s_at	NM_001076683 /// NM_001076684 /// NM_014233																				
4.47	4.19	0.28	1.49E-01	5.16E-01	ZNF687	zinc finger protein 687	chr1q21.2	234924_s_at	NM_020832																				
3.08	2.83	0.26	1.49E-01	5.16E-01	---	---	---	1557521_a_at	---																				
2.84	2.48	0.36	1.49E-01	5.16E-01	RBP4	Retinol binding protein 4, plasma	chr10q23-q24	222049_s_at	NM_006744																				
3.43	2.64	0.79	1.49E-01	5.16E-01	JMY	junction-mediating and regulatory protein	chr5q14.1	241985_at	NM_152405																				
5.06	4.53	0.53	1.49E-01	5.16E-01	CDKN2AIPNL	CDKN2A interacting protein N-terminal like	chr5q31.1	235006_at	NM_080656																				
4.76	4.49	0.26	1.49E-01	5.16E-01	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	chr20q11	207625_s_at	NM_001032999 /// NM_001039709 /// NM_005093																				
4.32	3.83	0.49	1.49E-01	5.16E-01	LOC338799	hypothetical locus LOC338799	chr12q24.31	226369_at	NR_002809																				
2.93	2.68	0.25	1.49E-01	5.16E-01	---	---	---	240451_at	---																				

3.56	3.32	0.24	1.49E-01	5.16E-01	NS3BP	NS3BP	chr11p15.5	1553943_at	XR_041088 /// XR_041089 /// XR_041090																			
3.02	2.76	0.26	1.49E-01	5.16E-01	LOC401588	hypothetical LOC401588	chrXp11.3	241972_at	NR_015378 /// XR_041728 /// XR_041729 /// XR_041730																			
8.71	8.37	0.34	1.49E-01	5.16E-01	C1orf122	chromosome 1 open reading frame 122	chr1p34.3	225480_at	NM_198446																			
2.73	2.54	0.19	1.49E-01	5.16E-01	GFRA4	GDNF family receptor alpha 4	chr20p13-p12	234868_s_at	NM_022139 /// NM_145762																			
7.19	6.77	0.42	1.49E-01	5.16E-01	TFDP2	Transcription factor Dp-2 (E2F dimerization partner 2)	chr3q23	226157_at	NM_006286																			
7.75	7.13	0.61	1.49E-01	5.16E-01	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	chrXq25	203875_at	NM_003069 /// NM_139035																			
3.69	3.44	0.25	1.49E-01	5.16E-01	---	---	---	1569963_at	---																			
7.84	7.51	0.34	1.49E-01	5.16E-01	TM2D2	TM2 domain containing 2	chr8p11.23	224413_s_at	NM_001024380 /// NM_001024381 /// NM_031940 /// NM_078473																			
5.08	4.59	0.48	1.49E-01	5.16E-01	PLA2G12A	phospholipase A2, group XIIA	chr4q25	221027_s_at	NM_030821																			
7.15	6.73	0.42	1.49E-01	5.16E-01	WASF3	WAS protein family, member 3	chr13q12	204042_at	NM_006646																			
6.46	6.14	0.33	1.49E-01	5.16E-01	TFCP2	transcription factor CP2	chr12q13	209338_at	NM_005653																			
3.12	2.89	0.23	1.49E-01	5.16E-01	LILRB1	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	chr19q13.4	229937_x_at	NM_001081637 /// NM_001081638 /// NM_001081639 /// NM_006669																			
8.71	8.38	0.34	1.49E-01	5.16E-01	MPRIP	myosin phosphatase Rho interacting protein	chr17p11.2	212197_x_at	NM_015134 /// NM_201274																			
4.90	4.42	0.48	1.49E-01	5.16E-01	FGD1	FYVE, RhoGEF and PH domain containing 1	chrXp11.21	204819_at	NM_004463																			
6.54	6.31	0.24	1.49E-01	5.16E-01	PREP	prolyl endopeptidase	chr6q22	204117_at	NM_002726																			
5.72	5.48	0.23	1.50E-01	5.16E-01	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	chr14q31.1	225986_x_at	NM_017437																			
3.91	3.52	0.39	1.50E-01	5.16E-01	F2R	coagulation factor II (thrombin) receptor	chr5q13	1569642_at	NM_001992																			
3.93	3.66	0.27	1.50E-01	5.16E-01	---	---	---	233266_at	---																			
2.67	2.21	0.46	1.50E-01	5.16E-01	---	---	---	1569362_at	---																			
2.31	2.13	0.19	1.50E-01	5.16E-01	LOC388076 /// RPS8	hypothetical LOC388076 /// ribosomal protein S8	chr15q11.2 /// chr1p34.1-p32	214089_at	NM_001012 /// XM_001722259 /// XM_001724648 /// XM_931016																			
3.59	3.39	0.21	1.50E-01	5.16E-01	---	---	---	1556984_at	---																			
6.29	5.94	0.34	1.50E-01	5.16E-01	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	chr11q13.3	202066_at	NM_003626 /// NM_177423																			
3.10	2.91	0.19	1.50E-01	5.16E-01	---	---	---	1570151_at	---																			
6.26	5.87	0.39	1.50E-01	5.16E-01	C6orf129	chromosome 6 open reading frame 129	chr6p21.2	225723_at	NM_138493																			
2.92	2.63	0.29	1.50E-01	5.16E-01	ASB3	Ankyrin repeat and SOCS box-containing 3	chr2p16-p14	1560219_at	NM_016115 /// NM_145863																			
2.27	2.10	0.17	1.50E-01	5.16E-01	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	chr14q32	1554364_at	NM_002719 /// NM_178586 /// NM_178587 /// NM_178588																			
4.28	3.50	0.78	1.50E-01	5.16E-01	CLEC4GP1	C-type lectin domain family 4, member G pseudogene 1	chr19p13.2	1559194_a_at	NR_002931																			
2.12	1.90	0.22	1.50E-01	5.16E-01	PPP4R1	Protein phosphatase 4, regulatory subunit 1	chr18p11.22	1563690_at	NM_001042388 /// NM_005134																			
3.79	3.45	0.34	1.50E-01	5.16E-01	C20orf196	chromosome 20 open reading frame 196	chr20p12.3	243507_s_at	NM_152504																			
4.51	4.21	0.30	1.50E-01	5.16E-01	FAM105B	family with sequence similarity 105, member B	chr5p15.2	229268_at	NM_138348																			
2.72	2.50	0.22	1.50E-01	5.16E-01	SF3B14	Splicing factor 3B, 14 kDa subunit	chr2pter-p25.1	1561923_a_at	NM_016047																			

6.58	6.14	0.44	1.50E-01	5.16E-01	TRAF7	TNF receptor-associated factor 7	chr16p13.3	223031_s_at	NM_032271
6.34	5.87	0.47	1.50E-01	5.16E-01	C17orf97	chromosome 17 open reading frame 97	chr17p13.3	229238_at	NM_001013672
6.00	5.59	0.41	1.50E-01	5.16E-01	PIGU	phosphatidylinositol glycan anchor biosynthesis, class U	chr20q11.22	225903_at	NM_080476
4.06	3.72	0.35	1.50E-01	5.16E-01	MGC16211	hypothetical protein MGC16211	chr2q35	238572_at	---
6.18	5.74	0.44	1.50E-01	5.16E-01	C6orf89	chromosome 6 open reading frame 89	chr6p21.2	224988_at	NM_152734
6.65	6.05	0.60	1.50E-01	5.16E-01	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	chr2p25	201566_x_at	NM_002166
4.13	3.73	0.40	1.50E-01	5.17E-01	---	---	---	1557242_at	---
6.66	6.30	0.36	1.50E-01	5.17E-01	ATG2A	ATG2 autophagy related 2 homolog A (S. cerevisiae)	chr11q13.1	213300_at	NM_015104
7.75	7.42	0.33	1.50E-01	5.17E-01	LSM12	LSM12 homolog (S. cerevisiae)	chr17q21.31	212532_s_at	NM_152344
7.74	7.34	0.40	1.51E-01	5.17E-01	PCNA	proliferating cell nuclear antigen	chr20pter-p12	201202_at	NM_002592 /// NM_182649
2.63	2.43	0.20	1.51E-01	5.17E-01	---	---	---	1557589_a_at	---
5.18	4.85	0.33	1.51E-01	5.17E-01	TAZ	tafazzin	chrXq28	203977_at	NM_000116 /// NM_181311 /// NM_181312 /// NM_181313 /// NR_024048
6.10	5.60	0.50	1.51E-01	5.17E-01	MLXIP	MLX interacting protein	chr12q24.31	225157_at	NM_014938
5.83	5.47	0.37	1.51E-01	5.17E-01	AGXT2L2	alanine-glyoxylate aminotransferase 2-like 2	chr5q35.3	226783_at	NM_153373
2.60	2.28	0.32	1.51E-01	5.17E-01	---	---	---	231285_at	---
3.69	3.41	0.29	1.51E-01	5.17E-01	MAX	MYC associated factor X	chr14q23	214108_at	NM_002382 /// NM_145112 /// NM_145113 /// NM_145114 /// NM_145116 /// NM_197957
4.02	3.39	0.63	1.51E-01	5.17E-01	---	---	---	235207_at	---
5.12	4.74	0.38	1.51E-01	5.18E-01	WFS1	Wolfram syndrome 1 (wolframin)	chr4p16	1555270_a_at	NM_006005
3.20	2.87	0.33	1.51E-01	5.18E-01	---	---	---	243918_at	---
5.75	5.42	0.33	1.51E-01	5.18E-01	BRD4	bromodomain containing 4	chr19p13.1	202103_at	NM_014299 /// NM_058243
2.88	2.55	0.33	1.51E-01	5.18E-01	---	---	---	229809_at	---
4.67	4.36	0.31	1.51E-01	5.18E-01	FBRS	fibrosin	chr16p11.2	242217_s_at	NM_001105079
6.25	5.76	0.49	1.51E-01	5.18E-01	FOXK2	forkhead box K2	chr17q25	226224_at	NM_004514
2.70	2.24	0.45	1.51E-01	5.18E-01	---	---	---	241883_x_at	---
6.48	5.79	0.69	1.51E-01	5.18E-01	IGFBP5	insulin-like growth factor binding protein 5	chr2q33-q36	211958_at	NM_000599
4.95	4.26	0.69	1.51E-01	5.18E-01	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	chr5q13	226290_at	NM_018429
5.26	4.50	0.76	1.51E-01	5.18E-01	RELN	reelin	chr7q22	205923_at	NM_005045 /// NM_173054
5.19	4.82	0.38	1.51E-01	5.18E-01	LOC401397	hypothetical LOC401397	chr7q31.1	224723_x_at	XR_040259 /// XR_040260 /// XR_040261 /// XR_040262
7.09	6.70	0.38	1.51E-01	5.18E-01	MYO7A	myosin VIIA	chr11q13.5	208189_s_at	NM_000260 /// NM_001127179 /// NM_001127180
8.43	7.51	0.92	1.51E-01	5.18E-01	GNG11	guanine nucleotide binding protein (G protein), gamma 11	chr7q21	204115_at	NM_004126
3.29	3.00	0.29	1.51E-01	5.18E-01	---	---	---	229011_at	---
7.03	5.31	1.72	1.51E-01	5.18E-01	SNF1LK	SNF1-like kinase	chr21q22.3	208078_s_at	NM_173354
6.87	6.61	0.26	1.51E-01	5.18E-01	RFK	riboflavin kinase	chr9q21.13	203224_at	NM_018339
3.25	3.04	0.21	1.51E-01	5.18E-01	KIF26B	kinesin family member 26B	chr1q44	220002_at	NM_018012
3.54	3.05	0.49	1.51E-01	5.18E-01	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	chr6q26	219693_at	NM_020133
5.63	5.36	0.27	1.51E-01	5.18E-01	GSK3A	glycogen synthase kinase 3 alpha	chr19q13.2	632_at	NM_019884
4.86	3.85	1.01	1.52E-01	5.18E-01	XIST	X (inactive)-specific transcript (non-protein coding)	chrXq13.2	214218_s_at	NR_001564
9.65	9.39	0.26	1.52E-01	5.18E-01	SNRPG	small nuclear ribonucleoprotein polypeptide G	chr2p14	205644_s_at	NM_003096

6.24	5.75	0.49	1.52E-01	5.18E-01	NUP153	nucleoporin 153kDa	chr6p22.3	202097_at	NM_005124
3.64	3.07	0.57	1.52E-01	5.18E-01	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	chr14q22.1	206993_at	NM_001003803 /// NM_001003805 /// NM_015684
2.57	2.33	0.24	1.52E-01	5.18E-01	GPR97	G protein-coupled receptor 97	chr16q13	1553723_at	NM_170776
6.56	6.03	0.53	1.52E-01	5.18E-01	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	chr16q22.1	227382_at	NM_030579
6.37	6.06	0.30	1.52E-01	5.18E-01	TOE1	target of EGR1, member 1 (nuclear)	---	204080_at	NM_025077
4.08	3.84	0.24	1.52E-01	5.18E-01	DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	chrXq13.1	212729_at	NM_020730 /// NM_021120
4.38	3.76	0.62	1.52E-01	5.18E-01	LOC285835	hypothetical protein LOC285835	chr6p21.32	230937_at	---
8.54	8.31	0.24	1.52E-01	5.19E-01	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	chr17p13	208827_at	NM_002798
6.21	5.81	0.40	1.52E-01	5.19E-01	DGKA	diacylglycerol kinase, alpha 80kDa	chr12q13.3	203385_at	NM_001345 /// NM_201444 /// NM_201445 /// NM_201554
4.62	4.31	0.31	1.52E-01	5.19E-01	ELL3	elongation factor RNA polymerase II-like 3	chr15q15.3	219517_at	NM_025165
7.27	6.96	0.31	1.52E-01	5.19E-01	ICT1	immature colon carcinoma transcript 1	chr17q25.1	204868_at	NM_001545
2.54	2.30	0.24	1.52E-01	5.19E-01	---	---	---	243572_at	---
2.74	2.51	0.23	1.52E-01	5.19E-01	---	---	---	237681_at	---
2.51	2.19	0.32	1.52E-01	5.19E-01	---	---	---	1557644_at	---
4.86	4.60	0.26	1.52E-01	5.19E-01	CROCCL1	ciliary rootlet coiled-coil, rootletin-like 1	chr1p36.13	1569293_x_at	XR_039823 /// XR_039824
6.57	6.27	0.31	1.52E-01	5.19E-01	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	208914_at	NM_015044
2.14	1.93	0.21	1.52E-01	5.19E-01	ZMYM5	zinc finger, MYM-type 5	chr13q12	235620_x_at	NM_001039649 /// NM_001039650
6.65	6.30	0.35	1.52E-01	5.19E-01	LOC440498	Hypothetical gene supported by AK001829	chr18q23	232594_at	XM_498704 /// XM_938817
6.12	5.85	0.27	1.52E-01	5.19E-01	---	---	---	220452_x_at	---
5.44	5.06	0.38	1.52E-01	5.19E-01	SFT2D3	SFT2 domain containing 3	chr2q14.3	226639_at	NM_032740
2.62	2.42	0.20	1.52E-01	5.19E-01	TXNDC2	thioredoxin domain-containing 2 (spermatozoa)	---	224168_at	NM_001098529 /// NM_001098530 /// NM_032243 /// XM_001721366 /// XM_001721367
7.06	6.02	1.04	1.52E-01	5.19E-01	CAB39L	calcium binding protein 39-like	chr13q14.2-q14.3	225915_at	NM_001079670 /// NM_030925
7.44	7.02	0.42	1.52E-01	5.19E-01	MSRA	methionine sulfoxide reductase A	chr8p23.1	219281_at	NM_012331
9.61	9.37	0.24	1.52E-01	5.19E-01	CSNK2B /// LY6G5B	casein kinase 2, beta polypeptide /// lymphocyte antigen 6 complex, locus G5B	chr6p21-p12|6p21.3 /// chr6p21.3	201390_s_at	NM_001320 /// NM_021221
5.55	4.90	0.64	1.53E-01	5.19E-01	REV1	REV1 homolog (S. cerevisiae)	chr2q11.1-q11.2	218428_s_at	NM_001037872 /// NM_016316
8.13	7.69	0.44	1.53E-01	5.19E-01	TESK1	testis-specific kinase 1	chr9p13	204106_at	NM_006285
7.14	6.36	0.78	1.53E-01	5.20E-01	RPL31	ribosomal protein L31	chr2q11.2	200962_at	NM_000993 /// NM_001098577 /// NM_001099693

3.85	3.50	0.35	1.53E-01	5.20E-01	ZNF837	zinc finger protein 837	chr19q13.43	241277_x_at	NM_001129730 /// NM_138466 /// XM_001725760 /// XM_001725797 /// XM_001726206 /// XM_001726207 /// XM_375665 /// XM_938741																				
4.03	3.75	0.29	1.53E-01	5.20E-01	AMAC1 /// AMAC1L2	acyl-malonyl condensing enzyme 1 /// acyl-malonyl condensing enzyme 1-like 2	chr17q12 /// chr8p23-p22	1553340_s_at	NM_054028 /// NM_152462																				
3.47	3.27	0.19	1.53E-01	5.20E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	234364_at	---																				
10.76	10.55	0.21	1.53E-01	5.20E-01	NONO	non-POU domain containing, octamer-binding	chrXq13.1	200057_s_at	NM_007363																				
2.56	2.30	0.26	1.53E-01	5.20E-01	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	chr5q31	222971_at	NM_002488																				
11.01	10.42	0.59	1.53E-01	5.20E-01	APOE	apolipoprotein E	chr19q13.2	212884_x_at	NM_000041																				
8.71	8.45	0.27	1.53E-01	5.20E-01	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	chr14q24.3	200929_at	NM_006827																				
5.44	5.09	0.35	1.53E-01	5.20E-01	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	chr18q22.3	1554239_s_at	NM_175907																				
4.16	3.88	0.28	1.53E-01	5.20E-01	NACAD	NAC alpha domain containing	chr7p13	213630_at	XM_001126176 /// XM_001133202 /// XM_001717181 /// XM_166571																				
9.32	9.00	0.32	1.53E-01	5.20E-01	BAT3	HLA-B associated transcript 3	chr6p21.3	210208_x_at	NM_001098534 /// NM_004639 /// NM_080702 /// NM_080703																				
5.96	5.65	0.31	1.53E-01	5.20E-01	KIAA0513	KIAA0513	chr16q24.1	204546_at	NM_014732																				
6.18	5.78	0.40	1.53E-01	5.20E-01	RPL31	ribosomal protein L31	chr2q11.2	221593_s_at	NM_000993 /// NM_001098577 /// NM_001099693																				
2.11	1.93	0.18	1.53E-01	5.20E-01	---	---	---	241029_at	---																				
5.31	4.98	0.33	1.53E-01	5.20E-01	IQSEC2	IQ motif and Sec7 domain 2	chrXp11.22	229840_at	NM_001111125 /// NM_015075 /// XM_001714411																				
6.81	6.38	0.44	1.53E-01	5.20E-01	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	chr22q13.33	205241_at	NM_005138																				
4.14	3.80	0.34	1.53E-01	5.20E-01	DMRTC1 /// LOC728656	DMRT-like family C1 /// doublesex-mab-3-like	chrXq13.1	1560300_a_at	NM_001080851 /// NM_033053																				
2.21	2.04	0.17	1.53E-01	5.20E-01	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	chr12p12.1-p11.2	1569788_at	NM_003034																				
6.37	6.11	0.27	1.53E-01	5.20E-01	C7orf44	chromosome 7 open reading frame 44	chr7p13	209445_x_at	NM_018224																				
2.43	2.19	0.23	1.53E-01	5.20E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	217065_at	---																				
4.40	4.11	0.29	1.53E-01	5.20E-01	EGLN1	egl nine homolog 1 (C. elegans)	chr1q42.1	224314_s_at	NM_022051																				
9.50	9.15	0.35	1.53E-01	5.20E-01	NOLA2	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs)	chr5q35.3	209104_s_at	NM_001034833 /// NM_017838																				
2.56	2.34	0.22	1.53E-01	5.20E-01	TM2D1	TM2 domain containing 1	chr1p31.3	213882_at	NM_032027																				
4.76	4.40	0.36	1.53E-01	5.20E-01	TOR2A	torsin family 2, member A	chr9q34.11	227972_at	NM_001085347 /// NM_001134430 /// NM_001134431 /// NM_130459																				

7.01	6.37	0.64	1.53E-01	5.20E-01	CTSC	cathepsin C	chr11q14.1-q14.3	225647_s_at	NM_001114173 /// NM_001814 /// NM_148170																				
3.55	3.31	0.24	1.53E-01	5.20E-01	---	---	---	1559808_at	---																				
3.07	2.84	0.22	1.54E-01	5.20E-01	DCST1	DC-STAMP domain containing 1	chr1q21.3	1553860_at	NM_152494																				
5.54	5.22	0.32	1.54E-01	5.21E-01	TBC1D7	TBC1 domain family, member 7	chr6p24.1	223461_at	NM_016495																				
2.41	2.22	0.19	1.54E-01	5.21E-01	---	---	---	1569703_a_at	---																				
3.88	3.61	0.26	1.54E-01	5.21E-01	LRRC14	leucine rich repeat containing 14	chr8q24.3	32062_at	NM_014665																				
8.29	7.92	0.38	1.54E-01	5.21E-01	KLHDC2	kelch domain containing 2	chr14q22.1	217906_at	NM_014315																				
5.20	4.78	0.42	1.54E-01	5.21E-01	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	chr17q21.32	241910_x_at	NM_001113738 /// NM_016632																				
2.30	2.12	0.18	1.54E-01	5.21E-01	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	chr2q24-q31	203397_s_at	NM_004482																				
7.08	6.48	0.60	1.54E-01	5.21E-01	NANS	N-acetylneuraminic acid synthase	chr9p24.1-p23	218189_s_at	NM_018946																				
5.45	5.05	0.40	1.54E-01	5.21E-01	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	chr7q22.1	205195_at	NM_001283 /// NM_057089																				
4.46	4.22	0.23	1.54E-01	5.21E-01	---	---	---	1561153_at	---																				
6.50	6.12	0.38	1.54E-01	5.21E-01	CHCHD5	coiled-coil-helix-coiled-coil-helix domain containing 5	chr2q13	223479_s_at	NM_032309																				
3.09	2.83	0.26	1.54E-01	5.21E-01	DAB2IP	DAB2 interacting protein	chr9q33.1-q33.3	228942_s_at	NM_032552 /// NM_138709																				
3.51	3.17	0.35	1.54E-01	5.21E-01	C9orf47	chromosome 9 open reading frame 47	chr9q22.1	231286_at	NM_001001938																				
6.26	5.98	0.28	1.54E-01	5.21E-01	THOC5	THO complex 5	chr22q12.2	209418_s_at	NM_001002877 /// NM_001002878 /// NM_001002879 /// NM_003678																				
4.43	4.01	0.42	1.54E-01	5.21E-01	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	chr8q23-q24	214708_at	NM_021021																				
3.96	3.55	0.40	1.54E-01	5.21E-01	LYNX1	Ly6/neurotoxin 1	chr8q24.3	1559388_a_at	NM_023946 /// NM_177457 /// NM_177458 /// NM_177476 /// NM_177477																				
4.74	4.40	0.34	1.54E-01	5.21E-01	C19orf6	chromosome 19 open reading frame 6	chr19p13.3	212575_at	NM_001033026 /// NM_033420																				
8.77	8.50	0.27	1.54E-01	5.21E-01	PRR13	proline rich 13	chr12q12	217794_at	NM_001005354 /// NM_018457																				
3.87	3.50	0.37	1.54E-01	5.21E-01	LCE1E	late cornified envelope 1E	chr1q21.3	1559224_at	NM_178353																				
7.41	7.00	0.41	1.54E-01	5.21E-01	ZBTB44	zinc finger and BTB domain containing 44	chr11q24.3	225845_at	NM_014155																				
7.32	6.73	0.59	1.54E-01	5.21E-01	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	chr6q23	202644_s_at	NM_006290																				
2.70	2.45	0.26	1.54E-01	5.21E-01	TAGAP	T-cell activation RhoGTPase activating protein	chr6q25.3	1552542_s_at	NM_054114 /// NM_138810 /// NM_152133																				
9.21	8.90	0.30	1.54E-01	5.21E-01	C19orf43	chromosome 19 open reading frame 43	chr19p13.13	223003_at	NM_024038																				
2.70	2.50	0.21	1.54E-01	5.21E-01	---	---	---	224051_at	---																				
5.17	4.73	0.44	1.54E-01	5.21E-01	TMCO6	transmembrane and coiled-coil domains 6	chr5q31.3	213550_s_at	NM_018502																				
4.24	3.98	0.26	1.54E-01	5.21E-01	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	chr1p36.2	211841_s_at	NM_001039664 /// NM_003790 /// NM_148965 /// NM_148966 /// NM_148967 /// NM_148970																				
6.15	5.68	0.47	1.54E-01	5.21E-01	AP4B1	adaptor-related protein complex 4, beta 1 subunit	chr1p13.2	231714_s_at	NM_006594																				
2.39	2.02	0.37	1.54E-01	5.21E-01	---	---	---	244820_at	---																				

4.14	3.54	0.60	1.54E-01	5.21E-01	RRAD	Ras-related associated with diabetes	chr16q22	204802_at	NM_001128850 /// NM_004165																				
9.59	8.80	0.79	1.54E-01	5.21E-01	UGCG	UDP-glucose ceramide glucosyltransferase	chr9q31	224967_at	NM_003358																				
2.72	2.45	0.27	1.55E-01	5.21E-01	SNHG10	small nucleolar RNA host gene 10 (non-protein coding)	chr14q32.13	238691_at	NR_001459 /// NR_003138																				
3.37	3.14	0.23	1.55E-01	5.21E-01	RBM41	RNA binding motif protein 41	chrXq22.1-q24	232860_x_at	NM_018301																				
3.98	3.61	0.36	1.55E-01	5.21E-01	---	---	---	231316_at	---																				
2.98	2.54	0.44	1.55E-01	5.22E-01	MYBPC1	myosin binding protein C, slow type	chr12q23.2	214087_s_at	NM_002465 /// NM_206819 /// NM_206820 /// NM_206821																				
3.96	3.67	0.28	1.55E-01	5.22E-01	LRRC14	leucine rich repeat containing 14	chr8q24.3	203495_at	NM_014665																				
6.85	6.58	0.27	1.55E-01	5.22E-01	ATXN2	ataxin 2	chr12q24.1	202622_s_at	NM_002973																				
2.27	1.82	0.45	1.55E-01	5.22E-01	EFCAB2	EF-hand calcium binding domain 2	chr1q44	223608_at	NM_032328																				
2.61	2.35	0.25	1.55E-01	5.22E-01	LOC439914	hypothetical gene supported by NM_175889	chr11q13.1	1556639_at	XR_000554 /// XR_000637																				
10.22	9.91	0.31	1.55E-01	5.22E-01	MRPS24	mitochondrial ribosomal protein S24	chr7p14	224948_at	NM_032014																				
4.39	4.07	0.32	1.55E-01	5.22E-01	TRAFD1	TRAF-type zinc finger domain containing 1	chr12q	243196_s_at	NM_006700																				
5.01	4.58	0.43	1.55E-01	5.22E-01	PLAUR	plasminogen activator, urokinase receptor	chr19q13	211924_s_at	NM_001005376 /// NM_001005377 /// NM_002659																				
3.35	3.01	0.34	1.55E-01	5.22E-01	NCDN	Neurochondrin	chr1p34.3	237002_at	NM_001014839 /// NM_001014841 /// NM_014284																				
7.33	6.87	0.45	1.55E-01	5.22E-01	PWWP2B	PWWP domain containing 2B	chr10q26.3	227999_at	NM_001098637 /// NM_138499																				
2.66	2.43	0.23	1.55E-01	5.22E-01	ITGB4	integrin, beta 4	chr17q25	211905_s_at	NM_000213 /// NM_001005619 /// NM_001005731																				
2.58	2.20	0.37	1.55E-01	5.23E-01	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	chr4q32.1	220317_at	NM_004744																				
2.49	2.05	0.43	1.55E-01	5.23E-01	TC2N	tandem C2 domains, nuclear	chr14q32.12	1553132_a_at	NM_001128595 /// NM_001128596 /// NM_152332																				
6.94	6.64	0.31	1.55E-01	5.23E-01	ATF5	activating transcription factor 5	chr19q13.3	204998_s_at	NM_012068																				
11.89	11.71	0.18	1.55E-01	5.23E-01	PPIA	peptidylprolyl isomerase A (cyclophilin A)	chr7p13	211378_x_at	NM_021130																				
2.41	2.21	0.19	1.55E-01	5.23E-01	LOC151121	hypothetical protein LOC151121	chr2q21.1	1560750_at	XR_017843 /// XR_017948 /// XR_041796																				
7.94	7.35	0.59	1.55E-01	5.23E-01	RALGDS	ral guanine nucleotide dissociation stimulator	chr9q34.3	209050_s_at	NM_001042368 /// NM_006266																				

3.24	3.05	0.19	1.56E-01	5.23E-01	GAGE1 /// GAGE12B /// GAGE12C /// GAGE12D /// GAGE12E /// GAGE12F /// GAGE12G /// GAGE12H /// GAGE12I /// GAGE12J /// GAGE13 /// GAGE2A /// GAGE2B /// GAGE2C /// GAGE2D /// GAGE2E /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7 /// GAGE8	G antigen 1 /// G antigen 12B /// G antigen 12C /// G antigen 12D /// G antigen 12E /// G antigen 12F /// G antigen 12G /// G antigen 12H /// G antigen 12I /// G antigen 12J /// G antigen 13 /// G antigen 2A /// G antigen 2B /// G antigen 2C /// G antigen 2D /// G antigen 2E /// G antigen 4 /// G antigen 5 /// G antigen 6 /// G antigen 7 /// G antigen 8	chrXp11.23 /// chrXp11.4-p11.2	207086_x_at	NM_001040663 /// NM_001085441 /// NM_001098405 /// NM_001098406 /// NM_001098407 /// NM_001098408 /// NM_001098409 /// NM_001098410 /// NM_001098411 /// NM_001098418 /// NM_001127199 /// NM_001127200 /// NM_001127212 /// NM_001127345 /// NM_001468 /// NM_001472 /// NM_001474 /// NM_001475 /// NM_001476 /// NM_001477 /// NM_012196 /// NM_021123 /// XM_001130991 /// XM_001713660 /// XM_001720189																				
3.93	3.70	0.22	1.56E-01	5.23E-01	WDR27	WD repeat domain 27	chr6q27	235576_at	NM_182552																				
3.18	2.81	0.37	1.56E-01	5.23E-01	KIAA0562	KIAA0562	chr1p36.32	204075_s_at	NM_014704																				
2.31	2.11	0.20	1.56E-01	5.23E-01	---	---	---	234666_at	---																				
4.58	4.17	0.41	1.56E-01	5.23E-01	ATF5	activating transcription factor 5	chr19q13.3	204999_s_at	NM_012068																				
5.45	4.99	0.47	1.56E-01	5.23E-01	TRIM35	tripartite motif-containing 35	chr8p21.2	227102_at	NM_171982																				
7.41	7.11	0.31	1.56E-01	5.23E-01	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	chr19p12	31807_at	NM_019070																				
2.78	2.62	0.16	1.56E-01	5.23E-01	---	---	---	1562068_at	---																				
4.56	3.93	0.63	1.56E-01	5.23E-01	ANKRD55	Ankyrin repeat domain 55	chr5q11.2	240456_at	NM_001039935 /// NM_024669																				

3.35	3.19	0.16	1.56E-01	5.23E-01	BRCA1	breast cancer 1, early onset	chr17q21	211851_x_at	NM_007294 /// NM_007295 /// NM_007296 /// NM_007297 /// NM_007298 /// NM_007299 /// NM_007300 /// NM_007302 /// NM_007303 /// NM_007304 /// NM_007305																				
2.36	2.11	0.25	1.56E-01	5.24E-01	---	---	---	1560855_at	---																				
3.65	3.33	0.32	1.56E-01	5.24E-01	NLRP3	NLR family, pyrin domain containing 3	chr1q44	207075_at	NM_001079821 /// NM_001127461 /// NM_001127462 /// NM_004895 /// NM_183395																				
8.60	8.32	0.27	1.56E-01	5.24E-01	PALLD	palladin, cytoskeletal associated protein	chr4q32.3	200897_s_at	NM_016081																				
7.63	7.20	0.43	1.56E-01	5.24E-01	ETHE1	ethylmalonic encephalopathy 1	chr19q13.31	204034_at	NM_014297																				
6.60	6.15	0.45	1.57E-01	5.24E-01	---	---	---	1566342_at	---																				
5.61	5.40	0.20	1.57E-01	5.24E-01	---	---	---	240984_at	---																				
4.31	4.00	0.30	1.57E-01	5.24E-01	---	---	---	231378_at	---																				
6.36	5.98	0.38	1.57E-01	5.24E-01	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	chr1q42.3	226233_at	NM_152490																				
3.38	2.97	0.41	1.57E-01	5.24E-01	---	---	---	233196_at	---																				
3.34	3.08	0.26	1.57E-01	5.24E-01	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr7p14.3	202903_at	NM_001130710 /// NM_012322																				
4.02	3.60	0.42	1.57E-01	5.24E-01	KIAA1704	KIAA1704	chr13q13-q14	226429_at	NM_018559																				
5.33	4.75	0.58	1.57E-01	5.25E-01	USP46	ubiquitin specific peptidase 46	chr4q12	203869_at	NM_001134223 /// NM_022832																				
8.29	7.96	0.32	1.57E-01	5.25E-01	METTL11A	methyltransferase like 11A	chr9q34.11	223368_s_at	NM_014064																				
2.34	2.09	0.25	1.57E-01	5.25E-01	B3GALTL	beta 1,3-galactosyltransferase-like	chr13q12.3	227083_at	NM_194318																				
2.52	2.22	0.30	1.57E-01	5.25E-01	SLC25A27	solute carrier family 25, member 27	chr6p11.2-q12	1552774_a_at	NM_004277																				
4.49	4.02	0.47	1.57E-01	5.25E-01	---	---	---	227437_at	---																				
6.94	6.61	0.33	1.57E-01	5.25E-01	GKLP /// SCYL1	telomerase regulation-associated protein /// SCY1-like 1 (S. cerevisiae)	chr11q12.1 /// chr11q13	223033_s_at	NM_001048218 /// NM_001134680 /// NM_020680																				
3.42	3.12	0.29	1.57E-01	5.25E-01	EFNA5	Ephrin-A5	chr5q21	214036_at	NM_001962																				
10.65	10.46	0.20	1.57E-01	5.25E-01	SUMO2	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	chr17q25.1	213881_x_at	NM_001005849 /// NM_006937																				
5.32	4.75	0.57	1.57E-01	5.25E-01	FKBP7	FK506 binding protein 7	chr2q31.2	224002_s_at	NM_181342																				
8.40	8.15	0.25	1.57E-01	5.25E-01	ZNHIT1	zinc finger, HIT type 1	chr7q22.1	201541_s_at	NM_006349																				
2.44	2.24	0.20	1.57E-01	5.25E-01	SCTR	secretin receptor	chr2q14.1	1565737_at	NM_002980																				
8.63	8.32	0.32	1.57E-01	5.25E-01	SURF4	surfeit 4	chr9q34.2	222978_at	NM_033161																				
2.28	2.06	0.22	1.57E-01	5.25E-01	TRIM59	tripartite motif-containing 59	chr3q26.1	227801_at	NM_173084																				
2.70	2.49	0.21	1.57E-01	5.25E-01	LOC92249	hypothetical LOC92249	chrXq11.2	216838_at	NR_015353																				
2.94	2.77	0.18	1.57E-01	5.25E-01	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	chr3q29	1553668_at	NM_032773																				
5.88	5.59	0.29	1.57E-01	5.25E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	216885_s_at	NM_015726																				
2.71	2.48	0.23	1.57E-01	5.25E-01	---	---	---	243156_at	---																				
8.22	8.01	0.21	1.57E-01	5.25E-01	GOLPH3	golgi phosphoprotein 3 (coat-protein)	chr5p13.3	217803_at	NM_022130																				
4.33	4.04	0.29	1.57E-01	5.25E-01	---	---	---	1563250_at	---																				
2.54	2.32	0.22	1.57E-01	5.25E-01	TIAM2	T-cell lymphoma invasion and metastasis 2	chr6q25.2	219950_s_at	NM_001010927 /// NM_012454																				
3.56	3.29	0.27	1.57E-01	5.25E-01	ARHGEF15	Rho guanine nucleotide exchange factor (GEF) 15	chr17p13.1	205507_at	NM_173728																				
6.88	6.17	0.71	1.58E-01	5.25E-01	ZNF711	zinc finger protein 711	chrXq21.1-q21.2	228988_at	NM_021998																				
3.43	3.23	0.19	1.58E-01	5.25E-01	---	---	---	234900_at	---																				

7.89	7.44	0.45	1.58E-01	5.25E-01	SIDT2	SID1 transmembrane family, member 2	chr11q23.3	56256_at	NM_001040455																				
4.14	3.94	0.20	1.58E-01	5.25E-01	TTC9B	tetratricopeptide repeat domain 9B	chr19q13.2	242484_at	NM_152479																				
6.27	5.79	0.48	1.58E-01	5.25E-01	ATXN1	ataxin 1	chr6p23	203232_s_at	NM_000332 /// NM_001128164																				
7.36	6.95	0.40	1.58E-01	5.25E-01	RBM15	RNA binding motif protein 15	chr1p13	219286_s_at	NM_022768																				
6.55	6.29	0.26	1.58E-01	5.25E-01	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	chr7q36	207622_s_at	NM_005692 /// NM_007189																				
5.64	5.27	0.37	1.58E-01	5.25E-01	GSR	glutathione reductase	chr8p21.1	205770_at	NM_000637																				
2.32	2.14	0.18	1.58E-01	5.25E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	210741_at	NM_015313																				
2.60	2.40	0.20	1.58E-01	5.26E-01	LGALS13	lectin, galactoside-binding, soluble, 13	chr19q13.1	220440_at	NM_013268																				
3.21	3.02	0.20	1.58E-01	5.26E-01	ARIH2	Ariadne homolog 2 (Drosophila)	chr3p21.2-p21.3	1559121_s_at	NM_006321																				
3.96	3.39	0.57	1.58E-01	5.26E-01	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	chr3q12.1	210942_s_at	NM_006100																				
2.05	1.86	0.19	1.58E-01	5.26E-01	CDH26	cadherin-like 26	chr20q13.2-q13.33	233662_at	NM_021810 /// NM_177980																				
4.05	3.57	0.48	1.58E-01	5.26E-01	TPCN2	two pore segment channel 2	chr11q13.2	229250_at	NM_139075																				
2.38	2.22	0.17	1.58E-01	5.26E-01	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	chr4q21	211494_s_at	NM_001098484 /// NM_001134742 /// NM_003759																				
3.29	3.03	0.26	1.58E-01	5.26E-01	ELMO2	engulfment and cell motility 2	chr20q13	1554857_at	NM_133171 /// NM_182764																				
8.86	8.42	0.44	1.58E-01	5.26E-01	WTAP	Wilms tumor 1 associated protein	chr6q25-q27	227621_at	NM_004906 /// NM_152857 /// NM_152858																				
9.03	8.47	0.56	1.58E-01	5.26E-01	FOSL2	FOS-like antigen 2	chr2p23.3	225262_at	NM_005253																				
4.46	4.13	0.32	1.58E-01	5.26E-01	PARP9	poly (ADP-ribose) polymerase family, member 9	chr3q13-q21	227807_at	NM_031458																				
2.53	2.35	0.18	1.58E-01	5.26E-01	---	---	---	238895_at	---																				
5.90	5.15	0.75	1.58E-01	5.26E-01	LMCD1	LIM and cysteine-rich domains 1	chr3p26-p24	218574_s_at	NM_014583																				
3.68	3.34	0.34	1.58E-01	5.26E-01	FAM119A	family with sequence similarity 119, member A	chr2q33.3	235177_at	NM_001127395 /// NM_145280																				
8.26	7.76	0.50	1.59E-01	5.27E-01	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	chr19p13.2	200664_s_at	NM_006145																				
7.08	6.68	0.40	1.59E-01	5.27E-01	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	chr7p13	207318_s_at	NM_003718 /// NM_031267																				
2.72	2.51	0.22	1.59E-01	5.27E-01	LOC100131096	Hypothetical protein LOC100131096	chr17q25.3	228591_at	XM_001720907 /// XM_001726205 /// XM_001726705																				
6.54	6.33	0.21	1.59E-01	5.27E-01	CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11p11	221742_at	NM_001025596 /// NM_006560 /// NM_198700																				
2.81	2.59	0.22	1.59E-01	5.27E-01	---	---	---	237010_at	---																				
6.13	5.70	0.42	1.59E-01	5.27E-01	SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	chr3q27.2	222523_at	NM_021627																				
2.26	2.09	0.18	1.59E-01	5.27E-01	ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif, 20	chr12q12	1553409_at	NM_025003																				
7.42	6.94	0.48	1.59E-01	5.27E-01	PCTK1	PCTAIRE protein kinase 1	chrXp11.3-p11.23	208824_x_at	NM_006201 /// NM_033018																				
2.76	2.53	0.23	1.59E-01	5.27E-01	CXorf24	chromosome X open reading frame 24	chrXp11.3	239034_at	XM_926772 /// XM_937342																				
2.32	2.11	0.21	1.59E-01	5.27E-01	---	---	---	215964_at	---																				
2.41	2.19	0.22	1.59E-01	5.27E-01	LOC150005	hypothetical protein LOC150005	chr21q21.1	1561342_at	---																				
3.01	2.68	0.33	1.59E-01	5.27E-01	C9orf126	chromosome 9 open reading frame 126	chr9q33.3	241754_at	NM_173690																				
5.27	5.05	0.22	1.59E-01	5.27E-01	HIST1H2AD /// HIST1H3D	histone cluster 1, H2ad /// histone cluster 1, H3d	chr6p21.3	214522_x_at	NM_003530 /// NM_021065																				
6.67	6.19	0.48	1.59E-01	5.27E-01	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	chr1p36	221892_at	NM_004285																				
5.77	5.41	0.36	1.59E-01	5.27E-01	---	---	---	226579_at	---																				
2.35	2.10	0.26	1.59E-01	5.27E-01	IGFBP7	insulin-like growth factor binding protein 7	chr4q12	213910_at	NM_001553																				
8.00	7.65	0.36	1.59E-01	5.27E-01	CBR1	carbonyl reductase 1	chr21q22.13	209213_at	NM_001757																				
7.51	7.07	0.45	1.59E-01	5.27E-01	SRP19	signal recognition particle 19kDa	chr5q21-q22	205335_s_at	NM_003135																				

4.05	3.76	0.29	1.59E-01	5.27E-01	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	chr22q12.2	211391_s_at	NM_014323 /// NM_032050 /// NM_032051 /// NM_032052																				
5.64	5.40	0.23	1.59E-01	5.27E-01	B9D1	B9 protein domain 1	chr17p11.2	205662_at	NM_015681																				
8.73	8.44	0.30	1.59E-01	5.27E-01	FAM96B	family with sequence similarity 96, member B	chr16q22.1-q22.3	218074_at	NM_016062																				
4.72	4.29	0.43	1.59E-01	5.27E-01	C16orf53	chromosome 16 open reading frame 53	chr16p11.2	231878_at	NM_024516																				
5.46	4.82	0.64	1.59E-01	5.28E-01	AXIN2	axin 2	chr17q23-q24	222696_at	NM_004655																				
3.58	3.19	0.39	1.60E-01	5.28E-01	CHKB /// CPT1B	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	chr22q13.33	210069_at	NM_004377 /// NM_005198 /// NM_152245 /// NM_152246 /// NM_152247 /// NM_152253																				
2.79	2.47	0.32	1.60E-01	5.28E-01	---	---	---	242645_at	---																				
2.65	2.47	0.17	1.60E-01	5.28E-01	hCG_1999814	hCG1999814	chr7q36.3	1564548_at	XM_001720548 /// XM_001726868 /// XM_926301 /// XM_942355																				
7.15	6.94	0.21	1.60E-01	5.28E-01	DTD1	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	chr20p11.23	234107_s_at	NM_080820																				
5.99	5.60	0.39	1.60E-01	5.28E-01	ARIH2	ariadne homolog 2 (Drosophila)	chr3p21.2-p21.3	201229_s_at	NM_006321																				
6.13	5.84	0.29	1.60E-01	5.28E-01	FDX1L	ferredoxin 1-like	chr19p13.2	226451_at	NM_001031734																				
7.73	7.13	0.60	1.60E-01	5.28E-01	---	---	---	229874_x_at	---																				
5.01	4.51	0.51	1.60E-01	5.28E-01	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	chr11p13	229666_s_at	NM_001033505 /// NM_001033506 /// NM_001326																				
3.71	3.49	0.23	1.60E-01	5.28E-01	SNED1	sushi, nidogen and EGF-like domains 1	chr2q37.3	1554798_at	NM_001080437																				
5.84	5.61	0.23	1.60E-01	5.28E-01	EZH1	enhancer of zeste homolog 1 (Drosophila)	chr17q21.1-q21.3	32259_at	NM_001991																				
2.12	1.91	0.21	1.60E-01	5.28E-01	---	---	---	1566468_at	---																				
4.61	4.35	0.27	1.60E-01	5.28E-01	---	---	---	243002_at	---																				
2.34	2.14	0.20	1.60E-01	5.28E-01	VSX1	visual system homeobox 1	chr20p11.23-p11.22	224075_s_at	NM_014588 /// NM_199425																				
3.63	3.26	0.38	1.60E-01	5.28E-01	RGL3	ral guanine nucleotide dissociation stimulator-like 3	chr19p13.2	1556355_x_at	NM_001035223																				
2.64	2.35	0.28	1.60E-01	5.28E-01	GNG2	guanine nucleotide binding protein (G protein), gamma 2	chr14q21	1555766_a_at	NM_053064																				
4.45	4.00	0.44	1.60E-01	5.28E-01	SCAND2	SCAN domain containing 2 pseudogene	chr15q25-q26	215670_s_at	NM_022050 /// NM_033633 /// NM_033634 /// NM_033635 /// NM_033636 /// NM_033640 /// NR_003654 /// NR_004859																				
6.65	6.09	0.56	1.60E-01	5.28E-01	NUDT4 /// NUDT4P1	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	chr12q21 /// chr1q21.1	212183_at	NM_019094 /// NM_199040 /// NR_002212																				
3.44	3.07	0.37	1.60E-01	5.29E-01	LRRC49	leucine rich repeat containing 49	chr15q23	219338_s_at	NM_017691																				
3.76	3.44	0.32	1.60E-01	5.29E-01	---	---	---	217647_at	---																				
2.16	1.97	0.19	1.60E-01	5.29E-01	ZNF826	zinc finger protein 826	chr19p12	1569191_at	NM_001039884																				

7.35	6.96	0.39	1.60E-01	5.29E-01	SIRPA	signal-regulatory protein alpha	chr20p13	202897_at	NM_001040022 /// NM_001040023 /// NM_080792																				
3.21	3.04	0.17	1.60E-01	5.29E-01	KIAA0494	KIAA0494	chr1pter-p22.1	1559023_a_at	NM_014774																				
8.25	7.81	0.45	1.60E-01	5.29E-01	HMGB1	high-mobility group box 1	chr13q12	224731_at	NM_002128																				
7.23	6.82	0.41	1.61E-01	5.29E-01	GPRASP2	G protein-coupled receptor associated sorting protein 2	chrXq22.1	228027_at	NM_001004051 /// NM_138437																				
3.41	3.07	0.34	1.61E-01	5.29E-01	ZNF664	Zinc finger protein 664	chr12q24.31	1569935_at	NM_152437																				
2.99	2.64	0.36	1.61E-01	5.29E-01	---	---	---	229347_at	---																				
2.82	2.45	0.37	1.61E-01	5.29E-01	SEC16B	SEC16 homolog B (S. cerevisiae)	chr1q25.2	228150_at	NM_033127																				
4.74	4.24	0.50	1.61E-01	5.29E-01	CAPN10	calpain 10	chr2q37.3	219333_s_at	NM_021251 /// NM_023083 /// NM_023085 /// NM_023089																				
4.53	4.11	0.42	1.61E-01	5.29E-01	IKZF5	IKAROS family zinc finger 5 (Pegasus)	chr10q26	220086_at	NM_022466																				
2.42	2.26	0.17	1.61E-01	5.29E-01	C21orf74	chromosome 21 open reading frame 74	chr21q21.1	1552605_s_at	XR_001010 /// XR_001423																				
2.13	1.94	0.19	1.61E-01	5.29E-01	LOC497256	hypothetical LOC497256	chr9q22.1	1560380_at	XR_001071																				
5.45	5.17	0.28	1.61E-01	5.29E-01	GGCX	gamma-glutamyl carboxylase	chr2p12	235413_at	NM_000821																				
2.23	2.02	0.21	1.61E-01	5.29E-01	CRAMP1L	Crm, cramped-like (Drosophila)	chr16p13.3	242355_at	NM_020825																				
7.62	7.29	0.33	1.61E-01	5.29E-01	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	chr8q22.2	202635_s_at	NM_005034																				
4.11	3.93	0.18	1.61E-01	5.29E-01	---	---	---	242842_at	---																				
6.19	5.86	0.33	1.61E-01	5.29E-01	MMD	monocyte to macrophage differentiation-associated	chr17q	203414_at	NM_012329																				
4.44	4.02	0.42	1.61E-01	5.29E-01	---	---	---	207688_s_at	---																				
2.61	2.34	0.27	1.61E-01	5.29E-01	---	---	---	1565722_at	---																				
5.36	5.02	0.34	1.61E-01	5.29E-01	CPT2	carnitine palmitoyltransferase II	chr1p32	204264_at	NM_000098																				
4.54	4.21	0.33	1.61E-01	5.29E-01	LSDP5	lipid storage droplet protein 5	chr19p13.3	1568667_s_at	NM_001013706																				
4.02	3.72	0.30	1.61E-01	5.29E-01	---	---	---	235423_at	---																				
2.32	2.16	0.16	1.61E-01	5.29E-01	TAS2R13	taste receptor, type 2, member 13	chr12p13	221395_at	NM_023920																				
6.25	5.98	0.27	1.61E-01	5.29E-01	NPY1R	neuropeptide Y receptor Y1	chr4q31.3-q32	205440_s_at	NM_000909																				
3.86	3.19	0.67	1.61E-01	5.29E-01	KIAA0101	KIAA0101	chr15q22.31	202503_s_at	NM_001029989 /// NM_014736																				
2.22	2.05	0.17	1.61E-01	5.29E-01	SLC44A5	solute carrier family 44, member 5	chr1p31.1	1552782_at	NM_001130058 /// NM_152697																				
7.92	7.34	0.58	1.61E-01	5.29E-01	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8p21-p12	209368_at	NM_001979																				
2.41	2.21	0.20	1.61E-01	5.29E-01	---	---	---	1558573_at	---																				
5.78	5.45	0.33	1.61E-01	5.30E-01	REEP3	receptor accessory protein 3	chr10q21.3	225785_at	NM_001001330																				
6.27	5.95	0.33	1.61E-01	5.30E-01	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	chr19p13.3	202354_s_at	NM_002096																				
2.73	2.51	0.22	1.61E-01	5.30E-01	---	---	---	238492_at	---																				
3.59	3.24	0.35	1.61E-01	5.30E-01	---	---	---	205316_at	---																				
6.95	6.49	0.46	1.61E-01	5.30E-01	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	chr7q31.3-q32	204169_at	NM_000883 /// NM_001102605 /// NM_183243																				
3.82	3.20	0.61	1.62E-01	5.30E-01	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	chr3q28	225612_s_at	NM_032047																				
5.14	4.84	0.30	1.62E-01	5.30E-01	MEF2A	myocyte enhancer factor 2A	chr15q26	214684_at	NM_001130926 /// NM_001130927 /// NM_001130928 /// NM_005587																				
5.88	5.52	0.35	1.62E-01	5.30E-01	GAS8	growth arrest-specific 8	chr16q24.3	204921_at	NM_001481 /// NR_023348																				
5.43	5.08	0.35	1.62E-01	5.30E-01	SLC15A4	solute carrier family 15, member 4	chr12q24.32	225057_at	NM_145648																				
7.02	6.75	0.27	1.62E-01	5.30E-01	CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11p11	209489_at	NM_001025596 /// NM_006560 /// NM_198700																				
2.19	2.03	0.17	1.62E-01	5.30E-01	---	---	---	1562216_at	---																				

4.98	4.54	0.45	1.62E-01	5.30E-01	PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	chr1p13.3	218040_at	NM_018061
2.78	2.27	0.51	1.62E-01	5.30E-01	HOXA13	homeobox A13	chr7p15-p14	231786_at	NM_000522
3.52	3.14	0.37	1.62E-01	5.30E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	208237_x_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723
8.80	8.53	0.27	1.62E-01	5.30E-01	COPE	coatomer protein complex, subunit epsilon	chr19p13.11	201264_at	NM_007263 /// NM_199442 /// NM_199444
7.51	6.98	0.53	1.62E-01	5.30E-01	MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	chr3q27	218440_at	NM_020166
9.26	9.00	0.26	1.62E-01	5.30E-01	BANF1	barrier to autointegration factor 1	chr11q13.1	210125_s_at	NM_003860
2.57	2.30	0.26	1.62E-01	5.30E-01	CRKRS	Cdc2-related kinase, arginine/serine-rich	chr17q12	213557_at	NM_015083 /// NM_016507
3.50	3.25	0.25	1.62E-01	5.30E-01	KIAA1755	KIAA1755	chr20q11.23	1561394_s_at	NM_001029864
3.45	2.93	0.51	1.62E-01	5.30E-01	---	---	---	227979_at	---
2.80	2.59	0.21	1.62E-01	5.30E-01	---	---	---	240640_at	---
3.42	3.20	0.22	1.62E-01	5.30E-01	PMFBP1	polyamine modulated factor 1 binding protein 1	chr16q22.3	221022_s_at	NM_031293
4.62	4.12	0.49	1.62E-01	5.30E-01	STARD10	StAR-related lipid transfer (START) domain containing 10	chr11q13	238911_at	NM_006645
2.24	2.08	0.17	1.62E-01	5.30E-01	SERGEF	secretion regulating guanine nucleotide exchange factor	chr11p14.3	223483_at	NM_012139
5.21	4.87	0.34	1.62E-01	5.30E-01	TRIM33	tripartite motif-containing 33	chr1p13.1	212435_at	NM_015906 /// NM_033020
4.11	3.84	0.26	1.62E-01	5.30E-01	LRRC57	leucine rich repeat containing 57	chr15q15.1	229232_at	NM_153260
5.71	5.23	0.49	1.62E-01	5.30E-01	ZNF238	zinc finger protein 238	chr1q44-qter	212774_at	NM_006352 /// NM_205768
2.24	2.08	0.16	1.62E-01	5.30E-01	---	---	---	244425_at	---
3.49	3.29	0.20	1.62E-01	5.30E-01	FBXL20	F-box and leucine-rich repeat protein 20	chr17q12	239224_at	NM_032875
8.54	7.91	0.63	1.62E-01	5.30E-01	HN1	hematological and neurological expressed 1	chr17q25.1	217755_at	NM_001002032 /// NM_001002033 /// NM_016185
2.25	2.08	0.18	1.62E-01	5.30E-01	---	---	---	224056_at	---
2.20	2.01	0.19	1.62E-01	5.30E-01	---	---	---	242404_at	---
3.84	3.47	0.37	1.62E-01	5.30E-01	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	chr1p36.11	1555499_a_at	NM_170743 /// NM_173064 /// NM_173065
2.41	2.24	0.17	1.62E-01	5.30E-01	MYH7B	myosin, heavy chain 7B, cardiac muscle, beta	chr20q11.22	215795_at	NM_020884
3.68	3.45	0.23	1.62E-01	5.30E-01	TMEM103	transmembrane protein 103	chr3p21.31	220600_at	NM_001031703
4.57	4.26	0.31	1.62E-01	5.30E-01	---	---	---	1559530_at	---
4.28	3.96	0.31	1.62E-01	5.30E-01	LOC442175	similar to hCG1811681	chr6p22.1	216490_x_at	XM_001130492 /// XM_001130871 /// XM_001719140
5.67	5.16	0.51	1.62E-01	5.30E-01	CHMP5	chromatin modifying protein 5	chr9p13.3	218085_at	NM_016410
10.35	10.08	0.27	1.62E-01	5.30E-01	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	chr7q34	218200_s_at	NM_004546
8.95	8.64	0.31	1.62E-01	5.31E-01	SF3B14	splicing factor 3B, 14 kDa subunit	chr2pter-p25.1	223416_at	NM_016047
4.98	4.57	0.41	1.62E-01	5.31E-01	SOX12	SRY (sex determining region Y)-box 12	chr20p13	204432_at	NM_006943
7.06	6.18	0.88	1.62E-01	5.31E-01	C7orf29	chromosome 7 open reading frame 29	chr7q36.1	227598_at	NM_138434
6.89	6.54	0.36	1.62E-01	5.31E-01	HDGFRP3	hepatoma-derived growth factor, related protein 3	chr15q25.2	209524_at	NM_016073
3.72	3.27	0.45	1.62E-01	5.31E-01	C7orf41	chromosome 7 open reading frame 41	chr7p15.1	226018_at	NM_152793
4.15	3.84	0.32	1.62E-01	5.31E-01	LPHN1	latrophilin 1	chr19p13.2	47560_at	NM_001008701 /// NM_014921
5.65	5.28	0.37	1.62E-01	5.31E-01	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	chr1q41-q42	217787_s_at	NM_004481
4.42	4.12	0.29	1.62E-01	5.31E-01	CNR1	cannabinoid receptor 1 (brain)	chr6q14-q15	213436_at	NM_016083 /// NM_033181
2.09	1.91	0.18	1.62E-01	5.31E-01	EREG	epiregulin	chr4q13.3	205767_at	NM_001432

7.39	6.56	0.83	1.62E-01	5.31E-01	KCTD14	potassium channel tetramerisation domain containing 14	chr11q14.1	219545_at	NM_023930																				
6.65	6.39	0.26	1.63E-01	5.31E-01	ERC1	ELKS/RAB6-interacting/CAST family member 1	chr12p13.3	226049_at	NM_015064 /// NM_178037 /// NM_178038 /// NM_178039 /// NM_178040																				
3.55	3.24	0.31	1.63E-01	5.31E-01	---	---	---	231249_at	---																				
3.37	2.99	0.38	1.63E-01	5.31E-01	FLJ10246	FLJ10246	chr5p12	220458_at	XR_001523 /// XR_001525																				
5.05	4.76	0.29	1.63E-01	5.31E-01	SLC35E1	solute carrier family 35, member E1	chr19p13.11	227518_at	NM_024881																				
7.06	6.75	0.31	1.63E-01	5.31E-01	CHPF	chondroitin polymerizing factor	chr2q35	202175_at	NM_024536																				
4.84	4.43	0.41	1.63E-01	5.31E-01	ELF2	E74-like factor 2 (ets domain transcription factor)	chr4q28	210361_s_at	NM_006874 /// NM_201999																				
9.09	8.77	0.32	1.63E-01	5.31E-01	GSTK1	glutathione S-transferase kappa 1	---	217751_at	NM_015917																				
4.74	3.35	1.40	1.63E-01	5.31E-01	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	chr7q21-q31	203789_s_at	NM_006379																				
2.66	2.48	0.17	1.63E-01	5.31E-01	C2orf13	chromosome 2 open reading frame 13	chr2p14	1555100_at	NM_173545																				
6.43	6.00	0.43	1.63E-01	5.31E-01	ARRDC1	arrestin domain containing 1	chr9q34.3	226405_s_at	NM_152285																				
4.07	3.78	0.29	1.63E-01	5.31E-01	CUGBP2	CUG triplet repeat, RNA binding protein 2	chr10p13	227178_at	NM_001025076 /// NM_001025077 /// NM_001083591 /// NM_006561																				
2.22	2.06	0.16	1.63E-01	5.31E-01	---	---	---	239365_at	---																				
3.06	2.70	0.36	1.63E-01	5.31E-01	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	chr5q35	221421_s_at	NM_030955																				
4.19	3.87	0.32	1.63E-01	5.31E-01	---	---	---	216554_s_at	---																				
2.73	2.51	0.22	1.63E-01	5.31E-01	GATM	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	chr15q21.1	231686_at	NM_001482																				
4.70	4.16	0.54	1.63E-01	5.31E-01	DPH3	DPH3, KTI11 homolog (S. cerevisiae)	chr3p24.3	225195_at	NM_001047434 /// NM_206831																				
5.14	4.78	0.37	1.63E-01	5.31E-01	SNX19	sorting nexin 19	chr11q25	202359_s_at	NM_014758																				
5.51	5.00	0.51	1.63E-01	5.31E-01	FAM44A	family with sequence similarity 44, member A	chr4p16.1	225821_s_at	NM_148894																				
2.91	2.69	0.22	1.63E-01	5.31E-01	---	---	---	229613_at	---																				
5.43	5.14	0.29	1.63E-01	5.31E-01	NVL	nuclear VCP-like	chr1q41-q42.2	207877_s_at	NM_002533 /// NM_206840																				
8.74	8.51	0.23	1.63E-01	5.31E-01	AP3S1	adaptor-related protein complex 3, sigma 1 subunit	chr5q22	202442_at	NM_001284																				
5.91	5.53	0.38	1.63E-01	5.31E-01	PAQR8	progestin and adipoQ receptor family member VIII	chr6p12.1	226423_at	NM_133367																				
3.25	2.90	0.36	1.63E-01	5.32E-01	LOC100133696 /// PCOTH	hypothetical protein LOC100133696 /// prostate collagen triple helix	chr13q12	222277_at	NM_001014442 /// XM_001717385																				
2.32	2.16	0.16	1.64E-01	5.32E-01	---	---	---	1569937_at	---																				
3.56	3.15	0.40	1.64E-01	5.32E-01	TSC22D4	TSC22 domain family, member 4	chr7p21-p15	1554501_at	NM_030935																				
10.75	10.19	0.56	1.64E-01	5.32E-01	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	chr6p21.3	211990_at	NM_033554																				
3.36	3.13	0.22	1.64E-01	5.32E-01	ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	chr12q24.12	237482_s_at	NM_025247																				
6.46	6.17	0.29	1.64E-01	5.32E-01	RNF170	ring finger protein 170	chr8p11.21	226104_at	NM_030954																				
5.08	4.71	0.37	1.64E-01	5.32E-01	C19orf39	chromosome 19 open reading frame 39	chr19p13.2	227352_at	NM_175871																				
10.14	9.86	0.27	1.64E-01	5.32E-01	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	chr5q31	209224_s_at	NM_002488																				
4.95	4.63	0.31	1.64E-01	5.32E-01	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	chr14q22.1	235113_at	NM_152329 /// NM_203467																				
6.71	6.38	0.33	1.64E-01	5.32E-01	CNPY3	canopy 3 homolog (zebrafish)	chr6pter-p12.1	217931_at	NM_006586																				
9.27	9.02	0.25	1.64E-01	5.32E-01	CCT7	chaperonin containing TCP1, subunit 7 (eta)	chr2p13.2	200812_at	NM_001009570 /// NM_006429																				
5.37	4.88	0.49	1.64E-01	5.32E-01	ZNF436	zinc finger protein 436	chr1p36	226114_at	NM_001077195 /// NM_030634																				
3.63	3.06	0.57	1.64E-01	5.32E-01	RNF166	ring finger protein 166	chr16q24.3	227726_at	NM_178841																				
4.84	4.49	0.35	1.64E-01	5.32E-01	ZNF337	zinc finger protein 337	chr20p11.21	37860_at	NM_015655																				
7.14	6.84	0.30	1.64E-01	5.32E-01	SDF2	stromal cell-derived factor 2	chr17q11.2	203090_at	NM_006923																				
6.86	6.48	0.38	1.64E-01	5.32E-01	MPI	mannose phosphate isomerase	chr15q22-qter	202472_at	NM_002435																				
7.11	6.79	0.32	1.64E-01	5.32E-01	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	chr1pter-q24	213296_at	NM_007033																				
8.01	7.61	0.39	1.64E-01	5.32E-01	TMEM165	transmembrane protein 165	chr4q12	218095_s_at	NM_018475																				

7.37	7.12	0.24	1.64E-01	5.32E-01	IGF2R	insulin-like growth factor 2 receptor	chr6q26	201393_s_at	NM_000876
6.05	5.60	0.46	1.64E-01	5.32E-01	C7orf43	chromosome 7 open reading frame 43	chr7q22.1	220659_s_at	NM_018275
2.31	2.08	0.23	1.64E-01	5.32E-01	---	---	---	231655_x_at	---
4.24	3.77	0.47	1.64E-01	5.32E-01	NBR2	neighbor of BRCA1 gene 2	chr17q21	1553992_s_at	NR_003108
6.55	6.32	0.22	1.64E-01	5.32E-01	VPS39	vacuolar protein sorting 39 homolog (S. cerevisiae)	chr15q15.1	212156_at	NM_015289
4.74	4.31	0.43	1.64E-01	5.32E-01	C19orf66	chromosome 19 open reading frame 66	chr19p13.2	1555491_a_at	NM_018381
5.76	5.31	0.45	1.64E-01	5.32E-01	STXBP2	syntaxin binding protein 2	chr19p13.3-p13.2	209367_at	NM_001127396 /// NM_006949
3.51	3.19	0.32	1.64E-01	5.32E-01	PFDN6	prefoldin subunit 6	chr6p21.3	242048_at	NM_014260
2.68	2.48	0.20	1.64E-01	5.32E-01	---	---	---	237019_at	---
3.26	2.87	0.39	1.64E-01	5.32E-01	FBP2	fructose-1,6-bisphosphatase 2	chr9q22.3	206844_at	NM_003837
6.76	6.55	0.21	1.64E-01	5.32E-01	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	chr3q26.33	225358_at	NM_145261
3.33	3.14	0.19	1.64E-01	5.32E-01	VWA3B	von Willebrand factor A domain containing 3B	chr2q11.2	1558470_at	NM_144992
2.67	2.44	0.23	1.64E-01	5.32E-01	CTA-221G9.4	KIAA1671 protein	chr22q11.23	1563478_at	XR_040421 /// XR_040422 /// XR_040423
4.24	3.86	0.39	1.64E-01	5.33E-01	MYO7A	myosin VIIA	chr11q13.5	211104_s_at	NM_000260 /// NM_001127179 /// NM_001127180
3.34	2.81	0.53	1.64E-01	5.33E-01	---	---	---	226641_at	---
4.27	3.50	0.76	1.65E-01	5.33E-01	---	---	---	240655_at	---
2.33	2.13	0.20	1.65E-01	5.33E-01	UNC5C	Unc-5 homolog C (C. elegans)	chr4q21-q23	240958_at	NM_003728
7.26	6.75	0.51	1.65E-01	5.33E-01	TSPAN14	tetraspanin 14	chr10q23.1	221002_s_at	NM_001128309 /// NM_030927
8.32	7.86	0.46	1.65E-01	5.33E-01	AKT1	v-akt murine thymoma viral oncogene homolog 1	chr14q32.32|14q32.32	207163_s_at	NM_001014431 /// NM_001014432 /// NM_005163
2.49	2.28	0.21	1.65E-01	5.33E-01	---	---	---	1557042_at	---
10.51	9.78	0.73	1.65E-01	5.33E-01	IGFBP5	insulin-like growth factor binding protein 5	chr2q33-q36	211959_at	NM_000599
6.08	5.84	0.24	1.65E-01	5.33E-01	ZNF446	zinc finger protein 446	chr19q13.43	219900_s_at	NM_017908
4.82	4.23	0.59	1.65E-01	5.33E-01	---	---	---	230604_at	---
2.18	2.03	0.16	1.65E-01	5.33E-01	OR1A2	olfactory receptor, family 1, subfamily A, member 2	chr17p13.3	221445_at	NM_012352
3.65	3.39	0.26	1.65E-01	5.33E-01	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	chr14q11.2	210321_at	NM_033423
2.39	2.22	0.17	1.65E-01	5.33E-01	GPR112	G protein-coupled receptor 112	chrXq26.3	1553006_at	NM_153834
4.01	3.83	0.19	1.65E-01	5.34E-01	WFDC8	WAP four-disulfide core domain 8	chr20q13.12	215276_at	NM_130896 /// NM_181510
2.70	2.49	0.21	1.65E-01	5.34E-01	SLC17A1	solute carrier family 17 (sodium phosphate), member 1	chr6p23-p21.3	206872_at	NM_005074
6.31	6.05	0.26	1.65E-01	5.34E-01	UBE3B	ubiquitin protein ligase E3B	chr12q24.11	212403_at	NM_130466 /// NM_183415
6.99	6.42	0.57	1.65E-01	5.34E-01	HIPK1	homeodomain interacting protein kinase 1	chr1p13.2	212293_at	NM_152696 /// NM_181358 /// NM_198268 /// NM_198269
2.10	1.94	0.16	1.65E-01	5.34E-01	---	---	---	241638_at	---
5.94	5.67	0.26	1.65E-01	5.34E-01	HEXDC	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	chr17q25.3	1555866_a_at	NM_173620
6.31	5.98	0.33	1.66E-01	5.34E-01	BCAR1	breast cancer anti-estrogen resistance 1	chr16q22-q23	223116_at	NM_014567
3.78	3.46	0.32	1.66E-01	5.34E-01	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	chr10p11.22-p11.21	221280_s_at	NM_019619
7.22	6.79	0.44	1.66E-01	5.34E-01	NECAB3	N-terminal EF-hand calcium binding protein 3	chr20q11.22	210720_s_at	NM_031231 /// NM_031232
1.96	1.80	0.16	1.66E-01	5.34E-01	---	---	---	241532_at	---
2.45	2.29	0.16	1.66E-01	5.34E-01	ZPBP	zona pellucida binding protein	chr7p14.3	207021_at	NM_007009
5.05	4.41	0.63	1.66E-01	5.34E-01	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	chr8p12	226150_at	NM_001102559 /// NM_001102560 /// NM_032483

6.65	5.97	0.68	1.66E-01	5.34E-01	C17orf81	chromosome 17 open reading frame 81	chr17p13.1	219260_s_at	NM_015362 /// NM_203413 /// NM_203414 /// NM_203415																			
2.81	2.58	0.24	1.66E-01	5.34E-01	TMEM67	transmembrane protein 67	chr8q22.1	1563646_a_at	NM_153704																			
3.02	2.80	0.22	1.66E-01	5.34E-01	MFN2	mitofusin 2	chr1p36.22	1566105_at	NM_001127660 /// NM_014874																			
6.66	6.33	0.32	1.66E-01	5.34E-01	WDR77	WD repeat domain 77	chr1p13.2	201420_s_at	NM_024102																			
2.52	2.36	0.17	1.66E-01	5.34E-01	FN1	fibronectin 1	chr2q34	1558199_at	NM_002026 /// NM_054034 /// NM_212474 /// NM_212475 /// NM_212476 /// NM_212478 /// NM_212482																			
2.15	1.92	0.23	1.66E-01	5.34E-01	---	---	---	236277_at	---																			
9.68	9.44	0.24	1.66E-01	5.34E-01	CAPNS1	calpain, small subunit 1	chr19q13.12	200001_at	NM_001003962 /// NM_001749																			
4.57	3.92	0.65	1.66E-01	5.35E-01	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	chr14q32.1	202833_s_at	NM_000295 /// NM_001002235 /// NM_001002236 /// NM_001127700 /// NM_001127701 /// NM_001127702 /// NM_001127703 /// NM_001127704 /// NM_001127705 /// NM_001127706 /// NM_001127707																			
3.58	2.68	0.89	1.66E-01	5.35E-01	RP13-347D8.3	KIAA1210 protein	chrXq24	232332_at	NM_020721																			
6.16	5.81	0.35	1.66E-01	5.35E-01	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	chr22q11.2|22q11.21	217427_s_at	NM_003325																			
4.65	4.25	0.41	1.66E-01	5.35E-01	DNALI1	dynein, axonemal, light intermediate chain 1	chr1p35.1	205186_at	NM_003462																			
2.59	2.23	0.35	1.66E-01	5.35E-01	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	chr12p12.1	208561_at	NM_005691 /// NM_020297 /// NM_020298																			
7.32	6.89	0.43	1.66E-01	5.35E-01	C8orf82	chromosome 8 open reading frame 82	chr8q24	226710_at	NM_001001795																			
7.25	6.84	0.41	1.66E-01	5.35E-01	GLUL	glutamate-ammonia ligase (glutamine synthetase)	chr1q31	217202_s_at	NM_001033044 /// NM_001033056 /// NM_002065																			
2.45	2.28	0.17	1.66E-01	5.35E-01	LOC100130741	hypothetical protein LOC100130741	chr7q36.3	215740_at	XM_001720074 /// XM_001720612 /// XM_001721890																			

5.72	5.27	0.45	1.66E-01	5.35E-01	DUSP10	dual specificity phosphatase 10	chr1q41	221563_at	NM_007207 /// NM_144728 /// NM_144729																				
6.46	6.14	0.32	1.67E-01	5.35E-01	KIAA0284	KIAA0284	chr14q32.33	213242_x_at	NM_001112726 /// NM_015005																				
4.32	4.05	0.27	1.67E-01	5.35E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	224517_at	NR_003655 /// XR_042143 /// XR_042182																				
2.30	2.12	0.19	1.67E-01	5.35E-01	PGM2L1	phosphoglucomutase 2-like 1	chr11q13.4	235149_at	NM_173582																				
5.84	5.55	0.29	1.67E-01	5.35E-01	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	chr1p36.13	221656_s_at	NM_001011722 /// NM_018125																				
8.03	7.85	0.18	1.67E-01	5.35E-01	MRPS14	mitochondrial ribosomal protein S14	chr1q23-q25	203800_s_at	NM_022100																				
5.27	4.46	0.81	1.67E-01	5.36E-01	MRPL43	mitochondrial ribosomal protein L43	chr10q24.31	230026_at	NM_032112 /// NM_176792 /// NM_176793 /// NM_176794																				
4.56	4.26	0.30	1.67E-01	5.36E-01	EMILIN2	elastin microfibril interfacer 2	chr18p11.3	224374_s_at	NM_032048																				
3.71	3.46	0.24	1.67E-01	5.36E-01	TAL1	T-cell acute lymphocytic leukemia 1	chr1p32	216925_s_at	NM_003189																				
6.28	5.79	0.49	1.67E-01	5.36E-01	CGGBP1	CGG triplet repeat binding protein 1	chr3p12-p11.1	206861_s_at	NM_001008390 /// NM_003663																				
3.09	2.80	0.30	1.67E-01	5.36E-01	---	---	---	1570329_at	---																				
5.06	4.77	0.29	1.67E-01	5.36E-01	C20orf177	chromosome 20 open reading frame 177	chr20q13.2-q13.33	225313_at	NM_022106																				
5.59	5.34	0.25	1.67E-01	5.37E-01	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	chr20q13.33	217888_s_at	NM_018209 /// NM_175609																				
5.15	4.79	0.36	1.67E-01	5.37E-01	ATP13A2	ATPase type 13A2	chr1p36	218608_at	NM_022089																				
4.40	4.16	0.25	1.67E-01	5.37E-01	RGS10	regulator of G-protein signaling 10	chr10q25	204316_at	NM_001005339 /// NM_002925																				
2.09	1.92	0.17	1.67E-01	5.37E-01	DLEU7	deleted in lymphocytic leukemia, 7	chr13q14.3	1566081_at	NM_198989																				
2.26	2.05	0.20	1.67E-01	5.37E-01	RBMY2FP	RNA binding motif protein, Y-linked, family 2, member F pseudogene	chrYq11.223	216544_at	NR_002193																				
10.51	10.30	0.22	1.67E-01	5.37E-01	LOC100128140 /// LOC390183 /// LOC442162 /// RPS4X	similar to ribosomal protein S4, X-linked /// similar to Ribosomal protein S4, X-linked /// hypothetical LOC442162 /// ribosomal protein S4, X-linked	chr11q12.1 /// chr17p13.3 /// chr6p23 /// chrXq13.1	216342_x_at	NM_001007 /// XR_016275 /// XR_016748 /// XR_018242 /// XR_018871 /// XR_037026 /// XR_037282 /// XR_039001 /// XR_039397 /// XR_039417																				
3.09	2.84	0.25	1.67E-01	5.37E-01	FBLN1	fibulin 1	chr22q13.31	207834_at	NM_001996 /// NM_006485 /// NM_006486 /// NM_006487																				
6.07	5.72	0.35	1.67E-01	5.37E-01	GIGYF1	GRB10 interacting GYF protein 1	chr7q22	226768_at	NM_022574																				
6.48	6.01	0.47	1.67E-01	5.37E-01	SPRYD4	SPRY domain containing 4	chr12q13.2	225616_at	NM_207344																				
2.30	2.09	0.21	1.67E-01	5.37E-01	---	---	---	1563487_at	---																				

2.08	1.92	0.16	1.68E-01	5.37E-01	LOC400590	hypothetical LOC400590	chr17q11.2	1560992_at	XR_042032 /// XR_042033 /// XR_042034																				
11.21	11.06	0.15	1.68E-01	5.37E-01	RPL35A	ribosomal protein L35a	chr3q29-qter	225190_x_at	NM_000996																				
2.13	1.97	0.15	1.68E-01	5.37E-01	FAM122C	family with sequence similarity 122C	chrXq26.3	1552322_at	NM_138819																				
2.51	2.31	0.20	1.68E-01	5.37E-01	---	---	---	240495_at	---																				
7.40	6.68	0.72	1.68E-01	5.37E-01	SOCS2	suppressor of cytokine signaling 2	chr12q	203373_at	NM_003877																				
6.85	6.47	0.38	1.68E-01	5.37E-01	MAP4	microtubule-associated protein 4	chr3p21	243_g_at	NM_001134364 /// NM_001134365 /// NM_002375 /// NM_030884 /// NM_030885																				
7.61	7.14	0.47	1.68E-01	5.37E-01	ARHGEF18	rho/rac guanine nucleotide exchange factor (GEF) 18	chr19p13.3	213039_at	NM_001130955 /// NM_015318																				
5.73	5.43	0.30	1.68E-01	5.37E-01	LUC7L2	LUC7-like 2 (S. cerevisiae)	chr7q34	217842_at	NM_016019																				
2.85	2.67	0.17	1.68E-01	5.37E-01	DKK3	dickkopf homolog 3 (Xenopus laevis)	chr11p15.2	230508_at	NM_001018057 /// NM_013253 /// NM_015881																				
3.57	3.13	0.44	1.68E-01	5.37E-01	---	---	---	242521_at	---																				
8.33	7.62	0.71	1.68E-01	5.37E-01	KCTD12	potassium channel tetramerisation domain containing 12	chr13q22.3	212192_at	NM_138444																				
2.90	2.71	0.20	1.68E-01	5.37E-01	MAP1D	methionine aminopeptidase 1D	chr2q31.1	1569029_at	NM_199227																				
6.63	6.32	0.32	1.68E-01	5.38E-01	MAN1B1	mannosidase, alpha, class 1B, member 1	chr9q34	218636_s_at	NM_016219																				
4.44	3.95	0.49	1.68E-01	5.38E-01	TET3	tet oncogene family member 3	chr2p13.1	235542_at	NM_144993																				
5.25	4.99	0.26	1.68E-01	5.38E-01	C9orf156	chromosome 9 open reading frame 156	chr9q22.33	47530_at	NM_016481																				
3.34	3.06	0.28	1.68E-01	5.38E-01	---	---	---	229136_s_at	---																				
5.74	5.31	0.43	1.68E-01	5.38E-01	CSRP2BP	CSRP2 binding protein	chr20p11.23	228543_at	NM_020536 /// NM_177926																				
7.24	6.96	0.29	1.68E-01	5.38E-01	LYPLA2	lysophospholipase II	chr1p36.12-p35.1	202292_x_at	NM_007260																				
3.35	3.14	0.21	1.68E-01	5.38E-01	LOC284551	hypothetical protein LOC284551	chr1p35.2	1563802_at	---																				
5.77	5.52	0.25	1.68E-01	5.38E-01	ZNF592	zinc finger protein 592	chr15q25.3	227507_at	NM_014630																				
6.63	6.23	0.40	1.68E-01	5.38E-01	ATRIP /// TREX1	ATR interacting protein /// three prime repair exonuclease 1	chr3p21.31	205875_s_at	NM_016381 /// NM_032166 /// NM_033629 /// NM_130384																				
3.32	3.07	0.25	1.68E-01	5.38E-01	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	chr1q31	209992_at	NM_001018053 /// NM_006212																				
6.26	5.90	0.35	1.68E-01	5.38E-01	CCDC93	coiled-coil domain containing 93	chr2q14.1	209688_s_at	NM_019044																				
3.68	3.49	0.19	1.68E-01	5.38E-01	HLCS	holocarboxylase synthetase (biotin-(proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)) ligase)	chr21q22.1|21q22.13	207833_s_at	NM_000411																				
7.16	6.56	0.60	1.69E-01	5.38E-01	NASP	nuclear autoantigenic sperm protein (histone-binding)	chr1p34.1	201970_s_at	NM_002482 /// NM_152298 /// NM_172164																				
3.06	2.90	0.16	1.69E-01	5.38E-01	---	---	---	1566475_at	---																				
6.52	5.98	0.54	1.69E-01	5.38E-01	RGPD4 /// RGPD5 /// RGPD6 /// RGPD8	RANBP2-like and GRIP domain containing 4 /// RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 6 /// RANBP2-like and GRIP domain containing 8	chr2q12.3 /// chr2q13	212842_x_at	NM_001123363 /// NM_005054 /// NM_032260 /// XM_001133591 /// XM_001721299 /// XM_001722279																				
2.87	2.58	0.28	1.69E-01	5.38E-01	OTUB2	OTU domain, ubiquitin aldehyde binding 2	chr14q32.13	222878_s_at	NM_023112																				
3.85	3.58	0.27	1.69E-01	5.38E-01	MSRB3	methionine sulfoxide reductase B3	chr12q14.3	238583_at	NM_001031679 /// NM_198080																				

4.84	4.56	0.28	1.69E-01	5.38E-01	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	chr17q11.1-q11.2	227891_s_at	NM_003487 /// NM_139215																				
4.24	3.18	1.06	1.69E-01	5.38E-01	NRK	Nik related kinase	chrXq22.3	232771_at	NM_198465																				
3.65	3.40	0.24	1.69E-01	5.38E-01	---	---	---	231379_at	---																				
6.64	6.46	0.17	1.69E-01	5.38E-01	PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha isoform	chr1q32.2-q32.3	202187_s_at	NM_006243																				
2.11	1.94	0.16	1.69E-01	5.39E-01	---	---	---	1561953_at	---																				
4.50	3.89	0.61	1.69E-01	5.39E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	212935_at	NM_001112732 /// NM_024979																				
3.86	3.46	0.41	1.69E-01	5.39E-01	C20orf196	chromosome 20 open reading frame 196	chr20p12.3	235063_at	NM_152504																				
5.70	5.49	0.22	1.69E-01	5.39E-01	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	chr17p11.2	238434_at	NM_144775																				
8.51	8.27	0.23	1.69E-01	5.39E-01	SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	chr3q21.3	217716_s_at	NM_013336																				
4.51	3.59	0.92	1.69E-01	5.39E-01	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	chr10q21.1	205249_at	NM_000399																				
4.97	4.66	0.30	1.69E-01	5.39E-01	AQP3	aquaporin 3 (Gill blood group)	chr9p13	203747_at	NM_004925																				
2.30	2.07	0.24	1.69E-01	5.39E-01	---	---	---	1568650_a_at	---																				
2.48	2.32	0.17	1.69E-01	5.39E-01	---	---	---	241511_at	---																				
3.26	2.92	0.34	1.69E-01	5.39E-01	LOC129293	hypothetical protein LOC129293	chr2p11.2	227867_at	NM_001080824																				
6.82	6.41	0.41	1.69E-01	5.39E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	212636_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855																				
7.81	7.46	0.35	1.69E-01	5.39E-01	ARID1A	AT rich interactive domain 1A (SWI-like)	chr1p35.3	212152_x_at	NM_006015 /// NM_139135																				
2.54	2.33	0.21	1.69E-01	5.39E-01	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	chr1p36.1	1570625_at	NM_003198																				
3.34	3.08	0.26	1.69E-01	5.39E-01	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	chr20q13.33	1553304_at	NM_144703																				
8.83	7.76	1.07	1.69E-01	5.39E-01	NPTX2	neuronal pentraxin II	chr7q21.3-q22.1	213479_at	NM_002523																				
3.15	2.81	0.33	1.69E-01	5.39E-01	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	chr3q13.11	227900_at	NM_170662																				
10.11	9.63	0.48	1.70E-01	5.39E-01	TOB1	transducer of ERBB2, 1	chr17q21	228834_at	NM_005749																				
2.28	2.11	0.18	1.70E-01	5.39E-01	GLS2	glutaminase 2 (liver, mitochondrial)	chr12q13	1564707_x_at	NM_013267																				
3.61	3.35	0.25	1.70E-01	5.39E-01	CXCR6	chemokine (C-X-C motif) receptor 6	chr3p21	206974_at	NM_006564																				
5.73	5.34	0.40	1.70E-01	5.39E-01	ADCY6	adenylate cyclase 6	chr12q12-q13	209195_s_at	NM_015270 /// NM_020983																				
8.29	7.99	0.30	1.70E-01	5.39E-01	UBAP2	ubiquitin associated protein 2	chr9p13.3	219192_at	NM_018449																				
2.48	2.25	0.23	1.70E-01	5.39E-01	C17orf64	chromosome 17 open reading frame 64	chr17q23.2	1555985_at	NM_181707																				
4.15	3.79	0.36	1.70E-01	5.39E-01	ANKRD16	ankyrin repeat domain 16	chr10p15.1	231423_s_at	NM_001009941 /// NM_001009942 /// NM_001009943 /// NM_019046																				
5.35	5.09	0.26	1.70E-01	5.39E-01	PARC	p53-associated parkin-like cytoplasmic protein	chr6p21.1	213204_at	NM_015089																				
3.20	2.85	0.35	1.70E-01	5.39E-01	TAPBP	TAP binding protein (tapasin)	chr6p21.3	210294_at	NM_003190 /// NM_172208 /// NM_172209																				
8.51	8.15	0.37	1.70E-01	5.39E-01	LOC401152	HCV F-transactivated protein 1	chr4q26	224604_at	NM_001001701																				
6.75	6.08	0.68	1.70E-01	5.40E-01	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	chr20p12	213222_at	NM_015192 /// NM_182734																				
7.18	6.90	0.28	1.70E-01	5.40E-01	BCL2L13	BCL2-like 13 (apoptosis facilitator)	chr22q11.1	217955_at	NM_015367																				
2.21	2.06	0.15	1.70E-01	5.40E-01	NRXN1	neurexin 1	chr2p16.3	216096_s_at	NM_004801 /// NM_138735																				
9.63	9.28	0.34	1.70E-01	5.40E-01	PLP2	proteolipid protein 2 (colonic epithelium-enriched)	chrXp11.23	201136_at	NM_002668																				
5.90	5.44	0.46	1.70E-01	5.40E-01	SAMD4B	sterile alpha motif domain containing 4B	chr19q13.2	229871_at	NM_018028																				
2.46	2.17	0.29	1.70E-01	5.40E-01	---	---	---	1565635_at	---																				
2.45	2.25	0.20	1.70E-01	5.40E-01	LEPR	leptin receptor	chr1p31	1556919_at	NM_001003679 /// NM_001003680 /// NM_002303																				
5.82	5.28	0.54	1.70E-01	5.40E-01	RNF19B	ring finger protein 19B	chr1p35.1	36564_at	NM_001127361 /// NM_153341																				

3.94	3.60	0.33	1.70E-01	5.40E-01	---	---	---	226234_at	---																			
6.24	5.74	0.49	1.70E-01	5.40E-01	ZNF608	zinc finger protein 608	chr5q23.2	229817_at	NM_020747																			
2.32	2.12	0.20	1.70E-01	5.40E-01	BTF3	basic transcription factor 3	chr5q13.2	217467_at	NM_001037637 /// NM_001207																			
3.55	3.20	0.35	1.70E-01	5.40E-01	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	chr12p13.3	202498_s_at	NM_006931																			
3.32	2.61	0.71	1.70E-01	5.40E-01	STK17B	serine/threonine kinase 17b	chr2q32.3	205214_at	NM_004226																			
4.37	4.07	0.30	1.70E-01	5.40E-01	MAPKAP1	mitogen-activated protein kinase associated protein 1	chr9q33.3	229845_at	NM_001006617 /// NM_001006618 /// NM_001006619 /// NM_001006620 /// NM_001006621 /// NM_024117																			
2.31	2.07	0.24	1.70E-01	5.41E-01	---	---	---	1557277_a_at	---																			
6.56	6.14	0.41	1.70E-01	5.41E-01	YPEL3	yippee-like 3 (Drosophila)	chr16p11.2	223179_at	NM_031477																			
6.92	6.04	0.88	1.71E-01	5.41E-01	KCTD14	potassium channel tetramerisation domain containing 14	chr11q14.1	58916_at	NM_023930																			
5.34	5.13	0.21	1.71E-01	5.41E-01	HMGB3	high-mobility group box 3	chrXq28	203744_at	NM_005342																			
7.31	6.85	0.46	1.71E-01	5.41E-01	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	chr10q24	209345_s_at	NM_018425																			
5.55	5.28	0.27	1.71E-01	5.41E-01	STK16	serine/threonine kinase 16	chr2q34-q37	209622_at	NM_001008910 /// NM_003691																			
3.01	2.77	0.24	1.71E-01	5.41E-01	---	---	---	1558381_a_at	---																			
6.10	5.61	0.50	1.71E-01	5.41E-01	PPM1F	protein phosphatase 1F (PP2C domain containing)	chr22q11.22	203063_at	NM_014634																			
6.35	5.96	0.38	1.71E-01	5.41E-01	TRAPPC2L	trafficking protein particle complex 2-like	chr16q24.3	238628_s_at	NM_016209																			
6.54	6.25	0.29	1.71E-01	5.41E-01	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	chr9p22.3	217707_x_at	NM_003070 /// NM_139045																			
6.70	6.27	0.43	1.71E-01	5.41E-01	HEL308	DNA helicase HEL308	chr4q21.23	1554342_s_at	NM_133636																			
2.74	2.51	0.23	1.71E-01	5.41E-01	---	---	---	243706_at	---																			
3.42	3.10	0.32	1.71E-01	5.41E-01	YPEL3	yippee-like 3 (Drosophila)	chr16p11.2	232077_s_at	NM_031477																			
5.73	5.35	0.38	1.71E-01	5.41E-01	PELI1	pellino homolog 1 (Drosophila)	chr2p13.3	218319_at	NM_020651																			
7.68	7.36	0.31	1.71E-01	5.41E-01	MED12	mediator complex subunit 12	chrXq13	216071_x_at	NM_005120																			
2.76	2.53	0.23	1.71E-01	5.41E-01	RRH	retinal pigment epithelium-derived rhodopsin homolog	chr4q25	208314_at	NM_006583																			
2.89	2.68	0.20	1.71E-01	5.41E-01	C9orf128	chromosome 9 open reading frame 128	chr9p13.3	240871_at	NM_001012446																			
5.21	4.57	0.64	1.71E-01	5.41E-01	NAP1L5	nucleosome assembly protein 1-like 5	chr4q22.1|4q21-q22	228062_at	NM_153757																			
2.90	2.65	0.24	1.71E-01	5.41E-01	ZNF383	zinc finger protein 383	chr19q13.12	235414_at	NM_152604																			
10.32	10.08	0.24	1.71E-01	5.41E-01	COMMD6	COMM domain containing 6	---	225312_at	NM_203495 /// NM_203497																			
9.07	8.74	0.33	1.71E-01	5.41E-01	BAT3	HLA-B associated transcript 3	chr6p21.3	213318_s_at	NM_001098534 /// NM_004639 /// NM_080702 /// NM_080703																			
3.61	3.26	0.34	1.72E-01	5.42E-01	PAQR5	progestin and adipoQ receptor family member V	chr15q23	220333_at	NM_001104554 /// NM_017705																			
7.19	6.99	0.19	1.72E-01	5.42E-01	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)	chr19p13.13	226428_at	NM_013433																			
7.46	7.08	0.38	1.72E-01	5.42E-01	PPHLN1	periphilin 1	chr12q12	225073_at	NM_016488 /// NM_201438 /// NM_201439 /// NM_201440 /// NM_201515																			
8.79	8.50	0.29	1.72E-01	5.42E-01	---	---	---	226297_at	---																			
2.36	2.14	0.22	1.72E-01	5.42E-01	---	---	---	240525_at	---																			
2.68	2.49	0.18	1.72E-01	5.42E-01	SPTBN5	Spectrin, beta, non-erythrocytic 5	chr15q21	1556839_s_at	NM_016642																			
2.72	2.46	0.26	1.72E-01	5.42E-01	PARP14	poly (ADP-ribose) polymerase family, member 14	chr3q21.1	232610_at	NM_017554																			
7.22	6.80	0.42	1.72E-01	5.42E-01	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	chr1q21.2	221505_at	NM_030920																			

7.74	7.37	0.38	1.72E-01	5.42E-01	BIN1	bridging integrator 1	chr2q14	210202_s_at	NM_004305 /// NM_139343 /// NM_139344 /// NM_139345 /// NM_139346 /// NM_139347 /// NM_139348 /// NM_139349 /// NM_139350 /// NM_139351																				
3.09	2.86	0.24	1.72E-01	5.42E-01	SPAG8	sperm associated antigen 8	chr9p13.3	206815_at	NM_001039592 /// NM_172312																				
2.75	2.45	0.30	1.72E-01	5.42E-01	---	---	---	234360_at	---																				
6.76	6.47	0.28	1.72E-01	5.42E-01	SPNS1	spinster homolog 1 (Drosophila)	chr16p11.2	223173_at	NM_032038																				
3.17	2.98	0.20	1.72E-01	5.42E-01	SCD5	stearoyl-CoA desaturase 5	chr4q21.22	220232_at	NM_001037582 /// NM_024906																				
5.13	4.65	0.48	1.72E-01	5.42E-01	CDK10	cyclin-dependent kinase 10	chr16q24	210622_x_at	NM_001098533 /// NM_052987 /// NM_052988																				
5.54	5.26	0.28	1.72E-01	5.42E-01	PPP1R3D	protein phosphatase 1, regulatory (inhibitor) subunit 3D	chr20q13.3	204554_at	NM_006242																				
3.37	2.95	0.41	1.72E-01	5.42E-01	---	---	---	236553_at	---																				
7.36	6.97	0.39	1.72E-01	5.42E-01	BCKDK	branched chain ketoacid dehydrogenase kinase	chr16p11.2	202030_at	NM_001122957 /// NM_005881																				
3.45	3.13	0.32	1.72E-01	5.42E-01	CXorf36	chromosome X open reading frame 36	chrXp11.3	1553584_at	NM_024689 /// NM_176819																				
6.58	6.22	0.37	1.72E-01	5.42E-01	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	chr20p13	209237_s_at	NM_005116 /// NM_203327																				
5.40	5.14	0.26	1.72E-01	5.43E-01	LBR	lamin B receptor	chr1q42.1	201795_at	NM_002296 /// NM_194442																				
4.32	3.95	0.37	1.72E-01	5.43E-01	PAOX	polyamine oxidase (exo-N4-amino)	chr10q26.3	50400_at	NM_152911 /// NM_207127 /// NM_207128																				
6.57	5.75	0.82	1.73E-01	5.43E-01	DKFZP564O0823	DKFZP564O0823 protein	chr4q13.3-q21.3	225809_at	NM_015393																				
7.06	6.66	0.40	1.73E-01	5.43E-01	NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	chr19q13.11	235384_at	NM_001105570																				
3.74	3.38	0.36	1.73E-01	5.43E-01	ATXN7	ataxin 7	chr3p21.1-p12	243259_at	NM_000333 /// NM_001128149																				
2.64	2.44	0.19	1.73E-01	5.43E-01	GTF2IRD2	GTF2I repeat domain containing 2	chr7q11.23	1557289_s_at	NM_173537 /// XM_001721289 /// XM_001722115																				
3.04	2.82	0.22	1.73E-01	5.43E-01	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	chr17q22	238681_at	NM_182569																				

9.07	8.85	0.22	1.73E-01	5.43E-01	LOC100127918 /// LOC100127922 /// SUMO2 /// SUMO4	similar to small ubiquitin-related modifier 2 /// similar to SMT3B protein /// SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) /// SMT3 suppressor of mif two 3 homolog 4 (S. cerevisiae)	chr17q25.1 /// chr4q21.1 /// chr5q35.2 /// chr6q25	208738_x_at	NM_001002255 /// NM_001005849 /// NM_006937 /// XR_038410 /// XR_038502 /// XR_038517 /// XR_038672 /// XR_038872 /// XR_039548																			
2.31	2.14	0.18	1.73E-01	5.43E-01	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	chr12q23.3	1559393_at	NM_001034173																				
5.99	5.64	0.35	1.73E-01	5.43E-01	---	---	---	1556582_at	---																				
8.41	7.96	0.44	1.73E-01	5.43E-01	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	chr5q35	221923_s_at	NM_001037738 /// NM_002520 /// NM_199185																				
2.58	2.29	0.29	1.73E-01	5.43E-01	FLJ10661	similar to CG7889-PA	chr8p23.1	1562903_at	XR_015342 /// XR_015555 /// XR_040164																				
3.42	3.07	0.35	1.73E-01	5.43E-01	MYO15B	myosin XVB pseudogene	chr17q25.1	227743_at	NR_003587																				
2.31	2.05	0.26	1.73E-01	5.43E-01	---	---	---	229455_at	---																				
3.57	3.33	0.24	1.73E-01	5.43E-01	PRUNE	prune homolog (Drosophila)	chr1q21	209599_s_at	NM_021222																				
2.25	2.06	0.20	1.73E-01	5.43E-01	RANBP17	RAN binding protein 17	chr5q34	244198_at	NM_022897																				
9.55	9.12	0.43	1.73E-01	5.43E-01	H2AFJ	H2A histone family, member J	chr12p12	225245_x_at	NM_177925																				
3.46	3.18	0.28	1.73E-01	5.43E-01	MYL4	myosin, light chain 4, alkali; atrial, embryonic	chr17q21-qter	217274_x_at	NM_001002841 /// NM_002476																				
6.52	6.24	0.28	1.73E-01	5.43E-01	MORC2	MORC family CW-type zinc finger 2	chr22q12.2	203956_at	NM_014941																				
12.85	12.71	0.14	1.73E-01	5.43E-01	hCG_21078 /// RPL27A	hCG21078 /// ribosomal protein L27a	chr11p15 /// chr6q25.2	203034_s_at	NM_000990 /// NM_001089587																				
2.76	2.54	0.21	1.73E-01	5.43E-01	LNPEP	leucyl/cystinyl aminopeptidase	chr5q15	207904_s_at	NM_005575 /// NM_175920																				
2.78	2.55	0.24	1.73E-01	5.43E-01	GAGE12F /// GAGE12G /// GAGE12I /// GAGE2A /// GAGE2B /// GAGE2E /// GAGE4 /// GAGE7	G antigen 12F /// G antigen 12G /// G antigen 12I /// G antigen 2A /// G antigen 2B /// G antigen 2E /// G antigen 4 /// G antigen 7	chrXp11.23 /// chrXp11.4-p11.2	208235_x_at	NM_001098405 /// NM_001098409 /// NM_001098411 /// NM_001127200 /// NM_001127212 /// NM_001474 /// NM_001477 /// NM_021123 /// XM_001130991																			
2.57	2.35	0.22	1.73E-01	5.44E-01	---	---	---	1557914_s_at	---																				
8.88	8.36	0.52	1.73E-01	5.44E-01	ZC3H11A	zinc finger CCCH-type containing 11A	chr1q32.1	205788_s_at	NM_014827																				
4.96	4.65	0.31	1.73E-01	5.44E-01	KLK3	Kallikrein-related peptidase 3	chr19q13.41	231629_x_at	NM_001030047 /// NM_001030048 /// NM_001030049 /// NM_001030050 /// NM_001648																				
3.51	3.19	0.32	1.73E-01	5.44E-01	IL17D	interleukin 17D	chr13q12.11	227401_at	NM_138284																				

3.35	3.18	0.17	1.73E-01	5.44E-01	LAMA3	laminin, alpha 3	chr18q11.2	1563772_a_at	NM_000227 /// NM_001127717 /// NM_001127718 /// NM_198129
6.58	6.07	0.51	1.74E-01	5.44E-01	RALGDS	ral guanine nucleotide dissociation stimulator	chr9q34.3	209051_s_at	NM_001042368 /// NM_006266
4.23	3.98	0.24	1.74E-01	5.44E-01	YY1	YY1 transcription factor	chr14q	201902_s_at	NM_003403
3.92	3.60	0.32	1.74E-01	5.44E-01	SNHG5 /// SNORD50A /// SNORD50B	small nucleolar RNA host gene 5 (non-protein coding) /// small nucleolar RNA, C/D box 50A /// small nucleolar RNA, C/D box 50B	chr6q14.3	244669_at	NR_002743 /// NR_003038 /// NR_003044
5.59	5.32	0.26	1.74E-01	5.44E-01	MR1	major histocompatibility complex, class I-related	chr1q25.3	210223_s_at	NM_001531
4.70	4.50	0.20	1.74E-01	5.44E-01	MYLPF	fast skeletal myosin light chain 2	chr16p11.2	205163_at	NM_013292
1.97	1.73	0.24	1.74E-01	5.44E-01	PPA2	Pyrophosphatase (inorganic) 2	chr4q25	1556284_at	NM_001034191 /// NM_006903 /// NM_176866 /// NM_176867 /// NM_176869
6.72	6.45	0.27	1.74E-01	5.44E-01	C20orf194	chromosome 20 open reading frame 194	chr20p13	225825_at	NM_001009984
8.45	8.15	0.30	1.74E-01	5.44E-01	TAPBP	TAP binding protein (tapasin)	chr6p21.3	208829_at	NM_003190 /// NM_172208 /// NM_172209
7.94	7.41	0.53	1.74E-01	5.44E-01	TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	chr10q25.3	226339_at	NM_139169
2.67	2.44	0.24	1.74E-01	5.44E-01	RAPSN	receptor-associated protein of the synapse	chr11p11.2-p11.1	211570_s_at	NM_005055 /// NM_032645
7.23	6.98	0.26	1.74E-01	5.44E-01	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	chr10q24.32	200720_s_at	NM_005736
6.34	5.68	0.66	1.74E-01	5.44E-01	---	---	---	226525_at	---
6.16	5.53	0.62	1.74E-01	5.44E-01	FAM91A2 /// FLJ39739	family with sequence similarity 91, member A2 /// hypothetical FLJ39739	chr1q21.1	1568609_s_at	XR_039904 /// XR_039905 /// XR_040635
2.91	2.66	0.25	1.74E-01	5.44E-01	SLAIN1	SLAIN motif family, member 1	chr13q22.3	225619_at	NM_001040153 /// NM_144595
4.77	4.26	0.51	1.74E-01	5.44E-01	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	chr6p25.2	209941_at	NM_003804
8.04	7.63	0.41	1.74E-01	5.44E-01	LASP1	LIM and SH3 protein 1	chr17q11-q21.3	200618_at	NM_006148
5.60	5.30	0.30	1.74E-01	5.44E-01	BOLA1	bolA homolog 1 (E. coli)	chr1p36.13-q31.3	219345_at	NM_016074
4.50	4.16	0.33	1.74E-01	5.45E-01	PLCD3	phospholipase C, delta 3	chr17q21.31	1552476_s_at	NM_133373
4.05	3.62	0.43	1.74E-01	5.45E-01	ZC3H8	zinc finger CCCH-type containing 8	chr2q13	223506_at	NM_032494
6.68	6.42	0.26	1.74E-01	5.45E-01	TBC1D5	TBC1 domain family, member 5	chr3p24.3	201814_at	NM_001134380 /// NM_001134381 /// NM_014744 /// XM_001716616 /// XM_001718151
2.84	2.64	0.20	1.74E-01	5.45E-01	HNF1A	HNF1 homeobox A	chr12q22-qter|12q24.2	216930_at	NM_000545

7.35	6.66	0.69	1.74E-01	5.45E-01	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	chr21q22.3	204567_s_at	NM_004915 /// NM_016818 /// NM_207174 /// NM_207627 /// NM_207628 /// NM_207629																					
2.73	2.50	0.23	1.74E-01	5.45E-01	---	---	---	244381_at	---																					
7.06	6.63	0.43	1.75E-01	5.45E-01	VEGFA	vascular endothelial growth factor A	chr6p12	212171_x_at	NM_001025366 /// NM_001025367 /// NM_001025368 /// NM_001025369 /// NM_001025370 /// NM_001033756 /// NM_003376																					
5.42	5.18	0.24	1.75E-01	5.45E-01	TGS1	trimethylguanosine synthase homolog (S. cerevisiae)	chr8q11	219231_at	NM_024831																					
2.80	2.59	0.21	1.75E-01	5.45E-01	ZNF789	zinc finger protein 789	chr7q22.1	1569194_at	NM_001013258 /// NM_213603																					
3.30	2.98	0.32	1.75E-01	5.45E-01	RPL23AP7	ribosomal protein L23a pseudogene 7	chr2q14	221634_at	NR_000029																					
5.82	5.62	0.20	1.75E-01	5.45E-01	ARHGAP10	Rho GTPase activating protein 10	chr4q31.23	219431_at	NM_024605																					
3.13	2.95	0.19	1.75E-01	5.45E-01	LOC285847	hypothetical protein LOC285847	chr6p21.31	1557724_a_at	XM_934928 /// XM_934929 /// XM_945988 /// XM_945990																					
4.97	4.19	0.78	1.75E-01	5.45E-01	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	chr11p14-p13	218326_s_at	NM_018490																					
7.47	7.22	0.25	1.75E-01	5.45E-01	C2orf47	chromosome 2 open reading frame 47	chr2q33.1	219176_at	NM_024520																					
5.87	5.67	0.20	1.75E-01	5.45E-01	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	chr10q22-q23	231763_at	NM_007055																					
4.95	4.66	0.29	1.75E-01	5.45E-01	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	chr6p21.2-p21.1	221662_s_at	NM_006672 /// NM_153320																					
3.39	3.15	0.24	1.75E-01	5.45E-01	---	---	---	1563142_at	---																					
8.11	7.79	0.32	1.75E-01	5.45E-01	NCOR2	nuclear receptor co-repressor 2	chr12q24	207760_s_at	NM_001077261 /// NM_006312																					
2.51	2.35	0.16	1.75E-01	5.45E-01	DOCK5	dedicator of cytokinesis 5	chr8p21.2	1569590_at	NM_024940																					
6.38	5.84	0.54	1.75E-01	5.45E-01	CHST14	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	chr15q15.1	226314_at	NM_130468																					
3.55	3.39	0.16	1.75E-01	5.45E-01	KIAA0999	KIAA0999 protein	chr11q23.3	1563455_at	NM_025164																					
3.15	2.78	0.37	1.75E-01	5.45E-01	---	---	---	211106_at	---																					
2.31	2.15	0.16	1.75E-01	5.45E-01	RMST	rhabdomyosarcoma 2 associated transcript (non-protein coding)	chr12q23.1|12q21	229782_at	NR_024037 /// XR_000219 /// XR_001330																					
2.95	2.60	0.35	1.75E-01	5.45E-01	ZNF26	zinc finger protein 26	chr12q24.33	1555325_s_at	NM_019591																					
3.19	2.96	0.23	1.75E-01	5.45E-01	---	---	---	1561733_at	---																					
5.52	4.95	0.57	1.75E-01	5.45E-01	PNN	pinin, desmosome associated protein	chr14q21.1	212037_at	NM_002687																					
2.45	2.28	0.17	1.75E-01	5.45E-01	TCTE3	t-complex-associated-testis-expressed 3	chr6q27	1554401_a_at	NM_174910																					
3.11	2.88	0.24	1.75E-01	5.46E-01	LOC340178	hypothetical protein LOC340178	chr6q27	244120_at	---																					
3.84	3.53	0.31	1.75E-01	5.46E-01	CCDC149	coiled-coil domain containing 149	chr4p15.2	1553839_at	NM_001130726 /// NM_173463																					
6.61	6.20	0.42	1.75E-01	5.46E-01	MRPL2	mitochondrial ribosomal protein L2	chr6p21.3	229884_s_at	NM_015950																					
3.05	2.87	0.18	1.75E-01	5.46E-01	LOC731424	hypothetical protein LOC731424	---	1569095_at	XM_001132858 /// XM_001723759																					
7.31	6.98	0.33	1.75E-01	5.46E-01	ATXN7L3	ataxin 7-like 3	chr17q21.31	224969_at	NM_001098833 /// NM_020218																					

9.54	8.92	0.63	1.75E-01	5.46E-01	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	chr2p25	201565_s_at	NM_002166																				
2.13	1.95	0.18	1.75E-01	5.46E-01	MAGEA2 /// MAGEA2B /// MAGEA6	melanoma antigen family A, 2 /// melanoma antigen family A, 2B /// melanoma antigen family A, 6	chrXq28	214603_at	NM_005361 /// NM_005363 /// NM_153488 /// NM_175742 /// NM_175743 /// NM_175868																				
7.68	7.30	0.38	1.76E-01	5.46E-01	TMEM203	transmembrane protein 203	chr9q34.3	225052_at	NM_053045																				
5.53	5.25	0.28	1.76E-01	5.46E-01	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	chr9q34	217876_at	NM_001122823 /// NM_012087																				
4.66	4.16	0.50	1.76E-01	5.46E-01	LOC100129965 /// PRDM11	hypothetical protein LOC100129965 /// PR domain containing 11	chr11p11 /// chr11p11.2	239763_at	NM_020229 /// XM_001721980 /// XM_001724363 /// XM_001724519																				
6.88	6.60	0.28	1.76E-01	5.46E-01	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	chr1p34-p33	210092_at	NM_002370																				
5.13	4.60	0.53	1.76E-01	5.46E-01	PILRA	paired immunoglobin-like type 2 receptor alpha	chr7q22.1	222218_s_at	NM_013439 /// NM_178272 /// NM_178273																				
3.27	3.08	0.19	1.76E-01	5.46E-01	ZDHHC4	Zinc finger, DHHC-type containing 4	chr7p22.1	230905_at	NM_001134387 /// NM_001134388 /// NM_001134389 /// NM_018106																				
5.09	4.84	0.25	1.76E-01	5.46E-01	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	chr2q35	210422_x_at	NM_000578																				
2.88	2.49	0.39	1.76E-01	5.46E-01	---	---	---	230177_at	---																				
6.03	5.52	0.51	1.76E-01	5.46E-01	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	chr11p15.1	210253_at	NM_001098520 /// NM_001098521 /// NM_001098522 /// NM_001098523 /// NM_006410																				
4.60	4.42	0.19	1.76E-01	5.46E-01	CAPN13	calpain 13	chr2p22-p21	229499_at	NM_144575																				
7.81	7.47	0.34	1.76E-01	5.46E-01	LOC552889	hypothetical LOC552889	chr12q21	212114_at	NR_015371 /// XR_040493 /// XR_040494 /// XR_040495																				
6.19	5.82	0.37	1.76E-01	5.46E-01	DDEF1	development and differentiation enhancing factor 1	chr8q24.1-q24.2	224790_at	NM_018482																				
7.05	6.80	0.24	1.76E-01	5.46E-01	VCP	valosin-containing protein	chr9p13.3	208648_at	NM_007126																				
4.16	3.96	0.20	1.76E-01	5.46E-01	PATL1	protein associated with topoisomerase II homolog 1 (yeast)	chr11q12.1	235235_s_at	NM_152716																				
7.67	7.26	0.40	1.76E-01	5.46E-01	KLHDC3	kelch domain containing 3	chr6p21.1	214383_x_at	NM_057161																				
3.13	2.86	0.27	1.76E-01	5.46E-01	---	---	---	237012_at	---																				
8.34	7.97	0.37	1.76E-01	5.46E-01	TUSC3	tumor suppressor candidate 3	chr8p22	213423_x_at	NM_006765 /// NM_178234																				
3.79	3.46	0.33	1.76E-01	5.46E-01	IL8RA	interleukin 8 receptor, alpha	chr2q35	207094_at	NM_000634																				
7.81	7.48	0.33	1.76E-01	5.46E-01	DCXR	dicarbonyl/L-xylulose reductase	chr17q25.3	217973_at	NM_016286																				

5.04	4.83	0.22	1.76E-01	5.46E-01	HFE	hemochromatosis	chr6p21.3	211332_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011																				
2.99	2.83	0.16	1.76E-01	5.46E-01	TOLLIP	Toll interacting protein	chr11p15.5	237342_at	NM_019009																				
6.51	6.09	0.42	1.76E-01	5.46E-01	TSEN54	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	chr17q25.1	225879_at	NM_207346																				
7.13	6.28	0.85	1.77E-01	5.47E-01	AXUD1	AXIN1 up-regulated 1	chr3p22	225557_at	NM_033027																				
2.54	2.31	0.23	1.77E-01	5.47E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	213960_at	NM_001007156 /// NM_001012338 /// NM_002530																				
3.64	3.17	0.47	1.77E-01	5.47E-01	PRMT3	protein arginine methyltransferase 3	chr11p15.1	213320_at	NM_005788																				
6.89	6.44	0.45	1.77E-01	5.47E-01	TMEM167A	transmembrane protein 167A	chr5q14.2	226276_at	NM_174909																				
5.75	5.14	0.61	1.77E-01	5.47E-01	TNRC6A	trinucleotide repeat containing 6A	chr16p11.2	224705_s_at	NM_014494																				
2.60	2.40	0.20	1.77E-01	5.47E-01	FBXL21	F-box and leucine-rich repeat protein 21	chr5q31	1553500_at	NM_012159																				
7.72	7.09	0.63	1.77E-01	5.47E-01	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle	chr12q13.13	204173_at	NM_002475																				
6.88	6.51	0.37	1.77E-01	5.47E-01	MGC21874	transcriptional adaptor 2 (ADA2 homolog, yeast)-beta	chr4p16.1	226240_at	NM_152293																				
4.85	4.48	0.37	1.77E-01	5.47E-01	C1orf56	chromosome 1 open reading frame 56	chr1q21.2	221222_s_at	NM_017860																				
2.20	2.01	0.19	1.77E-01	5.47E-01	---	---	---	1570618_at	---																				
4.99	4.70	0.30	1.77E-01	5.47E-01	CDYL	chromodomain protein, Y-like	chr6p25.1	203099_s_at	NM_004824 /// NM_170751 /// NM_170752																				
8.25	7.98	0.27	1.77E-01	5.47E-01	IFT20	intraflagellar transport 20 homolog (Chlamydomonas)	chr17q11.2	210312_s_at	NM_174887																				
5.81	5.45	0.36	1.77E-01	5.47E-01	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced	chr12q13	201332_s_at	NM_003153																				
2.52	2.31	0.21	1.77E-01	5.47E-01	---	---	---	239703_at	---																				
12.58	12.42	0.16	1.77E-01	5.47E-01	RPL7A	ribosomal protein L7a	chr9q34	217740_x_at	NM_000972 /// NR_000016 /// NR_000017 /// NR_002447 /// NR_002448																				
3.73	3.20	0.52	1.77E-01	5.47E-01	SHPRH	SNF2 histone linker PHD RING helicase	chr6q24.3	226366_at	NM_001042683 /// NM_173082																				
8.44	8.17	0.28	1.77E-01	5.47E-01	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	chr10q11.21-q11.23	225535_s_at	NM_006327																				
3.41	3.18	0.22	1.77E-01	5.47E-01	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	chrXq22.1	205217_at	NM_004085																				
7.50	7.16	0.34	1.77E-01	5.47E-01	NADK	NAD kinase	chr1p36.33-p36.21	208918_s_at	NM_023018																				
4.51	4.30	0.21	1.77E-01	5.47E-01	MYO19	myosin XIX	chr17q12	236022_at	NM_001033580 /// NM_025109																				
5.36	4.97	0.39	1.77E-01	5.47E-01	MCM2	minichromosome maintenance complex component 2	chr3q21	202107_s_at	NM_004526																				
4.87	4.41	0.46	1.77E-01	5.47E-01	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	chr2p16.1	210347_s_at	NM_018014 /// NM_022893 /// NM_138559																				
3.92	3.28	0.63	1.77E-01	5.47E-01	CSNK1A1	Casein kinase 1, alpha 1	chr5q32	1556006_s_at	NM_001025105 /// NM_001892																				
2.67	2.46	0.21	1.77E-01	5.48E-01	C14orf49	chromosome 14 open reading frame 49	chr14q32.13	1553644_at	NM_152592																				
5.89	5.55	0.34	1.77E-01	5.48E-01	TBC1D22A	TBC1 domain family, member 22A	chr22q13.3	33778_at	NM_014346																				

4.54	4.24	0.31	1.77E-01	5.48E-01	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	chr11q24.2	1554091_a_at	NM_001039661 /// NM_148910																				
6.20	5.65	0.55	1.77E-01	5.48E-01	SRPR	signal recognition particle receptor ('docking protein')	chr11q24.3	200917_s_at	NM_003139																				
8.07	7.75	0.32	1.78E-01	5.48E-01	C6orf108	chromosome 6 open reading frame 108	chr6p21.1	39817_s_at	NM_006443 /// NM_199184																				
10.91	10.70	0.21	1.78E-01	5.48E-01	H3F3A /// H3F3B /// LOC440926	H3 histone, family 3A /// H3 histone, family 3B (H3.3B) /// H3 histone, family 3A pseudogene	chr17q25 /// chr1q41 /// chr2q31.1	200080_s_at	NM_002107 /// NM_005324 /// NR_002315 /// XR_042136 /// XR_042137 /// XR_042155																				
5.85	5.46	0.39	1.78E-01	5.48E-01	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	chr10q24.1-q24.3	223494_at	NM_012215																				
3.40	3.13	0.26	1.78E-01	5.48E-01	TMEM79	transmembrane protein 79	chr1q22	223544_at	NM_032323																				
5.83	5.31	0.51	1.78E-01	5.48E-01	UHRF2	ubiquitin-like with PHD and ring finger domains 2	chr9p24.1	225610_at	NM_152896																				
5.21	4.93	0.27	1.78E-01	5.48E-01	ATP5H	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	chr17q25	1555998_at	NM_001003785 /// NM_006356																				
5.32	4.88	0.43	1.78E-01	5.48E-01	PQLC2	PQ loop repeat containing 2	chr1p36.13	1555781_at	NM_001040125 /// NM_001040126 /// NM_017765																				
2.26	2.06	0.20	1.78E-01	5.48E-01	LOC100133308	Ras suppressor protein 1 pseudogene	chr10q11.21	1557672_s_at	XM_001717581																				
3.03	2.86	0.17	1.78E-01	5.48E-01	PTPRE	Protein tyrosine phosphatase, receptor type, E	chr10q26	233978_at	NM_006504 /// NM_130435																				
5.53	5.23	0.30	1.78E-01	5.48E-01	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	chr9p13.3	205042_at	NM_001128227 /// NM_005476																				
5.21	4.76	0.45	1.78E-01	5.48E-01	TBRG1	transforming growth factor beta regulator 1	chr11q24.2	225818_s_at	NM_032811 /// NR_016021																				
6.27	5.86	0.41	1.78E-01	5.48E-01	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	chr1q42|17p13.2	209142_s_at	NM_003342																				
2.04	1.86	0.19	1.78E-01	5.48E-01	PEX13	peroxisomal biogenesis factor 13	chr2p14-p16	1558163_at	NM_002618																				
2.63	2.24	0.39	1.78E-01	5.48E-01	AREG /// AREGB	amphiregulin /// amphiregulin B	chr4q13-q21 /// chr4q13.3	205239_at	NM_001657 /// XM_001125684																				
6.64	6.30	0.34	1.78E-01	5.48E-01	C9orf89	chromosome 9 open reading frame 89	chr9q22.31	223398_at	NM_032310																				
6.23	5.81	0.42	1.78E-01	5.48E-01	---	---	---	241906_at	---																				
7.43	6.95	0.48	1.78E-01	5.48E-01	CHKB	choline kinase beta	chr22q13.33	204193_at	NM_005198 /// NM_152253																				
6.22	5.98	0.23	1.78E-01	5.48E-01	SAP130	Sin3A-associated protein, 130kDa	chr2q14.3	220367_s_at	NM_024545																				
2.25	2.09	0.16	1.78E-01	5.48E-01	---	---	---	239200_at	---																				
4.93	4.65	0.28	1.78E-01	5.48E-01	C10orf12	chromosome 10 open reading frame 12	chr10q24.1	226892_at	NM_015652																				
4.47	4.09	0.38	1.78E-01	5.48E-01	ATG16L2	ATG16 autophagy related 16-like 2 (S. cerevisiae)	chr11q13.4	229389_at	NM_033388																				
3.95	3.71	0.24	1.78E-01	5.48E-01	HUWE1	HECT, UBA and WWE domain containing 1	chrXp11.22	208599_at	NM_031407																				
4.03	3.70	0.33	1.78E-01	5.48E-01	ETNK2	ethanolamine kinase 2	chr1q32.1	219268_at	NM_018208																				
2.24	2.06	0.18	1.78E-01	5.48E-01	CLP1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	chr11q12	1566152_a_at	NM_006831																				
3.31	2.96	0.35	1.78E-01	5.48E-01	---	---	---	241890_at	---																				
5.07	4.74	0.33	1.78E-01	5.48E-01	RCOR1	REST corepressor 1	chr14q32.31-q32.32	212612_at	NM_015156																				
4.45	4.25	0.20	1.78E-01	5.48E-01	---	---	---	237868_x_at	---																				
2.19	1.97	0.22	1.78E-01	5.48E-01	LOC374491	TPTE and PTEN homologous inositol lipid phosphatase pseudogene	chr13q12.12	233675_s_at	NR_002815																				
6.03	5.67	0.36	1.79E-01	5.48E-01	ZNF330	zinc finger protein 330	chr4q31.1|4q31.1-q31.2	213760_s_at	NM_014487																				
3.41	3.16	0.25	1.79E-01	5.48E-01	---	---	---	1559494_at	---																				
2.58	2.27	0.31	1.79E-01	5.48E-01	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2	chr2p22.2-p22.1	237968_at	NM_022374																				
3.11	2.92	0.19	1.79E-01	5.49E-01	RREB1	ras responsive element binding protein 1	chr6p25	217411_s_at	NM_001003698 /// NM_001003699 /// NM_002955																				

2.26	2.08	0.18	1.79E-01	5.49E-01	LOC100130894	hypothetical LOC100130894	chr16q22.1	1564158_a_at	XM_001724211 /// XM_001724341 /// XM_001726728																			
3.38	3.07	0.31	1.79E-01	5.49E-01	SIX2	SIX homeobox 2	chr2p16-p15	206510_at	NM_016932																			
3.33	2.96	0.38	1.79E-01	5.49E-01	KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	chr5q34	209948_at	NM_004137																			
6.30	5.98	0.32	1.79E-01	5.49E-01	PEX16	peroxisomal biogenesis factor 16	chr11p11.2	221604_s_at	NM_004813 /// NM_057174																			
6.65	6.33	0.32	1.79E-01	5.49E-01	NUDT4 /// NUDT4P1	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	chr12q21 /// chr1q21.1	206303_s_at	NM_019094 /// NM_199040 /// NR_002212																			
2.35	2.18	0.17	1.79E-01	5.49E-01	SCAMPER	sphingolipid Ca2+ release mediating protein of endoplasmic reticulum	---	1555722_at	---																			
3.25	2.92	0.33	1.79E-01	5.49E-01	RHEB	Ras homolog enriched in brain	chr7q36	213409_s_at	NM_005614																			
1.92	1.72	0.19	1.79E-01	5.49E-01	UBE3C	ubiquitin protein ligase E3C	chr7q36.3	1554793_at	NM_014671																			
2.19	2.00	0.19	1.79E-01	5.49E-01	C4orf39	chromosome 4 open reading frame 39	chr4q32.3	1553711_a_at	NM_153027																			
6.33	6.08	0.25	1.79E-01	5.49E-01	CCDC94	coiled-coil domain containing 94	chr19p13.3	204335_at	NM_018074																			
3.63	3.39	0.24	1.79E-01	5.49E-01	---	---	---	230741_at	---																			
6.23	5.61	0.62	1.79E-01	5.49E-01	EMP2	epithelial membrane protein 2	chr16p13.2	225079_at	NM_001424																			
5.90	5.46	0.43	1.79E-01	5.49E-01	SPON1	spondin 1, extracellular matrix protein	chr11p15.2	209436_at	NM_006108																			
6.21	5.44	0.77	1.79E-01	5.49E-01	CREM	cAMP responsive element modulator	chr10p11.21	230511_at	NM_001881 /// NM_181571 /// NM_182717 /// NM_182718 /// NM_182719 /// NM_182720 /// NM_182721 /// NM_182722 /// NM_182723 /// NM_182724 /// NM_182725 /// NM_182769 /// NM_182770 /// NM_182771 /// NM_182772 /// NM_182850 /// NM_182853 /// NM_183011 /// NM_183012 /// NM_183013 /// NM_183060																			
8.85	8.49	0.36	1.79E-01	5.49E-01	MRPL53	mitochondrial ribosomal protein L53	chr2p13.1	225523_at	NM_053050																			
6.38	5.90	0.48	1.79E-01	5.49E-01	JMY	junction-mediating and regulatory protein	chr5q14.1	226352_at	NM_152405																			
3.67	3.40	0.28	1.80E-01	5.50E-01	SUFU	suppressor of fused homolog (Drosophila)	chr10q24.32	224201_s_at	NM_016169																			

3.10	2.57	0.53	1.80E-01	5.50E-01	DDX11 /// DDX12 /// LOC642846	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) /// DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 (CHL1-like helicase homolog, S. cerevisiae) /// DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11-like	chr12p11 /// chr12p13.31	213378_s_at	NM_004399 /// NM_030653 /// NM_152438 /// XM_001716130 /// XM_495908 /// XM_931833 /// XR_017754 /// XR_041429
2.40	2.19	0.21	1.80E-01	5.50E-01	---	---	---	243172_at	---
6.35	6.14	0.21	1.80E-01	5.50E-01	LETM1	Leucine zipper-EF-hand containing transmembrane protein 1	chr4p16.3	222006_at	NM_012318
4.71	4.32	0.40	1.80E-01	5.50E-01	CCNG2	cyclin G2	chr4q21.1	228081_at	NM_004354
2.99	2.76	0.23	1.80E-01	5.50E-01	ZDHHC2	Zinc finger, DHHC-type containing 2	chr8p21.3-p22	1563502_at	NM_016353
7.85	7.54	0.31	1.80E-01	5.50E-01	MRPS28	mitochondrial ribosomal protein S28	chr8q21.1-q21.2	219819_s_at	NM_014018
2.40	2.24	0.16	1.80E-01	5.50E-01	PACRG	PARK2 co-regulated	chr6q26	214204_at	NM_001080378 /// NM_001080379 /// NM_152410
6.82	6.55	0.27	1.80E-01	5.50E-01	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	chr5q31.2	201343_at	NM_003339 /// NM_181838
5.64	5.12	0.52	1.80E-01	5.50E-01	HERC4	hect domain and RLD 4	chr10q21.3	225988_at	NM_015601 /// NM_022079
2.89	2.67	0.22	1.80E-01	5.50E-01	GNMT	glycine N-methyltransferase	chr6p12	210328_at	NM_018960
3.93	3.61	0.32	1.80E-01	5.50E-01	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	chr20q11.23	1557394_at	NM_001042486 /// NM_014902 /// NM_183006
2.55	2.27	0.28	1.80E-01	5.50E-01	---	---	---	243911_at	---
2.30	2.12	0.18	1.80E-01	5.50E-01	---	---	---	237263_at	---
2.81	2.61	0.20	1.80E-01	5.50E-01	KLHL6	kelch-like 6 (Drosophila)	---	1560397_s_at	NM_130446
7.07	6.35	0.72	1.80E-01	5.50E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	208580_x_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054
5.69	5.10	0.59	1.80E-01	5.50E-01	---	---	---	231035_s_at	---
6.04	5.66	0.38	1.80E-01	5.51E-01	LOC100133916 /// MED18	hypothetical protein LOC100133916 /// mediator complex subunit 18	chr1p35.3	221650_s_at	NM_001127350 /// NM_017638 /// XM_001713715
4.16	3.96	0.20	1.80E-01	5.51E-01	---	---	---	233021_at	---

6.66	6.27	0.39	1.80E-01	5.51E-01	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	chr6q15	222435_s_at	NM_016021																				
2.81	2.58	0.23	1.80E-01	5.51E-01	ASB2	ankyrin repeat and SOCS box-containing 2	chr14q31-q32	233857_s_at	NM_016150																				
3.57	3.34	0.23	1.80E-01	5.51E-01	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	chr15q21.1	233801_s_at	NM_020858 /// NM_024966 /// NM_153616 /// NM_153617 /// NM_153618 /// NM_153619																				
2.87	2.59	0.28	1.80E-01	5.51E-01	LOC401320	Hypothetical LOC401320	chr7p15.1	239313_at	XM_379482 /// XM_380098 /// XM_938539																				
3.42	3.17	0.24	1.80E-01	5.51E-01	---	---	---	1560405_at	---																				
5.41	5.07	0.34	1.81E-01	5.51E-01	LMF1	lipase maturation factor 1	chr16p13.3	46142_at	NM_022773																				
5.99	5.80	0.18	1.81E-01	5.51E-01	IL10RB	interleukin 10 receptor, beta	chr21q22.1-q22.2|21q22.11	209575_at	NM_000628																				
4.63	4.20	0.43	1.81E-01	5.51E-01	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	chr7q22.1	226100_at	NM_018682 /// NM_182931																				
5.58	4.85	0.73	1.81E-01	5.51E-01	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	chr2p12	218696_at	NM_004836																				
2.36	2.19	0.17	1.81E-01	5.51E-01	---	---	---	240710_at	---																				
3.83	3.63	0.20	1.81E-01	5.51E-01	SHBG	sex hormone-binding globulin	chr17p13-p12	215689_s_at	NM_001040																				
3.71	3.44	0.27	1.81E-01	5.51E-01	STX6	syntaxin 6	chr1q25.3	212800_at	NM_005819																				
6.84	6.36	0.48	1.81E-01	5.51E-01	CTBP2	C-terminal binding protein 2	chr10q26.13	201219_at	NM_001083914 /// NM_001329 /// NM_022802																				
7.22	6.88	0.34	1.81E-01	5.51E-01	HADH	hydroxyacyl-Coenzyme A dehydrogenase	chr4q22-q26	201036_s_at	NM_005327																				
6.83	6.48	0.34	1.81E-01	5.51E-01	DRAM	damage-regulated autophagy modulator	chr12q23.2	218627_at	NM_018370																				
5.44	5.16	0.28	1.81E-01	5.51E-01	CLDN15	claudin 15	chr7q11.22	219640_at	NM_014343																				
2.81	2.58	0.23	1.81E-01	5.51E-01	LOC100128439	hypothetical protein LOC100128439	chr19p13.3	1558447_at	XM_001723279 /// XM_001726335 /// XM_001726390																				
7.29	7.09	0.20	1.81E-01	5.51E-01	CCNY	cyclin Y	chr10p11.21	224647_at	NM_145012 /// NM_181698																				
5.80	5.38	0.42	1.81E-01	5.51E-01	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	chr17p13	222841_s_at	NM_013337																				
2.65	2.48	0.17	1.81E-01	5.51E-01	OR6A2	olfactory receptor, family 6, subfamily A, member 2	chr11p15	221465_at	NM_003696																				
4.54	3.92	0.62	1.81E-01	5.51E-01	CHD2	chromodomain helicase DNA binding protein 2	chr15q26	1554014_at	NM_001042572 /// NM_001271																				
2.36	2.17	0.19	1.81E-01	5.51E-01	FKSG29	FKSG29	chr13q32.3	223896_at	NR_024013 /// XM_001719551 /// XM_001719891 /// XM_001721354																				
3.51	3.22	0.29	1.81E-01	5.51E-01	---	---	---	1565672_at	---																				
3.24	2.98	0.26	1.81E-01	5.52E-01	PRDM5	PR domain containing 5	chr4q25-q26	220792_at	NM_018699																				
4.66	4.18	0.48	1.82E-01	5.52E-01	ZFHX4	zinc finger homeobox 4	chr8q21.11	241700_at	NM_024721																				
6.04	5.78	0.26	1.82E-01	5.52E-01	RFT1	RFT1 homolog (S. cerevisiae)	chr3p21.1	226060_at	NM_052859																				
3.84	3.49	0.35	1.82E-01	5.52E-01	TMEM206	transmembrane protein 206	chr1q32.3	222752_s_at	NM_018252																				
5.47	5.18	0.29	1.82E-01	5.52E-01	ABI2	abl interactor 2	chr2q33	211793_s_at	NM_005759																				
5.58	4.78	0.80	1.82E-01	5.52E-01	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	chr2p13	201446_s_at	NM_022037 /// NM_022173																				
3.68	3.47	0.21	1.82E-01	5.52E-01	POU3F1	POU class 3 homeobox 1	chr1p34.1	208345_s_at	NM_002699																				
6.78	6.43	0.35	1.82E-01	5.52E-01	C3orf63	chromosome 3 open reading frame 63	chr3p14.3	209285_s_at	NM_001112736 /// NM_015224																				
3.03	2.84	0.19	1.82E-01	5.52E-01	SSH1	slingshot homolog 1 (Drosophila)	chr12q24.11	1555624_a_at	NM_018984																				
5.54	5.19	0.35	1.82E-01	5.52E-01	C19orf22	chromosome 19 open reading frame 22	chr19p13.3	221764_at	NM_138774																				
6.68	6.28	0.41	1.82E-01	5.52E-01	PREB	prolactin regulatory element binding	chr2p23.3	217861_s_at	NM_013388																				

2.74	2.47	0.26	1.82E-01	5.52E-01	---	---	---	239974_at	---
2.28	2.12	0.17	1.82E-01	5.52E-01	TREML3	triggering receptor expressed on myeloid cells-like 3	chr6p21.1	1557444_at	XM_001717580 /// XM_929970 /// XM_941488
4.51	4.31	0.19	1.82E-01	5.52E-01	MEI1	meiosis inhibitor 1	chr22q13.2	230011_at	NM_152513
2.30	2.14	0.16	1.82E-01	5.52E-01	---	---	---	1557295_a_at	---
7.68	7.38	0.30	1.82E-01	5.52E-01	WDR26	WD repeat domain 26	chr1q42.11	218107_at	NM_001115113 /// NM_025160
7.10	6.83	0.27	1.82E-01	5.52E-01	C11orf1	chromosome 11 open reading frame 1	chr11q13-q22	222785_x_at	NM_022761
3.01	2.61	0.40	1.82E-01	5.52E-01	UNC84A	unc-84 homolog A (C. elegans)	chr7p22.3	214169_at	NM_001130965 /// NM_025154
6.50	6.16	0.34	1.82E-01	5.52E-01	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	chr7p15.1	217784_at	NM_006555
6.22	5.92	0.31	1.82E-01	5.52E-01	FBXO28	F-box protein 28	chr1q42.11	1555971_s_at	NM_015176
8.89	8.46	0.43	1.82E-01	5.52E-01	---	---	---	226190_at	---
2.74	2.55	0.19	1.82E-01	5.52E-01	---	---	---	1569838_at	---
3.22	3.03	0.19	1.82E-01	5.53E-01	---	---	---	1562220_at	---
2.25	2.05	0.20	1.83E-01	5.53E-01	GPR87	G protein-coupled receptor 87	chr3q24	219936_s_at	NM_023915
4.05	3.66	0.40	1.83E-01	5.53E-01	TACC3	transforming, acidic coiled-coil containing protein 3	chr4p16.3	218308_at	NM_006342
7.07	6.32	0.76	1.83E-01	5.53E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	208228_s_at	NM_000141 /// NM_022970
4.54	3.99	0.56	1.83E-01	5.53E-01	LOC400642	hypothetical LOC400642	chr18p11.31	228160_at	---
3.32	3.06	0.26	1.83E-01	5.53E-01	---	---	---	1569515_a_at	---
4.25	3.89	0.36	1.83E-01	5.53E-01	PECR	peroxisomal trans-2-enoyl-CoA reductase	chr2q35	221142_s_at	NM_018441
2.45	2.25	0.20	1.83E-01	5.53E-01	---	---	---	1561034_at	---
2.78	2.60	0.18	1.83E-01	5.53E-01	TCL1A	T-cell leukemia/lymphoma 1A	chr14q32.1	39318_at	NM_001098725 /// NM_021966
3.05	2.81	0.24	1.83E-01	5.53E-01	---	---	---	216801_at	---
6.26	5.88	0.37	1.83E-01	5.53E-01	MGA	MAX gene associated	chr15q14	230848_s_at	NM_001080541
6.66	6.29	0.37	1.83E-01	5.54E-01	TFB1M	transcription factor B1, mitochondrial	chr6q25.1-q25.3	219169_s_at	NM_016020
2.40	2.23	0.17	1.83E-01	5.54E-01	KLF5	Kruppel-like factor 5 (intestinal)	chr13q22.1	209211_at	NM_001730
2.83	2.56	0.27	1.83E-01	5.54E-01	PDLIM7	PDZ and LIM domain 7 (enigma)	chr5q35.3	1569150_x_at	NM_005451 /// NM_203352 /// NM_213636
5.82	5.48	0.34	1.83E-01	5.54E-01	DGKZ	diacylglycerol kinase, zeta 104kDa	chr11p11.2	207556_s_at	NM_001105540 /// NM_003646 /// NM_201532 /// NM_201533
3.68	3.36	0.32	1.83E-01	5.54E-01	TMEM80	transmembrane protein 80	chr11p15.5	1559132_at	NM_001042463 /// NM_174940
3.80	3.36	0.44	1.83E-01	5.54E-01	OCC-1	overexpressed in colon carcinoma-1	chr12q23.3	225105_at	XR_040442 /// XR_040443 /// XR_040444
2.12	1.97	0.15	1.83E-01	5.54E-01	---	---	---	242127_at	---
3.86	3.68	0.18	1.83E-01	5.54E-01	CDK6	cyclin-dependent kinase 6	chr7q21-q22	207143_at	NM_001259
3.28	3.07	0.21	1.83E-01	5.54E-01	C11orf9	chromosome 11 open reading frame 9	chr11q12-q13.1	204073_s_at	NM_001127392 /// NM_013279
4.84	4.54	0.29	1.83E-01	5.54E-01	DNAJC17	DnaJ (Hsp40) homolog, subfamily C, member 17	chr15q15.1	219861_at	NM_018163
3.26	2.94	0.32	1.83E-01	5.54E-01	PSPC1	Paraspeckle component 1	chr13q12.11	222612_at	NM_001042414 /// NR_003272
2.83	2.61	0.22	1.83E-01	5.54E-01	RCVRN	recoverin	chr17p13.1	206203_at	NM_002903
3.22	2.82	0.40	1.83E-01	5.54E-01	SERP2	stress-associated endoplasmic reticulum protein family member 2	chr13q14.11	228044_at	NM_001010897
5.23	4.86	0.37	1.83E-01	5.54E-01	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	chr19q13.1	213076_at	NM_025194
4.79	4.42	0.37	1.84E-01	5.54E-01	ADRBK1	adrenergic, beta, receptor kinase 1	chr11q13.1	201401_s_at	NM_001619
7.57	7.33	0.24	1.84E-01	5.54E-01	TMEM218	transmembrane protein 218	chr11q24.2	226073_at	NM_001080546
3.68	3.37	0.31	1.84E-01	5.54E-01	LOC729088	hypothetical protein LOC729088	chr6q27	238833_at	XR_040995
6.39	6.03	0.36	1.84E-01	5.54E-01	FAM134A	family with sequence similarity 134, member A	chr2q35	222129_at	NM_024293
6.31	6.00	0.31	1.84E-01	5.54E-01	SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	chr11q23.3	202830_s_at	NM_001467

2.21	2.03	0.17	1.84E-01	5.55E-01	FAM47A	family with sequence similarity 47, member A	chrXp21.1	243700_x_at	NM_203408
6.51	6.24	0.27	1.84E-01	5.55E-01	MRPL44	mitochondrial ribosomal protein L44	chr2q36.1	222555_s_at	NM_022915
3.43	3.19	0.24	1.84E-01	5.55E-01	KLF7	Kruppel-like factor 7 (ubiquitous)	chr2q32	238482_at	NM_003709
3.95	3.55	0.40	1.84E-01	5.55E-01	HLA-F	major histocompatibility complex, class I, F	chr6p21.3	221978_at	NM_001098478 /// NM_001098479 /// NM_018950
2.82	2.63	0.19	1.84E-01	5.55E-01	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	chr1p36.12	1554310_a_at	NM_003760
2.53	2.36	0.17	1.84E-01	5.55E-01	LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	chr19q13.4	1555634_a_at	NM_021250 /// NM_181879 /// NM_181985 /// NM_181986
2.26	2.08	0.18	1.84E-01	5.55E-01	KLHL24	kelch-like 24 (Drosophila)	chr3q27.1	242088_at	NM_017644
2.71	2.40	0.31	1.84E-01	5.55E-01	SYF2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	chr1p36.11	1559979_at	NM_015484 /// NM_207170
9.66	9.26	0.40	1.84E-01	5.55E-01	UBA1	ubiquitin-like modifier activating enzyme 1	chrXp11.23	200964_at	NM_003334 /// NM_153280
4.61	4.06	0.55	1.84E-01	5.55E-01	OSR2	odd-skipped related 2 (Drosophila)	chr8q22.2	213568_at	NM_053001
3.61	3.10	0.51	1.84E-01	5.55E-01	FAM149A	family with sequence similarity 149, member A	chr4q35.2	214889_at	NM_001006655 /// NM_015398
6.63	6.30	0.33	1.84E-01	5.55E-01	CCDC44	coiled-coil domain containing 44	chr17q23.3	221069_s_at	NM_016360
4.86	4.50	0.36	1.84E-01	5.55E-01	---	---	---	242140_at	---
5.45	5.15	0.30	1.84E-01	5.55E-01	UBE2I	Ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	chr16p13.3	208760_at	NM_003345 /// NM_194259 /// NM_194260 /// NM_194261
10.30	9.90	0.40	1.84E-01	5.55E-01	FDXR	ferredoxin reductase	chr17q24-q25	207813_s_at	NM_004110 /// NM_024417
3.76	3.21	0.55	1.84E-01	5.55E-01	ABHD5	abhydrolase domain containing 5	chr3p21	213935_at	NM_016006
6.08	5.70	0.37	1.85E-01	5.55E-01	C17orf63	chromosome 17 open reading frame 63	chr17q11.2	218464_s_at	NM_001077498 /// NM_018182
5.38	4.94	0.44	1.85E-01	5.55E-01	ICAM1	intercellular adhesion molecule 1	chr19p13.3-p13.2	202637_s_at	NM_000201
9.28	9.09	0.19	1.85E-01	5.55E-01	PSMG2	proteasome (prosome, macropain) assembly chaperone 2	chr18p11.21	218467_at	NM_020232
5.28	4.95	0.33	1.85E-01	5.55E-01	THBS3	thrombospondin 3	chr1q21	209561_at	NM_007112
2.19	2.00	0.18	1.85E-01	5.55E-01	LOC339766	hypothetical protein LOC339766	chr2q37.1	1556167_at	XM_001721240 /// XM_291007 /// XM_939706
6.43	6.17	0.26	1.85E-01	5.56E-01	MTMR10	myotubularin related protein 10	chr15q13.3	225810_at	NM_017762
4.16	3.87	0.29	1.85E-01	5.56E-01	---	---	---	236139_at	---
8.30	8.05	0.25	1.85E-01	5.56E-01	KCMF1	potassium channel modulatory factor 1	chr2p11.2	217938_s_at	NM_020122
4.49	4.06	0.43	1.85E-01	5.56E-01	TBC1D16	TBC1 domain family, member 16	chr17q25.3	1554701_a_at	NM_019020
2.34	2.14	0.20	1.85E-01	5.56E-01	---	---	---	229781_at	---
8.71	8.48	0.23	1.85E-01	5.56E-01	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	chr8p12	201375_s_at	NM_001009552 /// NM_004156
5.49	5.05	0.44	1.85E-01	5.56E-01	IRF2	interferon regulatory factor 2	chr4q34.1-q35.1	203275_at	NM_002199
5.28	4.95	0.33	1.85E-01	5.56E-01	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	chr10q22	212757_s_at	NM_001222 /// NM_172169 /// NM_172170 /// NM_172171 /// NM_172173
3.25	2.99	0.26	1.85E-01	5.56E-01	---	---	---	1557897_at	---
2.46	2.27	0.19	1.85E-01	5.56E-01	FLJ13310	hypothetical protein FLJ13310	chr1q32.1	220916_at	---
2.33	2.15	0.18	1.85E-01	5.56E-01	---	---	---	220833_at	---
4.12	3.82	0.30	1.85E-01	5.56E-01	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	chr19q13.3	204815_s_at	NM_014681
5.00	4.31	0.69	1.85E-01	5.56E-01	SDC1	syndecan 1	chr2p24.1	201287_s_at	NM_001006946 /// NM_002997

2.64	2.40	0.24	1.85E-01	5.56E-01	DGCR14	DiGeorge syndrome critical region gene 14	chr22q11.21|22q11.2	239730_at	NM_022719
6.11	5.83	0.29	1.85E-01	5.56E-01	ARL16	ADP-ribosylation factor-like 16	chr17q25.3	234972_at	NM_001040025
5.30	5.01	0.29	1.85E-01	5.56E-01	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	chr14q22.1	213995_at	NM_001003803 /// NM_001003805 /// NM_015684
6.12	5.40	0.72	1.85E-01	5.56E-01	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	chr11q13.2	222759_at	NM_016028 /// NM_017635
5.35	4.57	0.78	1.85E-01	5.56E-01	TMEM49	transmembrane protein 49	chr17q23.1	1569003_at	NM_030938
3.46	3.23	0.23	1.86E-01	5.56E-01	LOC100131349 /// NT5C	hypothetical protein LOC100131349 /// 5', 3'-nucleotidase, cytosolic	chr17q25.1	1557303_at	NM_014595 /// XM_001718022 /// XM_001719279
6.12	5.82	0.30	1.86E-01	5.57E-01	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	chr11p15.5	49327_at	NM_001017524 /// NM_012239
7.21	6.86	0.34	1.86E-01	5.57E-01	COQ5	coenzyme Q5 homolog, methyltransferase (S. cerevisiae)	chr12q24.31	223114_at	NM_032314
3.73	3.38	0.35	1.86E-01	5.57E-01	MTMR3	myotubularin related protein 3	chr22q12.2	211507_s_at	NM_021090 /// NM_153050 /// NM_153051
6.56	6.03	0.53	1.86E-01	5.57E-01	INTS6	integrator complex subunit 6	chr13q14.12-q14.2	218819_at	NM_001039937 /// NM_001039938 /// NM_012141
5.00	4.58	0.41	1.86E-01	5.57E-01	ZNF621	zinc finger protein 621	chr3p22.1	1558620_at	NM_001098414 /// NM_198484
4.03	3.59	0.44	1.86E-01	5.57E-01	LOC652968 /// TBC1D10A	hypothetical protein LOC652968 /// TBC1 domain family, member 10A	chr22q12 /// chr22q12.1-qter	233528_s_at	NM_001037666 /// NM_031937
4.34	3.96	0.38	1.86E-01	5.57E-01	JMJD3	jumonji domain containing 3, histone lysine demethylase	chr17p13.1	213146_at	NM_001080424
3.18	2.94	0.25	1.86E-01	5.57E-01	SYNJ2	synaptojanin 2	chr6q25.3	1555009_a_at	NM_003898
6.47	6.24	0.23	1.86E-01	5.57E-01	RAB12	RAB12, member RAS oncogene family	chr18p11.22	239891_x_at	NM_001025300
6.67	6.37	0.31	1.86E-01	5.57E-01	VPS26B	vacuolar protein sorting 26 homolog B (S. pombe)	chr11q25	225483_at	NM_052875
5.08	4.69	0.38	1.86E-01	5.57E-01	TMC8	transmembrane channel-like 8	chr17q25.3	227353_at	NM_152468
4.75	4.53	0.22	1.86E-01	5.57E-01	NUB1	negative regulator of ubiquitin-like proteins 1	chr7q36	1569030_s_at	NM_016118
4.06	3.79	0.27	1.86E-01	5.57E-01	ZNF609	zinc finger protein 609	chr15q22.31	212617_at	NM_015042
3.96	3.51	0.45	1.86E-01	5.57E-01	LOC220594	TL132 protein	chr17p11.2	213510_x_at	NR_003554
6.22	5.92	0.30	1.86E-01	5.57E-01	RFNG	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	chr17q25	212968_at	NM_002917
8.57	8.27	0.31	1.86E-01	5.57E-01	ZNF207	zinc finger protein 207	chr17q11.2	200828_s_at	NM_001032293 /// NM_001098507 /// NM_003457
3.37	3.15	0.22	1.86E-01	5.57E-01	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	229557_at	NR_002766 /// NR_003530 /// NR_003531
5.89	5.37	0.52	1.86E-01	5.57E-01	---	---	---	241416_at	---
6.57	6.21	0.36	1.86E-01	5.57E-01	DAXX	death-domain associated protein	chr6p21.3	216038_x_at	NM_001350
8.68	8.27	0.41	1.86E-01	5.57E-01	VSIG4	V-set and immunoglobulin domain containing 4	chrXq12-q13.3	204787_at	NM_001100431 /// NM_007268
4.47	4.02	0.45	1.86E-01	5.57E-01	LTBP2	latent transforming growth factor beta binding protein 2	chr14q24	223690_at	NM_000428
5.88	5.53	0.34	1.86E-01	5.57E-01	ZNF281	Zinc finger protein 281	chr1q32.1	228785_at	NM_012482
9.03	8.80	0.23	1.86E-01	5.57E-01	LAMP1	lysosomal-associated membrane protein 1	chr13q34	201552_at	NM_005561
3.54	3.26	0.28	1.86E-01	5.57E-01	LONRF3	LON peptidase N-terminal domain and ring finger 3	chrXq24	220009_at	NM_001031855 /// NM_024778
4.12	3.90	0.22	1.86E-01	5.57E-01	DNASE1	deoxyribonuclease I	chr16p13.3	1558546_at	NM_005223
5.05	4.68	0.37	1.86E-01	5.57E-01	MDN1	MDN1, midasin homolog (yeast)	chr6q15	212693_at	NM_014611
4.21	3.94	0.27	1.86E-01	5.57E-01	TYSND1	Trypsin domain containing 1	chr10q22.1	231422_x_at	NM_001040273 /// NM_173555

6.94	6.60	0.34	1.86E-01	5.57E-01	TUBA4A	tubulin, alpha 4a	chr2q35	212242_at	NM_006000																			
5.23	4.47	0.76	1.86E-01	5.57E-01	---	---	---	222877_at	---																			
6.19	5.83	0.36	1.86E-01	5.57E-01	BOC	Boc homolog (mouse)	chr3q13.2	225990_at	NM_033254																			
6.45	6.19	0.26	1.87E-01	5.58E-01	MADD	MAP-kinase activating death domain	chr11p11.2	38398_at	NM_003682 /// NM_130470 /// NM_130471 /// NM_130472 /// NM_130473 /// NM_130474 /// NM_130475 /// NM_130476																			
5.54	5.34	0.20	1.87E-01	5.58E-01	ZHX3	zinc fingers and homeoboxes 3	chr20q12	212545_s_at	NM_015035																			
8.63	8.34	0.28	1.87E-01	5.58E-01	ACO2	aconitase 2, mitochondrial	chr22q11.2-q13.31|22q13.2|22q13.2-q13.31	200793_s_at	NM_001098																			
5.46	5.11	0.35	1.87E-01	5.58E-01	CASP6	caspase 6, apoptosis-related cysteine peptidase	chr4q25	209790_s_at	NM_001226 /// NM_032992																			
8.30	8.00	0.30	1.87E-01	5.58E-01	MYH10	myosin, heavy chain 10, non-muscle	chr17p13	212372_at	NM_005964																			
6.05	5.65	0.41	1.87E-01	5.58E-01	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	chr2q23-q24	203080_s_at	NM_013450																			
2.25	2.07	0.18	1.87E-01	5.58E-01	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	chrXq25	221098_x_at	NM_006649																			
5.71	5.27	0.44	1.87E-01	5.58E-01	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	chr16q22.1	203785_s_at	NM_018380																			
6.41	6.01	0.40	1.87E-01	5.58E-01	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	chr1p36.3-p36.2	209354_at	NM_003820																			
2.12	1.96	0.16	1.87E-01	5.58E-01	PIK3C3	phosphoinositide-3-kinase, class 3	chr18q12.3	1569272_at	NM_002647																			
5.57	5.26	0.31	1.87E-01	5.58E-01	ZBTB22	zinc finger and BTB domain containing 22	chr6p21.3	213081_at	NM_005453																			
2.52	2.33	0.19	1.87E-01	5.58E-01	FAM71F1	family with sequence similarity 71, member F1	chr7q32.1	231466_at	NM_032599																			
6.89	6.70	0.19	1.87E-01	5.58E-01	FTSJ2	FtsJ homolog 2 (E. coli)	chr7p22	222130_s_at	NM_013393																			
5.77	5.34	0.43	1.87E-01	5.58E-01	COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	chr17p12-p11.2	203858_s_at	NM_001303																			
9.35	9.12	0.23	1.87E-01	5.59E-01	PRCP	prolylcarboxypeptidase (angiotensinase C)	chr11q14	201494_at	NM_005040 /// NM_199418																			
4.75	4.49	0.27	1.87E-01	5.59E-01	CCDC21	coiled-coil domain containing 21	chr1p36.11	219611_s_at	NM_022778																			
4.04	3.29	0.74	1.88E-01	5.59E-01	C9orf72	chromosome 9 open reading frame 72	chr9p21.2	1553133_at	NM_018325 /// NM_145005																			
7.49	7.15	0.34	1.88E-01	5.59E-01	SF3A1	splicing factor 3a, subunit 1, 120kDa	chr22q12.2	216457_s_at	NM_001005409 /// NM_005877																			
5.61	5.27	0.34	1.88E-01	5.59E-01	TMEM170A	transmembrane protein 170A	chr16q23.1	227586_at	NM_145254																			
2.41	2.20	0.21	1.88E-01	5.59E-01	---	---	---	235841_at	---																			
3.85	3.69	0.15	1.88E-01	5.59E-01	MUPCDH	mucin-like protocadherin	chr11p15.5	219796_s_at	NM_021924 /// NM_031264																			
4.67	4.50	0.17	1.88E-01	5.59E-01	---	---	---	1566581_at	---																			
2.34	2.07	0.27	1.88E-01	5.59E-01	---	---	---	244867_at	---																			
3.19	2.96	0.24	1.88E-01	5.59E-01	TRPC1	transient receptor potential cation channel, subfamily C, member 1	chr3q22-q24	205802_at	NM_003304																			
7.29	7.01	0.28	1.88E-01	5.59E-01	POLD2	polymerase (DNA directed), delta 2, regulatory subunit 50kDa	chr7p13	201115_at	NM_001127218 /// NM_006230																			
5.49	4.61	0.87	1.88E-01	5.59E-01	JAM2	junctional adhesion molecule 2	chr21q21.2	229127_at	NM_021219																			
7.96	7.53	0.43	1.88E-01	5.59E-01	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	chr12q23-q24.1	212361_s_at	NM_001681 /// NM_170665																			
2.40	2.19	0.21	1.88E-01	5.59E-01	CRYGS	Crystallin, gamma S	chr3q25-qter	223643_at	NM_017541																			
3.42	2.87	0.55	1.88E-01	5.60E-01	LOC440944	Hypothetical gene supported by AK128398	chr3p25.3	1555858_at	XR_017845 /// XR_017949 /// XR_041324																			
8.53	8.20	0.33	1.88E-01	5.60E-01	CTBP1	C-terminal binding protein 1	chr4p16	212863_x_at	NM_001012614 /// NM_001328																			
2.14	2.01	0.13	1.88E-01	5.60E-01	SLC35E1	solute carrier family 35, member E1	chr19p13.11	1566798_at	NM_024881																			
5.85	5.29	0.55	1.88E-01	5.60E-01	CDAN1	congenital dyserythropoietic anemia, type I	chr15q15.2	228516_at	NM_138477																			

6.03	5.75	0.28	1.88E-01	5.60E-01	GOSR1	golgi SNAP receptor complex member 1	chr17q11	213021_at	NM_001007024 /// NM_001007025 /// NM_004871
1.85	1.70	0.16	1.88E-01	5.60E-01	MDGA2	MAM domain containing glycosylphosphatidylinositol anchor 2	chr14q21.3	239935_at	NM_001113498 /// NM_182830
6.07	5.62	0.45	1.89E-01	5.60E-01	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	chr16p11.2	205786_s_at	NM_000632
5.91	5.64	0.27	1.89E-01	5.60E-01	C20orf27	chromosome 20 open reading frame 27	chr20p13	218081_at	NM_001039140
7.63	7.42	0.21	1.89E-01	5.60E-01	TMEM106C	transmembrane protein 106C	chr12q13.1	201764_at	NM_024056
6.96	6.69	0.27	1.89E-01	5.60E-01	GTF3C1	general transcription factor IIIC, polypeptide 1, alpha 220kDa	chr16p12	202320_at	NM_001520
2.90	2.74	0.16	1.89E-01	5.60E-01	LOC644090	hypothetical LOC644090	chr7q36.1	1562749_at	XM_001719144 /// XM_931994 /// XM_945887
6.63	6.34	0.29	1.89E-01	5.60E-01	PL-5283	PL-5283 protein	chr7q33	224751_at	NM_001130929 /// XM_930101 /// XM_935586 /// XM_938850
4.99	4.60	0.39	1.89E-01	5.60E-01	NAT11	N-acetyltransferase 11	chr11q13.1	218734_at	NM_024771
6.70	6.33	0.37	1.89E-01	5.61E-01	TFB1M	transcription factor B1, mitochondrial	chr6q25.1-q25.3	228075_x_at	NM_016020
3.08	2.86	0.23	1.89E-01	5.61E-01	TAF1L	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	chr9p21.1	1553011_at	NM_153809
7.66	7.31	0.35	1.89E-01	5.61E-01	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	chr19p13.1	202801_at	NM_002730 /// NM_207518
2.22	1.97	0.25	1.89E-01	5.61E-01	F11	coagulation factor XI	chr4q35	1563160_at	NM_000128
3.48	3.10	0.38	1.89E-01	5.61E-01	GPR182	G protein-coupled receptor 182	chr12q13.3	1552440_at	NM_007264
6.93	6.69	0.24	1.89E-01	5.61E-01	M6PR	mannose-6-phosphate receptor (cation dependent)	chr12p13	200900_s_at	NM_002355
2.79	2.57	0.22	1.89E-01	5.61E-01	CDON	Cdon homolog (mouse)	chr11q23-q24	227526_at	NM_016952
2.26	2.10	0.15	1.89E-01	5.61E-01	---	---	---	232715_at	---
2.55	2.36	0.19	1.89E-01	5.61E-01	RDM1	RAD52 motif 1	chr17q11.2	239169_at	NM_001034836 /// NM_145654
7.64	7.18	0.46	1.89E-01	5.61E-01	CHSY1	chondroitin sulfate synthase 1	chr15q26.3	203044_at	NM_014918
2.43	2.24	0.20	1.89E-01	5.61E-01	FRY	furry homolog (Drosophila)	chr13q13.1	214319_at	NM_023037
2.17	2.01	0.16	1.89E-01	5.61E-01	C10orf108	chromosome 10 open reading frame 108	chr10p15.3	1557548_at	XR_041941 /// XR_041942 /// XR_041943 /// XR_041945 /// XR_041946
5.60	5.10	0.50	1.89E-01	5.61E-01	MID1IP1	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	chrXp11.4	218251_at	NM_001098790 /// NM_001098791 /// NM_021242
2.40	2.25	0.15	1.89E-01	5.61E-01	---	---	---	1559550_s_at	---
4.26	3.79	0.48	1.89E-01	5.61E-01	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	chrXp22.13	228933_at	NM_198270
5.48	5.18	0.30	1.89E-01	5.61E-01	NIP7	nuclear import 7 homolog (S. cerevisiae)	chr16q22.1	223397_s_at	NM_016101
4.86	4.62	0.24	1.89E-01	5.61E-01	---	---	---	235630_at	---
6.70	6.42	0.27	1.89E-01	5.61E-01	KLHDC3	kelch domain containing 3	chr6p21.1	208784_s_at	NM_057161
3.29	2.92	0.37	1.89E-01	5.61E-01	GOLGA8A /// GOLGA8B	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B	chr15q11.2 /// chr15q14	210424_s_at	NM_001023567 /// NM_181077 /// XM_001714558
5.37	5.03	0.35	1.90E-01	5.61E-01	SSH1	slingshot homolog 1 (Drosophila)	chr12q24.11	221753_at	NM_018984
2.47	2.29	0.18	1.90E-01	5.61E-01	EEF1E1	Eukaryotic translation elongation factor 1 epsilon 1	chr6p24.3-p25.1	213907_at	NM_004280
5.05	4.74	0.31	1.90E-01	5.61E-01	ZNF3	zinc finger protein 3	chr7q22.1	212684_at	NM_017715 /// NM_032924
6.51	6.13	0.38	1.90E-01	5.61E-01	PLA2G12A	phospholipase A2, group XIIA	chr4q25	223373_s_at	NM_030821

2.41	2.13	0.28	1.90E-01	5.61E-01	GAP43	growth associated protein 43	chr3q13.1-q13.2	204471_at	NM_001130064 /// NM_002045
3.01	2.86	0.15	1.90E-01	5.61E-01	PTPN21	protein tyrosine phosphatase, non-receptor type 21	chr14q31.3	40524_at	NM_007039
6.73	6.36	0.37	1.90E-01	5.61E-01	C11orf68	chromosome 11 open reading frame 68	chr11q13.1	221534_at	NM_031450
3.44	3.10	0.34	1.90E-01	5.61E-01	---	---	---	235452_at	---
6.52	6.18	0.35	1.90E-01	5.61E-01	LRP11	low density lipoprotein receptor-related protein 11	chr6q25.1	225060_at	NM_032832
2.64	2.44	0.19	1.90E-01	5.61E-01	CD209	CD209 molecule	chr19p13	1555729_a_at	NM_021155
2.83	2.53	0.30	1.90E-01	5.61E-01	RPS14	ribosomal protein S14	chr5q31-q33	214245_at	NM_001025070 /// NM_001025071 /// NM_005617
2.77	2.60	0.17	1.90E-01	5.61E-01	HHIPL1	HHIP-like 1	chr14q32	1556564_at	NM_001127258 /// NM_032425
3.95	3.57	0.38	1.90E-01	5.61E-01	KIAA1549	KIAA1549	chr7q34	223575_at	NM_020910
2.49	2.32	0.17	1.90E-01	5.62E-01	CHRNB3	cholinergic receptor, nicotinic, beta 3	chr8p11.2	207859_s_at	NM_000749
2.39	2.24	0.14	1.90E-01	5.62E-01	DOCK4	Dedicator of cytokinesis 4	chr7q31.1	241313_at	NM_014705
6.81	6.53	0.27	1.90E-01	5.62E-01	NR1H2	nuclear receptor subfamily 1, group H, member 2	chr19q13.3-q13.3	218215_s_at	NM_007121
2.23	2.03	0.20	1.90E-01	5.62E-01	---	---	---	230187_s_at	---
7.93	7.59	0.34	1.90E-01	5.62E-01	C14orf1	chromosome 14 open reading frame 1	chr14q24.3	202562_s_at	NM_007176
11.68	11.50	0.18	1.90E-01	5.62E-01	EEF2	eukaryotic translation elongation factor 2	chr19pter-q12	204102_s_at	NM_001961
3.83	3.63	0.20	1.90E-01	5.62E-01	FLJ32679 /// GOLGA8E /// GOLGA8G /// LOC100132565 /// LOC100132979 /// LOC729786	golgin-like hypothetical protein LOC440321 /// golgi autoantigen, golgin subfamily a, 8E /// golgi autoantigen, golgin subfamily a, 8G /// similar to golgi autoantigen, golgin subfamily a, 8G /// similar to golgi autoantigen, golgin subfamily a, 8A /// similar to golgi autoantigen, golgin subfamily a, 8G	chr15p13 /// chr15q11.2 /// chr5q13.1	222149_x_at	NM_001012420 /// NM_001012423 /// NM_001012452 /// XM_001723327 /// XM_001723328 /// XM_001723476 /// XM_001723478 /// XM_001724161 /// XM_001724162
4.34	3.95	0.40	1.91E-01	5.63E-01	SLCO3A1	solute carrier organic anion transporter family, member 3A1	chr15q26	219229_at	NM_013272
5.74	5.51	0.22	1.91E-01	5.63E-01	---	---	---	235989_at	---
7.72	7.47	0.25	1.91E-01	5.63E-01	GSS	glutathione synthetase	chr20q11.2	211630_s_at	NM_000178
4.42	4.14	0.29	1.91E-01	5.63E-01	C9orf127	chromosome 9 open reading frame 127	chr9p13.3	229729_at	NM_001042589 /// NM_001042590 /// NM_016446
5.05	4.80	0.25	1.91E-01	5.63E-01	ZNF343	zinc finger protein 343	chr20p13	227986_at	NM_024325
5.92	5.48	0.43	1.91E-01	5.63E-01	OCRL	oculocerebrorenal syndrome of Lowe	chrXq25-q26.1	208316_s_at	NM_000276 /// NM_001587
3.22	2.88	0.33	1.91E-01	5.63E-01	UGP2	UDP-glucose pyrophosphorylase 2	chr2p14-p13	232180_at	NM_001001521 /// NM_006759
4.83	4.55	0.27	1.91E-01	5.63E-01	BTNL9	butyrophilin-like 9	chr5q35.3	228434_at	NM_152547
6.09	5.58	0.51	1.91E-01	5.63E-01	CAPG	capping protein (actin filament), gelsolin-like	chr2p11.2	201850_at	NM_001747
2.94	2.69	0.26	1.91E-01	5.63E-01	JMJD2D	jumonji domain containing 2D	chr11q21	242788_at	NM_018039
3.14	2.99	0.15	1.91E-01	5.63E-01	SLC25A24	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	chr1p13.3	244481_at	NM_013386 /// NM_213651
8.00	7.12	0.87	1.91E-01	5.63E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	203638_s_at	NM_000141 /// NM_022970
2.60	2.40	0.21	1.91E-01	5.63E-01	---	---	---	1556160_a_at	---
8.39	8.11	0.27	1.91E-01	5.63E-01	SDF4	stromal cell derived factor 4	chr1p36.33	232032_x_at	NM_016176 /// NM_016547
3.01	2.80	0.21	1.91E-01	5.63E-01	BMP2	bone morphogenetic protein 2	chr20p12	205289_at	NM_001200
2.46	2.26	0.20	1.91E-01	5.63E-01	EHF	Ets homologous factor	chr11p12	225645_at	NM_012153
6.77	6.51	0.27	1.91E-01	5.63E-01	SLC25A44	solute carrier family 25, member 44	chr1q22	32091_at	NM_014655
4.86	4.48	0.38	1.91E-01	5.63E-01	---	---	---	239536_at	---
2.87	2.72	0.15	1.91E-01	5.63E-01	---	---	---	1563692_at	---
2.44	2.25	0.19	1.91E-01	5.63E-01	---	---	---	237994_at	---

2.48	2.26	0.22	1.91E-01	5.63E-01	C11orf44	chromosome 11 open reading frame 44	chr11q24.3	1553417_at	XR_039976 /// XR_039977 /// XR_039978																				
4.93	4.56	0.37	1.91E-01	5.63E-01	SLC2A4RG	SLC2A4 regulator	chr20q13.33	1555500_s_at	NM_020062																				
5.87	5.32	0.55	1.91E-01	5.63E-01	---	---	---	225055_at	---																				
3.91	3.21	0.70	1.91E-01	5.63E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	213933_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719																				
9.18	8.68	0.50	1.92E-01	5.63E-01	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	chrXp11.3-p11.23	201210_at	NM_001356																				
2.23	2.08	0.15	1.92E-01	5.63E-01	---	---	---	241204_at	---																				
7.08	6.87	0.21	1.92E-01	5.63E-01	MPP1	membrane protein, palmitoylated 1, 55kDa	chrXq28	202974_at	NM_002436																				
4.59	3.64	0.95	1.92E-01	5.63E-01	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	chr14q32.2	222895_s_at	NM_022898 /// NM_138576																				
2.51	2.32	0.19	1.92E-01	5.64E-01	LOC144776	hypothetical protein LOC144776	chr13q31.3	1564287_at	XM_375033 /// XM_936612																				
5.67	5.29	0.38	1.92E-01	5.64E-01	PCGF2	polycomb group ring finger 2	chr17q12	203793_x_at	NM_007144																				
5.34	5.06	0.28	1.92E-01	5.64E-01	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	chr1p36.22	212326_at	NM_015378 /// NM_018156																				
9.81	9.20	0.61	1.92E-01	5.64E-01	TPM2	tropomyosin 2 (beta)	chr9p13.2-p13.1	204083_s_at	NM_003289 /// NM_213674																				
2.16	2.02	0.14	1.92E-01	5.64E-01	OR9A1P	olfactory receptor, family 9, subfamily A, member 1 pseudogene	chr7q34	1567249_at	---																				
4.52	4.18	0.33	1.92E-01	5.64E-01	USP24	ubiquitin specific peptidase 24	chr1p32.3	212388_at	NM_015306																				
2.24	2.02	0.21	1.92E-01	5.64E-01	ZNF568	zinc finger protein 568	chr19q13.12	1561425_a_at	NM_198539																				
2.74	2.54	0.20	1.92E-01	5.64E-01	ADCK2	aarF domain containing kinase 2	chr7q32-q34	222117_s_at	NM_052853																				
2.13	1.96	0.16	1.92E-01	5.64E-01	---	---	---	1564718_at	---																				
3.84	3.64	0.20	1.92E-01	5.64E-01	---	---	---	1566474_at	---																				
5.88	5.48	0.41	1.92E-01	5.64E-01	NR2C2	nuclear receptor subfamily 2, group C, member 2	chr3p25	225477_s_at	NM_003298																				
6.47	6.09	0.39	1.92E-01	5.65E-01	RCOR3	REST corepressor 3	chr1q32.2-q32.3	222605_at	NM_018254																				
3.40	3.05	0.35	1.92E-01	5.65E-01	RNF24	ring finger protein 24	chr20p13-p12.1	204668_at	NM_001134337 /// NM_001134338 /// NM_007219																				
7.69	7.30	0.39	1.93E-01	5.65E-01	C5orf25	chromosome 5 open reading frame 25	chr5q35.2	228805_at	NM_198567																				
2.17	1.98	0.20	1.93E-01	5.65E-01	MCM10	minichromosome maintenance complex component 10	chr10p13	222962_s_at	NM_018518 /// NM_182751																				
7.91	7.65	0.25	1.93E-01	5.65E-01	C1orf212	chromosome 1 open reading frame 212	chr1p34.3	225404_at	NM_138428																				
2.43	2.21	0.22	1.93E-01	5.65E-01	TTC7A	Tetratricopeptide repeat domain 7A	chr2p21	240369_at	NM_020458																				
5.78	5.40	0.39	1.93E-01	5.65E-01	NKIRAS2	NFKB inhibitor interacting Ras-like 2	chr17q21.2	218240_at	NM_001001349 /// NM_017595																				
2.69	2.45	0.24	1.93E-01	5.65E-01	PGR	progesterone receptor	chr11q22-q23	208305_at	NM_000926																				
3.88	3.63	0.25	1.93E-01	5.65E-01	SFT2D2	SFT2 domain containing 2	chr1q24.2	214838_at	NM_199344																				
3.98	3.68	0.30	1.93E-01	5.65E-01	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	chr9q21.32	203220_s_at	NM_005077																				
2.78	2.47	0.30	1.93E-01	5.65E-01	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	chr4q31.1	222587_s_at	NM_017423																				
2.58	2.40	0.18	1.93E-01	5.65E-01	---	---	---	1563886_at	---																				
2.45	2.27	0.18	1.93E-01	5.65E-01	FNDC3A	fibronectin type III domain containing 3A	chr13q14.2	241611_s_at	NM_001079673 /// NM_014923																				

7.42	6.99	0.44	1.93E-01	5.65E-01	YTHDC1	YTH domain containing 1	chr4q13.2	212455_at	NM_001031732 /// NM_133370																				
6.41	5.91	0.50	1.93E-01	5.65E-01	FKBP11	FK506 binding protein 11, 19 kDa	chr12q13.12	219118_at	NM_016594																				
2.32	2.18	0.14	1.93E-01	5.65E-01	KCNJ10	potassium inwardly-rectifying channel, subfamily J, member 10	chr1q22-q23	206692_at	NM_002241																				
3.14	2.86	0.28	1.93E-01	5.65E-01	C11orf41	chromosome 11 open reading frame 41	chr11p13	235486_at	NM_012194																				
7.91	7.73	0.19	1.93E-01	5.65E-01	WDR82	WD repeat domain 82	chr3p21.1	201934_at	NM_025222																				
3.29	2.97	0.32	1.93E-01	5.65E-01	---	---	---	1556229_at	---																				
4.34	3.95	0.39	1.93E-01	5.65E-01	---	---	---	227709_at	---																				
5.56	5.09	0.47	1.93E-01	5.65E-01	SALL2	sal-like 2 (Drosophila)	chr14q11.1-q12	213283_s_at	NM_005407																				
2.33	2.18	0.15	1.93E-01	5.65E-01	GPC3	Glypican 3	chrXq26.1	243243_at	NM_004484																				
4.00	3.83	0.17	1.93E-01	5.65E-01	LOC642031	hypothetical protein LOC642031	---	239676_x_at	XM_936101																				
5.62	5.29	0.33	1.93E-01	5.65E-01	C22orf40	chromosome 22 open reading frame 40	chr22q13.31	227590_at	NM_207327																				
7.27	6.88	0.40	1.93E-01	5.65E-01	FADS3	fatty acid desaturase 3	chr11q12-q13.1	204257_at	NM_021727																				
3.06	2.66	0.41	1.93E-01	5.65E-01	LOC100130958	hypothetical protein LOC100130958	chr16q23.1	1559960_x_at	NM_001129979 /// XM_001717986 /// XM_001718777 /// XM_001719609																				
1.96	1.77	0.19	1.93E-01	5.65E-01	SMAD4	SMAD family member 4	chr18q21.1	1565702_at	NM_005359																				
2.07	1.81	0.26	1.93E-01	5.65E-01	LOC283483	hypothetical protein LOC283483	chr13q33.3	244119_at	---																				
2.53	2.29	0.23	1.93E-01	5.65E-01	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	chr2q32.1	229588_at	NM_018981																				
8.30	8.00	0.30	1.93E-01	5.66E-01	PGLS	6-phosphogluconolactonase	chr19p13.2	218388_at	NM_012088																				
6.58	6.32	0.26	1.93E-01	5.66E-01	SFRS2B	splicing factor, arginine/serine-rich 2B	chr11q22	228760_at	NM_032102																				
7.98	7.58	0.40	1.93E-01	5.66E-01	MRPL32	mitochondrial ribosomal protein L32	chr7p14	225260_s_at	NM_031903																				
7.03	6.80	0.23	1.94E-01	5.66E-01	SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	chr1p36.33	223053_x_at	NM_014188																				
4.64	4.25	0.39	1.94E-01	5.66E-01	GPATCH1	G patch domain containing 1	chr19q13.11	219818_s_at	NM_018025																				
2.64	2.34	0.30	1.94E-01	5.66E-01	ATR	ataxia telangiectasia and Rad3 related	chr3q22-q24	233288_at	NM_001184																				
2.98	2.72	0.25	1.94E-01	5.66E-01	ZNF345	zinc finger protein 345	chr19q13.12	207236_at	NM_003419																				
2.46	2.29	0.17	1.94E-01	5.66E-01	TIFA	TRAF-interacting protein with forkhead-associated domain	chr4q25	238858_at	NM_052864																				
5.02	4.64	0.38	1.94E-01	5.66E-01	SAMD4A	sterile alpha motif domain containing 4A	chr14q22.2	212845_at	NM_015589																				
3.97	3.59	0.39	1.94E-01	5.66E-01	DTX4	deltex 4 homolog (Drosophila)	chr11q12.1	212611_at	NM_015177																				
3.24	2.96	0.27	1.94E-01	5.66E-01	SOX21	SRY (sex determining region Y)-box 21	chr13q31-q32	208468_at	NM_007084																				
7.11	6.58	0.53	1.94E-01	5.66E-01	PHLDA1	pleckstrin homology-like domain, family A, member 1	chr12q15	225842_at	NM_007350																				
7.09	6.74	0.35	1.94E-01	5.66E-01	SEPX1	selenoprotein X, 1	chr16p13.3	217977_at	NM_016332																				
6.23	5.98	0.25	1.94E-01	5.66E-01	GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	chr12q24.2	216232_s_at	NM_006836																				
9.40	8.98	0.41	1.94E-01	5.66E-01	CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1	chr8q21	1552493_s_at	NM_000497 /// NM_001026213																				
7.07	6.84	0.23	1.94E-01	5.66E-01	TMEM60	transmembrane protein 60	chr7q11.23	223396_at	NM_032936																				
3.35	2.98	0.37	1.94E-01	5.66E-01	DPEP2	dipeptidase 2	chr16q22.1	219452_at	NM_022355																				
2.69	2.42	0.26	1.94E-01	5.66E-01	---	---	---	243695_at	---																				
2.54	2.35	0.19	1.94E-01	5.66E-01	TOP1MT	Topoisomerase (DNA) I, mitochondrial	chr8q24.3	1560757_at	NM_052963																				
2.21	2.05	0.15	1.94E-01	5.66E-01	---	---	---	217131_at	---																				
2.79	2.65	0.14	1.94E-01	5.66E-01	---	---	---	231631_at	---																				
6.27	5.99	0.29	1.94E-01	5.66E-01	CSNK2A1	casein kinase 2, alpha 1 polypeptide	chr20p13	212075_s_at	NM_001895 /// NM_177559 /// NM_177560																				
2.70	2.47	0.23	1.94E-01	5.66E-01	SLC11A2	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	chr12q13	237106_at	NM_000617																				
3.16	2.94	0.22	1.94E-01	5.66E-01	LOC441528	hypothetical protein LOC441528	chrXp22.33	1558046_x_at	XR_041386																				
5.81	5.36	0.45	1.94E-01	5.66E-01	ZFP36L2	zinc finger protein 36, C3H type-like 2	chr2p22.3-p21	201367_s_at	NM_006887																				
3.53	3.22	0.32	1.94E-01	5.66E-01	PRR5	proline rich 5 (renal)	chr22q13	219168_s_at	NM_001017528 /// NM_001017529 /// NM_001017530 /// NM_015366 /// NM_181333																				
2.41	2.20	0.21	1.94E-01	5.67E-01	LOC731157	Hypothetical LOC731157	chr5q14.3	233163_at	XR_015397 /// XR_037137 /// XR_037460																				
2.32	2.14	0.18	1.94E-01	5.67E-01	---	---	---	234502_at	---																				

8.70	8.46	0.24	1.95E-01	5.67E-01	C1orf43	chromosome 1 open reading frame 43	chr1q21.2	1555226_s_at	NM_001098616 /// NM_015449 /// NM_138740																				
5.02	4.55	0.47	1.95E-01	5.67E-01	KLHL8	kelch-like 8 (Drosophila)	chr4q22.1	242648_at	NM_020803																				
7.67	7.45	0.22	1.95E-01	5.67E-01	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	chr12q24.31	201632_at	NM_001414																				
2.38	2.21	0.17	1.95E-01	5.67E-01	---	---	---	241790_at	---																				
9.22	9.06	0.16	1.95E-01	5.67E-01	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	221481_x_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370																				
3.38	3.18	0.20	1.95E-01	5.67E-01	C1orf91	chromosome 1 open reading frame 91	chr1p36.11-p34.2	234006_s_at	NM_019118																				
3.84	3.57	0.27	1.95E-01	5.67E-01	EPHB6	EPH receptor B6	chr7q33-q35	204718_at	NM_004445																				
5.45	5.12	0.33	1.95E-01	5.67E-01	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	chr8p12	223568_s_at	NM_001102559 /// NM_001102560 /// NM_032483																				
3.28	2.98	0.30	1.95E-01	5.67E-01	AGER	advanced glycosylation end product-specific receptor	chr6p21.3	210081_at	NM_001136 /// NM_172197																				
3.05	2.82	0.23	1.95E-01	5.67E-01	LYG1	lysozyme G-like 1	chr2q11.2	236706_at	NM_174898																				
2.86	2.69	0.17	1.95E-01	5.67E-01	CLIP1	CAP-GLY domain containing linker protein 1	chr12q24.3	240444_x_at	NM_002956 /// NM_198240																				
4.37	4.14	0.23	1.95E-01	5.67E-01	TIGD1	tigger transposable element derived 1	chr2q37.1	1553099_at	NM_145702																				
7.45	7.15	0.30	1.95E-01	5.67E-01	FAM65A	family with sequence similarity 65, member A	chr16q22.1	45749_at	NM_024519																				
10.72	10.50	0.22	1.95E-01	5.67E-01	COX5B	cytochrome c oxidase subunit Vb	chr2cen-q13	211025_x_at	NM_001862																				
3.84	3.43	0.41	1.95E-01	5.67E-01	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10q25.3	212762_s_at	NM_030756																				
8.40	7.33	1.07	1.95E-01	5.67E-01	---	---	---	238835_at	---																				
4.28	4.00	0.28	1.95E-01	5.67E-01	PIGG	phosphatidylinositol glycan anchor biosynthesis, class G	chr4p16.3	1563842_at	NM_001127178 /// NM_017733																				
8.18	7.92	0.26	1.95E-01	5.67E-01	SMS	spermine synthase	chrXp22.1	202043_s_at	NM_004595																				
5.50	5.25	0.25	1.95E-01	5.67E-01	POLL	polymerase (DNA directed), lambda	chr10q23	221049_s_at	NM_013274																				
2.16	2.02	0.14	1.95E-01	5.67E-01	---	---	---	237907_at	---																				
7.99	7.44	0.55	1.95E-01	5.68E-01	GLIPR2	GLI pathogenesis-related 2	chr9p13-p12	225602_at	NM_022343																				
5.41	5.14	0.27	1.95E-01	5.68E-01	LOH12CR1	loss of heterozygosity, 12, chromosomal region 1	chr12p12	227723_at	NM_058169																				
8.00	7.64	0.35	1.95E-01	5.68E-01	FAM54B	family with sequence similarity 54, member B	chr1p36.11	224280_s_at	NM_001099625 /// NM_001099626 /// NM_001099627 /// NM_019557																				
5.75	5.40	0.34	1.95E-01	5.68E-01	MLXIP	MLX interacting protein	chr12q24.31	202519_at	NM_014938																				
2.08	1.94	0.15	1.96E-01	5.68E-01	LOC646470	similar to proteaseome (prosome, macropain) 28 subunit, 3	chr1q23.3	243581_at	XR_017682 /// XR_019649 /// XR_040951																				
3.30	2.92	0.37	1.96E-01	5.68E-01	ABCB10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	chr1q42.13	223320_s_at	NM_012089																				
2.44	2.13	0.31	1.96E-01	5.68E-01	PPIL4 /// ZC3H12D	peptidylprolyl isomerase (cyclophilin)-like 4 /// zinc finger CCCH-type containing 12D	chr6q24-q25 /// chr6q25.1	1559263_s_at	NM_139126 /// NM_207360																				
3.37	3.04	0.34	1.96E-01	5.68E-01	LAT /// SPNS1	linker for activation of T cells /// spinster homolog 1 (Drosophila)	chr16p11.2	211005_at	NM_001014987 /// NM_001014988 /// NM_001014989 /// NM_014387 /// NM_032038																				
2.87	2.71	0.17	1.96E-01	5.68E-01	H6PD	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	chr1p36	1555685_at	NM_004285																				
2.59	2.43	0.16	1.96E-01	5.68E-01	FAM153B	family with sequence similarity 153, member B	chr5q35.2	1555485_s_at	NM_001079529																				
8.56	8.00	0.57	1.96E-01	5.68E-01	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	chr1p36.12	218309_at	NM_018584																				

2.11	1.97	0.15	1.96E-01	5.68E-01	RS1	retinoschisin 1	chrXp22.2-p22.1	207363_at	NM_000330																				
6.01	5.53	0.48	1.96E-01	5.69E-01	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	chr22q12.2	209494_s_at	NM_014323 /// NM_032050 /// NM_032051 /// NM_032052																				
6.97	6.73	0.24	1.96E-01	5.69E-01	LOC220906 /// RPL7L1	hypothetical protein LOC220906 /// ribosomal protein L7-like 1	chr10p11.23 /// chr6p21.1	225515_s_at	NM_198486 /// XM_001716346 /// XM_001716412																				
4.55	4.24	0.31	1.96E-01	5.69E-01	TBC1D12	TBC1 domain family, member 12	chr10q23.33	221858_at	NM_015188																				
5.99	5.65	0.35	1.96E-01	5.69E-01	MSL3L1	male-specific lethal 3-like 1 (Drosophila)	chrXp22.3	207551_s_at	NM_006800 /// NM_078628 /// NM_078629 /// NM_078630																				
3.12	2.83	0.29	1.96E-01	5.69E-01	ZNF341	zinc finger protein 341	chr20q11.22	233362_at	NM_032819																				
8.35	8.16	0.19	1.96E-01	5.69E-01	NUTF2	nuclear transport factor 2	chr16q22.1	202397_at	NM_005796																				
6.63	6.32	0.30	1.96E-01	5.69E-01	RBM17	RNA binding motif protein 17	chr10p15.1	224781_s_at	NM_032905																				
2.70	2.46	0.25	1.96E-01	5.69E-01	---	---	---	1557325_at	---																				
7.75	7.27	0.48	1.96E-01	5.69E-01	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	chr5q31	208951_at	NM_001182																				
4.30	4.02	0.29	1.97E-01	5.69E-01	SPPL2B	signal peptide peptidase-like 2B	chr19p13.3	225249_at	NM_001077238 /// NM_152988																				
3.59	3.27	0.32	1.97E-01	5.69E-01	CLEC7A	C-type lectin domain family 7, member A	chr12p13.2	1554406_a_at	NM_022570 /// NM_197947 /// NM_197948 /// NM_197949 /// NM_197950 /// NM_197954																				
2.28	2.13	0.16	1.97E-01	5.69E-01	PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	chr20q13.13	214827_at	NM_032521																				
2.60	2.42	0.18	1.97E-01	5.69E-01	FLJ31485	hypothetical gene supported by AK056047; AK056281; AK123838	chr12q24.33	243351_at	XM_001128937 /// XM_001133168 /// XM_001715676																				
5.38	5.05	0.33	1.97E-01	5.69E-01	KLF15	Kruppel-like factor 15	chr3q13-q21	231015_at	NM_014079																				
5.61	5.22	0.38	1.97E-01	5.70E-01	---	---	---	239896_at	---																				
2.51	2.37	0.14	1.97E-01	5.70E-01	LUZP1	leucine zipper protein 1	chr1p36	1553224_at	NM_033631																				
4.41	3.94	0.47	1.97E-01	5.70E-01	SUZ12 /// SUZ12P	suppressor of zeste 12 homolog (Drosophila) /// suppressor of zeste 12 homolog pseudogene	chr17q11.2	213971_s_at	NM_015355																				
5.29	4.69	0.60	1.97E-01	5.70E-01	TMEM163	transmembrane protein 163	chr2q21.3	1552626_a_at	NM_030923																				
9.69	9.49	0.20	1.97E-01	5.70E-01	ARF4	ADP-ribosylation factor 4	chr3p21.2-p21.1	201097_s_at	NM_001660																				
6.97	6.71	0.26	1.97E-01	5.70E-01	TBL1X	transducin (beta)-like 1X-linked	chrXp22.3	213400_s_at	NM_005647																				
2.31	2.16	0.15	1.97E-01	5.70E-01	---	---	---	240678_at	---																				
2.69	2.50	0.18	1.97E-01	5.70E-01	LOC100131039	Hypothetical protein LOC100131039	chr2q31.2	1556043_a_at	XM_001722439 /// XM_001722454 /// XM_001726001																				
2.79	2.57	0.22	1.97E-01	5.70E-01	RFFL	ring finger and FYVE-like domain containing 1	chr17q12	1552649_a_at	NM_001017368 /// NM_057178																				
11.24	11.07	0.17	1.98E-01	5.71E-01	RPL35A	ribosomal protein L35a	chr3q29-qter	213687_s_at	NM_000996																				
3.64	3.28	0.37	1.98E-01	5.71E-01	ABAT	4-aminobutyrate aminotransferase	chr16p13.2	206527_at	NM_000663 /// NM_001127448 /// NM_020686																				

8.73	8.47	0.26	1.98E-01	5.71E-01	TRIOBP	TRIO and F-actin binding protein	chr22q13.1	216210_x_at	NM_001039141 /// NM_007032 /// NM_138632																				
2.50	2.18	0.32	1.98E-01	5.71E-01	---	---	---	242388_x_at	---																				
2.97	2.75	0.22	1.98E-01	5.71E-01	ILDR1	immunoglobulin-like domain containing receptor 1	chr3q13.33	1553545_at	NM_175924																				
6.46	6.12	0.33	1.98E-01	5.71E-01	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	chr6p21.3	202307_s_at	NM_000593																				
6.14	5.69	0.46	1.98E-01	5.71E-01	ARID1A	AT rich interactive domain 1A (SWI-like)	chr1p35.3	210649_s_at	NM_006015 /// NM_139135																				
4.31	4.13	0.18	1.98E-01	5.71E-01	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	chr12q24.31	204590_x_at	NM_022916																				
6.53	6.29	0.25	1.98E-01	5.71E-01	NADK	NAD kinase	chr1p36.33-p36.21	213607_x_at	NM_023018																				
6.20	5.88	0.31	1.98E-01	5.71E-01	MAP2K2	mitogen-activated protein kinase kinase 2	chr19p13.3	213490_s_at	NM_030662																				
5.85	5.61	0.24	1.98E-01	5.71E-01	TRAK1	trafficking protein, kinesin binding 1	chr3p25.3-p24.1	202080_s_at	NM_001042646 /// NM_014965																				
3.36	3.12	0.24	1.98E-01	5.71E-01	LOC201229	Hypothetical protein LOC201229	chr17q11.2	1560703_at	NM_001076680																				
6.53	6.27	0.26	1.98E-01	5.71E-01	---	---	---	213474_at	---																				
5.69	5.08	0.61	1.98E-01	5.71E-01	NLK	nemo-like kinase	chr17q11.2	218318_s_at	NM_016231																				
2.80	2.42	0.38	1.98E-01	5.71E-01	LOC150759	hypothetical protein LOC150759	chr2q11.2	213703_at	XR_000661																				
6.34	5.96	0.38	1.98E-01	5.72E-01	THAP11	THAP domain containing 11	chr16q22.1	212910_at	NM_020457																				
6.50	5.75	0.75	1.98E-01	5.72E-01	CRLF1	cytokine receptor-like factor 1	chr19p12	206315_at	NM_004750																				
2.37	2.11	0.26	1.98E-01	5.72E-01	---	---	---	228289_at	---																				
5.27	4.96	0.31	1.98E-01	5.72E-01	SPRED1	sprouty-related, EVH1 domain containing 1	chr15q14	235074_at	NM_152594																				
5.41	5.24	0.17	1.98E-01	5.72E-01	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	chr19q13.2	1558407_at	NM_022835																				
7.85	6.47	1.39	1.99E-01	5.72E-01	ZNF331	zinc finger protein 331	chr19q13.41	227613_at	NM_001079906 /// NM_001079907 /// NM_018555																				
3.66	3.36	0.30	1.99E-01	5.72E-01	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	chr5q31.2	227166_at	NM_152686																				
4.80	4.45	0.35	1.99E-01	5.72E-01	FAIM	Fas apoptotic inhibitory molecule	chr3q22.3	220643_s_at	NM_001033030 /// NM_001033031 /// NM_001033032 /// NM_018147																				
4.63	4.40	0.23	1.99E-01	5.72E-01	C11orf84	chromosome 11 open reading frame 84	chr11q13.1	227292_at	NM_138471																				
2.60	2.43	0.17	1.99E-01	5.72E-01	---	---	---	1566499_at	---																				
2.28	2.09	0.19	1.99E-01	5.72E-01	ITGB8	integrin, beta 8	chr7p15.3	205816_at	NM_002214																				
2.65	2.46	0.20	1.99E-01	5.72E-01	C14orf64	chromosome 14 open reading frame 64	chr14q32.2	1564211_at	NR_015430																				
2.91	2.47	0.43	1.99E-01	5.72E-01	---	---	---	235428_at	---																				
2.73	2.52	0.21	1.99E-01	5.73E-01	APOC2	Apolipoprotein C-II	chr19q13.2	231562_at	NM_000483																				
3.87	3.29	0.59	1.99E-01	5.73E-01	TMEM200B	transmembrane protein 200B	chr1p35	227386_s_at	NM_001003682																				
6.93	6.70	0.23	1.99E-01	5.73E-01	UBFD1	ubiquitin family domain containing 1	chr16p12	224878_at	NM_019116																				
4.08	3.70	0.38	1.99E-01	5.73E-01	IMMT	Inner membrane protein, mitochondrial (mitofilin)	chr2p11.2|2	242361_at	NM_001100169 /// NM_001100170 /// NM_006839																				
6.01	5.67	0.34	1.99E-01	5.73E-01	CRYZL1	crystallin, zeta (quinone reductase)-like 1	chr21q21.3	1552347_at	NM_145858																				
3.85	3.56	0.29	1.99E-01	5.73E-01	SNAP25	synaptosomal-associated protein, 25kDa	chr20p12-p11.2	202507_s_at	NM_003081 /// NM_130811																				
4.05	3.79	0.26	1.99E-01	5.73E-01	RABL5	RAB, member RAS oncogene family-like 5	chr7q22.1	218785_s_at	NM_001130820 /// NM_001130821 /// NM_001130822 /// NM_022777																				
5.38	5.15	0.23	1.99E-01	5.73E-01	CRELD1	cysteine-rich with EGF-like domains 1	chr3p25.3	203368_at	NM_001031717 /// NM_001077415 /// NM_015513																				
5.99	5.64	0.35	1.99E-01	5.73E-01	RSPH3	radial spoke 3 homolog (Chlamydomonas)	chr6q25.3	1568613_at	NM_031924																				
2.69	2.49	0.20	1.99E-01	5.73E-01	SOX4	SRY (sex determining region Y)-box 4	chr6p22.3	1567906_at	NM_003107																				

2.79	2.53	0.26	2.00E-01	5.73E-01	USP33	ubiquitin specific peptidase 33	chr1p31.1	217441_at	NM_015017 /// NM_201624 /// NM_201626																				
5.63	5.34	0.29	2.00E-01	5.73E-01	OBFC2B	oligonucleotide/oligosaccharide-binding fold containing 2B	chr12q13.2	218903_s_at	NM_024068																				
5.71	5.44	0.27	2.00E-01	5.73E-01	CNTROB	centrobin, centrosomal BRCA2 interacting protein	chr17p13.1	228633_s_at	NM_001037144 /// NM_053051																				
4.49	4.23	0.25	2.00E-01	5.73E-01	SRPK1	SFRS protein kinase 1	chr6p21.3-p21.2	202199_s_at	NM_003137																				
7.76	7.22	0.54	2.00E-01	5.73E-01	GLIS2	GLIS family zinc finger 2	chr16p13.3	223378_at	NM_032575																				
7.72	7.51	0.20	2.00E-01	5.73E-01	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	chr2q35	208758_at	NM_004044																				
8.64	8.28	0.36	2.00E-01	5.73E-01	MAPRE1	microtubule-associated protein, RP/EB family, member 1	chr20q11.1-q11.23	200713_s_at	NM_012325																				
6.49	6.22	0.27	2.00E-01	5.73E-01	HSPBP1	hsp70-interacting protein	chr19q13.42	202415_s_at	NM_001130106 /// NM_012267																				
4.80	4.56	0.24	2.00E-01	5.73E-01	DUSP18	dual specificity phosphatase 18	chr22q12.2	227098_at	NM_152511																				
3.86	3.49	0.37	2.00E-01	5.73E-01	KIAA0922	KIAA0922	chr4q31.3	209760_at	NM_001131007 /// NM_015196																				
4.55	4.25	0.29	2.00E-01	5.73E-01	---	---	---	227010_at	---																				
2.74	2.57	0.17	2.00E-01	5.73E-01	PP13439	hypothetical LOC100128046	chr3q26.31	1569660_at	XM_001723263 /// XM_001726081 /// XM_001726374																				
4.97	4.43	0.55	2.00E-01	5.73E-01	INTS6	integrator complex subunit 6	chr13q14.12-q14.2	222239_s_at	NM_001039937 /// NM_001039938 /// NM_012141																				
3.50	3.20	0.30	2.00E-01	5.73E-01	CCDC96	coiled-coil domain containing 96	chr4p16.1	238682_at	NM_153376																				
3.22	2.90	0.32	2.00E-01	5.73E-01	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	chr13q11-q12	230348_at	NM_014572																				
2.73	2.56	0.17	2.00E-01	5.73E-01	---	---	---	217688_at	---																				
2.81	2.68	0.14	2.00E-01	5.73E-01	---	---	---	1569724_at	---																				
3.07	2.83	0.24	2.00E-01	5.73E-01	FAM90A1	family with sequence similarity 90, member A1	chr12p13.31	220535_at	NM_018088																				
3.91	3.61	0.30	2.00E-01	5.74E-01	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	chr5p12	225984_at	NM_006251 /// NM_206907																				
4.05	3.80	0.25	2.00E-01	5.74E-01	TOP3A	topoisomerase (DNA) III alpha	chr17p12-p11.2	204946_s_at	NM_004618																				
2.91	2.72	0.18	2.00E-01	5.74E-01	---	---	---	1565894_at	---																				
3.69	3.27	0.43	2.00E-01	5.74E-01	SIGLEC16	sialic acid binding Ig-like lectin 16 (gene/pseudogene)	chr19q13.33	1561880_a_at	NR_002825																				
7.17	6.84	0.33	2.00E-01	5.74E-01	PNPO	pyridoxamine 5'-phosphate oxidase	chr17q21.32	222653_at	NM_018129																				
3.07	2.88	0.19	2.00E-01	5.74E-01	TUB	tubby homolog (mouse)	chr11p15.5	228883_at	NM_003320 /// NM_177972																				
3.04	2.78	0.26	2.00E-01	5.74E-01	ZNF496	zinc finger protein 496	chr1q44	225349_at	NM_032752																				
2.03	1.89	0.14	2.01E-01	5.74E-01	DAZL	deleted in azoospermia-like	chr3p24.3	206588_at	NM_001351																				
3.67	2.81	0.86	2.01E-01	5.74E-01	SFRS5	splicing factor, arginine/serine-rich 5	chr14q24	210077_s_at	NM_001039465 /// NM_006925																				
3.18	2.93	0.25	2.01E-01	5.74E-01	---	---	---	239434_at	---																				
4.52	4.22	0.30	2.01E-01	5.74E-01	CARD8	caspase recruitment domain family, member 8	chr19q13.32	1554479_a_at	NM_014959																				
3.12	2.81	0.31	2.01E-01	5.74E-01	TEAD4	TEA domain family member 4	chr12p13.3-p13.2	41037_at	NM_003213 /// NM_201441 /// NM_201443																				
9.16	8.91	0.25	2.01E-01	5.74E-01	HLA-G	major histocompatibility complex, class I, G	chr6p21.3	211529_x_at	NM_002127																				
2.03	1.88	0.15	2.01E-01	5.74E-01	AFAP1	actin filament associated protein 1	chr4p16	203563_at	NM_001134647 /// NM_021638 /// NM_198595																				
3.93	3.74	0.20	2.01E-01	5.74E-01	TGM5	transglutaminase 5	chr15q15.2	207911_s_at	NM_004245 /// NM_201631																				
2.50	2.25	0.26	2.01E-01	5.74E-01	SOCS6	suppressor of cytokine signaling 6	chr18q22.2	206020_at	NM_004232																				
7.05	6.77	0.28	2.01E-01	5.74E-01	C11orf1	chromosome 11 open reading frame 1	chr11q13-q22	231530_s_at	NM_022761																				
3.78	3.46	0.32	2.01E-01	5.74E-01	NPY6R	neuropeptide Y receptor Y6 (pseudogene)	chr5q31	210444_at	NR_002713																				
3.31	3.06	0.25	2.01E-01	5.74E-01	PTPN7	protein tyrosine phosphatase, non-receptor type 7	chr1q32.1	1554860_at	NM_002832 /// NM_080588																				

4.97	4.77	0.20	2.01E-01	5.74E-01	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	chr7q36.1	222582_at	NM_001040633 /// NM_016203 /// NM_024429																				
4.06	3.58	0.48	2.01E-01	5.74E-01	PAQR8	progestin and adipoQ receptor family member VIII	chr6p12.1	227626_at	NM_133367																				
2.20	2.04	0.17	2.01E-01	5.74E-01	---	---	---	238410_x_at	---																				
2.11	1.97	0.14	2.01E-01	5.75E-01	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	chr2q32.3-q33.1	243080_at	NM_020760																				
4.56	4.21	0.35	2.01E-01	5.75E-01	KIAA0999	KIAA0999 protein	chr11q23.3	204157_s_at	NM_025164																				
2.51	2.32	0.18	2.01E-01	5.75E-01	KIAA0409	KIAA0409	chr11p15.4	203170_at	NM_015324																				
8.15	7.21	0.93	2.01E-01	5.75E-01	BTG2	BTG family, member 2	chr1q32	201236_s_at	NM_006763																				
2.44	2.30	0.14	2.02E-01	5.75E-01	---	---	---	1557118_a_at	---																				
6.81	6.55	0.25	2.02E-01	5.75E-01	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	chr7q22.1	209635_at	NM_001283 /// NM_057089																				
3.44	3.23	0.21	2.02E-01	5.75E-01	WDR8	WD repeat domain 8	chr1p36.3	236382_at	NM_017818																				
7.27	7.07	0.20	2.02E-01	5.75E-01	PPP2R2D	protein phosphatase 2, regulatory subunit B, delta isoform	chr10q26.3	221772_s_at	NM_001003656 /// NM_018461																				
6.58	6.26	0.32	2.02E-01	5.75E-01	LOC441461	hypothetical gene supported by BC030123	chr9q31.1	1558688_at	XR_041357 /// XR_041358 /// XR_041359																				
5.69	5.28	0.42	2.02E-01	5.75E-01	ZFYVE16	zinc finger, FYVE domain containing 16	chr5q14	203651_at	NM_001105251 /// NM_014733																				
2.07	1.94	0.13	2.02E-01	5.75E-01	LOC401220	hypothetical gene supported by BC036933	chr5q35.3	1559760_at	XM_379378 /// XM_945580																				
7.73	7.31	0.43	2.02E-01	5.75E-01	RGS3	regulator of G-protein signaling 3	chr9q32	203823_at	NM_017790 /// NM_021106 /// NM_130795 /// NM_134427 /// NM_144488 /// NM_144489																				
9.82	9.47	0.35	2.02E-01	5.75E-01	C2CD2	C2 calcium-dependent domain containing 2	chr21q22.3	212875_s_at	NM_015500 /// NM_199050																				
4.84	3.64	1.20	2.02E-01	5.76E-01	CXCL2	chemokine (C-X-C motif) ligand 2	chr4q21	209774_x_at	NM_002089																				
2.73	2.51	0.23	2.02E-01	5.76E-01	LOC791120 /// ZNF783	hypothetical LOC791120 /// zinc finger family member 783	chr7q36.1	1556224_a_at	NM_001004302 /// NR_015357 /// XR_039872 /// XR_039873 /// XR_039874 /// XR_039875																				
7.95	7.56	0.39	2.02E-01	5.76E-01	TTC19	tetratricopeptide repeat domain 19	chr17p12	217964_at	NM_017775																				
8.60	8.42	0.18	2.02E-01	5.76E-01	COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	chr7q22.1	201405_s_at	NM_006833																				
2.51	2.30	0.20	2.02E-01	5.76E-01	RAD51L3	RAD51-like 3 (S. cerevisiae)	chr17q11	37793_r_at	NM_002878 /// NM_133629																				
3.00	2.75	0.26	2.02E-01	5.76E-01	KLF12	Kruppel-like factor 12	chr13q22	214276_at	NM_007249																				
2.68	2.49	0.20	2.02E-01	5.76E-01	---	---	---	239764_at	---																				
5.29	4.89	0.39	2.02E-01	5.76E-01	WDFY3	WD repeat and FYVE domain containing 3	chr4q21.23	212606_at	NM_014991 /// NM_178583 /// NM_178585																				
2.35	2.20	0.16	2.02E-01	5.76E-01	---	---	---	217290_at	---																				
5.18	4.87	0.31	2.02E-01	5.76E-01	ARID1B	AT rich interactive domain 1B (SWI1-like)	chr6q25.1	1566990_x_at	NM_017519 /// NM_020732 /// NM_175863																				

2.83	2.65	0.18	2.02E-01	5.76E-01	GPR161	G protein-coupled receptor 161	chr1q24.2	230369_at	NM_007369 /// NM_153832																				
6.16	5.86	0.30	2.02E-01	5.76E-01	ESRRA	estrogen-related receptor alpha	chr11q13	1487_at	NM_004451																				
2.65	2.45	0.20	2.02E-01	5.76E-01	---	---	---	239554_at	---																				
5.27	4.87	0.40	2.03E-01	5.76E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	206111_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447																			
2.87	2.70	0.17	2.03E-01	5.76E-01	PPOX	protoporphyrinogen oxidase	chr1q22	238118_s_at	NM_000309 /// NM_001122764																				
3.56	2.34	1.22	2.03E-01	5.76E-01	CCNL1	Cyclin L1	chr3q25.32	1555827_at	NM_020307																				
2.75	2.53	0.21	2.03E-01	5.77E-01	TRD@	T cell receptor delta locus	chr14q11.2	213830_at	---																				
8.34	8.12	0.22	2.03E-01	5.77E-01	AHNAK	AHNAK nucleoprotein	chr11q12.2	211986_at	NM_001620 /// NM_024060																				
4.83	4.24	0.58	2.03E-01	5.77E-01	---	---	---	229822_at	---																				
2.38	2.18	0.20	2.03E-01	5.77E-01	HERC3	hect domain and RLD 3	chr4q21	1554290_at	NM_014606																				
3.05	2.84	0.21	2.03E-01	5.77E-01	LOC92497	hypothetical LOC92497	chr12q23.1	232611_at	XM_931850 /// XM_944913																				
2.69	2.48	0.21	2.03E-01	5.77E-01	CNIH3	cornichon homolog 3 (Drosophila)	chr1q42.12	214841_at	NM_152495																				
3.67	3.37	0.30	2.03E-01	5.77E-01	LOC401577	hypothetical protein LOC401577	chrXp22.33;Yp11.31	232172_at	XM_001714655 /// XM_001716015 /// XM_001717305 /// XM_379694																				

4.59	3.98	0.61	2.03E-01	5.77E-01	GSTO2	glutathione S-transferase omega 2	chr10q25.1	227163_at	NM_183239
5.58	5.32	0.26	2.03E-01	5.77E-01	DNASE2	deoxyribonuclease II, lysosomal	chr19p13.2	214992_s_at	NM_001375
6.13	5.73	0.41	2.03E-01	5.77E-01	KIRREL	kin of IRRE like (Drosophila)	chr1q21-q25	225303_at	NM_018240
4.22	3.86	0.36	2.03E-01	5.77E-01	---	---	---	236580_at	---
4.38	3.97	0.41	2.03E-01	5.77E-01	MFAP2	microfibrillar-associated protein 2	chr1p36.1-p35	203417_at	NM_002403 /// NM_017459
5.95	5.56	0.39	2.03E-01	5.77E-01	PNPLA4	patatin-like phospholipase domain containing 4	chrXp22.3	209740_s_at	NM_004650
4.03	3.61	0.42	2.03E-01	5.77E-01	ERO1LB	ERO1-like beta (S. cerevisiae)	chr1q42.2-q43	231944_at	NM_019891
4.31	4.09	0.21	2.03E-01	5.77E-01	ARS2	arsenate resistance protein 2	chr7q21	201679_at	NM_001128852 /// NM_001128853 /// NM_001128854 /// NM_015908 /// NM_182800
2.17	1.99	0.18	2.03E-01	5.77E-01	---	---	---	241077_at	---
7.55	6.51	1.04	2.03E-01	5.77E-01	---	---	---	235739_at	---
2.11	1.96	0.16	2.03E-01	5.77E-01	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	chr10p11.23	211264_at	NM_000818 /// NM_001134366
2.75	2.60	0.15	2.03E-01	5.77E-01	PHF21B	PHD finger protein 21B	chr22q13.31	1562309_s_at	NM_138415
5.05	4.69	0.35	2.03E-01	5.77E-01	C8orf30A	chromosome 8 open reading frame 30A	chr8q24.3	221629_x_at	NM_016458
3.36	2.94	0.42	2.03E-01	5.77E-01	STRC	stereocilin	chr15q15.3	1561306_s_at	NM_153700 /// XM_001715128 /// XM_001718339
2.78	2.60	0.18	2.03E-01	5.78E-01	KRT18P33	Keratin 18 pseudogene 33	chr2p14	1559940_s_at	XM_001719210 /// XR_017456 /// XR_019330
3.74	3.22	0.52	2.04E-01	5.78E-01	SENP6	SUMO1/sentrin specific peptidase 6	chr6q13-q14.3	214790_at	NM_001100409 /// NM_015571
8.86	8.63	0.22	2.04E-01	5.78E-01	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	chr1p34.2	200039_s_at	NM_002794
4.24	4.04	0.20	2.04E-01	5.78E-01	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	chr6p21.2-p21.1	1555553_a_at	NM_006672 /// NM_153320
4.81	4.51	0.30	2.04E-01	5.78E-01	C16orf86	chromosome 16 open reading frame 86	chr16q22.1	231153_at	NM_001012984
6.37	5.99	0.38	2.04E-01	5.78E-01	TSC2	tuberous sclerosis 2	chr16p13.3	215735_s_at	NM_000548 /// NM_001077183 /// NM_001114382
5.33	5.06	0.27	2.04E-01	5.78E-01	NPEPL1 /// STX16	aminopeptidase-like 1 /// syntaxin 16	chr20q13.32	218822_s_at	NM_001001433 /// NM_003763 /// NM_024663
8.65	8.39	0.26	2.04E-01	5.78E-01	MYEOV2	myeloma overexpressed 2	chr2q37.3	226845_s_at	NM_138336
4.76	4.55	0.21	2.04E-01	5.78E-01	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	chr1p22.2	202270_at	NM_002053
4.47	4.13	0.35	2.04E-01	5.78E-01	CENPN	centromere protein N	chr16q23.2	219555_s_at	NM_001100624 /// NM_001100625 /// NM_018455
7.23	6.26	0.97	2.04E-01	5.78E-01	CX3CR1	chemokine (C-X3-C motif) receptor 1	chr3p21|3p21.3	205898_at	NM_001337
6.53	6.23	0.30	2.04E-01	5.78E-01	RNF10	ring finger protein 10	chr12q24.31	208632_at	NM_014868
2.38	2.20	0.17	2.04E-01	5.78E-01	---	---	---	1568656_at	---
5.54	5.08	0.46	2.04E-01	5.78E-01	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	chr22q13.31-q13.33	226501_at	NM_022098
2.09	1.93	0.16	2.04E-01	5.78E-01	LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	chr1p13.1	242164_s_at	NM_014813
2.87	2.70	0.17	2.04E-01	5.78E-01	OSTbeta	organic solute transporter beta	chr15q22.31	230830_at	NM_178859
2.52	2.38	0.14	2.04E-01	5.78E-01	---	---	---	243102_at	---
2.14	1.96	0.18	2.04E-01	5.78E-01	---	---	---	231490_at	---
4.81	4.50	0.30	2.04E-01	5.78E-01	INO80D	INO80 complex subunit D	chr2q33.3	227924_at	NM_017759
3.75	3.15	0.60	2.04E-01	5.78E-01	MEX3D	mex-3 homolog D (C. elegans)	chr19p13.3	91816_f_at	NM_001085363 /// NM_203304

4.96	4.70	0.26	2.04E-01	5.78E-01	PHF21A	PHD finger protein 21A	chr11p11.2	1554153_a_at	NM_001101802 /// NM_016621																				
4.69	4.19	0.50	2.04E-01	5.78E-01	---	---	---	241494_at	---																				
4.35	4.12	0.22	2.04E-01	5.78E-01	FAM71A	Family with sequence similarity 71, member A	chr1q32.3	1564112_at	NM_153606																				
3.45	3.29	0.16	2.04E-01	5.78E-01	RECQL5	RecQ protein-like 5	chr17q25.2-q25.3	34063_at	NM_001003715 /// NM_001003716 /// NM_004259																				
2.36	2.16	0.20	2.04E-01	5.78E-01	ASCL1	achaete-scute complex homolog 1 (Drosophila)	chr12q23.2	209987_s_at	NM_004316																				
6.11	5.68	0.43	2.04E-01	5.79E-01	AMOTL2	angiomotin like 2	chr3q21-q22	203002_at	NM_016201																				
5.96	5.71	0.25	2.04E-01	5.79E-01	CD40	CD40 molecule, TNF receptor superfamily member 5	chr20q12-q13.2	35150_at	NM_001250 /// NM_152854																				
3.43	3.19	0.24	2.05E-01	5.79E-01	---	---	---	235756_at	---																				
8.03	7.57	0.46	2.05E-01	5.79E-01	---	---	---	225811_at	---																				
2.35	2.19	0.16	2.05E-01	5.79E-01	GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	chr5q12	220831_at	NM_016591																				
2.11	1.94	0.17	2.05E-01	5.79E-01	RABGAP1L	RAB GTPase activating protein 1-like	chr1q24	1554725_at	NM_001035230 /// NM_014857																				
2.18	2.04	0.14	2.05E-01	5.79E-01	DEFB122	defensin, beta 122 (pseudogene)	chr20q11.1	1562167_a_at	NR_002577																				
7.67	7.41	0.26	2.05E-01	5.79E-01	IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	chr2q21.1	212411_at	NM_033416																				
5.87	5.56	0.31	2.05E-01	5.79E-01	YDJC	YdjC homolog (bacterial)	chr22q11.21	227042_at	NM_001017964																				
10.14	9.96	0.19	2.05E-01	5.79E-01	EIF3K	eukaryotic translation initiation factor 3, subunit K	chr19q13.2	210501_x_at	NM_013234																				
4.71	4.33	0.38	2.05E-01	5.79E-01	C4orf42	chromosome 4 open reading frame 42	chr4p16.3	232066_x_at	NM_052861																				
6.33	6.08	0.24	2.05E-01	5.79E-01	PNO1	partner of NOB1 homolog (S. cerevisiae)	chr2p14	211697_x_at	NM_020143																				
7.30	7.12	0.17	2.05E-01	5.79E-01	PA2G4	proliferation-associated 2G4, 38kDa	chr12q13.2	208676_s_at	NM_006191																				
5.55	5.10	0.45	2.05E-01	5.79E-01	SYNGAP1 /// ZBTB9	synaptic Ras GTPase activating protein 1 homolog (rat) /// zinc finger and BTB domain containing 9	chr6p21.3 /// chr6p21.32	226163_at	NM_001130066 /// NM_006772 /// NM_152735																				
8.24	7.87	0.38	2.05E-01	5.79E-01	YPEL5	yippee-like 5 (Drosophila)	chr2p23.1	222408_s_at	NM_001127399 /// NM_001127400 /// NM_001127401 /// NM_016061																				
3.75	3.55	0.20	2.05E-01	5.79E-01	LOC100128443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	chr5q12.3	243575_at	NM_015183 /// NM_198828 /// XM_001720470 /// XM_001720479 /// XM_001722488																				
8.21	7.70	0.52	2.05E-01	5.79E-01	HLA-DMA	major histocompatibility complex, class II, DM alpha	chr6p21.3	217478_s_at	NM_006120																				
3.11	2.63	0.48	2.05E-01	5.79E-01	C1orf71	chromosome 1 open reading frame 71	chr1q44	1554660_a_at	NM_152609																				
3.86	3.55	0.31	2.05E-01	5.79E-01	PBX2	pre-B-cell leukemia homeobox 2	chr6p21.3	211097_s_at	NM_002586																				
3.65	3.28	0.37	2.05E-01	5.79E-01	RC3H2	ring finger and CCCH-type zinc finger domains 2	chr9q34	220201_at	NM_001100588 /// NM_018835																				
6.00	5.73	0.27	2.05E-01	5.79E-01	MED20	mediator complex subunit 20	chr6p21.1	212872_s_at	NM_004275																				
7.20	7.00	0.20	2.05E-01	5.79E-01	ARPC5L	actin related protein 2/3 complex, subunit 5-like	chr9q33.3	226915_s_at	NM_030978																				
6.22	5.92	0.30	2.05E-01	5.79E-01	---	---	---	225652_at	---																				
4.32	4.05	0.27	2.05E-01	5.79E-01	NR4A1	nuclear receptor subfamily 4, group A, member 1	chr12q13	210226_at	NM_002135 /// NM_173157																				
2.34	2.05	0.28	2.05E-01	5.79E-01	C6orf170	chromosome 6 open reading frame 170	chr6q22.31	232038_at	NM_152730																				
2.94	2.71	0.23	2.05E-01	5.79E-01	ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	chr17p13.2	207190_at	NM_015113 /// XM_001127649 /// XM_001719617 /// XM_001723898																				
2.30	2.11	0.18	2.05E-01	5.79E-01	---	---	---	1559483_at	---																				
2.17	2.04	0.13	2.05E-01	5.80E-01	---	---	---	1562669_at	---																				

6.85	6.43	0.42	2.05E-01	5.80E-01	TAF6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	chr7q22.1	203572_s_at	NM_005641 /// NM_139122 /// NM_139123 /// NM_139315																				
6.32	5.93	0.39	2.05E-01	5.80E-01	C1D	nuclear DNA-binding protein	chr2p13-p12	200056_s_at	NM_006333 /// NM_173177																				
6.43	5.99	0.43	2.06E-01	5.80E-01	ZCCHC3	zinc finger, CCHC domain containing 3	chr20p13-p12.2	225091_at	NM_033089																				
2.74	2.59	0.15	2.06E-01	5.80E-01	---	---	---	240025_x_at	---																				
2.95	2.80	0.14	2.06E-01	5.80E-01	CLECL1	C-type lectin-like 1	chr12p13.31	1561899_at	NM_172004																				
4.20	3.67	0.53	2.06E-01	5.80E-01	KCTD13	potassium channel tetramerisation domain containing 13	chr16p11.2	221889_at	NM_178863																				
6.10	5.86	0.23	2.06E-01	5.80E-01	RASSF7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	chr11p15.5	40359_at	NM_003475																				
9.40	9.03	0.37	2.06E-01	5.80E-01	H2AFJ	H2A histone family, member J	chr12p12	224301_x_at	NM_177925																				
2.48	2.28	0.19	2.06E-01	5.80E-01	KIAA1529	KIAA1529	chr9q22.33	229627_at	NM_020893																				
4.33	3.94	0.40	2.06E-01	5.80E-01	---	---	---	230456_at	---																				
3.04	2.70	0.35	2.06E-01	5.80E-01	ZNF107	zinc finger protein 107	chr7q11.2	205739_x_at	NM_001013746 /// NM_016220																				
3.05	2.86	0.19	2.06E-01	5.80E-01	ZNF570	zinc finger protein 570	chr19q13.12	1552562_at	NM_144694																				
4.91	4.24	0.67	2.06E-01	5.80E-01	---	---	---	213686_at	---																				
2.22	2.05	0.18	2.06E-01	5.80E-01	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	chr7p15.3	243167_at	NM_178559																				
5.56	5.34	0.23	2.06E-01	5.80E-01	MGC3207	hypothetical protein MGC3207	chr19p13.13	223770_x_at	NM_001031727 /// NM_032285																				
5.57	5.32	0.25	2.06E-01	5.80E-01	---	---	---	230407_at	---																				
3.36	2.66	0.70	2.06E-01	5.80E-01	LGALS8	lectin, galactoside-binding, soluble, 8	chr1q42-q43	210732_s_at	NM_006499 /// NM_201543 /// NM_201544 /// NM_201545																				
3.37	3.01	0.36	2.06E-01	5.81E-01	MGC13005	hypothetical LOC84771	chr9p24.3	223777_at	NR_024004 /// NR_024005 /// XM_376814																				
3.28	3.04	0.23	2.06E-01	5.81E-01	PHLDB1	pleckstrin homology-like domain, family B, member 1	chr11q23.3	216102_at	NM_015157																				
4.09	3.83	0.26	2.06E-01	5.81E-01	U2AF1	U2 small nuclear RNA auxiliary factor 1	chr21q22.3	231904_at	NM_001025203 /// NM_001025204 /// NM_006758																				
4.79	4.22	0.57	2.06E-01	5.81E-01	THBS4	thrombospondin 4	chr5q13	204776_at	NM_003248																				
2.58	2.28	0.31	2.06E-01	5.81E-01	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	chr2q24.1	210007_s_at	NM_000408 /// NM_001083112																				
6.59	6.27	0.32	2.06E-01	5.81E-01	XKR8	XK, Kell blood group complex subunit-related family, member 8	chr1p35.3	218753_at	NM_018053																				
2.55	2.40	0.15	2.06E-01	5.81E-01	---	---	---	1562598_at	---																				
7.02	6.75	0.26	2.06E-01	5.81E-01	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1	chr6p21.33	200045_at	NM_001025091 /// NM_001090																				
2.84	2.55	0.29	2.06E-01	5.81E-01	ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)	chr3p25.3-p25.2	1569827_at	NM_006395																				
5.60	5.37	0.23	2.06E-01	5.81E-01	SYT15	synaptotagmin XV	chr10q11.1	1560878_at	NM_031912 /// NM_181519 /// XM_001720092																				
3.03	2.77	0.26	2.07E-01	5.81E-01	---	---	---	231085_s_at	---																				
2.34	2.07	0.26	2.07E-01	5.81E-01	---	---	---	243788_at	---																				
7.38	7.03	0.34	2.07E-01	5.81E-01	FADS3	fatty acid desaturase 3	chr11q12-q13.1	216080_s_at	NM_021727																				

2.77	2.54	0.23	2.07E-01	5.81E-01	KRIT1	KRIT1, ankyrin repeat containing	chr7q21-q22	216713_at	NM_001013406 /// NM_004912 /// NM_194454 /// NM_194455 /// NM_194456
3.95	3.72	0.22	2.07E-01	5.81E-01	MYLK3	myosin light chain kinase 3	chr16q11.2	1562411_at	NM_182493
2.98	2.73	0.25	2.07E-01	5.81E-01	---	---	---	244486_at	---
4.62	4.41	0.21	2.07E-01	5.81E-01	PLXND1	plexin D1	chr3q21.3	1563657_at	NM_015103
8.58	8.40	0.18	2.07E-01	5.81E-01	VCP	valosin-containing protein	chr9p13.3	208649_s_at	NM_007126
4.17	3.94	0.23	2.07E-01	5.81E-01	ADIG	adipogenin	chr20q11.23	1554128_at	NM_001018082
2.83	2.60	0.23	2.07E-01	5.81E-01	---	---	---	230729_at	---
2.91	2.72	0.19	2.07E-01	5.81E-01	---	---	---	1559876_at	---
8.24	7.75	0.48	2.07E-01	5.81E-01	PHACTR2	phosphatase and actin regulator 2	chr6q24.2	227947_at	NM_001100164 /// NM_001100165 /// NM_001100166 /// NM_014721
2.67	2.46	0.21	2.07E-01	5.81E-01	---	---	---	229795_at	---
4.68	4.34	0.35	2.07E-01	5.81E-01	NOM1	nucleolar protein with MIF4G domain 1	chr7q36.3	227161_at	NM_138400
2.27	2.10	0.16	2.07E-01	5.81E-01	C9orf144	chromosome 9 open reading frame 144	chr9p13.2	216084_at	XR_040555 /// XR_040556 /// XR_040557
5.47	4.97	0.51	2.07E-01	5.81E-01	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	chr19q13.1	204039_at	NM_004364
2.62	2.45	0.18	2.07E-01	5.81E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	206616_s_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723
6.20	5.71	0.49	2.07E-01	5.82E-01	SOCS7	Suppressor of cytokine signaling 7	chr17q12	228662_at	NM_014598
3.03	2.84	0.18	2.07E-01	5.82E-01	ZNF589	zinc finger protein 589	chr3p21	210061_at	NM_016089
7.30	6.85	0.45	2.07E-01	5.82E-01	MFGE8	milk fat globule-EGF factor 8 protein	chr15q25	210605_s_at	NM_001114614 /// NM_005928
6.55	6.20	0.35	2.07E-01	5.82E-01	DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	chr9q34.13	209391_at	NM_003863
4.68	4.33	0.35	2.07E-01	5.82E-01	RIOK1	RIO kinase 1 (yeast)	chr6p24.3	224450_s_at	NM_031480 /// NM_153005
4.48	3.94	0.54	2.07E-01	5.82E-01	C11orf31	chromosome 11 open reading frame 31	chr11q12.1	1557799_at	NM_170746
2.49	2.32	0.18	2.08E-01	5.82E-01	---	---	---	242061_at	---
5.26	4.85	0.41	2.08E-01	5.82E-01	TTC7A	tetratricopeptide repeat domain 7A	chr2p21	224923_at	NM_020458
5.36	5.02	0.34	2.08E-01	5.82E-01	PRRX2	paired related homeobox 2	chr9q34.1	219729_at	NM_016307
2.63	2.49	0.14	2.08E-01	5.82E-01	---	---	---	242419_at	---
5.08	4.77	0.31	2.08E-01	5.82E-01	NUP62	nucleoporin 62kDa	chr19q13.33	207740_s_at	NM_012346 /// NM_016553 /// NM_153718 /// NM_153719
2.81	2.61	0.21	2.08E-01	5.82E-01	SYT9	synaptotagmin IX	chr11p15.4	1555052_a_at	NM_175733
8.70	8.48	0.22	2.08E-01	5.82E-01	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	chr9q22.32	201305_x_at	NM_006401
6.70	6.38	0.32	2.08E-01	5.82E-01	WSB2	WD repeat and SOCS box-containing 2	chr12q24.23	213734_at	NM_018639
2.87	2.63	0.24	2.08E-01	5.82E-01	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	chr2p23.1	1560180_at	NM_024572
5.01	4.80	0.22	2.08E-01	5.82E-01	---	---	---	1564129_a_at	---
7.11	6.74	0.37	2.08E-01	5.82E-01	PHC3	polyhomeotic homolog 3 (Drosophila)	chr3q26.2	226508_at	NM_024947

2.46	2.22	0.24	2.08E-01	5.82E-01	MDM2	Mdm2 p53 binding protein homolog (mouse)	chr12q14.3-q15	205386_s_at	NM_002392 /// NM_006878 /// NM_006879 /// NM_006881 /// NM_006882																			
3.40	3.09	0.31	2.08E-01	5.82E-01	GPR161	G protein-coupled receptor 161	chr1q24.2	214104_at	NM_007369 /// NM_153832																			
6.12	5.82	0.30	2.08E-01	5.82E-01	SAE1	SUMO1 activating enzyme subunit 1	chr19q13.32	1555618_s_at	NM_005500																			
6.11	5.73	0.38	2.08E-01	5.82E-01	KIAA1602	KIAA1602	chr12q13.13	231865_at	NM_020941																			
6.31	5.92	0.40	2.08E-01	5.82E-01	OXCT1	3-oxoacid CoA transferase 1	chr5p13.1	202780_at	NM_000436																			
5.33	5.10	0.23	2.08E-01	5.82E-01	HPS4	Hermansky-Pudlak syndrome 4	chr22cen-q12.3	1552652_at	NM_022081 /// NM_152841																			
9.86	9.56	0.30	2.08E-01	5.82E-01	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	chr11q14.1	218101_s_at	NM_004549																			
4.85	4.23	0.63	2.08E-01	5.82E-01	PKP4	plakophilin 4	chr2q23-q31	201929_s_at	NM_001005476 /// NM_003628																			
2.83	2.63	0.20	2.08E-01	5.82E-01	---	---	---	1555855_at	---																			
3.74	3.17	0.57	2.08E-01	5.82E-01	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	chr19p13.2-p13.1	214933_at	NM_000068 /// NM_001127221 /// NM_001127222 /// NM_023035																			
6.03	5.61	0.42	2.08E-01	5.82E-01	LOC648390 /// RPS27A /// UBB /// UBC	similar to ubiquitin B /// ribosomal protein S27a /// ubiquitin B /// ubiquitin C	chr12q24.3 /// chr17p12-p11.2 /// chr2p16 /// chr2q22.1	217144_at	NM_002954 /// NM_018955 /// NM_021009 /// XR_018377 /// XR_037845																			
8.14	7.85	0.30	2.08E-01	5.82E-01	POLDIP2	polymerase (DNA-directed), delta interacting protein 2	chr17q11.2	217806_s_at	NM_015584																			
5.17	5.01	0.16	2.08E-01	5.82E-01	C22orf27	chromosome 22 open reading frame 27	chr22q12.2	230566_at	XR_041215 /// XR_041216 /// XR_041217																			
6.95	6.71	0.24	2.08E-01	5.82E-01	RBM22	RNA binding motif protein 22	chr5q33.1	224068_x_at	NM_018047																			
3.26	2.74	0.52	2.08E-01	5.82E-01	RBM26	RNA binding motif protein 26	chr13q31.1	229433_at	NM_022118																			
8.36	8.03	0.32	2.08E-01	5.82E-01	MPRIP	myosin phosphatase Rho interacting protein	chr17p11.2	214771_x_at	NM_015134 /// NM_201274																			
4.42	3.73	0.69	2.08E-01	5.82E-01	RBP4	retinol binding protein 4, plasma	chr10q23-q24	219140_s_at	NM_006744																			
3.78	3.60	0.18	2.08E-01	5.82E-01	HEATR1	HEAT repeat containing 1	chr1q43	228351_at	NM_018072																			
2.73	2.55	0.18	2.08E-01	5.82E-01	MBL1P1	mannose-binding lectin (protein A) 1, pseudogene 1	chr10q22.2-q22.3	215110_at	NR_002724																			
2.57	2.41	0.17	2.08E-01	5.82E-01	CCRL1	chemokine (C-C motif) receptor-like 1	chr3q22	220351_at	NM_016557 /// NM_178445																			
2.31	2.14	0.17	2.09E-01	5.82E-01	LOC400680	hypothetical gene supported by AK097381; BC040866	chr19p12	1562348_at	XM_378783 /// XM_943659																			
3.02	2.69	0.33	2.09E-01	5.82E-01	L3MBTL	l(3)mbt-like (Drosophila)	chr20q13.12	210306_at	NM_015478 /// NM_032107																			
5.76	5.31	0.46	2.09E-01	5.83E-01	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	chr5q31.1	230078_at	NM_016340																			
5.75	5.35	0.39	2.09E-01	5.83E-01	AGXT2L2	alanine-glyoxylate aminotransferase 2-like 2	chr5q35.3	232488_at	NM_153373																			
6.94	6.58	0.36	2.09E-01	5.83E-01	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	chr17q23-q24	201827_at	NM_001098426 /// NM_003077																			
3.50	3.24	0.26	2.09E-01	5.83E-01	---	---	---	239302_s_at	---																			
3.74	3.41	0.33	2.09E-01	5.83E-01	CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	chrXq13.1	207144_s_at	NM_004143																			
7.48	7.23	0.25	2.09E-01	5.83E-01	UNC45A	unc-45 homolog A (C. elegans)	chr15q26.1	221708_s_at	NM_001039675 /// NM_018671																			

2.71	2.51	0.20	2.09E-01	5.83E-01	FBXW8	F-box and WD repeat domain containing 8	chr12q24.22|tdb9938	231883_at	NM_012174 /// NM_153348
6.76	6.36	0.40	2.09E-01	5.83E-01	KPNA2 /// LOC728860	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) /// karyopherin alpha-2 subunit like	chr17q24.2	211762_s_at	NM_002266 /// XM_001722955 /// XM_001722957
2.99	2.74	0.25	2.09E-01	5.83E-01	TMEM194A	transmembrane protein 194A	chr12q13.3	212619_at	NM_001130963 /// NM_015257
2.74	2.48	0.25	2.09E-01	5.83E-01	ERAP1	endoplasmic reticulum aminopeptidase 1	chr5q15	209701_at	NM_001040458 /// NM_016442
5.83	5.28	0.55	2.09E-01	5.83E-01	ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	chr11p13	213497_at	NM_145804
3.80	3.58	0.21	2.09E-01	5.83E-01	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	chr12q24.3-qter	215437_x_at	NM_013449
2.32	2.13	0.20	2.09E-01	5.83E-01	CXCL5	chemokine (C-X-C motif) ligand 5	chr4q12-q13	214974_x_at	NM_002994
6.76	6.38	0.38	2.09E-01	5.83E-01	CREB3L1	cAMP responsive element binding protein 3-like 1	chr11p11.2	213059_at	NM_052854
6.35	5.88	0.47	2.09E-01	5.83E-01	PYCARD	PYD and CARD domain containing	chr16p12-p11.2	221666_s_at	NM_013258 /// NM_145182
5.90	5.74	0.17	2.09E-01	5.83E-01	THSD4	thrombospondin, type I, domain containing 4	chr15q23	226506_at	NM_024817
2.78	2.50	0.29	2.09E-01	5.83E-01	USP46	ubiquitin specific peptidase 46	chr4q12	222941_at	NM_001134223 /// NM_022832
5.96	5.62	0.34	2.09E-01	5.83E-01	SPAG9	sperm associated antigen 9	chr17q21.33	225339_at	NM_001130528 /// NM_003971
4.74	4.38	0.36	2.09E-01	5.84E-01	ZNF526	zinc finger protein 526	chr19q13.2	228229_at	NM_133444
6.83	6.47	0.36	2.09E-01	5.84E-01	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	chr12q24.3-qter	201353_s_at	NM_013449
2.77	2.58	0.19	2.10E-01	5.84E-01	SEC14L3	SEC14-like 3 (S. cerevisiae)	chr22q12.2	240699_at	NM_174975
5.52	5.07	0.45	2.10E-01	5.84E-01	HEYL	hairy/enhancer-of-split related with YRPW motif-like	chr1p34.3	226828_s_at	NM_014571
8.41	7.97	0.43	2.10E-01	5.84E-01	CHPT1	choline phosphotransferase 1	chr12q	221675_s_at	NM_020244
2.98	2.79	0.19	2.10E-01	5.84E-01	QDPR	Quinoid dihydropteridine reductase	chr4p15.31	238616_at	NM_000320
2.09	1.91	0.17	2.10E-01	5.84E-01	---	---	---	222886_at	---
5.03	4.76	0.27	2.10E-01	5.84E-01	LOC100130886 /// TMEM164	hypothetical protein LOC100130886 /// transmembrane protein 164	chrXq22.3	223201_s_at	NM_032227 /// XM_001714477
5.04	4.58	0.46	2.10E-01	5.84E-01	---	---	---	217347_at	---
2.95	2.70	0.25	2.10E-01	5.84E-01	LOC285771	hypothetical protein LOC285771	chr6p25.2	237870_at	---
3.75	3.55	0.20	2.10E-01	5.84E-01	---	---	---	1570483_at	---
5.85	5.55	0.29	2.10E-01	5.84E-01	BCAM	basal cell adhesion molecule (Lutheran blood group)	chr19q13.2	40093_at	NM_001013257 /// NM_005581
2.65	2.44	0.21	2.10E-01	5.84E-01	---	---	---	241823_at	---
7.96	7.74	0.22	2.10E-01	5.84E-01	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	chr10q21.3	210686_x_at	NM_152707
3.32	3.01	0.31	2.10E-01	5.84E-01	C11orf72	chromosome 11 open reading frame 72	chr11q13.2	1553438_at	NM_173578
4.99	4.73	0.26	2.10E-01	5.84E-01	---	---	---	239389_at	---
2.15	1.98	0.17	2.10E-01	5.84E-01	PSMA8	proteasome (prosome, macropain) subunit, alpha type, 8	chr18q11.2	240091_at	NM_001025096 /// NM_001025097 /// NM_144662
6.20	5.67	0.52	2.10E-01	5.84E-01	TMEM41B	transmembrane protein 41B	chr11p15.4	212623_at	NM_015012
5.09	4.74	0.35	2.10E-01	5.84E-01	GDPD5	glycerophosphodiester phosphodiesterase domain containing 5	chr11q13.4-q13.5	213343_s_at	NM_030792
2.13	1.98	0.15	2.10E-01	5.84E-01	---	---	---	215801_at	---
3.04	2.76	0.28	2.10E-01	5.84E-01	MYCBPAP	MYCBP associated protein	chr17q21.33	223731_at	NM_032133
6.64	6.28	0.36	2.10E-01	5.85E-01	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	chr22q13	221516_s_at	NM_019008
3.23	3.00	0.24	2.10E-01	5.85E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	208226_x_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723
3.45	3.26	0.19	2.10E-01	5.85E-01	---	---	---	236913_at	---

3.65	3.37	0.28	2.11E-01	5.85E-01	SERHL /// SERHL2	serine hydrolase-like /// serine hydrolase-like 2	chr22q13 /// chr22q13.2-q13.31	217276_x_at	NM_014509 /// NM_170694 /// XM_001719595
5.40	4.92	0.49	2.11E-01	5.85E-01	HKR1	GLI-Kruppel family member HKR1	chr19q13.12	231836_at	NM_181786
8.75	8.33	0.42	2.11E-01	5.85E-01	SIAH2	seven in absentia homolog 2 (Drosophila)	chr3q25	209339_at	NM_005067
2.33	2.15	0.19	2.11E-01	5.85E-01	TFDP1	Transcription factor Dp-1	chr13q34	242538_at	NM_007111
5.64	4.90	0.74	2.11E-01	5.85E-01	NCAM1	neural cell adhesion molecule 1	chr11q23.1	209968_s_at	NM_000615 /// NM_001076682 /// NM_181351
2.35	2.18	0.17	2.11E-01	5.85E-01	TPPP	Tubulin polymerization promoting protein	chr5p15.3	230197_s_at	NM_007030
5.63	4.81	0.82	2.11E-01	5.85E-01	JUN	jun oncogene	chr1p32-p31	201466_s_at	NM_002228
3.30	3.13	0.17	2.11E-01	5.85E-01	---	---	---	1565535_x_at	---
8.11	7.54	0.58	2.11E-01	5.85E-01	QPRT	quinolinate phosphoribosyltransferase	chr16p11.2	204044_at	NM_014298
3.57	3.33	0.23	2.11E-01	5.85E-01	PLEKHA8	Pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	chr7p21-p11.2	227247_at	NM_032639
3.50	3.32	0.18	2.11E-01	5.86E-01	KRT78	keratin 78	chr12q13.13	1553212_at	NM_173352
6.06	5.76	0.30	2.11E-01	5.86E-01	GALNAC4S-6ST	B cell RAG associated protein	chr10q26	203066_at	NM_015892
4.01	3.77	0.24	2.11E-01	5.86E-01	MCART1	mitochondrial carrier triple repeat 1	chr9p13.3-p12	232092_at	NM_033412
3.92	3.44	0.49	2.11E-01	5.86E-01	MFSD8	major facilitator superfamily domain containing 8	chr4q28.1-q28.2	229509_at	NM_152778
2.91	2.75	0.16	2.11E-01	5.86E-01	CABP1	calcium binding protein 1	chr12q24.31	208320_at	NM_001033677 /// NM_004276 /// NM_031205
5.07	4.86	0.21	2.11E-01	5.86E-01	ATAD3A /// ATAD3B /// ATAD3C /// LOC732419	ATPase family, AAA domain containing 3A /// ATPase family, AAA domain containing 3B /// ATPase family, AAA domain containing 3C /// similar to AAA-ATPase TOB3	chr1p36.33	1552641_s_at	NM_001039211 /// NM_018188 /// NM_031921 /// XM_001718658
2.27	2.10	0.17	2.11E-01	5.86E-01	---	---	---	1559573_at	---
3.09	2.87	0.21	2.11E-01	5.86E-01	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	chr7q21.1	207773_x_at	NM_022820 /// NM_057095 /// NM_057096
3.23	3.03	0.20	2.11E-01	5.86E-01	KIF2C	kinesin family member 2C	chr1p34.1	209408_at	NM_006845
2.79	2.61	0.18	2.11E-01	5.86E-01	---	---	---	1561305_at	---
2.42	2.23	0.19	2.11E-01	5.86E-01	LOC348808	BC048124	chr3q22.1	1556887_at	NR_002811
4.84	4.60	0.23	2.11E-01	5.86E-01	CES3	carboxylesterase 3	chr16q22.1	220335_x_at	NM_024922
3.86	3.64	0.22	2.11E-01	5.86E-01	KLF15	Kruppel-like factor 15	chr3q13-q21	221302_at	NM_014079
2.71	2.46	0.25	2.11E-01	5.86E-01	---	---	---	231433_at	---
4.19	3.95	0.24	2.11E-01	5.86E-01	TRIM16L	Tripartite motif-containing 16-like	chr17p11.2	1559682_at	NM_001037330
4.15	3.92	0.23	2.11E-01	5.86E-01	TTC12	tetratricopeptide repeat domain 12	chr11q23.1	1554531_at	NM_017868
2.71	2.48	0.23	2.12E-01	5.86E-01	---	---	---	214388_at	---
6.37	6.17	0.20	2.12E-01	5.86E-01	PIGV	phosphatidylinositol glycan anchor biosynthesis, class V	chr1p36.11	51146_at	NM_017837
1.93	1.78	0.15	2.12E-01	5.86E-01	BTC	betacellulin	chr4q13-q21	241412_at	NM_001729
2.61	2.47	0.14	2.12E-01	5.86E-01	---	---	---	1556706_at	---
10.67	10.53	0.14	2.12E-01	5.86E-01	MGC87895 /// RPS14	similar to ribosomal protein S14 /// ribosomal protein S14	chr1p36.13 /// chr5q31-q33	208646_at	NM_001025070 /// NM_001025071 /// NM_005617 /// XM_001720055 /// XM_930106 /// XM_942712
2.16	1.99	0.18	2.12E-01	5.86E-01	ABHD12B	abhydrolase domain containing 12B	chr14q22.1	1564357_at	NM_181533 /// NM_181814
3.36	3.18	0.17	2.12E-01	5.86E-01	LOC100133471 /// LOC285103	hypothetical protein LOC100133471 /// hypothetical protein LOC285103	chr2q21.2	1561433_at	XM_001723145
2.71	2.13	0.58	2.12E-01	5.87E-01	SUZ12P	Suppressor of zeste 12 homolog pseudogene	chr17q11.2	236386_at	---
7.92	7.68	0.24	2.12E-01	5.87E-01	FBXO7	F-box protein 7	chr22q12-q13	1554423_a_at	NM_001033024 /// NM_012179

2.15	1.95	0.20	2.12E-01	5.87E-01	---	---	---	220729_at	---
6.24	5.87	0.37	2.12E-01	5.87E-01	KLC4	kinesin light chain 4	chr6p21.1	225596_at	NM_138343 /// NM_201521 /// NM_201522 /// NM_201523
2.42	2.27	0.15	2.12E-01	5.87E-01	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	chr16p13.11	1560013_at	NM_015027
2.39	2.24	0.14	2.12E-01	5.87E-01	---	---	---	241947_at	---
3.88	3.59	0.29	2.12E-01	5.87E-01	---	---	---	239070_at	---
4.38	4.12	0.26	2.12E-01	5.87E-01	IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	chr16p13.3	204792_s_at	NM_014714
2.75	2.53	0.22	2.12E-01	5.87E-01	SNORA68	small nucleolar RNA, H/ACA box 68	chr19p13	1566402_at	NR_000012
4.82	4.49	0.34	2.13E-01	5.88E-01	LOC100131110	hypothetical protein LOC100131110	chr13q32.3	240616_at	XM_001714494 /// XM_001714771 /// XM_001715750
2.87	2.64	0.23	2.13E-01	5.88E-01	FNIP1	folliculin interacting protein 1	chr5q23.3	223997_at	NM_001008738 /// NM_133372
8.71	8.50	0.21	2.13E-01	5.88E-01	LOC732160 /// NDUFA10	similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa precursor /// NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	chr2q37.3	217860_at	NM_004544 /// XR_016073
11.67	11.47	0.20	2.13E-01	5.88E-01	RPL35	ribosomal protein L35	chr9q34.1	200002_at	NM_007209
4.41	4.09	0.33	2.13E-01	5.88E-01	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	chr4p14	213983_s_at	NM_001100399 /// NM_001100400 /// NM_015200
6.67	6.13	0.53	2.13E-01	5.88E-01	C19orf48	chromosome 19 open reading frame 48	chr19q13.33	224468_s_at	NM_199249 /// NM_199250
5.74	5.37	0.37	2.13E-01	5.88E-01	SMPD2	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	chr6q21	205622_at	NM_003080
4.55	4.10	0.45	2.13E-01	5.88E-01	BIK	BCL2-interacting killer (apoptosis-inducing)	chr22q13.31	205780_at	NM_001197
8.11	7.91	0.20	2.13E-01	5.88E-01	---	---	---	213879_at	---
6.39	6.12	0.27	2.13E-01	5.88E-01	TMEM131	transmembrane protein 131	chr2q11.2	212507_at	NM_015348
2.56	2.37	0.19	2.13E-01	5.88E-01	---	---	---	234518_at	---
11.71	11.22	0.49	2.13E-01	5.88E-01	C3	complement component 3	chr19p13.3-p13.2	217767_at	NM_000064
3.95	3.74	0.21	2.13E-01	5.88E-01	DUSP8	dual specificity phosphatase 8	chr11p15.5	206374_at	NM_004420
5.05	4.86	0.19	2.13E-01	5.88E-01	ZNF561	zinc finger protein 561	chr19p13.2	235200_at	NM_152289
3.06	2.79	0.28	2.14E-01	5.89E-01	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	chr16q22.1	220236_at	NM_017990
4.45	4.25	0.20	2.14E-01	5.89E-01	LOC284798	hypothetical protein LOC284798	chr20p11.21	1561978_at	---
10.39	10.16	0.23	2.14E-01	5.89E-01	CUTA	cutA divalent cation tolerance homolog (E. coli)	chr6pter-p21.31	221488_s_at	NM_001014433 /// NM_001014837 /// NM_001014838 /// NM_001014840 /// NM_015921
6.64	6.33	0.31	2.14E-01	5.89E-01	CHMP1A	chromatin modifying protein 1A	chr16q24.3	201933_at	NM_001083314 /// NM_002768
2.43	2.27	0.15	2.14E-01	5.89E-01	---	---	---	239793_at	---
7.82	7.59	0.23	2.14E-01	5.89E-01	SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	chr20p13	225252_at	NM_080725
7.48	7.16	0.32	2.14E-01	5.89E-01	MRPL4	mitochondrial ribosomal protein L4	chr19p13.2	218105_s_at	NM_015956 /// NM_146387 /// NM_146388
2.74	2.59	0.15	2.14E-01	5.89E-01	---	---	---	1557404_at	---
4.14	3.73	0.41	2.14E-01	5.89E-01	TUFM	Tu translation elongation factor, mitochondrial	chr16p11.2	238190_at	NM_003321
8.33	7.51	0.82	2.14E-01	5.89E-01	RND3	Rho family GTPase 3	chr2q23.3	212724_at	NM_005168
5.58	5.10	0.48	2.14E-01	5.89E-01	C16orf70	chromosome 16 open reading frame 70	chr16q22.1	223440_at	NM_025187
2.94	2.70	0.24	2.14E-01	5.89E-01	KLHDC7A	kelch domain containing 7A	chr1p36.13	1553437_at	NM_152375
6.01	5.71	0.30	2.14E-01	5.89E-01	SFRS16	splicing factor, arginine/serine-rich 16	chr19q13.3	204978_at	NM_007056

3.68	3.29	0.39	2.14E-01	5.89E-01	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	chr2p23	244428_at	NM_022552 /// NM_153759 /// NM_175629 /// NM_175630																				
4.06	3.71	0.35	2.14E-01	5.89E-01	BANK1	B-cell scaffold protein with ankyrin repeats 1	chr4q24	1558662_s_at	NM_001083907 /// NM_001127507 /// NM_017935																				
2.88	2.67	0.21	2.14E-01	5.89E-01	---	---	---	239310_at	---																				
2.60	2.42	0.18	2.14E-01	5.89E-01	TCP11L2	T-complex 11 (mouse)-like 2	chr12q23.3	1565527_x_at	NM_152772																				
5.75	5.11	0.64	2.14E-01	5.89E-01	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	chr9p21-p12	204310_s_at	NM_003995																				
2.72	2.55	0.17	2.14E-01	5.89E-01	ATXN3	Ataxin 3	chr14q24.3-q32.2	233182_x_at	NM_001127696 /// NM_001127697 /// NM_004993 /// NM_030660																				
6.87	6.53	0.34	2.14E-01	5.89E-01	CENTG3	centaurin, gamma 3	chr7q36.1	225789_at	NM_001042535 /// NM_031946																				
2.90	2.71	0.19	2.14E-01	5.89E-01	LOC100131177	hypothetical protein LOC100131177	chr2q37.2	231468_at	XM_001714098 /// XM_001716855																				
1.98	1.81	0.17	2.14E-01	5.89E-01	FLJ41455	hypothetical gene supported by AK123449; BX641014	chr9q12	244395_at	---																				
2.32	2.13	0.19	2.14E-01	5.89E-01	MLXIP	MLX interacting protein	chr12q24.31	211789_s_at	NM_014938																				
4.51	4.08	0.43	2.14E-01	5.89E-01	ZNF467	zinc finger protein 467	chr7q36.1	214746_s_at	NM_207336																				
4.62	4.20	0.42	2.14E-01	5.89E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	209152_s_at	NM_003200																				
2.51	2.26	0.25	2.14E-01	5.89E-01	OR4C1P	olfactory receptor, family 4, subfamily C, member 1 pseudogene	chr11q11	1567271_at	---																				
6.72	6.45	0.27	2.15E-01	5.89E-01	NIF3L1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	chr2q33	218133_s_at	NM_021824																				
4.78	4.59	0.19	2.15E-01	5.89E-01	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	chr17q21-q22	210185_at	NM_000723 /// NM_199247 /// NM_199248																				
2.78	2.60	0.18	2.15E-01	5.89E-01	SEC14L5	SEC14-like 5 (S. cerevisiae)	chr16p13.3	210169_at	NM_014692																				
2.65	2.43	0.22	2.15E-01	5.89E-01	---	---	---	214376_at	---																				
4.59	4.24	0.35	2.15E-01	5.89E-01	SPATA2	spermatogenesis associated 2	chr20q13.1-q13.2	204433_s_at	NM_006038																				
8.38	8.14	0.24	2.15E-01	5.89E-01	CTBP2	C-terminal binding protein 2	chr10q26.13	210554_s_at	NM_001083914 /// NM_001329 /// NM_022802																				
3.55	3.36	0.18	2.15E-01	5.89E-01	---	---	---	237824_at	---																				
5.09	4.83	0.26	2.15E-01	5.89E-01	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	chr1q32	215050_x_at	NM_004759 /// NM_032960																				
2.36	2.03	0.33	2.15E-01	5.89E-01	---	---	---	235771_at	---																				
2.43	2.28	0.15	2.15E-01	5.89E-01	LOC643650	hypothetical protein LOC643650	chr10q11.22	1563742_at	XM_931714																				
2.59	2.37	0.22	2.15E-01	5.90E-01	---	---	---	1560262_at	---																				
2.89	2.65	0.24	2.15E-01	5.90E-01	MYF6	myogenic factor 6 (herculin)	chr12q21	206372_at	NM_002469																				
2.43	2.20	0.23	2.15E-01	5.90E-01	---	---	---	234301_s_at	---																				
6.56	6.27	0.30	2.15E-01	5.90E-01	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	chr3q13.11	209682_at	NM_170662																				
7.88	7.58	0.30	2.15E-01	5.90E-01	BAT2D1	BAT2 domain containing 1	chr1q23.3	211946_s_at	NM_015172																				
6.67	6.32	0.35	2.15E-01	5.90E-01	FMNL2	formin-like 2	chr2q23.3	226184_at	NM_052905																				
2.42	2.17	0.25	2.15E-01	5.90E-01	CNTN4	contactin 4	chr3p26-p25	229084_at	NM_175607 /// NM_175612 /// NM_175613																				
6.48	6.26	0.22	2.15E-01	5.90E-01	ZGPAT	zinc finger, CCCH-type with G patch domain	chr20q13.3	221848_at	NM_001083113 /// NM_032527 /// NM_181485																				
5.62	5.40	0.22	2.15E-01	5.90E-01	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	chr19q13.42	202407_s_at	NM_015629																				

6.46	5.86	0.60	2.15E-01	5.90E-01	FAM43B	family with sequence similarity 43, member B	chr1p36.12	1569256_a_at	NM_207334
5.21	4.77	0.44	2.15E-01	5.90E-01	MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	chr1p34.1	211774_s_at	NM_015506
2.80	2.61	0.19	2.15E-01	5.90E-01	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	chr2p15	230148_at	NM_152392
2.54	2.36	0.18	2.15E-01	5.90E-01	WNT1	wingless-type MMTV integration site family, member 1	chr12q13	208570_at	NM_005430
4.42	4.12	0.30	2.15E-01	5.90E-01	IMAA /// LOC440345 /// LOC440354 /// LOC595101 /// LOC641298 /// LOC728423 /// SLC7A5P1	SLC7A5 pseudogene /// hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1 /// hypothetical LOC728423 /// solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 pseudogene 1	chr16p11.2 /// chr16p12.1 /// chr16p12.2	208118_x_at	NR_002453 /// NR_002473 /// NR_002593 /// NR_002594 /// XR_015617 /// XR_015786 /// XR_041850 /// XR_042165
5.18	4.86	0.32	2.16E-01	5.90E-01	RBM15B	RNA binding motif protein 15B	chr3p21.2	226987_at	NM_013286
3.43	2.88	0.55	2.16E-01	5.90E-01	PAWR	PRKC, apoptosis, WT1, regulator	chr12q21	204005_s_at	NM_002583
7.76	7.48	0.28	2.16E-01	5.90E-01	MANBAL	mannosidase, beta A, lysosomal-like	chr20q11.23-q12	224689_at	NM_001003897 /// NM_022077
6.58	6.11	0.46	2.16E-01	5.90E-01	EPOR	erythropoietin receptor	chr19p13.3-p13.2	396_f_at	NM_000121
2.43	2.25	0.18	2.16E-01	5.90E-01	C3orf65	Chromosome 3 open reading frame 65	chr3q27.2	1563208_s_at	NM_001039788
4.66	3.89	0.77	2.16E-01	5.90E-01	FAM65C	family with sequence similarity 65, member C	chr20q13.13	227654_at	NM_080829
6.44	6.16	0.27	2.16E-01	5.90E-01	RNASEH1	ribonuclease H1	chr2p25	218497_s_at	NM_002936
8.03	7.65	0.38	2.16E-01	5.90E-01	M6PRBP1	mannose-6-phosphate receptor binding protein 1	chr19p13.3	202122_s_at	NM_005817
6.18	5.76	0.42	2.16E-01	5.91E-01	ERAL1	Era G-protein-like 1 (E. coli)	chr17q11.2	212087_s_at	NM_005702
4.73	4.45	0.28	2.16E-01	5.91E-01	QRICH1	Glutamine-rich 1	chr3p21.31	229806_at	NM_017730 /// NM_198880
6.76	6.45	0.31	2.16E-01	5.91E-01	B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	chr5q35.2-q35.3	53076_at	NM_007255
7.31	6.81	0.50	2.16E-01	5.91E-01	---	---	---	226134_s_at	---
3.50	3.34	0.16	2.16E-01	5.91E-01	TMEM63A	Transmembrane protein 63A	chr1q42.12	228549_at	NM_014698
5.55	5.13	0.42	2.16E-01	5.91E-01	---	---	---	235424_at	---
2.31	2.13	0.19	2.16E-01	5.91E-01	KIAA2022	KIAA2022	chrXq13.3	234333_at	NM_001008537
4.90	4.50	0.40	2.16E-01	5.91E-01	SEMA4G	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	chr10q24.31	219194_at	NM_017893
6.39	5.90	0.49	2.16E-01	5.91E-01	ELF1	E74-like factor 1 (ets domain transcription factor)	chr13q13	212418_at	NM_172373
2.24	2.04	0.20	2.16E-01	5.91E-01	FKBP4	FK506 binding protein 4, 59kDa	chr12p13.33	1560303_at	NM_002014
2.38	2.17	0.20	2.16E-01	5.91E-01	PPM1F	protein phosphatase 1F (PP2C domain containing)	chr22q11.22	1555091_at	NM_014634
2.51	2.20	0.31	2.16E-01	5.91E-01	---	---	---	234997_x_at	---
8.10	7.59	0.52	2.16E-01	5.91E-01	FLJ10357	hypothetical protein FLJ10357	chr14q11.2	220326_s_at	NM_018071
5.53	5.24	0.29	2.16E-01	5.91E-01	SBF1	SET binding factor 1	chr22q13.33	39835_at	NM_002972
3.39	3.19	0.19	2.16E-01	5.91E-01	ZNF425	zinc finger protein 425	chr7q36.1	242684_at	NM_001001661
3.41	3.10	0.31	2.17E-01	5.91E-01	RAD9A	RAD9 homolog A (S. pombe)	chr11q13.1-q13.2	204828_at	NM_004584
2.69	2.53	0.16	2.17E-01	5.91E-01	---	---	---	232539_at	---
6.74	6.51	0.24	2.17E-01	5.91E-01	ING4	inhibitor of growth family, member 4	chr12p13.31	218234_at	NM_001127582 /// NM_001127583 /// NM_001127584 /// NM_001127585 /// NM_001127586 /// NM_016162
7.16	6.90	0.26	2.17E-01	5.91E-01	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	chrXp11.4-p11.21	38964_r_at	NM_000377
6.96	6.64	0.32	2.17E-01	5.91E-01	AIG1	androgen-induced 1	chr6q24.2	223136_at	NM_016108
2.65	2.45	0.20	2.17E-01	5.91E-01	---	---	---	231147_at	---
2.44	2.26	0.18	2.17E-01	5.91E-01	PRICKLE1	Prickle homolog 1 (Drosophila)	chr12q12	232811_x_at	NM_153026
7.61	7.36	0.25	2.17E-01	5.92E-01	RILP	Rab interacting lysosomal protein	chr17p13.3	227366_at	NM_031430
4.93	4.47	0.45	2.17E-01	5.92E-01	ZFP36L1	zinc finger protein 36, C3H type-like 1	chr14q22-q24	211965_at	NM_004926
2.74	2.49	0.25	2.17E-01	5.92E-01	ZDHHC11	zinc finger, DHHC-type containing 11	chr5p15.33	1552283_s_at	NM_024786

7.41	6.88	0.53	2.17E-01	5.92E-01	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	chr21q22.3	202803_s_at	NM_000211 /// NM_001127491
8.15	7.86	0.29	2.17E-01	5.92E-01	WDR61	WD repeat domain 61	chr15q25.1	221532_s_at	NM_025234
3.55	3.23	0.32	2.17E-01	5.92E-01	LPCAT4	lysophosphatidylcholine acyltransferase 4	chr15q14	213078_x_at	NM_153613
2.59	2.40	0.19	2.17E-01	5.92E-01	ZNF131	zinc finger protein 131	chr5p12-p11	225916_at	NM_003432
4.18	3.88	0.30	2.17E-01	5.92E-01	LASS6	LAG1 homolog, ceramide synthase 6	chr2q24.3	212446_s_at	NM_203463
2.96	2.74	0.22	2.17E-01	5.92E-01	ANPEP	Alanyl (membrane) aminopeptidase	chr15q25-q26	234576_at	NM_001150
6.15	5.87	0.28	2.17E-01	5.92E-01	KIAA0859	KIAA0859	chr1q24-q25.3	206468_s_at	NM_001007239 /// NM_014955 /// NM_015935
2.74	2.47	0.27	2.18E-01	5.92E-01	---	---	---	217503_at	---
6.05	5.81	0.23	2.18E-01	5.92E-01	PMS2L3	postmeiotic segregation increased 2-like 3	chr7q11.23	216111_x_at	NM_001003686 /// NM_005395 /// XM_001716315
8.59	8.35	0.24	2.18E-01	5.92E-01	VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)	chr8q24.3	218679_s_at	NM_016208 /// NM_183057
4.59	4.31	0.28	2.18E-01	5.92E-01	SH3BP2	SH3-domain binding protein 2	chr4p16.3	209370_s_at	NM_001122681 /// NM_003023
8.08	7.65	0.42	2.18E-01	5.92E-01	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	chr19q13.2-q13.4	1568629_s_at	NM_005027
4.78	4.52	0.26	2.18E-01	5.92E-01	ZBTB24	zinc finger and BTB domain containing 24	chr6q21	205340_at	NM_014797
10.69	10.48	0.21	2.18E-01	5.92E-01	TUBA1B	tubulin, alpha 1b	chr12q13.12	201090_x_at	NM_006082
2.42	2.25	0.17	2.18E-01	5.92E-01	LOC645452	similar to hCG1782414	chr6p22.2	217340_at	XM_001714101 /// XM_928485 /// XM_939733
5.75	5.35	0.40	2.18E-01	5.92E-01	SARM1	sterile alpha and TIR motif containing 1	chr17q11	213259_s_at	NM_015077
7.86	7.62	0.24	2.18E-01	5.92E-01	CLPTM1L	CLPTM1-like	chr5pter-p15.3	226935_s_at	NM_030782 /// XM_001722978
2.68	2.49	0.20	2.18E-01	5.92E-01	---	---	---	1560589_a_at	---
1.94	1.81	0.13	2.18E-01	5.92E-01	LOC645513	Hypothetical LOC645513	chr4q26-q27	1556257_at	XM_001714125 /// XM_001714854 /// XM_001717939
2.38	2.23	0.15	2.18E-01	5.92E-01	---	---	---	1562523_at	---
3.54	3.26	0.28	2.18E-01	5.92E-01	---	---	---	236148_at	---
3.72	3.48	0.25	2.18E-01	5.92E-01	USP18	ubiquitin specific peptidase 18	chr22q11.21	219211_at	NM_017414
7.43	7.16	0.27	2.18E-01	5.93E-01	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	chr17q24-q25|17q25.1	227962_at	NM_004035 /// NM_007292
8.02	7.70	0.31	2.18E-01	5.93E-01	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	chr5q23-q31	202334_s_at	NM_003337
3.55	3.35	0.20	2.18E-01	5.93E-01	---	---	---	1561919_at	---
4.71	4.47	0.25	2.18E-01	5.93E-01	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	chr11q13	223371_s_at	NM_005528
2.10	1.95	0.15	2.18E-01	5.93E-01	---	---	---	1558947_at	---
2.95	2.70	0.26	2.18E-01	5.93E-01	TPCN2	Two pore segment channel 2	chr11q13.2	242554_at	NM_139075
3.28	3.13	0.15	2.18E-01	5.93E-01	---	---	---	217708_x_at	---
2.54	2.35	0.19	2.18E-01	5.93E-01	TBC1D26 /// ZNF286A	TBC1 domain family, member 26 /// zinc finger protein 286A	chr17p11.2	1569751_at	NM_001130842 /// NM_020652 /// NM_178571
4.56	4.25	0.31	2.18E-01	5.93E-01	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	chr3p21	205851_at	NM_005793
6.94	6.72	0.22	2.18E-01	5.93E-01	RABEPK	Rab9 effector protein with kelch motifs	chr9q33.3	203150_at	NM_005833
6.55	6.23	0.32	2.18E-01	5.93E-01	EML3	echinoderm microtubule associated protein like 3	chr11q12.3	203442_x_at	NM_153265
4.99	4.69	0.30	2.19E-01	5.93E-01	C17orf82	chromosome 17 open reading frame 82	chr17q23.2	1555478_at	NM_203425
6.24	6.01	0.23	2.19E-01	5.93E-01	SGSM3	small G protein signaling modulator 3	chr22q13.1-q13.2	203014_x_at	NM_015705
2.46	2.27	0.19	2.19E-01	5.93E-01	MGC70870	C-terminal binding protein 2 pseudogene	---	242136_x_at	NR_003682
5.16	4.96	0.20	2.19E-01	5.93E-01	TBL1X	transducin (beta)-like 1X-linked	chrXp22.3	201869_s_at	NM_005647

6.68	6.40	0.29	2.19E-01	5.93E-01	PLCD1	phospholipase C, delta 1	chr3p22-p21.3	205125_at	NM_001130964 /// NM_006225 /// NR_024071																				
2.27	2.09	0.18	2.19E-01	5.93E-01	---	---	---	1564670_at	---																				
7.36	7.07	0.29	2.19E-01	5.93E-01	GSS	glutathione synthetase	chr20q11.2	201415_at	NM_000178																				
4.95	4.63	0.33	2.19E-01	5.93E-01	C14orf101	chromosome 14 open reading frame 101	chr14q23.1	225675_at	NM_017799																				
5.21	4.92	0.28	2.19E-01	5.93E-01	HERC4	hect domain and RLD 4	chr10q21.3	225989_at	NM_015601 /// NM_022079																				
2.49	2.29	0.19	2.19E-01	5.93E-01	IVD	isovaleryl Coenzyme A dehydrogenase	chr15q14-q15	203681_at	NM_002225																				
3.17	2.95	0.23	2.19E-01	5.93E-01	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	chr22q13.2	232857_at	NM_001018050 /// NM_001018052 /// NM_138338																				
6.13	5.92	0.22	2.19E-01	5.93E-01	C1orf35	chromosome 1 open reading frame 35	chr1q42.13	219063_at	NM_024319																				
2.71	2.49	0.22	2.19E-01	5.93E-01	---	---	---	224417_at	---																				
6.48	6.07	0.41	2.19E-01	5.93E-01	POLRMT	polymerase (RNA) mitochondrial (DNA directed)	chr19p13.3	203782_s_at	NM_005035																				
4.61	4.31	0.29	2.19E-01	5.94E-01	RINT1	RAD50 interactor 1	chr7q22.2	218598_at	NM_021930																				
6.59	6.37	0.22	2.19E-01	5.94E-01	WDR77	WD repeat domain 77	chr1p13.2	201421_s_at	NM_024102																				
3.80	3.56	0.24	2.19E-01	5.94E-01	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	chr2p13.1	210124_x_at	NM_004263																				
8.10	7.83	0.27	2.19E-01	5.94E-01	GSPT1	G1 to S phase transition 1	chr16p13.1	215438_x_at	NM_001130006 /// NM_001130007 /// NM_002094																				
3.52	3.24	0.28	2.19E-01	5.94E-01	LOC100133577	hypothetical protein LOC100133577	---	226014_at	XM_001716788																				
5.57	4.97	0.60	2.19E-01	5.94E-01	CLDND1	claudin domain containing 1	chr3q12.1	208925_at	NM_001040181 /// NM_001040182 /// NM_001040183 /// NM_001040199 /// NM_001040200 /// NM_019895																				
2.19	2.05	0.15	2.19E-01	5.94E-01	---	---	---	1558481_s_at	---																				
2.46	2.29	0.17	2.20E-01	5.94E-01	XKR6	XK, Kell blood group complex subunit-related family, member 6	chr8p23.1	1557436_at	NM_173683																				
8.05	7.77	0.29	2.20E-01	5.94E-01	FIBP	fibroblast growth factor (acidic) intracellular binding protein	chr11q13.1	202041_s_at	NM_004214 /// NM_198897																				
3.10	2.89	0.21	2.20E-01	5.94E-01	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	chr19q13	204230_s_at	NM_020309																				
5.39	5.02	0.37	2.20E-01	5.94E-01	ITGB5	integrin, beta 5	chr3q21.2	201124_at	NM_002213																				
5.16	4.84	0.32	2.20E-01	5.94E-01	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	chr6q25.1	231094_s_at	NM_015440																				
2.24	2.11	0.14	2.20E-01	5.94E-01	---	---	---	243317_at	---																				
7.87	7.58	0.29	2.20E-01	5.94E-01	COMMD4	COMM domain containing 4	chr15q24.2	206441_s_at	NM_017828																				
7.42	7.17	0.25	2.20E-01	5.94E-01	C19orf50	chromosome 19 open reading frame 50	chr19p13.11	200076_s_at	NM_024069																				
4.85	4.65	0.21	2.20E-01	5.94E-01	SFMBT1	Scm-like with four mbt domains 1	chr3p21.1	213370_s_at	NM_001005158 /// NM_001005159 /// NM_016329																				
6.10	5.75	0.35	2.20E-01	5.94E-01	FRAG1	FGF receptor activating protein 1	chr11p15.5	215293_s_at	NM_014489																				
2.27	2.11	0.17	2.20E-01	5.94E-01	---	---	---	238269_at	---																				
5.00	4.68	0.31	2.20E-01	5.94E-01	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	chr1p22.1	216652_s_at	NM_001938																				
2.37	2.16	0.20	2.20E-01	5.94E-01	COMMD10	COMM domain containing 10	chr5q23.1	235481_at	NM_016144																				
6.19	5.86	0.33	2.20E-01	5.94E-01	CUL7	cullin 7	chr6p21.1	203558_at	NM_014780																				
7.32	6.94	0.37	2.20E-01	5.94E-01	RAP2B	RAP2B, member of RAS oncogene family	chr3q25.2	213923_at	NM_002886																				
2.37	2.22	0.15	2.20E-01	5.94E-01	---	---	---	1556502_at	---																				
6.46	6.16	0.30	2.20E-01	5.94E-01	MAN2A2	mannosidase, alpha, class 2A, member 2	chr15q26.1	202032_s_at	NM_006122																				
2.30	2.11	0.19	2.20E-01	5.94E-01	---	---	---	237557_at	---																				
2.34	2.19	0.14	2.20E-01	5.94E-01	RP11-251J8.3	hypothetical LOC646871	chr13q13.3	232605_s_at	XM_001132009 /// XM_001714513 /// XM_929830																				

5.68	5.11	0.57	2.20E-01	5.94E-01	ENO2	enolase 2 (gamma, neuronal)	chr12p13	201313_at	NM_001975
2.35	2.20	0.15	2.20E-01	5.94E-01	WDR52	WD repeat domain 52	chr3q13.2	230152_at	NM_018338
5.37	5.18	0.19	2.20E-01	5.95E-01	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	chr20q13.33	234001_s_at	NM_018209 /// NM_175609
9.58	9.37	0.21	2.20E-01	5.95E-01	COX6B1	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	chr19q13.1	201441_at	NM_001863
4.89	4.62	0.27	2.20E-01	5.95E-01	C16orf35	chromosome 16 open reading frame 35	chr16p13.3	203289_s_at	NM_001039476 /// NM_001077350
2.19	2.01	0.18	2.21E-01	5.95E-01	---	---	---	238098_at	---
4.34	4.08	0.27	2.21E-01	5.95E-01	C7orf13	chromosome 7 open reading frame 13	chr7q36	223630_at	XR_040519 /// XR_040520 /// XR_040521 /// XR_040522
7.27	6.96	0.31	2.21E-01	5.95E-01	PEPD	peptidase D	chr19q12-q13.2	202108_at	NM_000285
3.81	3.59	0.22	2.21E-01	5.95E-01	PRDM15	PR domain containing 15	chr21q22.3	231931_at	NM_001040424 /// NM_022115
2.14	2.01	0.13	2.21E-01	5.95E-01	DNAH12	dynein, axonemal, heavy chain 12	chr3p21.1	1563097_at	---
6.26	5.94	0.33	2.21E-01	5.95E-01	CYB561D2	cytochrome b-561 domain containing 2	chr3p21.3	209665_at	NM_007022
3.38	3.13	0.25	2.21E-01	5.95E-01	C10orf140	chromosome 10 open reading frame 140	chr10p12.31	1559266_s_at	NM_207371
4.06	3.80	0.26	2.21E-01	5.95E-01	---	---	---	216301_at	---
6.76	6.54	0.22	2.21E-01	5.95E-01	SSRP1	structure specific recognition protein 1	chr11q12	200957_s_at	NM_003146
6.57	6.21	0.36	2.21E-01	5.95E-01	RPP14	ribonuclease P/MRP 14kDa subunit	chr3p14.3	227005_at	NM_001098783 /// NM_007042
5.04	4.38	0.66	2.21E-01	5.95E-01	SCML1	sex comb on midleg-like 1 (Drosophila)	chrXp22.2-p22.1	218793_s_at	NM_001037535 /// NM_001037536 /// NM_001037540 /// NM_006746
4.57	3.95	0.62	2.21E-01	5.95E-01	IL1B	interleukin 1, beta	chr2q14	205067_at	NM_000576
4.33	3.82	0.51	2.21E-01	5.95E-01	---	---	---	239307_at	---
6.75	6.40	0.35	2.21E-01	5.96E-01	UBAC1	UBA domain containing 1	chr9q34.3	202151_s_at	NM_016172
6.18	5.96	0.21	2.21E-01	5.96E-01	---	---	---	227122_at	---
5.74	5.19	0.56	2.21E-01	5.96E-01	RBM25	RNA binding motif protein 25	chr14q24.3	212031_at	NM_021239
2.90	2.67	0.23	2.21E-01	5.96E-01	---	---	---	243343_at	---
4.67	4.39	0.28	2.22E-01	5.96E-01	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	chr7q22	203731_s_at	NM_014569 /// NM_145102
5.76	5.36	0.41	2.22E-01	5.96E-01	PCBP4	poly(rC) binding protein 4	chr3p21	209361_s_at	NM_020418 /// NM_033008 /// NM_033009 /// NM_033010
11.15	10.73	0.42	2.22E-01	5.96E-01	FDX1	ferredoxin 1	chr11q22	203647_s_at	NM_004109
7.63	7.30	0.33	2.22E-01	5.96E-01	MLX	MAX-like protein X	chr17q21.1	213708_s_at	NM_170607 /// NM_198204 /// NM_198205
6.96	6.63	0.33	2.22E-01	5.96E-01	C17orf81	chromosome 17 open reading frame 81	chr17p13.1	223286_at	NM_015362 /// NM_203413 /// NM_203414 /// NM_203415
5.31	4.92	0.38	2.22E-01	5.96E-01	PDCD2	programmed cell death 2	chr6q27	204025_s_at	NM_002598 /// NM_144781
3.23	3.05	0.18	2.22E-01	5.96E-01	PACS1	phosphofurin acidic cluster sorting protein 1	chr11q13.1	220557_s_at	NM_018026
4.56	4.15	0.41	2.22E-01	5.96E-01	ZNRF1	zinc and ring finger 1	chr16q23.1	225959_s_at	NM_032268
2.31	2.14	0.17	2.22E-01	5.96E-01	RUNDC2B	RUN domain containing 2B	chr16p12.2	1559297_at	NM_001012391 /// XM_001714307
2.49	2.35	0.15	2.22E-01	5.96E-01	---	---	---	1567100_at	---

4.64	4.32	0.31	2.22E-01	5.96E-01	MCM4	minichromosome maintenance complex component 4	chr8q11.2	222036_s_at	NM_005914 /// NM_182746
4.60	3.87	0.73	2.22E-01	5.96E-01	PION	pigeon homolog (Drosophila)	chr7q11.23	213142_x_at	NM_017439
3.17	2.96	0.21	2.22E-01	5.96E-01	---	---	---	240851_at	---
3.26	3.05	0.21	2.22E-01	5.96E-01	FLJ37035	FLJ37035 protein	chr10q26.13	239483_at	XR_000880 /// XR_000881 /// XR_001301 /// XR_001302
2.86	2.67	0.19	2.22E-01	5.96E-01	LOC100129206	Hypothetical protein LOC100129206	chr11q23.3	244301_at	XM_001718438 /// XM_001719091 /// XM_001719130
4.89	4.42	0.47	2.22E-01	5.96E-01	RCP9	calcitonin gene-related peptide-receptor component protein	chr7q11.21	203898_at	NM_001040647 /// NM_001040648 /// NM_014478
8.09	7.48	0.61	2.22E-01	5.96E-01	TNXB	tenascin XB	chr6p21.3	208609_s_at	NM_019105 /// NM_032470
2.21	2.06	0.15	2.22E-01	5.96E-01	hCG_1646157	hCG1646157	chr12q24.33	1569283_at	XR_040663 /// XR_040664 /// XR_040665
3.40	3.21	0.19	2.22E-01	5.96E-01	OOEP	oocyte expressed protein homolog (dog)	chr6q13	238218_at	NM_001080507
6.30	5.82	0.48	2.22E-01	5.96E-01	DKK3	dickkopf homolog 3 (Xenopus laevis)	chr11p15.2	202196_s_at	NM_001018057 /// NM_013253 /// NM_015881
2.84	2.68	0.16	2.22E-01	5.96E-01	SCD5	stearoyl-CoA desaturase 5	chr4q21.22	224019_at	NM_001037582 /// NM_024906
4.21	3.99	0.21	2.22E-01	5.96E-01	ASB16	ankyrin repeat and SOCS box-containing 16	chr17q21.31	1553253_at	NM_080863
2.78	2.58	0.20	2.22E-01	5.96E-01	---	---	---	1562055_at	---
4.97	4.52	0.45	2.22E-01	5.96E-01	ISG20	interferon stimulated exonuclease gene 20kDa	chr15q26	204698_at	NM_002201
6.64	6.44	0.20	2.22E-01	5.96E-01	TERF2	telomeric repeat binding factor 2	chr16q22.1	203611_at	NM_005652
6.08	5.73	0.35	2.23E-01	5.96E-01	KIAA1109	KIAA1109	chr4q27	212779_at	NM_015312
3.82	3.37	0.46	2.23E-01	5.96E-01	FRMD8	FERM domain containing 8	chr11q13	1554903_at	NM_031904
3.75	3.34	0.41	2.23E-01	5.96E-01	CPEB2	cytoplasmic polyadenylation element binding protein 2	chr4p15.33	235479_at	NM_182485 /// NM_182646
4.86	4.64	0.22	2.23E-01	5.96E-01	TBCD	tubulin folding cofactor D	chr17q25.3	201759_at	NM_005993
5.49	4.97	0.52	2.23E-01	5.96E-01	FCGR1A /// FCGR1C	Fc fragment of IgG, high affinity Ia, receptor (CD64) /// Fc fragment of IgG, high affinity Ic, receptor (CD64)	chr1q21.1 /// chr1q21.2-q21.3	216950_s_at	NM_000566 /// NM_001128589 /// XM_001714386 /// XR_039082
6.46	6.09	0.37	2.23E-01	5.96E-01	MPHOSPH8	M-phase phosphoprotein 8	chr13q12.11	221771_s_at	NM_017520
4.29	4.02	0.26	2.23E-01	5.96E-01	RRP1B	ribosomal RNA processing 1 homolog B (S. cerevisiae)	chr21q22.3	212844_at	NM_015056
2.03	1.90	0.13	2.23E-01	5.96E-01	---	---	---	1561740_at	---
6.74	6.41	0.32	2.23E-01	5.96E-01	TAGLN	Transgelin	chr11q23.2	226523_at	NM_001001522 /// NM_003186
8.23	7.93	0.30	2.23E-01	5.96E-01	COPZ1	coatomer protein complex, subunit zeta 1	chr12q13.2-q13.3	217726_at	NM_016057
6.12	5.61	0.51	2.23E-01	5.96E-01	---	---	---	1566968_at	---
6.96	6.64	0.32	2.23E-01	5.97E-01	TNIP2	TNFAIP3 interacting protein 2	chr4p16.3	218335_x_at	NM_024309
6.20	5.93	0.27	2.23E-01	5.97E-01	LPPR2	lipid phosphate phosphatase-related protein type 2	chr19p13.2	64899_at	NM_022737
6.17	5.43	0.74	2.23E-01	5.97E-01	MNDA	myeloid cell nuclear differentiation antigen	chr1q22	204959_at	NM_002432
3.65	3.25	0.40	2.23E-01	5.97E-01	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2	chr15q11-q12	209871_s_at	NM_001130414 /// NM_005503
5.19	4.95	0.24	2.23E-01	5.97E-01	C21orf70	chromosome 21 open reading frame 70	chr21q22.3	243750_x_at	NM_058190
3.30	2.91	0.39	2.23E-01	5.97E-01	KLF11	Kruppel-like factor 11	chr2p25	1553137_s_at	NM_003597
3.64	3.41	0.23	2.23E-01	5.97E-01	GATA4	GATA binding protein 4	chr8p23.1-p22	1553131_a_at	NM_002052
6.07	5.79	0.28	2.23E-01	5.97E-01	PTPN9	protein tyrosine phosphatase, non-receptor type 9	chr15q24.2	202958_at	NM_002833

2.48	2.32	0.16	2.23E-01	5.97E-01	OR2L2	olfactory receptor, family 2, subfamily L, member 2	chr1q44	1567238_at	NM_001004686																				
6.58	6.29	0.29	2.24E-01	5.97E-01	LOC285359 /// PDCL3	phosducin-like 3 pseudogene /// phosducin-like 3	chr2q11.2 /// chr3q12.3	219043_s_at	NM_024065 /// NR_002941																				
2.64	2.49	0.15	2.24E-01	5.97E-01	---	---	---	220569_at	---																				
5.21	4.81	0.40	2.24E-01	5.97E-01	ISG20	interferon stimulated exonuclease gene 20kDa	chr15q26	33304_at	NM_002201																				
6.16	5.73	0.43	2.24E-01	5.97E-01	FXN	frataxin	chr9q13-q21.1	205565_s_at	NM_000144 /// NM_181425																				
7.00	6.64	0.35	2.24E-01	5.98E-01	OCEL1	occludin/ELL domain containing 1	chr19p13.11	205441_at	NM_024578																				
8.07	7.50	0.57	2.24E-01	5.98E-01	OBSL1	obscurin-like 1	chr2q35	212775_at	NM_015311																				
4.16	3.83	0.33	2.24E-01	5.98E-01	PDGFRL	platelet-derived growth factor receptor-like	chr8p22-p21.3	205226_at	NM_006207																				
6.90	6.64	0.26	2.24E-01	5.98E-01	ZBTB40	zinc finger and BTB domain containing 40	chr1pter-q31.3	203959_s_at	NM_001083621 /// NM_014870																				
7.63	7.36	0.27	2.24E-01	5.98E-01	C22orf9	chromosome 22 open reading frame 9	chr22q13.31	217118_s_at	NM_001009880 /// NM_015264																				
2.51	2.37	0.15	2.24E-01	5.98E-01	FLJ31104	Hypothetical gene supported by AK055666; BC039324	chr5q11.2	1557466_at	---																				
7.19	6.97	0.23	2.24E-01	5.98E-01	LARP5	La ribonucleoprotein domain family, member 5	chr10p15.3	208954_s_at	NM_015155																				
5.79	5.46	0.33	2.24E-01	5.98E-01	CABIN1	calcineurin binding protein 1	chr22q11.23	202624_s_at	NM_012295																				
2.44	2.26	0.18	2.24E-01	5.98E-01	---	---	---	1562029_at	---																				
3.26	2.92	0.34	2.24E-01	5.98E-01	RPS15A	ribosomal protein S15a	chr16p	229882_at	NM_001019 /// NM_001030009																				
2.98	2.82	0.15	2.24E-01	5.98E-01	---	---	---	244201_at	---																				
2.00	1.83	0.16	2.24E-01	5.98E-01	---	---	---	244004_at	---																				
2.70	2.43	0.26	2.24E-01	5.98E-01	---	---	---	231074_at	---																				
2.29	2.09	0.20	2.24E-01	5.98E-01	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	239936_at	NR_002612																				
7.07	6.70	0.37	2.24E-01	5.98E-01	TFB2M	transcription factor B2, mitochondrial	chr1q44	218605_at	NM_022366																				
4.97	4.63	0.34	2.24E-01	5.98E-01	NPEPL1	aminopeptidase-like 1	chr20q13.32	218821_at	NM_024663																				
5.01	4.70	0.32	2.24E-01	5.98E-01	KIF22	kinesin family member 22	chr16p11.2	202183_s_at	NM_007317																				
4.52	3.90	0.62	2.25E-01	5.98E-01	ZNF326	zinc finger protein 326	chr1p22.2	227680_at	NM_182975 /// NM_182976																				
2.16	1.96	0.20	2.25E-01	5.98E-01	C6orf123 /// LOC100133056	chromosome 6 open reading frame 123 /// similar to HGC6.2	chr6q27	1555095_at	XM_001723741 /// XR_039813 /// XR_039814 /// XR_039815																				
6.74	6.44	0.29	2.25E-01	5.98E-01	USP30	ubiquitin specific peptidase 30	chr12q24.11	227572_at	NM_032663																				
7.45	7.16	0.30	2.25E-01	5.98E-01	LSM2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr6p21.3	209449_at	NM_021177																				
10.75	10.55	0.20	2.25E-01	5.98E-01	COX5B	cytochrome c oxidase subunit Vb	chr2cen-q13	202343_x_at	NM_001862																				
3.50	2.97	0.53	2.25E-01	5.99E-01	ZNF10	zinc finger protein 10	chr12q24.33	216350_s_at	NM_015394																				
6.60	6.25	0.35	2.25E-01	5.99E-01	ICAM3	intercellular adhesion molecule 3	chr19p13.3-p13.2	204949_at	NM_002162																				
4.18	3.92	0.27	2.25E-01	5.99E-01	KIR2DS5	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5	chr19q13.4	208203_x_at	NM_014513																				
3.63	3.22	0.41	2.25E-01	5.99E-01	NUMA1	nuclear mitotic apparatus protein 1	chr11q13	214250_at	NM_006185																				
3.58	3.42	0.17	2.25E-01	5.99E-01	CENPL	centromere protein L	chr1q25.1	232065_x_at	NM_001127181 /// NM_033319																				
6.24	5.61	0.64	2.25E-01	5.99E-01	MCOLN2	mucolipin 2	chr1p22	230110_at	NM_153259																				
3.09	2.87	0.22	2.25E-01	5.99E-01	SOX1	SRY (sex determining region Y)-box 1	chr13q34	230982_at	NM_005986																				
5.55	5.11	0.43	2.25E-01	5.99E-01	PDCD6	Aryl-hydrocarbon receptor repressor	chr5p15.33	222380_s_at	NM_013232 /// XM_001714855 /// XM_001720072 /// XM_001723249																				
2.31	2.15	0.17	2.25E-01	5.99E-01	---	---	---	243737_at	---																				
6.58	6.33	0.25	2.25E-01	5.99E-01	MAP2K5	mitogen-activated protein kinase kinase 5	chr15q23	204756_at	NM_002757 /// NM_145160																				

6.49	6.15	0.34	2.25E-01	5.99E-01	ZFP64	zinc finger protein 64 homolog (mouse)	chr20q13.2	218968_s_at	NM_018197 /// NM_022088 /// NM_199426 /// NM_199427																				
3.36	3.20	0.17	2.25E-01	5.99E-01	PLK3	Polo-like kinase 3 (Drosophila)	chr1p34.1	229825_at	NM_004073																				
4.49	3.97	0.52	2.25E-01	5.99E-01	DUSP2	dual specificity phosphatase 2	chr2q11	204794_at	NM_004418																				
2.09	1.93	0.16	2.26E-01	5.99E-01	---	---	---	1562086_at	---																				
2.27	2.13	0.13	2.26E-01	5.99E-01	---	---	---	1559316_at	---																				
1.98	1.84	0.15	2.26E-01	5.99E-01	---	---	---	1567859_at	---																				
3.29	3.05	0.24	2.26E-01	5.99E-01	---	---	---	1560577_at	---																				
2.63	2.43	0.20	2.26E-01	6.00E-01	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	chr4p15.1	1569141_a_at	NM_013261																				
3.24	2.96	0.28	2.26E-01	6.00E-01	ENC1	ectodermal-neural cortex (with BTB-like domain)	chr5q12-q13.3	201340_s_at	NM_003633																				
6.45	5.98	0.47	2.26E-01	6.00E-01	ANKHD1 /// EIF4EBP3	ankyrin repeat and KH domain containing 1 /// eukaryotic translation initiation factor 4E binding protein 3	chr5q31.3	219081_at	NM_003732 /// NM_017747 /// NM_017978 /// NM_024668																				
4.28	3.89	0.38	2.26E-01	6.00E-01	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	chr17q11.2	1556053_at	NM_003315																				
5.08	4.59	0.49	2.26E-01	6.00E-01	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	chr12q23.1	218395_at	NM_022496																				
1.98	1.83	0.14	2.27E-01	6.00E-01	---	---	---	228792_at	---																				
7.29	7.03	0.25	2.27E-01	6.00E-01	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	chr6p21.3	209040_s_at	NM_004159 /// NM_148919																				
2.77	2.51	0.26	2.27E-01	6.00E-01	FNTB	Farnesyltransferase, CAAX box, beta	chr14q23-q24	1568865_at	NM_002028																				
3.02	2.76	0.26	2.27E-01	6.00E-01	ATAD2	ATPase family, AAA domain containing 2	chr8q24.13	222740_at	NM_014109																				
2.51	2.31	0.20	2.27E-01	6.00E-01	LOC100128262	hypothetical LOC100128262	chr3q29	1565784_at	XM_001714083 /// XM_001716158 /// XM_001716783																				
6.90	6.15	0.75	2.27E-01	6.00E-01	TMEM47	transmembrane protein 47	chrXp11.4	209656_s_at	NM_031442																				
6.19	5.91	0.29	2.27E-01	6.01E-01	RAB4A	RAB4A, member RAS oncogene family	chr1q42-q43	203582_s_at	NM_004578																				
6.19	5.82	0.37	2.27E-01	6.01E-01	---	---	---	244753_at	---																				
3.33	3.10	0.22	2.27E-01	6.01E-01	KIR2DL3 /// KIR3DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3 /// killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	chr19q13.4 /// chr19q13.42	216676_x_at	NM_014511 /// NM_015868 /// NM_153443																				
2.35	2.14	0.21	2.27E-01	6.01E-01	STK4	serine/threonine kinase 4	chr20q11.2-q13.2	223746_at	NM_006282																				
3.02	2.85	0.17	2.27E-01	6.01E-01	---	---	---	211388_s_at	---																				
2.90	2.75	0.15	2.27E-01	6.01E-01	LOC642393 /// MRPL20	similar to mitochondrial ribosomal protein L20 /// mitochondrial ribosomal protein L20	chr1p36.3-p36.2	224803_s_at	NM_017971 /// XM_001724426 /// XM_001724427 /// XM_001724428 /// XM_001724433																				
4.22	3.88	0.35	2.27E-01	6.01E-01	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	chr3q22.3	234295_at	NM_016216																				
3.29	2.96	0.34	2.27E-01	6.01E-01	AOF2	amine oxidase (flavin containing) domain 2	chr1p36.12	1555897_at	NM_015013																				
2.44	2.30	0.13	2.27E-01	6.01E-01	---	---	---	239418_x_at	---																				
2.18	2.03	0.15	2.27E-01	6.01E-01	hCG_2019139	hCG2019139	chr20p11.23	1564758_at	XR_041858 /// XR_041859 /// XR_041860																				
2.69	2.53	0.16	2.27E-01	6.01E-01	SPERT	spermatid associated	chr13q14.12	1553847_a_at	NM_152719																				
2.25	2.09	0.16	2.27E-01	6.01E-01	---	---	---	241162_at	---																				
3.50	3.31	0.19	2.27E-01	6.01E-01	---	---	---	1561481_at	---																				
6.44	6.14	0.30	2.27E-01	6.01E-01	BAHD1	bromo adjacent homology domain containing 1	chr15q15.1	203051_at	NM_014952																				
4.64	4.26	0.38	2.27E-01	6.01E-01	STX16	syntaxin 16	chr20q13.32	1558249_s_at	NM_001001433 /// NM_003763																				
5.14	4.82	0.32	2.27E-01	6.02E-01	---	---	---	230703_at	---																				
5.27	5.05	0.21	2.27E-01	6.02E-01	HPS4	Hermansky-Pudlak syndrome 4	chr22cen-q12.3	218402_s_at	NM_022081 /// NM_152841																				

7.07	6.63	0.43	2.28E-01	6.02E-01	AMZ2	Archaelysin family metallopeptidase 2	chr17q24.2	227567_at	NM_001033569 /// NM_001033570 /// NM_001033571 /// NM_001033572 /// NM_001033574 /// NM_016627																				
4.44	4.06	0.37	2.28E-01	6.02E-01	C1orf107	chromosome 1 open reading frame 107	chr1q32.2	204700_x_at	NM_014388																				
6.10	5.75	0.34	2.28E-01	6.02E-01	RNASEH1	ribonuclease H1	chr2p25	218496_at	NM_002936																				
2.92	2.65	0.27	2.28E-01	6.02E-01	---	---	---	1568781_at	---																				
2.64	2.39	0.25	2.28E-01	6.02E-01	---	---	---	242155_x_at	---																				
7.33	7.01	0.32	2.28E-01	6.02E-01	ACBD5	acyl-Coenzyme A binding domain containing 5	chr10p12.1	225663_at	NM_001042473 /// NM_145698																				
2.93	2.71	0.22	2.28E-01	6.02E-01	N4BP2	NEDD4 binding protein 2	chr4p14	228242_at	NM_018177																				
2.49	2.34	0.15	2.28E-01	6.02E-01	GPR6	G protein-coupled receptor 6	chr6q21	214655_at	NM_005284																				
5.32	5.08	0.24	2.28E-01	6.02E-01	TCOF1	Treacher Collins-Franceschetti syndrome 1	chr5q32-q33.1	202385_s_at	NM_000356 /// NM_001008656 /// NM_001008657																				
5.43	5.24	0.19	2.28E-01	6.02E-01	HTT	huntingtin	chr4p16.3	202389_s_at	NM_002111																				
3.23	2.88	0.35	2.28E-01	6.02E-01	PLAGL2	pleiomorphic adenoma gene-like 2	chr20q11.21	202924_s_at	NM_002657																				
2.47	2.21	0.25	2.28E-01	6.02E-01	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	chr1q42.3	1561714_a_at	NM_152490																				
7.14	6.71	0.43	2.28E-01	6.02E-01	AMIGO3 /// GMPPB	adhesion molecule with Ig-like domain 3 /// GDP-mannose pyrophosphorylase B	chr3p21 /// chr3p21.31	219920_s_at	NM_013334 /// NM_021971 /// NM_198722																				
6.66	6.40	0.25	2.28E-01	6.02E-01	TRAF3IP2	TRAF3 interacting protein 2	chr6q21	215411_s_at	NM_147200 /// NM_147686																				
4.07	3.75	0.32	2.28E-01	6.02E-01	LTBP1	latent transforming growth factor beta binding protein 1	chr2p22-p21	202728_s_at	NM_000627 /// NM_206943																				
3.01	2.72	0.29	2.28E-01	6.02E-01	CPM	carboxypeptidase M	chr12q14.3	241765_at	NM_001005502 /// NM_001874 /// NM_198320																				
5.55	5.18	0.36	2.28E-01	6.02E-01	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	chr9q22-q31	203528_at	NM_006378																				
5.76	5.26	0.50	2.28E-01	6.02E-01	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	chr2q31.2	211930_at	NM_194247																				
5.28	4.90	0.38	2.28E-01	6.02E-01	AKAP7	A kinase (PRKA) anchor protein 7	chr6q23	211172_x_at	NM_004842 /// NM_016377 /// NM_138633																				
2.88	2.72	0.16	2.28E-01	6.02E-01	IL24	interleukin 24	chr1q32	206569_at	NM_006850 /// NM_181339																				
7.72	7.40	0.32	2.28E-01	6.02E-01	MAF1	MAF1 homolog (S. cerevisiae)	chr8q24.3	222998_at	NM_032272																				
2.26	2.11	0.15	2.28E-01	6.02E-01	---	---	---	240858_at	---																				
2.20	2.05	0.15	2.28E-01	6.02E-01	---	---	---	1568794_at	---																				
2.67	2.49	0.18	2.28E-01	6.02E-01	ATXN7L1	ataxin 7-like 1	chr7q22.2	214343_s_at	NM_020725 /// NM_152749																				
2.44	2.28	0.16	2.28E-01	6.02E-01	---	---	---	216132_at	---																				
2.75	2.50	0.25	2.28E-01	6.02E-01	THNSL2	threonine synthase-like 2 (S. cerevisiae)	chr2p11.2	239949_at	NM_018271																				
2.60	2.44	0.16	2.28E-01	6.02E-01	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	chr14q32.2	224310_s_at	NM_022898 /// NM_138576																				
4.10	3.81	0.29	2.28E-01	6.02E-01	---	---	---	227210_at	---																				
5.64	5.30	0.34	2.29E-01	6.02E-01	MGA	MAX gene associated	chr15q14	212945_s_at	NM_001080541																				
5.51	5.05	0.45	2.29E-01	6.02E-01	HSPA14	heat shock 70kDa protein 14	chr10p13	219212_at	NM_016299																				

2.72	2.54	0.18	2.29E-01	6.02E-01	NRP2	Neuropilin 2	chr2q33.3	228699_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279																				
3.89	3.62	0.26	2.29E-01	6.02E-01	MYO19	myosin XIX	chr17q12	219320_at	NM_001033580 /// NM_025109																				
3.37	3.11	0.26	2.29E-01	6.02E-01	RASL10A	RAS-like, family 10, member A	chr22q12.2	206850_at	NM_001007279 /// NM_006477																				
3.50	3.25	0.24	2.29E-01	6.02E-01	---	---	---	1561393_at	---																				
3.13	2.90	0.22	2.29E-01	6.02E-01	RAB33B	RAB33B, member RAS oncogene family	chr4q28	221014_s_at	NM_031296																				
4.39	4.14	0.25	2.29E-01	6.02E-01	---	---	---	1557409_at	---																				
2.36	2.21	0.15	2.29E-01	6.02E-01	ATP11B	ATPase, class VI, type 11B	chr3q27	238811_at	NM_014616																				
2.26	1.98	0.27	2.29E-01	6.02E-01	NOVA1	neuro-oncological ventral antigen 1	chr14q	207437_at	NM_002515 /// NM_006489 /// NM_006491																				
6.31	5.92	0.39	2.29E-01	6.02E-01	ASL	argininosuccinate lyase	chr7cen-q11.2	204608_at	NM_000048 /// NM_001024943 /// NM_001024944 /// NM_001024946																				
7.35	7.18	0.17	2.29E-01	6.02E-01	WASH1 /// WASH2P	WAS protein family homolog 1 /// WAS protein family homolog 2 pseudogene	chr2q14.1 /// chr9p24.3	225995_x_at	NM_182905 /// NR_024077 /// XR_040204																				
7.56	7.17	0.39	2.29E-01	6.02E-01	CBX3 /// LOC653972	chromobox homolog 3 (HP1 gamma homolog, Drosophila) /// similar to chromobox homolog 3	chr7p15.2	200037_s_at	NM_007276 /// NM_016587 /// XM_938779																				
2.78	2.54	0.24	2.29E-01	6.02E-01	CSE1L	CSE1 chromosome segregation 1-like (yeast)	chr20q13	210765_at	NM_001316																				
2.16	1.98	0.17	2.29E-01	6.03E-01	RFPL1	ret finger protein-like 1	chr22q12.2	207934_at	NM_021026																				
5.31	5.04	0.26	2.29E-01	6.03E-01	TRIM21	tripartite motif-containing 21	chr11p15.5	204804_at	NM_003141																				
6.27	6.10	0.17	2.29E-01	6.03E-01	INO80B /// WBP1	INO80 complex subunit B /// WW domain binding protein 1	chr2p12 /// chr2p13.1	221251_x_at	NM_012477 /// NM_031288																				
5.65	5.34	0.30	2.29E-01	6.03E-01	KPTN	kaptin (actin binding protein)	chr19q13.32	220160_s_at	NM_007059																				
3.05	2.72	0.33	2.29E-01	6.03E-01	LINS1	lines homolog 1 (Drosophila)	chr15q26.3	1554455_at	NM_001040614 /// NM_001040615 /// NM_001040616 /// NM_018148																				
3.23	2.96	0.26	2.29E-01	6.03E-01	EFCAB6	EF-hand calcium binding domain 6	chr22q13.1-q13.33	233345_at	NM_022785 /// NM_198856																				
6.33	5.64	0.69	2.29E-01	6.03E-01	IVNS1ABP	influenza virus NS1A binding protein	chr1q25.1-q31.1	206245_s_at	NM_006469																				
2.13	1.98	0.15	2.30E-01	6.03E-01	---	---	---	241544_at	---																				
10.74	10.54	0.20	2.30E-01	6.03E-01	TUBA1B	tubulin, alpha 1b	chr12q13.12	213646_x_at	NM_006082																				
8.68	8.24	0.45	2.30E-01	6.03E-01	CXorf48 /// MGC39606	chromosome X open reading frame 48 /// hypothetical protein MGC39606	chrXq26.3	227909_at	NM_001031705 /// NM_017863 /// XM_001127817 /// XM_001129116 /// XM_001721183																				
2.92	2.75	0.17	2.30E-01	6.03E-01	ZFYVE20	zinc finger, FYVE domain containing 20	chr3p24.3	1569714_at	NM_022340																				
2.69	2.40	0.30	2.30E-01	6.03E-01	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	chr18q21.32	204285_s_at	NM_021127																				

2.94	2.79	0.15	2.30E-01	6.03E-01	---	---	---	1559563_at	---
5.18	4.72	0.46	2.30E-01	6.03E-01	CHIC1	cysteine-rich hydrophobic domain 1	chrXq13-q21	228345_at	NM_001039840
5.91	5.67	0.24	2.30E-01	6.03E-01	HMG20B	high-mobility group 20B	chr19p13.3	209113_s_at	NM_006339
6.13	5.75	0.38	2.30E-01	6.03E-01	TMEM168	transmembrane protein 168	chr7q31.32	218962_s_at	NM_022484
2.68	2.53	0.15	2.30E-01	6.03E-01	---	---	---	242087_x_at	---
3.08	2.90	0.18	2.30E-01	6.03E-01	TMEM201	transmembrane protein 201	chr1p36.22	228671_at	NM_001010866 /// NM_001130924
2.19	1.99	0.20	2.30E-01	6.03E-01	LOC285692	hypothetical protein LOC285692	chr5p15.31	1561650_s_at	---
4.47	4.24	0.23	2.30E-01	6.03E-01	ATP8B1	ATPase, class I, type 8B, member 1	chr18q21-q22|18q21.31	238055_at	NM_005603
5.22	4.92	0.30	2.30E-01	6.03E-01	WDR79	WD repeat domain 79	chr17p13.1	44563_at	NM_018081
2.65	2.44	0.21	2.30E-01	6.04E-01	---	---	---	1570536_at	---
6.17	5.95	0.22	2.30E-01	6.04E-01	SNX11	sorting nexin 11	chr17q21.32	53912_at	NM_013323 /// NM_152244
2.21	2.07	0.15	2.30E-01	6.04E-01	---	---	---	1566978_at	---
2.28	2.12	0.16	2.30E-01	6.04E-01	KRTAP4-12	keratin associated protein 4-12	chr17q12-q21	224269_at	NM_031854
3.73	3.37	0.36	2.30E-01	6.04E-01	ZNF700	zinc finger protein 700	chr19p13.2	223590_at	NM_144566
2.35	2.15	0.19	2.30E-01	6.04E-01	---	---	---	1557869_at	---
7.61	7.22	0.39	2.30E-01	6.04E-01	C16orf14	chromosome 16 open reading frame 14	chr16p13.3	225861_at	NM_138418
2.88	2.59	0.28	2.30E-01	6.04E-01	C3orf31	Chromosome 3 open reading frame 31	chr3p25.2	231958_at	NM_138807
5.34	5.00	0.35	2.30E-01	6.04E-01	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	chr8p23	222874_s_at	NM_018941
3.10	2.83	0.27	2.30E-01	6.04E-01	BTNL2	butyrophilin-like 2 (MHC class II associated)	chr6p21.3	221457_s_at	NM_019602
2.10	1.97	0.13	2.31E-01	6.04E-01	---	---	---	1560846_at	---
6.61	6.18	0.43	2.31E-01	6.04E-01	LOC150166	hypothetical protein LOC150166	chr22q11.21	229295_at	---
2.52	2.36	0.16	2.31E-01	6.04E-01	C7orf4	chromosome 7 open reading frame 4	chr7q36	237088_at	---
3.36	3.00	0.37	2.31E-01	6.04E-01	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	chr3q23	226570_at	NM_001679
5.61	5.31	0.31	2.31E-01	6.04E-01	MESP1	mesoderm posterior 1 homolog (mouse)	chr15q26.1	224476_s_at	NM_018670
2.09	1.93	0.17	2.31E-01	6.04E-01	HTR7 /// HTR7P	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) /// 5-hydroxytryptamine (serotonin) receptor 7 pseudogene	chr10q21-q24 /// chr12p13.1	216098_s_at	NM_000872 /// NM_019859 /// NM_019860 /// NR_002774
2.10	1.98	0.13	2.31E-01	6.04E-01	---	---	---	1563486_at	---
4.70	4.29	0.42	2.31E-01	6.04E-01	C13orf27	chromosome 13 open reading frame 27	chr13q33.1	213346_at	NM_138779
2.44	2.31	0.13	2.31E-01	6.04E-01	SLC15A2	solute carrier family 15 (H+/peptide transporter), member 2	chr3q13.33	205317_s_at	NM_021082
3.47	3.22	0.24	2.31E-01	6.04E-01	---	---	---	1569444_at	---
3.35	3.07	0.29	2.31E-01	6.05E-01	CBWD1 /// CBWD2 /// CBWD3 /// CBWD5 /// CBWD6	COBW domain containing 1 /// COBW domain containing 2 /// COBW domain containing 3 /// COBW domain containing 5 /// COBW domain containing 6	chr2q14.1 /// chr9p24.3 /// chr9q12 /// chr9q13	229804_x_at	NM_001024916 /// NM_001085457 /// NM_018491 /// NM_172003 /// NM_201453 /// XM_001716392
2.68	2.54	0.14	2.31E-01	6.05E-01	GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	chr12q21.3-q22	231832_at	NM_003774
6.48	6.21	0.27	2.32E-01	6.05E-01	SMG5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr1q21.2	34868_at	NM_015327
3.29	3.06	0.22	2.32E-01	6.05E-01	PPM1H	protein phosphatase 1H (PP2C domain containing)	chr12q14.1-q14.2	212686_at	NM_020700
2.17	2.04	0.13	2.32E-01	6.05E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	233621_s_at	NM_015313
4.64	4.45	0.20	2.32E-01	6.05E-01	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	chr19q13.4	211336_x_at	NM_001081637 /// NM_001081638 /// NM_001081639 /// NM_006669
5.82	5.59	0.23	2.32E-01	6.05E-01	DUSP6	dual specificity phosphatase 6	chr12q22-q23	208893_s_at	NM_001946 /// NM_022652
6.63	6.41	0.22	2.32E-01	6.05E-01	LLGL1	lethal giant larvae homolog 1 (Drosophila)	chr17p11.2	236594_at	NM_004140
3.35	3.19	0.16	2.32E-01	6.05E-01	---	---	---	242160_at	---
3.85	3.61	0.24	2.32E-01	6.05E-01	CDK2	cyclin-dependent kinase 2	chr12q13	211804_s_at	NM_001798 /// NM_052827

2.86	2.63	0.24	2.32E-01	6.05E-01	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3	chr3p21.1	219714_s_at	NM_018398
5.41	5.14	0.27	2.32E-01	6.06E-01	MAP3K12	mitogen-activated protein kinase kinase kinase 12	chr12q13	205448_s_at	NM_006301
6.39	6.16	0.23	2.32E-01	6.06E-01	BCL2L11	BCL2-like 11 (apoptosis facilitator)	chr2q13	225606_at	NM_006538 /// NM_138621 /// NM_207002
3.35	3.14	0.21	2.32E-01	6.06E-01	TRAPPC10	trafficking protein particle complex 10	chr21q22.3	1555446_s_at	NM_001001723 /// NM_003274
4.17	3.97	0.20	2.32E-01	6.06E-01	CIB3	calcium and integrin binding family member 3	chr19p13.12	1552751_a_at	NM_054113
2.92	2.76	0.16	2.32E-01	6.06E-01	TMEM207	transmembrane protein 207	chr3q28	237639_at	NM_207316
2.85	2.70	0.16	2.33E-01	6.06E-01	---	---	---	227881_s_at	---
2.57	2.39	0.18	2.33E-01	6.07E-01	GOLGA3	golgi autoantigen, golgin subfamily a, 3	chr12q24.33	1554987_at	NM_005895
2.45	2.31	0.14	2.33E-01	6.07E-01	---	---	---	1562099_at	---
2.51	2.30	0.21	2.33E-01	6.07E-01	FGD6	FYVE, RhoGEF and PH domain containing 6	chr12q22	1555136_at	NM_018351
5.26	4.96	0.30	2.33E-01	6.07E-01	ARHGAP4	Rho GTPase activating protein 4	chrXq28	204425_at	NM_001666
4.15	3.83	0.32	2.33E-01	6.07E-01	ZFPL1	zinc finger protein-like 1	chr11q13	214310_s_at	NM_006782
8.24	7.86	0.38	2.33E-01	6.07E-01	ANXA11	annexin A11	chr10q23	206200_s_at	NM_001157 /// NM_145868 /// NM_145869
4.60	4.19	0.41	2.33E-01	6.08E-01	LMAN1L	lectin, mannose-binding, 1 like	chr15q24.1	220420_at	NM_021819
2.43	2.22	0.21	2.33E-01	6.08E-01	---	---	---	1557769_at	---
4.78	4.50	0.28	2.34E-01	6.08E-01	MAP3K3	mitogen-activated protein kinase kinase kinase 3	chr17q23.3	203514_at	NM_002401 /// NM_203351
4.94	4.60	0.34	2.34E-01	6.08E-01	LOC147727	hypothetical LOC147727	chr19p13.2	235014_at	XR_041067 /// XR_041068 /// XR_041069
3.68	3.44	0.24	2.34E-01	6.08E-01	WFIKKN1	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1	chr16p13.3	1552811_at	NM_053284
2.34	2.19	0.15	2.34E-01	6.08E-01	---	---	---	244139_s_at	---
2.37	2.17	0.20	2.34E-01	6.08E-01	ZNF599	zinc finger protein 599	chr19q13.11	243747_at	NM_001007248
8.35	7.94	0.41	2.34E-01	6.08E-01	FBXO21	F-box protein 21	chr12q24.22	212231_at	NM_015002 /// NM_033624
2.44	2.25	0.18	2.34E-01	6.09E-01	---	---	---	1562673_at	---
2.34	2.19	0.14	2.34E-01	6.09E-01	---	---	---	1563693_at	---
7.49	6.92	0.57	2.34E-01	6.09E-01	KLF6	Kruppel-like factor 6	chr10p15	208961_s_at	NM_001300
7.16	6.77	0.39	2.34E-01	6.09E-01	ZNF395	zinc finger protein 395	chr8p21.1	218149_s_at	NM_018660
3.00	2.66	0.34	2.34E-01	6.09E-01	---	---	---	242245_at	---
6.31	5.87	0.44	2.34E-01	6.09E-01	WDR33	WD repeat domain 33	chr2q14.3	222763_s_at	NM_001006622 /// NM_001006623 /// NM_018383
2.83	2.66	0.17	2.34E-01	6.09E-01	---	---	---	1561480_a_at	---
2.48	2.27	0.21	2.34E-01	6.09E-01	---	---	---	1567575_at	---
2.04	1.91	0.14	2.34E-01	6.09E-01	---	---	---	244454_at	---
2.46	2.23	0.23	2.34E-01	6.09E-01	VPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)	chr20p13-p12	215216_at	NM_022575 /// NM_080413 /// NM_080414
4.02	3.65	0.36	2.34E-01	6.09E-01	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	chr10q11.21	218871_x_at	NM_018590
2.46	2.33	0.13	2.34E-01	6.09E-01	---	---	---	1557768_at	---
2.53	2.33	0.20	2.34E-01	6.09E-01	ASB15	ankyrin repeat and SOCS box-containing 15	chr7q31.31	1564679_at	NM_080928
7.41	7.23	0.18	2.35E-01	6.09E-01	DIABLO	diablo homolog (Drosophila)	chr12q24.31	219350_s_at	NM_019887 /// NM_138929 /// NM_138930
7.34	6.84	0.50	2.35E-01	6.09E-01	C1orf142	chromosome 1 open reading frame 142	chr1q42.13	225244_at	NM_053052
2.79	2.63	0.16	2.35E-01	6.09E-01	POLG	polymerase (DNA directed), gamma	chr15q25	217636_at	NM_001126131 /// NM_002693
3.54	3.35	0.20	2.35E-01	6.09E-01	---	---	---	240934_at	---
6.23	5.79	0.44	2.35E-01	6.09E-01	FUK	fucokinase	chr16q22.1	226072_at	NM_145059
2.26	2.06	0.21	2.35E-01	6.09E-01	---	---	---	1562802_at	---
6.86	6.47	0.39	2.35E-01	6.09E-01	TRAF4	TNF receptor-associated factor 4	chr17q11-q12	202871_at	NM_004295
3.30	3.05	0.25	2.35E-01	6.09E-01	PRUNE	prune homolog (Drosophila)	chr1q21	232490_s_at	NM_021222

6.82	6.65	0.17	2.35E-01	6.09E-01	MRTO4	mRNA turnover 4 homolog (S. cerevisiae)	chr1p36.13	220688_s_at	NM_016183
2.35	2.17	0.18	2.35E-01	6.09E-01	MGC2889	hypothetical protein MGC2889	chr3q29	211718_at	---
5.48	5.12	0.35	2.35E-01	6.09E-01	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	chr9q34.3	225738_at	NM_005312 /// NM_198679
3.03	2.82	0.21	2.35E-01	6.09E-01	NKAIN4	Na+/K+ transporting ATPase interacting 4	chr20q13.33	228017_s_at	NM_152864
5.06	4.44	0.62	2.35E-01	6.09E-01	C5orf13	chromosome 5 open reading frame 13	chr5q22.1	230424_at	NM_004772
4.61	4.39	0.22	2.35E-01	6.09E-01	---	---	---	224375_at	---
2.92	2.64	0.28	2.35E-01	6.09E-01	SLC25A29	Solute carrier family 25, member 29	chr14q32.2	232280_at	NM_001039355
2.57	2.40	0.17	2.35E-01	6.09E-01	PCCA	Propionyl Coenzyme A carboxylase, alpha polypeptide	chr13q32	232376_at	NM_000282 /// NM_001127692
7.73	7.33	0.40	2.35E-01	6.09E-01	SON	SON DNA binding protein	chr21q22.1-q22.2|21q22.11	214988_s_at	NM_032195 /// NM_138927
3.14	2.99	0.16	2.35E-01	6.09E-01	KIAA0391	KIAA0391	chr14q13.2	202714_s_at	NM_014672
5.84	5.62	0.21	2.35E-01	6.09E-01	NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	chr19q13.1	214448_x_at	NM_001001716 /// NM_002503
4.87	4.57	0.30	2.35E-01	6.09E-01	KIAA0133	KIAA0133	chr1q42.13	205284_at	NM_014777
3.59	3.28	0.30	2.35E-01	6.09E-01	GNG2	guanine nucleotide binding protein (G protein), gamma 2	chr14q21	224965_at	NM_053064
2.41	2.25	0.16	2.35E-01	6.09E-01	---	---	---	1569243_at	---
4.78	4.51	0.27	2.35E-01	6.09E-01	KIAA1787	KIAA1787 protein	chr17p13	226703_at	NM_001005408 /// NM_032442
4.93	4.48	0.46	2.35E-01	6.09E-01	TBC1D24	TBC1 domain family, member 24	chr16p13.3	227908_at	NM_020705
2.09	1.95	0.13	2.35E-01	6.10E-01	---	---	---	1565874_at	---
7.80	7.56	0.24	2.35E-01	6.10E-01	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	chr3p21.3-p21.2	204842_x_at	NM_004157
2.37	2.21	0.16	2.35E-01	6.10E-01	---	---	---	1556235_at	---
2.28	2.14	0.15	2.35E-01	6.10E-01	hCG_1654703	hCG1654703	chr1q23.1	1568746_a_at	XM_001722850 /// XM_933506 /// XM_943630
2.87	2.68	0.19	2.35E-01	6.10E-01	---	---	---	1556938_a_at	---
8.72	8.52	0.20	2.35E-01	6.10E-01	CTBP2	C-terminal binding protein 2	chr10q26.13	210835_s_at	NM_001083914 /// NM_001329 /// NM_022802
7.65	7.25	0.40	2.36E-01	6.10E-01	FLJ35348	FLJ35348	chr9q34	212547_at	XR_041460 /// XR_041461 /// XR_041462
5.85	5.24	0.61	2.36E-01	6.10E-01	RBBP8	retinoblastoma binding protein 8	chr18q11.2	203344_s_at	NM_002894 /// NM_203291 /// NM_203292
4.26	4.05	0.21	2.36E-01	6.10E-01	ANK1	ankyrin 1, erythrocytic	chr8p11.1	207087_x_at	NM_000037 /// NM_020475 /// NM_020476 /// NM_020477 /// NM_020478 /// NM_020480
3.10	2.89	0.21	2.36E-01	6.10E-01	LOC100129407 /// LOC100132304	similar to hCG1993257 /// similar to hCG1993257	chrXq13.1	236758_at	XM_001715478 /// XM_001715870 /// XM_001716654 /// XM_001716677
2.76	2.57	0.18	2.36E-01	6.10E-01	---	---	---	239326_at	---
6.04	5.64	0.40	2.36E-01	6.10E-01	GPR157	G protein-coupled receptor 157	chr1p36.23	227970_at	NM_024980
3.09	2.81	0.29	2.36E-01	6.10E-01	ZNF529	Zinc finger protein 529	chr19q13.13	215307_at	NM_020951
2.42	2.21	0.21	2.36E-01	6.10E-01	---	---	---	241397_at	---
7.93	7.60	0.33	2.36E-01	6.10E-01	MRPL15	mitochondrial ribosomal protein L15	chr8q11.2-q13	218027_at	NM_014175

3.40	2.98	0.42	2.36E-01	6.10E-01	LOC100133130	PRO1102	chr10q11.21	223766_at	XM_001724485
8.09	7.80	0.30	2.36E-01	6.10E-01	MRPL14	mitochondrial ribosomal protein L14	chr6p21.3	225201_s_at	NM_032111
4.68	4.44	0.24	2.36E-01	6.10E-01	EME2	Essential meiotic endonuclease 1 homolog 2 (S. pombe)	chr16p13.3	1556024_at	NM_001010865
2.21	2.03	0.18	2.36E-01	6.10E-01	ATP9B	ATPase, class II, type 9B	chr18q23	1568723_at	NM_198531
2.24	2.10	0.14	2.36E-01	6.10E-01	CBY3	Chibby homolog 3 (Drosophila)	chr5q35.3	238138_at	XM_001724133 /// XM_928982 /// XM_936994
4.68	4.36	0.32	2.36E-01	6.10E-01	DOCK6	dedicator of cytokinesis 6	chr19p13.2	221794_at	NM_020812
7.76	7.44	0.31	2.36E-01	6.10E-01	RBBP4	retinoblastoma binding protein 4	chr1p35.1	217301_x_at	NM_005610
5.50	5.09	0.41	2.36E-01	6.10E-01	PGPEP1	pyroglutamyl-peptidase I	chr19p13.11	223469_at	NM_017712
3.12	2.92	0.20	2.36E-01	6.10E-01	---	---	---	242850_at	---
4.49	4.25	0.24	2.36E-01	6.10E-01	FLJ27365 /// LOC150381	FLJ27365 protein /// hypothetical protein LOC150381	chr22q13.31	1557342_a_at	XR_041674 /// XR_041675 /// XR_041676
2.51	2.32	0.19	2.36E-01	6.11E-01	---	---	---	239944_at	---
8.13	7.69	0.44	2.36E-01	6.11E-01	MED25	mediator complex subunit 25	chr19q13.3	1553993_s_at	NM_030973
8.66	8.50	0.16	2.37E-01	6.11E-01	FBXO7	F-box protein 7	chr22q12-q13	201178_at	NM_001033024 /// NM_012179
2.56	2.38	0.19	2.37E-01	6.11E-01	C7orf25	chromosome 7 open reading frame 25	chr7p14-p11.2	53202_at	NM_001099858 /// NM_024054
5.79	5.58	0.21	2.37E-01	6.11E-01	KBTBD4	kelch repeat and BTB (POZ) domain containing 4	chr11p11.2	218569_s_at	NM_016506 /// NM_018095
5.91	5.61	0.30	2.37E-01	6.11E-01	TULP4	tubby like protein 4	chr6q25-q26	218184_at	NM_001007466 /// NM_020245
5.61	5.02	0.60	2.37E-01	6.11E-01	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	chr3q25.31	1554148_a_at	NM_004733
2.17	2.02	0.15	2.37E-01	6.11E-01	---	---	---	244891_x_at	---
3.75	3.41	0.34	2.37E-01	6.12E-01	---	---	---	1558019_at	---
6.04	5.66	0.38	2.37E-01	6.12E-01	LOC100132969 /// TMEM185A	hypothetical protein LOC100132969 /// transmembrane protein 185A	chrXq28	227880_s_at	NM_032508 /// XM_001720980
2.49	2.34	0.15	2.37E-01	6.12E-01	---	---	---	1569953_at	---
3.47	3.11	0.36	2.37E-01	6.12E-01	---	---	---	244532_x_at	---
3.18	2.92	0.27	2.37E-01	6.12E-01	DUOX1	Dual oxidase 1	chr15q15.3	1565797_at	NM_017434 /// NM_175940
5.21	4.77	0.43	2.37E-01	6.12E-01	PLD1	phospholipase D1, phosphatidylcholine-specific	chr3q26	177_at	NM_001130081 /// NM_002662
2.84	2.49	0.35	2.37E-01	6.12E-01	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	chr6p21.3	215779_s_at	NM_003518 /// NM_003522 /// NM_003523 /// NM_003525 /// NM_003526
2.10	1.97	0.13	2.37E-01	6.12E-01	---	---	---	1563704_at	---
2.82	2.64	0.19	2.37E-01	6.12E-01	CECR2	cat eye syndrome chromosome region, candidate 2	chr22q11.2	233695_s_at	NM_031413
2.06	1.93	0.12	2.37E-01	6.12E-01	---	---	---	1568749_at	---
4.77	4.12	0.66	2.37E-01	6.12E-01	MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	chr1q21	214056_at	NM_021960 /// NM_182763
2.52	2.32	0.21	2.38E-01	6.12E-01	---	---	---	228983_at	---
2.33	2.14	0.19	2.38E-01	6.12E-01	FLJ45244	hypothetical locus FLJ45244	chr14q32.13	1557063_at	NM_207443
7.29	6.82	0.46	2.38E-01	6.13E-01	LST1	leukocyte specific transcript 1	chr6p21.3	214181_x_at	NM_007161 /// NM_205837 /// NM_205838 /// NM_205839 /// NM_205840

2.67	2.43	0.23	2.38E-01	6.13E-01	C19orf55	chromosome 19 open reading frame 55	chr19q13.12	242640_at	NM_001039887																				
2.75	2.59	0.16	2.38E-01	6.13E-01	RTTN	rotatin	chr18q22.2	1557388_at	NM_173630																				
6.26	6.06	0.20	2.38E-01	6.13E-01	MLL	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	226981_at	NM_005933																				
2.96	2.81	0.15	2.38E-01	6.13E-01	---	---	---	214019_at	---																				
7.71	7.24	0.48	2.38E-01	6.13E-01	SRGAP2P1	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 1	chr1p11.2	229067_at	---																				
7.00	6.81	0.19	2.38E-01	6.13E-01	TUBA3C /// TUBA3D	tubulin, alpha 3c /// tubulin, alpha 3d	chr13q11 /// chr2q21.1	210527_x_at	NM_006001 /// NM_080386																				
4.52	4.37	0.15	2.38E-01	6.13E-01	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	chr14q22.1	242154_x_at	NM_152329 /// NM_203467																				
3.28	3.13	0.15	2.38E-01	6.13E-01	C16orf57	chromosome 16 open reading frame 57	chr16q13	1554119_at	NM_024598																				
3.56	3.27	0.29	2.38E-01	6.13E-01	TRAF1	TNF receptor-associated factor 1	chr9q33-q34	205599_at	NM_005658																				
2.21	2.05	0.16	2.38E-01	6.13E-01	LOC729178	hypothetical protein LOC729178	chr6q24.3	1557891_s_at	XR_041025 /// XR_041026 /// XR_041027																				
6.75	6.37	0.39	2.38E-01	6.13E-01	INTS9	integrator complex subunit 9	chr8p21.1	203941_at	NM_018250																				
2.12	1.97	0.15	2.38E-01	6.13E-01	---	---	---	242729_at	---																				
2.39	2.24	0.15	2.38E-01	6.13E-01	LOC100131176	Similar to hCG1991662	chr7q36.1	1560147_at	XM_001716908 /// XM_001719421 /// XM_001720767																				
2.78	2.56	0.22	2.39E-01	6.13E-01	---	---	---	242374_at	---																				
4.86	4.67	0.19	2.39E-01	6.13E-01	ZBTB47	zinc finger and BTB domain containing 47	chr3p22.1	234338_s_at	NM_145166																				
6.37	6.15	0.22	2.39E-01	6.13E-01	LARP5	La ribonucleoprotein domain family, member 5	chr10p15.3	208952_s_at	NM_015155																				
3.81	3.49	0.31	2.39E-01	6.13E-01	JRK	jerky homolog (mouse)	chr8q24.3	1568605_at	NM_001077527 /// NM_003724																				
2.67	2.41	0.26	2.39E-01	6.13E-01	JMJD2B	Jumonji domain containing 2B	chr19p13.3	1559073_at	NM_015015																				
5.50	5.22	0.28	2.39E-01	6.13E-01	PPP3R1 /// WDR92	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform /// WD repeat domain 92	chr2p14 /// chr2p15	204506_at	NM_000945 /// NM_138458																				
2.55	2.40	0.15	2.39E-01	6.13E-01	OR52A1	olfactory receptor, family 52, subfamily A, member 1	chr11p15.5	221329_at	NM_012375																				
3.30	3.06	0.24	2.39E-01	6.13E-01	---	---	---	216006_at	---																				
6.06	5.86	0.20	2.39E-01	6.13E-01	KIF9	kinesin family member 9	chr3p21.31	228429_x_at	NM_022342 /// NM_182902 /// NM_182903																				
3.87	3.63	0.24	2.39E-01	6.13E-01	C5orf39	chromosome 5 open reading frame 39	chr5p12	227877_at	NM_001014279																				
5.91	5.69	0.21	2.39E-01	6.13E-01	SYS1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	chr20q13.12	224668_at	NM_033542																				
4.68	4.23	0.46	2.39E-01	6.13E-01	C18orf50	chromosome 18 open reading frame 50	---	1570552_at	---																				
3.53	3.29	0.24	2.39E-01	6.13E-01	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	chr12q	38158_at	NM_012291																				
7.30	7.13	0.17	2.39E-01	6.13E-01	EIF4E2	eukaryotic translation initiation factor 4E family member 2	chr2q37.1	209393_s_at	NM_004846																				
2.84	2.65	0.19	2.39E-01	6.13E-01	CCNY	cyclin Y	chr10p11.21	1554694_at	NM_145012 /// NM_181698																				
5.51	5.13	0.38	2.39E-01	6.13E-01	LDLRAD3	low density lipoprotein receptor class A domain containing 3	chr11p13	234985_at	NM_174902																				
4.03	3.49	0.54	2.39E-01	6.13E-01	YAF2	YY1 associated factor 2	chr12q12	206238_s_at	NM_005748																				
7.32	6.71	0.61	2.39E-01	6.13E-01	FGF9	fibroblast growth factor 9 (glia-activating factor)	chr13q11-q12	206404_at	NM_002010																				
8.91	8.66	0.25	2.39E-01	6.13E-01	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	chr13q31.2-q32.3	208855_s_at	NM_001032296 /// NM_003576																				
7.72	7.27	0.45	2.39E-01	6.13E-01	HNRNPA3 /// HNRNPA3P1	heterogeneous nuclear ribonucleoprotein A3 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	chr10q11.21 /// chr2q31.2	211931_s_at	NM_194247 /// NR_002726																				
3.22	2.68	0.54	2.39E-01	6.13E-01	---	---	---	242397_at	---																				
3.34	3.04	0.30	2.39E-01	6.13E-01	CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	chr1p21	36499_at	NM_001408																				
9.06	8.63	0.43	2.39E-01	6.13E-01	PGM5	phosphoglucomutase 5	chr9q13	226303_at	NM_021965																				

3.34	3.02	0.32	2.39E-01	6.13E-01	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	chr11q23	206011_at	NM_001223 /// NM_033292 /// NM_033293 /// NM_033294 /// NM_033295
2.35	2.16	0.20	2.39E-01	6.13E-01	CNTLN	centlein, centrosomal protein	chr9p22.2	1559005_s_at	NM_001114395 /// NM_017738
8.26	7.99	0.27	2.39E-01	6.13E-01	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	chr16q24.2	208786_s_at	NM_022818
3.70	3.47	0.23	2.39E-01	6.13E-01	IL12RB1	interleukin 12 receptor, beta 1	chr19p13.1	206890_at	NM_005535 /// NM_153701
5.97	5.70	0.27	2.39E-01	6.13E-01	BMP1	bone morphogenetic protein 1	chr8p21.3	207595_s_at	NM_001199 /// NM_006128 /// NM_006129
2.16	2.01	0.15	2.39E-01	6.13E-01	ARMC9	armadillo repeat containing 9	chr2q37.1	220754_at	NM_025139
5.24	4.86	0.37	2.39E-01	6.13E-01	MON1B	MON1 homolog B (yeast)	chr16q23.1	203644_s_at	NM_014940
5.42	5.00	0.42	2.40E-01	6.14E-01	CBLN4	cerebellin 4 precursor	chr20q13.13-q13.33	242524_at	NM_080617
3.18	2.93	0.25	2.40E-01	6.14E-01	LOC158402	hypothetical protein LOC158402	chr9q32	236769_at	---
4.45	4.10	0.35	2.40E-01	6.14E-01	---	---	---	242873_at	---
6.03	5.68	0.34	2.40E-01	6.14E-01	BICD2	bicaudal D homolog 2 (Drosophila)	chr9q22.31	213154_s_at	NM_001003800 /// NM_015250
2.24	2.09	0.15	2.40E-01	6.14E-01	KIAA1486	KIAA1486 protein	chr2q36.3	233916_at	NM_020864
5.12	4.46	0.65	2.40E-01	6.14E-01	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	chrXq13	212307_s_at	NM_181672 /// NM_181673
5.17	4.86	0.31	2.40E-01	6.14E-01	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	chr9q32	238765_at	NM_004888
8.63	8.42	0.21	2.40E-01	6.14E-01	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	chr11q13	200846_s_at	NM_001008709 /// NM_002708 /// NM_206873
7.77	7.60	0.17	2.40E-01	6.14E-01	ZBTB4	zinc finger and BTB domain containing 4	chr17p13.1	227047_x_at	NM_001128833 /// NM_020899
7.76	7.48	0.28	2.40E-01	6.14E-01	WTAP	Wilms tumor 1 associated protein	chr6q25-q27	203137_at	NM_004906 /// NM_152857 /// NM_152858
5.69	5.35	0.34	2.40E-01	6.14E-01	PCBP2	Poly(rC) binding protein 2	chr12q13.12-q13.13	229467_at	NM_001098620 /// NM_001128911 /// NM_001128912 /// NM_001128913 /// NM_001128914 /// NM_005016 /// NM_031989
3.79	3.63	0.16	2.40E-01	6.14E-01	MRPS15	mitochondrial ribosomal protein S15	chr1p35-p34.1	223291_at	NM_031280
6.02	5.64	0.38	2.40E-01	6.14E-01	LOC339290	hypothetical protein LOC339290	chr18p11.31	226235_at	XR_017922 /// XR_017997 /// XR_041986
2.82	2.65	0.17	2.40E-01	6.14E-01	TPM3	tropomyosin 3	chr1q21.2	214365_at	NM_001043351 /// NM_001043352 /// NM_001043353 /// NM_152263 /// NM_153649

7.09	6.78	0.31	2.40E-01	6.14E-01	BTBD6	BTB (POZ) domain containing 6	chr14q32	225389_at	NM_033271
5.09	4.76	0.33	2.40E-01	6.14E-01	USP53	ubiquitin specific peptidase 53	chr4q26	230083_at	NM_019050
6.12	5.72	0.40	2.40E-01	6.14E-01	TSKU	tsukushin	chr11q13.5	218245_at	NM_015516
2.64	2.49	0.15	2.40E-01	6.14E-01	---	---	---	1566609_at	---
5.17	4.65	0.51	2.40E-01	6.14E-01	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	chrXq13	207563_s_at	NM_181672 /// NM_181673
2.54	2.34	0.20	2.40E-01	6.14E-01	ZNF672	zinc finger protein 672	chr1q44	222509_s_at	NM_024836
5.64	5.36	0.28	2.40E-01	6.14E-01	C7orf52	Chromosome 7 open reading frame 52	chr7q22.1	1564658_at	NM_198571
4.94	4.69	0.26	2.40E-01	6.14E-01	GBP4	guanylate binding protein 4	chr1p22.2	235175_at	NM_052941
2.17	2.03	0.14	2.41E-01	6.15E-01	---	---	---	244270_at	---
2.22	2.06	0.16	2.41E-01	6.15E-01	LOC285972	hypothetical protein LOC285972	chr7q36.1	1560762_at	---
2.81	2.58	0.23	2.41E-01	6.15E-01	C1orf106	chromosome 1 open reading frame 106	chr1q32.1	219010_at	NM_018265
2.59	2.42	0.17	2.41E-01	6.15E-01	CXorf59	chromosome X open reading frame 59	chrXp21.1	1553466_at	NM_173695
2.30	2.15	0.15	2.41E-01	6.15E-01	CNR1	Cannabinoid receptor 1 (brain)	chr6q14-q15	1560225_at	NM_016083 /// NM_033181
3.93	3.74	0.18	2.41E-01	6.15E-01	VEZT	vezatin, adherens junctions transmembrane protein	chr12q22	207263_x_at	NM_017599
3.79	3.55	0.24	2.41E-01	6.15E-01	C2orf37	chromosome 2 open reading frame 37	chr2q31.1	231921_at	NM_025000
2.84	2.60	0.24	2.41E-01	6.15E-01	RBPMS /// SDHALP2	RNA binding protein with multiple splicing /// succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	chr3q29 /// chr8p12-p11	1557223_at	NM_001008710 /// NM_001008711 /// NM_001008712 /// NM_006867 /// NR_003265 /// XR_015171
3.36	3.13	0.23	2.41E-01	6.15E-01	---	---	---	228932_at	---
3.60	3.32	0.28	2.41E-01	6.15E-01	NFKBID	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	chr19q13.12	230052_s_at	NM_139239
3.24	3.05	0.20	2.41E-01	6.15E-01	---	---	---	1557507_at	---
7.22	7.08	0.13	2.41E-01	6.15E-01	FKSG49	FKSG49	chr5q13.3	211454_x_at	XR_041698
4.54	4.35	0.20	2.41E-01	6.15E-01	C9orf123	chromosome 9 open reading frame 123	chr9p24.1	224860_at	NM_033428
3.93	3.39	0.54	2.41E-01	6.15E-01	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	chr18p11.2	217425_at	NM_000529
7.92	7.52	0.40	2.41E-01	6.16E-01	MEIS2	Meis homeobox 2	chr15q14	207480_s_at	NM_002399 /// NM_170674 /// NM_170675 /// NM_170676 /// NM_170677 /// NM_172315 /// NM_172316
2.37	2.19	0.18	2.41E-01	6.16E-01	LOC91948	hypothetical LOC91948	chr15q26.2	234017_at	XR_040449 /// XR_040450 /// XR_040451
4.33	4.05	0.28	2.42E-01	6.16E-01	---	---	---	240765_at	---
2.83	2.70	0.14	2.42E-01	6.16E-01	ZXDA /// ZXDB	zinc finger, X-linked, duplicated A /// zinc finger, X-linked, duplicated B	chrXp11.1 /// chrXp11.21	215263_at	NM_007156 /// NM_007157
5.37	5.13	0.24	2.42E-01	6.16E-01	SFN	stratifin	chr1p36.11	33322_i_at	NM_006142
2.69	2.54	0.15	2.42E-01	6.16E-01	CENPL	centromere protein L	chr1q25.1	1554271_a_at	NM_001127181 /// NM_033319
2.29	2.13	0.16	2.42E-01	6.16E-01	RNF168	ring finger protein 168	chr3q29	1553127_a_at	NM_152617
2.07	1.92	0.15	2.42E-01	6.16E-01	---	---	---	215796_at	---
2.81	2.64	0.17	2.42E-01	6.16E-01	---	---	---	243067_at	---
8.77	7.55	1.21	2.42E-01	6.16E-01	ZNF331	zinc finger protein 331	chr19q13.41	219228_at	NM_001079906 /// NM_001079907 /// NM_018555

4.91	4.68	0.23	2.42E-01	6.16E-01	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	chr14q24.3	203988_s_at	NM_004480 /// NM_178154 /// NM_178155 /// NM_178156 /// NM_178157																				
5.55	5.28	0.27	2.42E-01	6.16E-01	FAM165B	family with sequence similarity 165, member B	chr21q22.12	1554432_x_at	NM_058182																				
2.69	2.56	0.13	2.42E-01	6.16E-01	---	---	---	215057_at	---																				
6.49	6.23	0.25	2.42E-01	6.16E-01	PPP1R8	protein phosphatase 1, regulatory (inhibitor) subunit 8	chr1p35	207830_s_at	NM_002713 /// NM_014110 /// NM_138558																				
5.67	5.36	0.30	2.42E-01	6.17E-01	TMEM8	transmembrane protein 8 (five membrane-spanning domains)	chr16p13.3	222718_at	NM_021259																				
2.39	2.24	0.15	2.42E-01	6.17E-01	NUP210L	nucleoporin 210kDa-like	chr1q21.3	232598_at	NM_207308																				
5.84	4.76	1.07	2.42E-01	6.17E-01	MCF2	MCF.2 cell line derived transforming sequence	chrXq27	217004_s_at	NM_001099855 /// NM_005369																				
2.17	2.04	0.13	2.43E-01	6.17E-01	C21orf131	chromosome 21 open reading frame 131	---	1557481_a_at	NR_024090																				
5.55	5.17	0.38	2.43E-01	6.17E-01	BNIP2	BCL2/adenovirus E1B 19kDa interacting protein 2	chr15q22.2	209308_s_at	NM_004330																				
2.91	2.58	0.33	2.43E-01	6.17E-01	EML1	echinoderm microtubule associated protein like 1	chr14q32	204796_at	NM_001008707 /// NM_004434																				
3.43	3.16	0.27	2.43E-01	6.17E-01	---	---	---	240368_at	---																				
3.37	3.18	0.20	2.43E-01	6.17E-01	LOC644165 /// LOC728216	similar to breakpoint cluster region /// hypothetical LOC728216	chr22q11.21 /// chr22q11.23	1553592_x_at	XM_001128283 /// XM_001721519 /// XM_933701																				
5.68	5.25	0.42	2.43E-01	6.17E-01	C6orf211	chromosome 6 open reading frame 211	chr6q25.1	218195_at	NM_024573																				
3.50	3.34	0.16	2.43E-01	6.17E-01	---	---	---	234388_at	---																				
6.17	5.88	0.29	2.43E-01	6.17E-01	TLR2	toll-like receptor 2	chr4q32	204924_at	NM_003264																				
2.52	2.32	0.20	2.43E-01	6.17E-01	---	---	---	1565740_at	---																				
6.21	5.89	0.31	2.43E-01	6.17E-01	ZYX	zyxin	chr7q32	200808_s_at	NM_001010972 /// NM_003461																				
2.86	2.61	0.26	2.43E-01	6.17E-01	BPI	bactericidal/permeability-increasing protein	chr20q11.23-q12	205557_at	NM_001725																				
6.85	6.56	0.29	2.43E-01	6.17E-01	HP1BP3	heterochromatin protein 1, binding protein 3	chr1p36.12	220633_s_at	NM_016287																				
7.60	7.38	0.21	2.43E-01	6.17E-01	PIGT	phosphatidylinositol glycan anchor biosynthesis, class T	chr20q12-q13.12	217770_at	NM_015937																				
2.16	2.00	0.16	2.43E-01	6.17E-01	PMP2	peripheral myelin protein 2	chr8q21.3-q22.1	235127_at	NM_002677																				
2.42	2.16	0.26	2.43E-01	6.17E-01	MFAP5	microfibrillar associated protein 5	chr12p13.1-p12.3	213764_s_at	NM_003480																				
6.06	5.61	0.45	2.43E-01	6.17E-01	RNASEH2C	ribonuclease H2, subunit C	chr11q13.1	227543_at	NM_032193																				
7.06	6.80	0.25	2.43E-01	6.17E-01	KAT5	K(lysine) acetyltransferase 5	chr11q13	214258_x_at	NM_006388 /// NM_182709 /// NM_182710																				
2.83	2.63	0.20	2.43E-01	6.17E-01	---	---	---	231670_at	---																				
3.49	3.28	0.21	2.43E-01	6.17E-01	SFT2D3	SFT2 domain containing 3	chr2q14.3	229023_at	NM_032740																				
3.37	3.14	0.24	2.43E-01	6.17E-01	---	---	---	1566502_at	---																				
3.31	3.05	0.26	2.43E-01	6.17E-01	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	chr20q13.13	215927_at	NM_006420																				
10.46	10.33	0.13	2.43E-01	6.17E-01	EIF1	eukaryotic translation initiation factor 1	chr17q21.2	202021_x_at	NM_005801																				
3.69	3.31	0.38	2.44E-01	6.18E-01	GLCCI1	glucocorticoid induced transcript 1	chr7p21.3	225706_at	NM_138426																				
7.40	6.98	0.42	2.44E-01	6.18E-01	IVD	isovaleryl Coenzyme A dehydrogenase	chr15q14-q15	225311_at	NM_002225																				
4.46	4.00	0.46	2.44E-01	6.18E-01	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	chr1p31	203708_at	NM_001037339 /// NM_001037340 /// NM_001037341 /// NM_002600																				
5.17	4.93	0.24	2.44E-01	6.18E-01	RBM15	RNA binding motif protein 15	chr1p13	1555761_x_at	NM_022768																				
2.18	2.07	0.12	2.44E-01	6.18E-01	TRIM26	Tripartite motif-containing 26	chr6p21.3	242618_at	NM_003449																				
2.40	2.24	0.16	2.44E-01	6.18E-01	DCDC2	doublecortin domain containing 2	chr6p22.1	222925_at	NM_016356																				
4.92	4.57	0.35	2.44E-01	6.18E-01	RPUSD2	RNA pseudouridylate synthase domain containing 2	chr15q13.3	221940_at	NM_152260																				
10.22	9.97	0.25	2.44E-01	6.18E-01	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	chr6q12	201597_at	NM_001865																				

2.33	2.16	0.17	2.44E-01	6.18E-01	GIGYF2	GRB10 interacting GYF protein 2	chr2q37.1	1558305_at	NM_001103146 /// NM_001103147 /// NM_001103148 /// NM_015575																			
6.83	6.49	0.34	2.44E-01	6.18E-01	C17orf76	chromosome 17 open reading frame 76	chr17p11.2	229889_at	NM_001113567 /// NM_207387																			
3.88	3.39	0.49	2.44E-01	6.18E-01	CXorf57	chromosome X open reading frame 57	chrXq22.3	219355_at	NM_018015																			
3.55	3.40	0.15	2.44E-01	6.18E-01	---	---	---	214232_at	---																			
4.44	4.18	0.27	2.44E-01	6.18E-01	GMIP	GEM interacting protein	chr19p12-p11	218913_s_at	NM_016573																			
7.85	7.59	0.26	2.44E-01	6.18E-01	FLJ21865	endo-beta-N-acetylglucosaminidase	chr17q25.3	65635_at	NM_001042573																			
4.46	4.15	0.31	2.44E-01	6.18E-01	ZNF248	zinc finger protein 248	---	213269_at	NM_021045																			
3.21	3.03	0.18	2.44E-01	6.19E-01	C10orf18	chromosome 10 open reading frame 18	chr10p15.1	238795_at	NM_017782																			
6.85	6.65	0.20	2.44E-01	6.19E-01	PIGS	phosphatidylinositol glycan anchor biosynthesis, class S	chr17p13.2	223148_at	NM_033198																			
5.10	4.87	0.23	2.45E-01	6.19E-01	TAGAP	T-cell activation RhoGTPase activating protein	chr6q25.3	1552541_at	NM_054114 /// NM_138810 /// NM_152133																			
4.08	3.80	0.28	2.45E-01	6.19E-01	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	chr17q25	202855_s_at	NM_001042422 /// NM_001042423 /// NM_004207																			
2.22	2.09	0.13	2.45E-01	6.19E-01	LRRC59	leucine rich repeat containing 59	chr17q21.33	234812_at	NM_018509																			
3.18	2.82	0.36	2.45E-01	6.19E-01	ETNK1	ethanolamine kinase 1	chr12p12.1	224453_s_at	NM_001039481 /// NM_018638																			
2.59	2.42	0.17	2.45E-01	6.19E-01	LOC100131053	hypothetical LOC100131053	chr1p36.13	239546_at	XM_001720101 /// XM_001722035 /// XM_001722493																			
2.51	2.28	0.24	2.45E-01	6.19E-01	---	---	---	224172_at	---																			
8.58	8.43	0.15	2.45E-01	6.19E-01	CTBP2	C-terminal binding protein 2	chr10q26.13	201220_x_at	NM_001083914 /// NM_001329 /// NM_022802																			
5.79	5.34	0.45	2.45E-01	6.19E-01	NAT14	N-acetyltransferase 14	chr19q13.42	223284_at	NM_020378																			
3.44	3.20	0.24	2.45E-01	6.19E-01	C5orf24	chromosome 5 open reading frame 24	chr5q31.1	1553107_s_at	NM_152409																			
2.47	2.32	0.15	2.45E-01	6.19E-01	FLJ32063	hypothetical protein LOC150538	chr2q33.1	1560010_a_at	XR_041743 /// XR_041744 /// XR_041745																			
9.75	9.54	0.21	2.45E-01	6.19E-01	---	---	---	227432_s_at	---																			
2.67	2.48	0.18	2.45E-01	6.19E-01	---	---	---	240843_at	---																			
3.74	3.54	0.20	2.45E-01	6.19E-01	RFFL	ring finger and FYVE-like domain containing 1	chr17q12	1566171_at	NM_001017368 /// NM_057178																			
2.68	2.43	0.24	2.45E-01	6.19E-01	---	---	---	240466_at	---																			
2.67	2.40	0.27	2.45E-01	6.19E-01	---	---	---	231979_at	---																			
3.13	2.90	0.23	2.45E-01	6.19E-01	FLT4	fms-related tyrosine kinase 4	chr5q35.3	210316_at	NM_002020 /// NM_182925																			
3.80	3.56	0.25	2.45E-01	6.19E-01	PVR	poliovirus receptor	chr19q13.2	216283_s_at	NM_006505																			
9.29	9.05	0.24	2.45E-01	6.19E-01	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	chr17q21.3	200759_x_at	NM_003204																			
6.40	5.97	0.43	2.45E-01	6.19E-01	C14orf169	chromosome 14 open reading frame 169	chr14q24.3	219526_at	NM_024644																			
5.84	5.49	0.36	2.45E-01	6.19E-01	FERMT1	fermitin family homolog 1 (Drosophila)	chr20p12.3	229545_at	NM_017671																			
2.82	2.67	0.15	2.45E-01	6.20E-01	GLOD5	glyoxalase domain containing 5	chrXp11.23	231052_at	NM_001080489																			
3.75	3.52	0.23	2.46E-01	6.20E-01	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	chr16q22.3	220446_s_at	NM_005769																			
8.02	7.71	0.31	2.46E-01	6.20E-01	C17orf89	chromosome 17 open reading frame 89	chr17q25.3	225967_s_at	NM_001086521																			
3.88	3.61	0.27	2.46E-01	6.20E-01	C3orf38	chromosome 3 open reading frame 38	chr3p11.2	1569129_s_at	NM_173824																			

2.22	2.08	0.14	2.46E-01	6.20E-01	DIO1	deiodinase, iodothyronine, type I	chr1p33-p32	206457_s_at	NM_000792 /// NM_001039715 /// NM_001039716 /// NM_213593																				
3.04	2.85	0.19	2.46E-01	6.20E-01	ONECUT3	one cut homeobox 3	chr19p13.3	234109_x_at	NM_001080488																				
8.67	8.40	0.26	2.46E-01	6.20E-01	ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	chr2q33.1	223266_at	NM_018571																				
7.43	7.22	0.21	2.46E-01	6.20E-01	MAPKAP1	mitogen-activated protein kinase associated protein 1	chr9q33.3	217808_s_at	NM_001006617 /// NM_001006618 /// NM_001006619 /// NM_001006620 /// NM_001006621 /// NM_024117																				
2.60	2.34	0.26	2.46E-01	6.20E-01	TBRG1	transforming growth factor beta regulator 1	chr11q24.2	230681_at	NM_032811 /// NR_016021																				
5.10	4.86	0.24	2.46E-01	6.20E-01	MED16	mediator complex subunit 16	chr19p13.3	221418_s_at	NM_005481																				
5.92	5.57	0.35	2.46E-01	6.20E-01	CNNM3	cyclin M3	chr2p12-p11.2	220739_s_at	NM_017623 /// NM_199078																				
3.20	3.02	0.17	2.46E-01	6.20E-01	LOC283932	hypothetical LOC283932	chr16p11.2	1553586_at	XR_040474 /// XR_040475 /// XR_040476																				
3.10	2.96	0.14	2.46E-01	6.20E-01	EVX1	even-skipped homeobox 1	chr7p15-p14	231706_s_at	NM_001989																				
4.57	4.33	0.24	2.46E-01	6.20E-01	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	chr14q23.3	212823_s_at	NM_015549																				
2.74	2.46	0.28	2.46E-01	6.20E-01	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	chr2q31	205278_at	NM_000817 /// NM_013445																				
6.28	6.03	0.25	2.46E-01	6.20E-01	COMT	catechol-O-methyltransferase	chr22q11.21-q11.23|22q11.21	213981_at	NM_000754 /// NM_007310																				
4.88	4.63	0.26	2.46E-01	6.20E-01	SFRS11	splicing factor, arginine/serine-rich 11	chr1p31	213742_at	NM_004768																				
2.55	2.36	0.19	2.46E-01	6.20E-01	LOC221710	hypothetical protein LOC221710	chr6p24.1	235707_at	XM_001720414 /// XM_001724989 /// XM_001725361																				
3.81	3.52	0.29	2.46E-01	6.20E-01	TSEN2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	chr3p25.1	219581_at	NM_025265																				
2.42	2.14	0.28	2.47E-01	6.21E-01	---	---	---	232997_at	---																				
6.17	5.84	0.33	2.47E-01	6.21E-01	---	---	---	1556507_at	---																				
7.91	7.78	0.13	2.47E-01	6.21E-01	C20orf43	chromosome 20 open reading frame 43	chr20q13.31	234926_s_at	NM_016407																				
3.96	3.75	0.21	2.47E-01	6.21E-01	COX5A	cytochrome c oxidase subunit Va	chr15q24.1	229426_at	NM_004255																				
2.87	2.71	0.16	2.47E-01	6.21E-01	---	---	---	227943_at	---																				
2.91	2.74	0.17	2.47E-01	6.21E-01	LOC145945	hypothetical protein LOC145945	chr15q26.2	232577_at	---																				
6.95	6.73	0.22	2.47E-01	6.21E-01	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	chr14q24.3	204290_s_at	NM_005589																				
6.38	6.10	0.29	2.47E-01	6.21E-01	OTUD7B	OTU domain containing 7B	chr1q21.2	227436_at	NM_020205																				
2.24	2.09	0.15	2.47E-01	6.21E-01	COX7B2	cytochrome c oxidase subunit VIIb2	chr4p12	231265_at	NM_130902																				
2.54	2.35	0.19	2.47E-01	6.21E-01	---	---	---	1569419_at	---																				
10.99	10.73	0.26	2.47E-01	6.21E-01	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	chr2q33.3	201193_at	NM_005896																				
2.33	2.18	0.14	2.47E-01	6.21E-01	---	---	---	233205_at	---																				
6.31	5.89	0.42	2.47E-01	6.21E-01	RAB28	RAB28, member RAS oncogene family	chr4p15.33	227003_at	NM_001017979 /// NM_004249																				
5.30	4.99	0.32	2.47E-01	6.21E-01	CHFR	checkpoint with forkhead and ring finger domains	chr12q24.33	223931_s_at	NM_018223																				
2.91	2.66	0.26	2.47E-01	6.21E-01	TEAD2	TEA domain family member 2	chr19q13.3	238323_at	NM_003598																				
3.44	3.19	0.25	2.47E-01	6.21E-01	LOC100132815	Hypothetical protein LOC100132815	chr19p12	227234_at	XM_001720961 /// XM_001726067 /// XM_001726889																				
2.51	2.34	0.17	2.47E-01	6.21E-01	---	---	---	1561310_at	---																				
4.00	3.59	0.41	2.47E-01	6.21E-01	TXNDC16	thioredoxin domain containing 16	chr14q22.1	226747_at	NM_020784																				

10.78	10.60	0.18	2.47E-01	6.21E-01	C4orf46 /// TOMM7	chromosome 4 open reading frame 46 /// translocase of outer mitochondrial membrane 7 homolog (yeast)	chr4q32.1 /// chr7p15.3	201812_s_at	NM_001008393 /// NM_019059																					
2.34	2.18	0.16	2.47E-01	6.21E-01	C17orf99	chromosome 17 open reading frame 99	---	236981_at	---																					
12.52	12.38	0.14	2.47E-01	6.21E-01	RPS15	ribosomal protein S15	chr19p13.3	200819_s_at	NM_001018																					
5.28	5.01	0.27	2.48E-01	6.21E-01	ZNF346	zinc finger protein 346	chr5q35.2	222884_at	NM_012279																					
2.64	2.45	0.20	2.48E-01	6.21E-01	---	---	---	232781_at	---																					
8.10	7.82	0.27	2.48E-01	6.21E-01	KIAA0664	KIAA0664	chr17p13.3	212456_at	NM_015229																					
4.23	3.89	0.34	2.48E-01	6.22E-01	LOC283070	hypothetical protein LOC283070	chr10p14	226382_at	---																					
2.32	2.14	0.18	2.48E-01	6.22E-01	---	---	---	1555204_at	---																					
5.65	5.40	0.26	2.48E-01	6.22E-01	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr1q25	218578_at	NM_024529																					
3.00	2.72	0.28	2.48E-01	6.22E-01	NUDT13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	chr10q22.1	214136_at	NM_015901																					
3.39	3.02	0.36	2.48E-01	6.22E-01	ZNF217	zinc finger protein 217	chr20q13.2	203739_at	NM_006526																					
3.27	3.06	0.21	2.48E-01	6.22E-01	---	---	---	236658_at	---																					
2.74	2.45	0.29	2.48E-01	6.22E-01	GPR84	G protein-coupled receptor 84	chr12q13.13	223767_at	NM_020370																					
3.56	3.32	0.24	2.48E-01	6.22E-01	ADAMTSL1	ADAMTS-like 1	chr9p22.2-p22.1	224371_at	NM_001040272 /// NM_052866																					
2.44	2.30	0.14	2.48E-01	6.22E-01	LOC338817	hypothetical protein LOC338817	chr12p13.2	1557826_at	---																					
3.82	3.43	0.39	2.48E-01	6.22E-01	---	---	---	235150_at	---																					
3.47	3.26	0.20	2.48E-01	6.22E-01	UBE2CBP	ubiquitin-conjugating enzyme E2C binding protein	chr6q14.1	227790_at	NM_198920																					
3.51	3.31	0.20	2.48E-01	6.22E-01	---	---	---	1559110_at	---																					
3.93	3.65	0.27	2.48E-01	6.22E-01	---	---	---	240094_at	---																					
3.32	3.05	0.28	2.48E-01	6.22E-01	CRYGS	crystallin, gamma S	chr3q25-qter	223644_s_at	NM_017541																					
3.65	3.45	0.21	2.48E-01	6.22E-01	YIPF4	Yip1 domain family, member 4	chr2p22.3	209551_at	NM_032312																					
2.65	2.46	0.18	2.48E-01	6.22E-01	NOX5	NADPH oxidase, EF-hand calcium binding domain 5	chr15q23	1553023_a_at	NM_024505																					
3.21	2.95	0.27	2.48E-01	6.22E-01	LOC284542	hypothetical protein LOC284542	chr1p33	230920_at	---																					
5.77	5.53	0.24	2.48E-01	6.22E-01	ZNF710	zinc finger protein 710	chr15q26.1	213542_at	NM_198526																					
2.49	2.35	0.14	2.49E-01	6.22E-01	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	chr2p21	243650_at	NM_172069																					
5.89	5.62	0.27	2.49E-01	6.22E-01	MMP11	matrix metallopeptidase 11 (stromelysin 3)	chr22q11.2|22q11.23	203878_s_at	NM_005940																					
4.62	4.43	0.20	2.49E-01	6.23E-01	TUBGCP2	Tubulin, gamma complex associated protein 2	chr10q26.3	213563_s_at	NM_006659																					
2.77	2.56	0.21	2.49E-01	6.23E-01	CTTNBP2	cortactin binding protein 2	chr7q31	232136_s_at	NM_033427																					
1.98	1.86	0.12	2.49E-01	6.23E-01	---	---	---	1569819_at	---																					
2.88	2.69	0.19	2.49E-01	6.23E-01	---	---	---	232223_at	---																					
6.21	5.92	0.29	2.49E-01	6.23E-01	FAM116A	family with sequence similarity 116, member A	chr3p14.3	226965_at	NM_152678																					
3.81	3.53	0.28	2.49E-01	6.23E-01	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	chr8p23	219340_s_at	NM_018941																					
5.28	5.11	0.18	2.49E-01	6.23E-01	FBXO42	F-box protein 42	chr1p36.23-p36.11	221812_at	NM_018994																					
4.57	4.26	0.31	2.49E-01	6.23E-01	WIPF1	WAS/WASL interacting protein family, member 1	chr2q31.1	202665_s_at	NM_001077269 /// NM_003387																					
3.31	3.08	0.22	2.49E-01	6.23E-01	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	chr18q22.1	207037_at	NM_003839																					
4.69	4.48	0.21	2.49E-01	6.23E-01	LOC388906	hypothetical gene supported by BC039496	chr22q13.2	1561537_at	XM_001716802 /// XM_001718421 /// XM_001719590																					
3.63	3.46	0.17	2.49E-01	6.23E-01	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	chr11q25	220677_s_at	NM_007037																					
4.36	4.07	0.29	2.49E-01	6.23E-01	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	chr19p13.3	228689_at	NM_175614																					
2.48	2.31	0.17	2.49E-01	6.23E-01	C4orf47	chromosome 4 open reading frame 47	chr4q35.1	236915_at	NM_001114357 /// XM_001720135 /// XM_001723753 /// XM_001723780																					
2.98	2.48	0.50	2.49E-01	6.23E-01	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	chr4p16.3	209569_x_at	NM_001040101 /// NM_014392																					
2.70	2.54	0.17	2.49E-01	6.23E-01	PDAP1	PDGFA associated protein 1	chr7q22.1	217624_at	NM_014891																					
3.51	3.31	0.20	2.49E-01	6.23E-01	CCDC125	coiled-coil domain containing 125	chr5q13.2	229082_at	NM_176816																					
4.92	4.48	0.44	2.49E-01	6.23E-01	---	---	---	242859_at	---																					
6.25	5.85	0.39	2.49E-01	6.23E-01	EVL	Enah/Vasp-like	chr14q32.2	217838_s_at	NM_016337																					
4.18	3.69	0.49	2.50E-01	6.23E-01	PTN	pleiotrophin	chr7q33-q34	211737_x_at	NM_002825																					
2.20	2.05	0.14	2.50E-01	6.23E-01	---	---	---	1569812_at	---																					

6.57	6.21	0.36	2.50E-01	6.23E-01	MYO7A	myosin VIIA	chr11q13.5	33197_at	NM_000260 /// NM_001127179 /// NM_001127180																				
5.60	5.11	0.48	2.50E-01	6.23E-01	C2orf56	chromosome 2 open reading frame 56	chr2p22.2	223560_s_at	NM_001083946 /// NM_144736																				
2.18	2.04	0.14	2.50E-01	6.23E-01	---	---	---	1560957_at	---																				
5.56	5.10	0.46	2.50E-01	6.23E-01	CPLX3 /// LMAN1L	complexin 3 /// lectin, mannose-binding, 1 like	chr15q24.1	219775_s_at	NM_001030005 /// NM_021819																				
2.08	1.95	0.14	2.50E-01	6.23E-01	---	---	---	240472_at	---																				
2.47	2.31	0.16	2.50E-01	6.23E-01	ALG10B	asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	chr12q12	238475_at	NM_001013620																				
6.88	6.58	0.30	2.50E-01	6.23E-01	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	chr19q13.2	209675_s_at	NM_007040 /// NM_144732																				
2.25	2.03	0.22	2.50E-01	6.23E-01	SIP1	survival of motor neuron protein interacting protein 1	chr14q13	205063_at	NM_001009182 /// NM_001009183 /// NM_003616																				
6.33	6.07	0.26	2.50E-01	6.23E-01	TRIM69	tripartite motif-containing 69	chr15q21.1	1568592_at	NM_080745 /// NM_182985																				
3.49	3.33	0.15	2.50E-01	6.23E-01	MZF1	myeloid zinc finger 1	chr19q13.2|19q13.2-q13.4	204138_s_at	NM_003422 /// NM_198055																				
3.06	2.89	0.17	2.50E-01	6.23E-01	TMC2	transmembrane channel-like 2	chr20p13	1553019_at	NM_080751																				
1.94	1.81	0.14	2.50E-01	6.23E-01	ABCA13	ATP-binding cassette, sub-family A (ABC1), member 13	chr7p12.3	1553605_a_at	NM_152701																				
7.04	6.78	0.27	2.50E-01	6.24E-01	AMBRA1	autophagy/beclin-1 regulator 1	chr11p11.2	219141_s_at	NM_017749																				
2.37	2.22	0.15	2.50E-01	6.24E-01	LOC339260	hypothetical protein LOC339260	chr17p11.2	1562754_at	---																				
2.56	2.36	0.20	2.50E-01	6.24E-01	LOC400960	hypothetical gene supported by BC040598	chr2p14	235137_at	XM_934552 /// XM_945536																				
6.70	6.32	0.38	2.50E-01	6.24E-01	PGP	phosphoglycolate phosphatase	chr16p13.3	222622_at	NM_001042371																				
2.28	2.13	0.15	2.50E-01	6.24E-01	LIN54	lin-54 homolog (C. elegans)	chr4q21.22	235809_at	NM_001115007 /// NM_001115008 /// NM_194282																				
2.35	2.08	0.27	2.50E-01	6.24E-01	ZNF493	zinc finger protein 493	chr19p12	211064_at	NM_001076678 /// NM_175910																				
3.62	3.46	0.16	2.50E-01	6.24E-01	PLA2G2E	phospholipase A2, group IIE	chr1p36.13	221389_at	NM_014589																				
2.79	2.61	0.18	2.50E-01	6.24E-01	---	---	---	1560955_at	---																				
8.35	8.18	0.16	2.50E-01	6.24E-01	PHB	prohibitin	chr17q21	200658_s_at	NM_002634																				
3.65	3.30	0.35	2.51E-01	6.24E-01	LACTB	lactamase, beta	chr15q22.1	1552485_at	NM_032857 /// NM_171846																				
2.82	2.63	0.18	2.51E-01	6.24E-01	RCAN1	Regulator of calcineurin 1	chr21q22.1-q22.2|21q22.12	215254_at	NM_004414 /// NM_203417 /// NM_203418																				
2.68	2.42	0.26	2.51E-01	6.24E-01	C8orf5	chromosome 8 open reading frame 5	chr8p23.1	236047_at	---																				
3.69	3.47	0.22	2.51E-01	6.24E-01	SPIRE2	spire homolog 2 (Drosophila)	chr16q24	243594_x_at	NM_032451																				
2.63	2.43	0.20	2.51E-01	6.24E-01	SLC35F2	solute carrier family 35, member F2	chr11q22.3	218826_at	NM_017515																				
4.80	4.14	0.65	2.51E-01	6.25E-01	TMEM108	transmembrane protein 108	chr3q21	223523_at	NM_023943																				
6.53	6.23	0.30	2.51E-01	6.25E-01	CYP4V2	cytochrome P450, family 4, subfamily V, polypeptide 2	chr4q35.2	226745_at	NM_207352																				
11.99	11.84	0.14	2.51E-01	6.25E-01	PPIA	peptidylprolyl isomerase A (cyclophilin A)	chr7p13	201293_x_at	NM_021130																				

6.32	5.91	0.41	2.51E-01	6.25E-01	PCBP2	poly(rC) binding protein 2	chr12q13.12-q13.13	213517_at	NM_001098620 /// NM_001128911 /// NM_001128912 /// NM_001128913 /// NM_001128914 /// NM_005016 /// NM_031989
2.38	2.18	0.20	2.51E-01	6.25E-01	---	---	---	238314_x_at	---
7.90	7.57	0.34	2.51E-01	6.25E-01	SEPW1	selenoprotein W, 1	chr19q13.3	201194_at	NM_003009
4.73	4.20	0.53	2.51E-01	6.25E-01	RNF157	ring finger protein 157	chr17q25.1	226433_at	NM_052916
2.74	2.57	0.17	2.51E-01	6.25E-01	STK4	serine/threonine kinase 4	chr20q11.2-q13.2	205411_at	NM_006282
9.30	8.91	0.39	2.51E-01	6.25E-01	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	chr3q23	208836_at	NM_001679
3.88	3.71	0.17	2.51E-01	6.25E-01	WNK2	WNK lysine deficient protein kinase 2	chr9q22.3	1557536_at	NM_006648
2.44	2.28	0.17	2.51E-01	6.25E-01	TMEM106B	transmembrane protein 106B	chr7p21.3	233666_at	NM_001134232 /// NM_018374
2.90	2.75	0.15	2.51E-01	6.25E-01	---	---	---	239255_at	---
3.29	3.01	0.28	2.51E-01	6.25E-01	---	---	---	229366_at	---
3.16	2.82	0.34	2.51E-01	6.25E-01	ZNF167	zinc finger protein 167	chr3p22.3-p21.1	206314_at	NM_018651 /// NM_025169
6.41	5.92	0.49	2.51E-01	6.25E-01	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	chr10q22.1	209834_at	NM_004273
5.05	4.82	0.23	2.51E-01	6.25E-01	---	---	---	43511_s_at	---
4.28	4.09	0.19	2.52E-01	6.26E-01	FMO4	flavin containing monooxygenase 4	chr1q23-q25	206263_at	NM_002022
2.41	2.27	0.15	2.52E-01	6.26E-01	MMP16	matrix metallopeptidase 16 (membrane-inserted)	chr8q21	208166_at	NM_005941 /// NM_022564
4.53	4.29	0.24	2.52E-01	6.26E-01	---	---	---	1559452_a_at	---
10.78	10.61	0.17	2.52E-01	6.26E-01	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	chr14q32.1	209443_at	NM_000624
2.34	2.15	0.20	2.52E-01	6.26E-01	NLRP10	NLR family, pyrin domain containing 10	chr11p15.4	1553534_at	NM_176821
8.96	8.24	0.72	2.52E-01	6.26E-01	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	chr19q13.1	201531_at	NM_003407
2.60	2.43	0.17	2.52E-01	6.26E-01	ENDOGL1	endonuclease G-like 1	chr3p21.3	206902_s_at	NM_005107
7.80	7.62	0.18	2.52E-01	6.26E-01	CDC123	cell division cycle 123 homolog (S. cerevisiae)	chr10p13	201725_at	NM_006023
7.27	7.09	0.18	2.52E-01	6.26E-01	BAG1	BCL2-associated athanogene	chr9p12	202387_at	NM_004323
7.46	7.18	0.28	2.52E-01	6.26E-01	ILF3	interleukin enhancer binding factor 3, 90kDa	chr19p13.2	217804_s_at	NM_004516 /// NM_012218 /// NM_153464
6.56	6.22	0.34	2.52E-01	6.26E-01	BRF2	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	chr8p12	218955_at	NM_018310
2.94	2.75	0.18	2.52E-01	6.26E-01	DKFZp451B082	hypothetical gene supported by AL831931	chr6q26	1563511_at	---
6.60	6.19	0.41	2.52E-01	6.27E-01	TUBG1	tubulin, gamma 1	chr17q21	201714_at	NM_001070
3.48	3.20	0.28	2.52E-01	6.27E-01	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	chr17q25	1569268_at	NM_000835
2.53	2.39	0.14	2.53E-01	6.27E-01	LOC344405	hypothetical LOC344405	chr2p16.1	237291_at	XR_042020 /// XR_042021 /// XR_042022
7.35	7.02	0.33	2.53E-01	6.27E-01	PHF3	PHD finger protein 3	chr6q12	217954_s_at	NM_015153
7.99	7.72	0.27	2.53E-01	6.27E-01	CCNDBP1	cyclin D-type binding-protein 1	chr15q14-q15	223084_s_at	NM_012142 /// NM_037370
2.24	2.09	0.16	2.53E-01	6.27E-01	VWA1	Von Willebrand factor A domain containing 1	chr1p36.33	225983_s_at	NM_022834 /// NM_199121
7.77	7.10	0.68	2.53E-01	6.27E-01	DAAM2	dishevelled associated activator of morphogenesis 2	chr6p21.2	212793_at	NM_015345
5.91	5.68	0.23	2.53E-01	6.27E-01	SPATA2L	spermatogenesis associated 2-like	chr16q24.3	214965_at	NM_152339
1.93	1.78	0.15	2.53E-01	6.27E-01	PDZK1P1	PDZ domain containing 1 pseudogene 1	chr1q21.1	240634_x_at	NR_003377
5.82	5.57	0.25	2.53E-01	6.27E-01	MSRB3	methionine sulfoxide reductase B3	chr12q14.3	1554126_at	NM_001031679 /// NM_198080
4.17	3.86	0.31	2.53E-01	6.27E-01	LASS4	LAG1 homolog, ceramide synthase 4	chr19p13.2	218922_s_at	NM_024552
2.74	2.54	0.20	2.53E-01	6.27E-01	LOC133874	hypothetical gene LOC133874	chr5q35.1	1554115_at	NM_001102609
6.90	6.35	0.56	2.53E-01	6.27E-01	JMJD2B	jumonji domain containing 2B	chr19p13.3	212492_s_at	NM_015015
3.78	3.59	0.19	2.53E-01	6.27E-01	FAM43A	family with sequence similarity 43, member A	chr3q29	1558174_at	NM_153690
5.58	5.12	0.46	2.53E-01	6.27E-01	---	---	---	240307_at	---

12.25	12.09	0.16	2.53E-01	6.27E-01	RPL7A	ribosomal protein L7a	chr9q34	224930_x_at	NM_000972 /// NR_000016 /// NR_000017 /// NR_002447 /// NR_002448																				
2.49	2.29	0.20	2.53E-01	6.27E-01	FNBP4	formin binding protein 4	chr11p11.2	235101_at	NM_015308																				
8.06	7.83	0.22	2.53E-01	6.27E-01	ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	chr16p13.3	200954_at	NM_001694																				
4.15	3.88	0.27	2.53E-01	6.27E-01	PLCXD1	phosphatidylinositol-specific phospholipase C, X domain containing 1	chrXp22.33; Yp11.32	218951_s_at	NM_018390																				
3.95	3.64	0.31	2.53E-01	6.27E-01	ZNF638	zinc finger protein 638	chr2p13.2-p13.1	1554248_at	NM_001014972 /// NM_014497																				
2.57	2.34	0.23	2.53E-01	6.27E-01	ZNF503	zinc finger protein 503	chr10q22.2	232178_at	NM_032772																				
4.29	4.14	0.15	2.53E-01	6.27E-01	ADCY9	adenylate cyclase 9	chr16p13.3	204498_s_at	NM_001116																				
6.36	6.03	0.33	2.53E-01	6.27E-01	FLYWCH1	FLYWCH-type zinc finger 1	chr16p13.3	223950_s_at	NM_020912 /// NM_032296																				
6.46	6.09	0.36	2.53E-01	6.27E-01	ST8SIA5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	chr18q21.1	206258_at	NM_013305																				
3.92	3.62	0.30	2.53E-01	6.27E-01	WHSC1	Wolf-Hirschhorn syndrome candidate 1	chr4p16.3	223472_at	NM_001042424 /// NM_007331 /// NM_133330 /// NM_133331 /// NM_133334 /// NM_133335																				
11.50	10.70	0.80	2.53E-01	6.27E-01	HBB	hemoglobin, beta	chr11p15.5	211696_x_at	NM_000518																				
2.87	2.42	0.45	2.54E-01	6.27E-01	WSB1	WD repeat and SOCS box-containing 1	chr17q11.1	201295_s_at	NM_015626 /// NM_134265																				
3.50	3.24	0.26	2.54E-01	6.28E-01	CCDC99	coiled-coil domain containing 99	chr5q35.1	221685_s_at	NM_017785																				
2.84	2.62	0.22	2.54E-01	6.28E-01	C1orf128	chromosome 1 open reading frame 128	chr1p36.11	223123_s_at	NM_020362																				
8.16	7.87	0.29	2.54E-01	6.28E-01	NIT1	nitrilase 1	chr1q21-q22	202891_at	NM_005600																				
3.46	3.28	0.18	2.54E-01	6.28E-01	ATAD2	ATPase family, AAA domain containing 2	chr8q24.13	228401_at	NM_014109																				
3.56	3.42	0.14	2.54E-01	6.28E-01	CALCA	calcitonin-related polypeptide alpha	chr11p15.2-p15.1	210727_at	NM_001033952 /// NM_001033953 /// NM_001741																				
4.76	4.32	0.44	2.54E-01	6.28E-01	KCTD11	potassium channel tetramerisation domain containing 11	chr17p13.1	235857_at	NM_001002914																				
2.82	2.62	0.20	2.54E-01	6.28E-01	---	---	---	233900_at	---																				
3.21	3.03	0.18	2.54E-01	6.28E-01	---	---	---	217391_x_at	---																				
2.10	1.97	0.13	2.54E-01	6.28E-01	---	---	---	1568898_at	---																				
7.60	7.11	0.49	2.54E-01	6.28E-01	SFRS1	splicing factor, arginine/serine-rich 1	chr17q21.3-q22	201742_x_at	NM_001078166 /// NM_006924																				
3.13	2.96	0.17	2.54E-01	6.28E-01	CCDC57	coiled-coil domain containing 57	chr17q25.3	1554554_at	NM_198082																				
9.58	9.33	0.25	2.54E-01	6.28E-01	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	chr7q32	201527_at	NM_004231																				
5.80	5.39	0.41	2.54E-01	6.28E-01	UBE3B	ubiquitin protein ligase E3B	chr12q24.11	213822_s_at	NM_130466 /// NM_183415																				
2.39	2.21	0.18	2.54E-01	6.28E-01	KRT7	keratin 7	chr12q12-q13	1558394_s_at	NM_005556																				
4.29	3.85	0.44	2.54E-01	6.28E-01	EAF2	ELL associated factor 2	chr3q13.33	219551_at	NM_018456																				
2.80	2.01	0.79	2.55E-01	6.28E-01	SELE	selectin E	chr1q22-q25	206211_at	NM_000450																				
9.47	9.16	0.31	2.55E-01	6.28E-01	SFRS3	splicing factor, arginine/serine-rich 3	chr6p21	208672_s_at	NM_003017																				
3.24	3.08	0.16	2.55E-01	6.29E-01	FLJ36116	hypothetical locus LOC388666	chr1p13.2	1564413_at	XR_017774 /// XR_017904																				
7.33	6.87	0.46	2.55E-01	6.29E-01	PLCL2	phospholipase C-like 2	chr3p24.3	213309_at	NM_015184																				
3.53	3.02	0.50	2.55E-01	6.29E-01	LOC389834	hypothetical LOC389834	---	244631_at	NM_001013655 /// XM_001726968																				

9.81	9.22	0.58	2.55E-01	6.29E-01	ABLIM1	actin binding LIM protein 1	chr10q25	200965_s_at	NM_001003407 /// NM_001003408 /// NM_002313 /// NM_006720																				
2.34	2.19	0.15	2.55E-01	6.29E-01	VN1R4	vomeronasal 1 receptor 4	chr19q13.41	1553560_at	NM_173857																				
3.72	3.23	0.48	2.55E-01	6.29E-01	BDH2	3-hydroxybutyrate dehydrogenase, type 2	chr4q24	235155_at	NM_020139																				
3.04	2.84	0.21	2.55E-01	6.29E-01	TRIM65	Tripartite motif-containing 65	chr17q25.1	239374_at	NM_173547																				
11.71	11.52	0.19	2.55E-01	6.29E-01	RPL36A	ribosomal protein L36a	chrXq22.1	201406_at	NM_021029																				
4.86	4.28	0.58	2.55E-01	6.29E-01	POMZP3	POM (POM121 homolog, rat) and ZP3 fusion	chr7q11.23	210910_s_at	NM_012230 /// NM_152992																				
5.82	5.46	0.36	2.55E-01	6.29E-01	---	---	---	242264_at	---																				
6.69	6.49	0.20	2.55E-01	6.29E-01	CKS1B	CDC28 protein kinase regulatory subunit 1B	chr1q21.2	201897_s_at	NM_001826																				
4.33	4.11	0.22	2.55E-01	6.29E-01	SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	chr2pter-p25.1	201836_s_at	NM_014860																				
3.20	2.91	0.30	2.55E-01	6.29E-01	C6orf201	Chromosome 6 open reading frame 201	chr6p25.2	242739_at	NM_001085401																				
1.93	1.78	0.15	2.56E-01	6.30E-01	TXNDC9	thioredoxin domain containing 9	chr2q11.2	1554047_at	NM_005783																				
8.01	7.86	0.16	2.56E-01	6.30E-01	AARS	alanyl-tRNA synthetase	chr16q22	201000_at	NM_001605																				
2.45	2.32	0.14	2.56E-01	6.30E-01	---	---	---	233989_at	---																				
12.19	12.04	0.15	2.56E-01	6.30E-01	PPIA	peptidylprolyl isomerase A (cyclophilin A)	chr7p13	212661_x_at	NM_021130																				
5.92	5.73	0.19	2.56E-01	6.30E-01	TMEM62	transmembrane protein 62	chr15q15.2	218776_s_at	NM_024956																				
2.10	1.97	0.12	2.56E-01	6.30E-01	HYALP1	hyaluronoglucosaminidase pseudogene 1	chr7q31.3	1564777_at	NR_002731																				
2.63	2.44	0.19	2.56E-01	6.30E-01	LOC100133283	Hypothetical protein LOC100133283	chr2q33.2	227631_at	XM_001716973 /// XM_001717429																				
7.78	7.58	0.19	2.56E-01	6.30E-01	HUWE1	HECT, UBA and WWE domain containing 1	chrXp11.22	208598_s_at	NM_031407																				
3.18	2.76	0.42	2.56E-01	6.30E-01	KLHL7	kelch-like 7 (Drosophila)	chr7p15.3	220238_s_at	NM_001031710 /// NM_018846																				
2.47	2.29	0.18	2.56E-01	6.30E-01	FOXF1	forkhead box F1	chr16q24	205935_at	NM_001451																				
2.41	2.17	0.24	2.56E-01	6.30E-01	---	---	---	227499_at	---																				
2.14	1.98	0.16	2.56E-01	6.30E-01	---	---	---	234123_at	---																				
5.69	5.45	0.25	2.56E-01	6.30E-01	JRK	jerky homolog (mouse)	chr8q24.3	37872_at	NM_001077527 /// NM_003724																				
3.80	3.58	0.21	2.56E-01	6.30E-01	ARHGAP9	Rho GTPase activating protein 9	chr12q14	226906_s_at	NM_001080156 /// NM_001080157 /// NM_032496																				
2.99	2.68	0.32	2.56E-01	6.30E-01	ACSBG2	acyl-CoA synthetase bubblegum family member 2	chr19p13.3	221716_s_at	NM_030924																				
8.43	8.25	0.19	2.56E-01	6.30E-01	RAB8A	RAB8A, member RAS oncogene family	chr19p13.1	208819_at	NM_005370																				
7.45	7.20	0.25	2.56E-01	6.30E-01	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	chr1p36.22	200827_at	NM_000302 /// XM_001715762 /// XM_001720424 /// XM_001721275																				
7.07	6.73	0.34	2.56E-01	6.30E-01	PARP10	poly (ADP-ribose) polymerase family, member 10	chr8q24.3	229350_x_at	NM_032789																				
4.40	4.23	0.18	2.56E-01	6.30E-01	---	---	---	1557690_x_at	---																				
2.25	2.11	0.13	2.56E-01	6.30E-01	---	---	---	237105_at	---																				
3.93	3.69	0.25	2.56E-01	6.30E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	226503_at	NM_018151																				
2.59	2.45	0.13	2.57E-01	6.30E-01	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	chr10q24.1-q24.3	216058_s_at	NM_000769																				
6.50	5.88	0.62	2.57E-01	6.30E-01	JOSD3	Josephin domain containing 3	chr11q21	221580_s_at	NM_024116																				
3.91	3.73	0.18	2.57E-01	6.30E-01	---	---	---	235280_at	---																				
3.20	3.00	0.20	2.57E-01	6.31E-01	---	---	---	238425_at	---																				
3.06	2.87	0.18	2.57E-01	6.31E-01	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	chr1q42.13	233029_at	NM_001098623 /// NM_052843																				
7.60	7.23	0.36	2.57E-01	6.31E-01	SON	SON DNA binding protein	chr21q22.1-q22.2|21q22.11	201086_x_at	NM_032195 /// NM_138927																				
7.84	7.58	0.27	2.57E-01	6.31E-01	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	chr20p13	221827_at	NM_006462 /// NM_031229																				

2.56	2.37	0.19	2.57E-01	6.31E-01	KIR2DL2 /// KIR2DL3 /// KIR2DS1 /// KIR2DS2 /// KIR2DS4 /// KIR2DS5	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5	chr19q13.4	211532_x_at	NM_012312 /// NM_012314 /// NM_014219 /// NM_014511 /// NM_014512 /// NM_014513 /// NM_015868 /// XM_001713705																			
3.55	3.11	0.43	2.57E-01	6.31E-01	SCLY	selenocysteine lyase	chr2q37.3	221575_at	NM_016510																				
8.10	7.80	0.30	2.57E-01	6.32E-01	EXOSC4	exosome component 4	chr8q24.3	218695_at	NM_019037																				
3.68	3.43	0.25	2.57E-01	6.32E-01	LOC440895	LIM and senescent cell antigen-like domains 3-like	chr2q13	215247_at	XM_001726941 /// XM_496582																				
2.13	2.01	0.12	2.58E-01	6.32E-01	---	---	---	1560959_a_at	---																				
4.65	4.38	0.27	2.58E-01	6.32E-01	DOCK6	dedicator of cytokinesis 6	chr19p13.2	55583_at	NM_020812																				
2.82	2.65	0.17	2.58E-01	6.32E-01	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	chr4q13	207392_x_at	NM_001076																				
6.42	6.03	0.38	2.58E-01	6.32E-01	ACP6	acid phosphatase 6, lysophosphatidic	chr1q21	218795_at	NM_016361																				
4.53	4.34	0.19	2.58E-01	6.32E-01	C2orf44	chromosome 2 open reading frame 44	chr2p23.3	219120_at	NM_025203																				
8.88	8.61	0.27	2.58E-01	6.32E-01	TUBB	tubulin, beta	chr6p21.33	212320_at	NM_178014																				
3.64	3.44	0.20	2.58E-01	6.32E-01	SNF1LK2	SNF1-like kinase 2	chr11q23.1	1556056_at	NM_015191																				
7.06	6.85	0.22	2.58E-01	6.32E-01	PFDN6	prefoldin subunit 6	chr6p21.3	222029_x_at	NM_014260																				
2.64	2.48	0.16	2.58E-01	6.32E-01	---	---	---	1562764_at	---																				
2.52	2.35	0.17	2.58E-01	6.32E-01	---	---	---	1565866_a_at	---																				
4.35	4.10	0.25	2.58E-01	6.32E-01	KIAA1553	KIAA1553	chr6q21	227920_at	NM_001080450																				
2.71	2.58	0.12	2.58E-01	6.32E-01	FGF8	fibroblast growth factor 8 (androgen-induced)	chr10q24	208449_s_at	NM_006119 /// NM_033163 /// NM_033164 /// NM_033165																				
6.48	6.16	0.32	2.58E-01	6.32E-01	SIDT2	SID1 transmembrane family, member 2	chr11q23.3	218765_at	NM_001040455																				
8.24	7.93	0.31	2.58E-01	6.32E-01	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	chr11q13	202418_at	NM_020470																				
3.66	3.47	0.19	2.58E-01	6.32E-01	TFB2M	transcription factor B2, mitochondrial	chr1q44	1566932_x_at	NM_022366																				
2.26	2.11	0.15	2.58E-01	6.32E-01	---	---	---	1562546_at	---																				
3.96	3.77	0.19	2.58E-01	6.32E-01	C18orf51	chromosome 18 open reading frame 51	chr18q22.3	229645_at	NM_001044369																				
3.82	3.55	0.27	2.58E-01	6.32E-01	---	---	---	229564_at	---																				
4.21	3.85	0.36	2.58E-01	6.32E-01	TRIM6	tripartite motif-containing 6	chr11p15.4	223599_at	NM_001003818 /// NM_058166																				
4.43	4.23	0.20	2.58E-01	6.32E-01	POLRMT	polymerase (RNA) mitochondrial (DNA directed)	chr19p13.3	203783_x_at	NM_005035																				
11.39	11.25	0.14	2.58E-01	6.32E-01	RPS25	ribosomal protein S25	chr11q23.3	200091_s_at	NM_001028																				
6.22	5.98	0.24	2.58E-01	6.33E-01	EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)	chr16p12.1	225993_at	NM_001083614 /// NR_003501																				
4.68	4.37	0.31	2.59E-01	6.33E-01	RFC2	replication factor C (activator 1) 2, 40kDa	chr7q11.23	1053_at	NM_002914 /// NM_181471																				
7.78	7.54	0.24	2.59E-01	6.33E-01	GUK1	guanylate kinase 1	chr1q32-q41	200075_s_at	NM_000858																				
7.37	7.17	0.20	2.59E-01	6.33E-01	OTUB1	OTU domain, ubiquitin aldehyde binding 1	chr11q13.1	38710_at	NM_017670 /// NR_003089																				
6.68	6.46	0.23	2.59E-01	6.33E-01	C16orf35	chromosome 16 open reading frame 35	chr16p13.3	214273_x_at	NM_001039476 /// NM_001077350																				
5.36	5.07	0.30	2.59E-01	6.33E-01	LOC100129550	hypothetical protein LOC100129550	chr3q21.1	229699_at	NM_001123328 /// XM_001719333 /// XM_001722536 /// XM_001723371																				

1.99	1.85	0.13	2.59E-01	6.33E-01	RBM33	RNA binding motif protein 33	chr7q36.3	1554096_a_at	NM_001008408 /// NM_053043
2.27	2.12	0.15	2.59E-01	6.33E-01	---	---	---	1569569_x_at	---
2.98	2.79	0.19	2.59E-01	6.33E-01	---	---	---	237823_at	---
2.91	2.78	0.14	2.59E-01	6.33E-01	---	---	---	242535_at	---
2.39	2.19	0.20	2.59E-01	6.33E-01	C1orf145	chromosome 1 open reading frame 145	chr1q42.13	1560554_a_at	NM_001025495
4.68	4.47	0.22	2.59E-01	6.33E-01	NR6A1	nuclear receptor subfamily 6, group A, member 1	chr9q33-q34.1	210392_x_at	NM_001489 /// NM_033334
8.02	7.76	0.27	2.59E-01	6.33E-01	HYPK /// SERF2	Huntingtin interacting protein K /// small EDRK-rich factor 2	chr15q15.3	226692_at	NM_001018108 /// NM_016400
4.18	3.77	0.41	2.59E-01	6.33E-01	MEX3C	mex-3 homolog C (C. elegans)	chr18q21.2	222567_s_at	NM_016626
2.58	2.43	0.15	2.59E-01	6.33E-01	KIAA1467	KIAA1467	chr12p13.1	213232_at	NM_020853
8.04	7.76	0.28	2.59E-01	6.33E-01	FLJ14154	hypothetical protein FLJ14154	chr16p13.3	45526_g_at	NM_001083600 /// NM_001083601 /// NM_024845
2.41	2.29	0.12	2.59E-01	6.33E-01	TCP11L2	t-complex 11 (mouse)-like 2	chr12q23.3	1569207_s_at	NM_152772
5.32	5.12	0.21	2.59E-01	6.33E-01	AVIL	advillin	chr12q14.1	233333_x_at	NM_006576
3.58	3.40	0.18	2.59E-01	6.33E-01	PSMC3IP	PSMC3 interacting protein	chr17q12-q21	213951_s_at	NM_013290 /// NM_016556
5.13	4.94	0.19	2.59E-01	6.33E-01	WDR4	WD repeat domain 4	chr21q22.3	221632_s_at	NM_018669 /// NM_033661
3.38	3.16	0.22	2.59E-01	6.33E-01	WIPF2	WAS/WASL interacting protein family, member 2	chr17q21.2	231251_at	NM_133264
2.91	2.60	0.31	2.59E-01	6.33E-01	CC2D1B	coiled-coil and C2 domain containing 1B	chr1p32.3	242487_at	NM_032449
5.76	5.51	0.25	2.59E-01	6.33E-01	PDCD2	programmed cell death 2	chr6q27	213581_at	NM_002598 /// NM_144781
2.35	2.21	0.14	2.59E-01	6.33E-01	---	---	---	1568921_at	---
2.12	1.99	0.13	2.59E-01	6.33E-01	UBA6	ubiquitin-like modifier activating enzyme 6	chr4q13.2	1555441_at	NM_018227
8.56	8.42	0.15	2.59E-01	6.34E-01	ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	chr7q22.1	200950_at	NM_006409
2.50	2.35	0.14	2.59E-01	6.34E-01	TTC26	tetratricopeptide repeat domain 26	chr7q34	1554672_at	NM_024926
3.35	3.20	0.15	2.59E-01	6.34E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	1562271_x_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735
10.99	10.80	0.19	2.60E-01	6.34E-01	PPIB	peptidylprolyl isomerase B (cyclophilin B)	chr15q21-q22	200967_at	NM_000942
2.91	2.67	0.24	2.60E-01	6.34E-01	RNF180	ring finger protein 180	chr5q12.2	242985_x_at	NM_001113561 /// NM_178532
2.44	2.26	0.18	2.60E-01	6.34E-01	LOC400238	hypothetical gene supported by AK093266	chr14q32.12	1561728_a_at	---
5.59	5.36	0.22	2.60E-01	6.34E-01	ZNF512	zinc finger protein 512	chr2p23	1553218_a_at	NM_032434
4.65	4.45	0.19	2.60E-01	6.34E-01	LOC100132273	Hypothetical protein LOC100132273	chr22q13.2	228117_at	XM_001716798
2.87	2.67	0.20	2.60E-01	6.34E-01	---	---	---	221955_at	---
2.46	2.24	0.22	2.60E-01	6.34E-01	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	chr1p36.1-p35	1554728_at	NM_003047
5.92	5.65	0.27	2.60E-01	6.34E-01	ABI3	ABI gene family, member 3	chr17q21.3	223615_at	NM_016428
10.74	10.56	0.18	2.60E-01	6.34E-01	TUBA1B	tubulin, alpha 1b	chr12q13.12	211058_x_at	NM_006082
4.20	4.04	0.16	2.60E-01	6.34E-01	DTNA	dystrobrevin, alpha	chr18q12	210736_x_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981

3.79	3.53	0.26	2.60E-01	6.34E-01	MPI	mannose phosphate isomerase	chr15q22-qter	230524_at	NM_002435
2.07	1.95	0.12	2.60E-01	6.34E-01	---	---	---	236469_at	---
2.40	2.22	0.18	2.60E-01	6.34E-01	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	chr8q24	204932_at	NM_002546
4.63	4.29	0.34	2.60E-01	6.34E-01	DCTN5	dynactin 5 (p25)	chr16p12.1	209231_s_at	NM_032486
2.16	2.01	0.15	2.60E-01	6.35E-01	LOC400581	GRB2-related adaptor protein-like	chr17p11.2	1559688_at	NM_001129778 /// XM_001720657 /// XM_001723190
5.74	5.51	0.23	2.60E-01	6.35E-01	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6	chr15q13-q15	226741_at	NM_001042494 /// NM_001042495 /// NM_001042496 /// NM_001042497 /// NM_005135 /// NM_133647
3.10	2.91	0.19	2.60E-01	6.35E-01	LOC100133287	hypothetical protein LOC100133287	chr21q22.3	1570432_at	XM_001718686 /// XM_001722338 /// XM_001726128
5.55	5.33	0.22	2.61E-01	6.35E-01	CHD1L	chromodomain helicase DNA binding protein 1-like	chr1q12	1556988_s_at	NM_004284
3.01	2.82	0.19	2.61E-01	6.35E-01	ZNF382	zinc finger protein 382	chr19q13.12	1557260_a_at	NM_032825
6.84	6.46	0.38	2.61E-01	6.35E-01	QSER1	glutamine and serine rich 1	chr11p13	226265_at	NM_001076786
7.46	6.92	0.53	2.61E-01	6.35E-01	FXYD6	FXYD domain containing ion transport regulator 6	chr11q23.3	217897_at	NM_022003
2.42	2.18	0.24	2.61E-01	6.35E-01	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	chr4p14	1569566_at	NM_015173
7.70	7.34	0.35	2.61E-01	6.35E-01	ORAI3	ORAI calcium release-activated calcium modulator 3	chr16p11.2	221864_at	NM_152288
4.92	4.75	0.17	2.61E-01	6.35E-01	PVR	poliovirus receptor	chr19q13.2	214444_s_at	NM_006505
3.01	2.33	0.68	2.61E-01	6.35E-01	CYorf15B	chromosome Y open reading frame 15B	chrYq11.222	223645_s_at	NM_032576
2.61	2.45	0.16	2.61E-01	6.35E-01	OR2A4	olfactory receptor, family 2, subfamily A, member 4	chr6q23	233493_at	NM_030908
7.54	7.31	0.23	2.61E-01	6.35E-01	MLX	MAX-like protein X	chr17q21.1	217910_x_at	NM_170607 /// NM_198204 /// NM_198205
4.10	3.84	0.26	2.61E-01	6.35E-01	---	---	---	234713_x_at	---
3.92	3.62	0.30	2.61E-01	6.35E-01	---	---	---	212920_at	---
6.79	6.52	0.28	2.61E-01	6.35E-01	PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	chr12q13.3	218942_at	NM_024779
5.93	5.63	0.30	2.61E-01	6.35E-01	MAP3K11	mitogen-activated protein kinase kinase kinase 11	chr11q13.1-q13.3	203652_at	NM_002419
2.77	2.59	0.18	2.61E-01	6.35E-01	PROSC	Proline synthetase co-transcribed homolog (bacterial)	chr8p11.2	227315_x_at	NM_007198
3.32	2.86	0.47	2.61E-01	6.35E-01	SDHALP1	succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1	chr3q29	230077_at	NR_003264 /// XR_042174
5.76	5.27	0.49	2.61E-01	6.35E-01	GAS1	growth arrest-specific 1	chr9q21.3-q22	204457_s_at	NM_002048
6.21	5.88	0.33	2.61E-01	6.35E-01	SLC43A1	solute carrier family 43, member 1	chr11p11.2-p11.1	204394_at	NM_003627
6.06	5.46	0.60	2.61E-01	6.35E-01	PDK1	pyruvate dehydrogenase kinase, isozyme 1	chr2q31.1	226452_at	NM_002610
3.87	3.64	0.23	2.61E-01	6.35E-01	C17orf70	chromosome 17 open reading frame 70	chr17q25.3	225322_s_at	NM_001109760 /// NM_025161
6.95	6.65	0.30	2.61E-01	6.35E-01	RBM42	RNA binding motif protein 42	chr19q13.12	205740_s_at	NM_024321
7.22	7.03	0.19	2.61E-01	6.35E-01	C7orf42	chromosome 7 open reading frame 42	chr7q11.21	224688_at	NM_017994
2.78	2.57	0.20	2.61E-01	6.35E-01	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	chr4q13	216687_x_at	NM_001076
2.22	2.08	0.14	2.61E-01	6.35E-01	---	---	---	232277_at	---
2.42	2.29	0.14	2.61E-01	6.35E-01	GINS4	GINS complex subunit 4 (Sld5 homolog)	chr8p11.21	1554356_at	NM_032336
3.25	3.04	0.21	2.61E-01	6.35E-01	GTPBP2	GTP binding protein 2	chr6p21-p12	223789_s_at	NM_019096
2.86	2.68	0.18	2.61E-01	6.35E-01	RNF34	ring finger protein 34	chr12q24.31	229855_at	NM_025126 /// NM_194271
2.59	2.46	0.13	2.61E-01	6.35E-01	LOC200261	hypothetical protein LOC200261	chr20p11.21	1554382_at	XR_041194 /// XR_041195 /// XR_041196
2.91	2.69	0.21	2.62E-01	6.35E-01	---	---	---	1565579_at	---
2.77	2.58	0.19	2.62E-01	6.35E-01	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	chr11p15.2	207786_at	NM_024514
3.67	3.50	0.17	2.62E-01	6.35E-01	GPR37L1	G protein-coupled receptor 37 like 1	chr1q32.1	207055_at	NM_004767
8.95	8.66	0.28	2.62E-01	6.35E-01	GNG10	guanine nucleotide binding protein (G protein), gamma 10	chr9q31.3	201921_at	NM_001017998
2.92	2.80	0.12	2.62E-01	6.35E-01	---	---	---	241848_x_at	---

8.12	7.92	0.20	2.62E-01	6.35E-01	LOC285550	hypothetical protein LOC285550	chr4p15.33-p15.32	227466_at	XR_017764 /// XR_017908 /// XR_040763																			
6.76	6.48	0.28	2.62E-01	6.35E-01	ZDHHC4	zinc finger, DHHC-type containing 4	chr7p22.1	220261_s_at	NM_001134387 /// NM_001134388 /// NM_001134389 /// NM_018106																			
3.57	3.35	0.23	2.62E-01	6.35E-01	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	chr12q24.13	226539_s_at	NM_001111322 /// NM_024072																			
9.25	8.98	0.28	2.62E-01	6.35E-01	CTSB	cathepsin B	chr8p22	213275_x_at	NM_001908 /// NM_147780 /// NM_147781 /// NM_147782 /// NM_147783																			
2.97	2.70	0.27	2.62E-01	6.36E-01	RHOC	Ras homolog gene family, member C	chr1p13.1	235742_at	NM_001042678 /// NM_001042679 /// NM_175744																			
6.66	6.47	0.19	2.62E-01	6.36E-01	LMO4	LIM domain only 4	chr1p22.3	209205_s_at	NM_006769																			
3.40	3.23	0.17	2.62E-01	6.36E-01	SLC5A10	solute carrier family 5 (sodium/glucose cotransporter), member 10	chr17p11.2	239707_at	NM_001042450 /// NM_152351																			
2.40	2.26	0.14	2.62E-01	6.36E-01	PCDHB18	protocadherin beta 18 pseudogene	chr5q31	234479_at	NR_001281																			
6.11	5.87	0.24	2.62E-01	6.36E-01	DTYMK /// LOC727761	deoxythymidylate kinase (thymidylate kinase) /// similar to Deoxythymidylate kinase (thymidylate kinase)	chr2q37.3	203270_at	NM_012145 /// XM_001126163 /// XM_001126184 /// XM_001126211																			
12.38	12.24	0.13	2.62E-01	6.36E-01	RPS14	ribosomal protein S14	chr5q31-q33	208645_s_at	NM_001025070 /// NM_001025071 /// NM_005617																			
2.04	1.88	0.16	2.62E-01	6.36E-01	---	---	---	1564003_at	---																			
10.78	10.60	0.17	2.62E-01	6.36E-01	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	chr8q24.3	203113_s_at	NM_001130053 /// NM_001130054 /// NM_001130055 /// NM_001130056 /// NM_001130057 /// NM_001960 /// NM_032378																			
3.54	3.38	0.15	2.62E-01	6.36E-01	SHPK /// TRPV1	sedoheptulokinase /// transient receptor potential cation channel, subfamily V, member 1	chr17p13 /// chr17p13.3	219712_s_at	NM_013276 /// NM_018727 /// NM_080704 /// NM_080705 /// NM_080706																			
3.68	3.46	0.23	2.62E-01	6.36E-01	LOC92497	hypothetical LOC92497	chr12q23.1	233198_at	XM_931850 /// XM_944913																			
8.66	8.38	0.28	2.63E-01	6.36E-01	LSMD1	LSM domain containing 1	chr17p13.1	224512_s_at	NM_032356																			
2.76	2.58	0.17	2.63E-01	6.36E-01	---	---	---	243587_x_at	---																			
2.81	2.62	0.20	2.63E-01	6.36E-01	---	---	---	1561318_at	---																			

7.02	6.85	0.18	2.63E-01	6.36E-01	SNAP29	synaptosomal-associated protein, 29kDa	chr22q11.21	218327_s_at	NM_004782
2.09	1.96	0.14	2.63E-01	6.36E-01	---	---	---	237829_at	---
3.92	3.73	0.19	2.63E-01	6.36E-01	---	---	---	229811_at	---
6.40	6.00	0.40	2.63E-01	6.36E-01	GPR56	G protein-coupled receptor 56	chr16q12.2-q21	212070_at	NM_005682 /// NM_201524 /// NM_201525
5.56	5.21	0.35	2.63E-01	6.36E-01	AMBRA1	autophagy/beclin-1 regulator 1	chr11p11.2	52731_at	NM_017749
2.99	2.83	0.16	2.63E-01	6.37E-01	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	chr5q33.1	238427_at	NM_152407
3.67	3.44	0.24	2.63E-01	6.37E-01	LOC339290	hypothetical protein LOC339290	chr18p11.31	243426_at	XR_017922 /// XR_017997 /// XR_041986
6.54	6.01	0.53	2.63E-01	6.37E-01	LOC645166	similar to lymphocyte-specific protein 1	chr1q21.1	228158_at	XM_001129441
2.03	1.85	0.17	2.63E-01	6.37E-01	---	---	---	233711_at	---
3.14	2.94	0.20	2.63E-01	6.37E-01	UROS	uroporphyrinogen III synthase	chr10q25.2-q26.3	232560_at	NM_000375
2.09	1.98	0.11	2.63E-01	6.37E-01	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	chr6p21.3	215666_at	NM_021983 /// XM_001723414 /// XM_001723417 /// XM_001723419
5.42	5.25	0.17	2.63E-01	6.37E-01	ZC3H7B	zinc finger CCCH-type containing 7B	chr22q13.2	213323_s_at	NM_017590
4.25	4.00	0.25	2.63E-01	6.37E-01	PCSK7	Proprotein convertase subtilisin/kexin type 7	chr11q23-q24	232248_at	NM_004716
3.45	3.14	0.31	2.63E-01	6.37E-01	---	---	---	241658_at	---
2.49	2.34	0.16	2.63E-01	6.37E-01	---	---	---	229954_at	---
2.80	2.59	0.22	2.63E-01	6.37E-01	SYN2	synapsin II	chr3p25	1553037_a_at	NM_003178 /// NM_133625
3.97	3.75	0.22	2.63E-01	6.37E-01	MKS1	Meckel syndrome, type 1	chr17q22	1555820_a_at	NM_017777
4.20	3.87	0.33	2.63E-01	6.37E-01	---	---	---	226392_at	---
5.54	5.04	0.50	2.64E-01	6.37E-01	---	---	---	226550_at	---
2.39	2.19	0.20	2.64E-01	6.37E-01	METTL4	methyltransferase like 4	chr18p11.32	232194_at	NM_022840
4.33	4.00	0.33	2.64E-01	6.37E-01	LYPD3	LY6/PLAUR domain containing 3	chr19q13.31	204952_at	NM_014400
2.58	2.40	0.17	2.64E-01	6.37E-01	---	---	---	243828_at	---
6.03	5.66	0.37	2.64E-01	6.37E-01	TRIM32	tripartite motif-containing 32	chr9q33.1	203846_at	NM_001099679 /// NM_012210
3.95	3.55	0.40	2.64E-01	6.37E-01	PERP	PERP, TP53 apoptosis effector	chr6q24	217744_s_at	NM_022121
7.31	7.01	0.29	2.64E-01	6.37E-01	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	chr6p21.3	32836_at	NM_006411 /// NM_032741
3.29	3.07	0.22	2.64E-01	6.37E-01	CTBS	chitobiase, di-N-acetyl-	chr1p22	218923_at	NM_004388
2.94	2.80	0.14	2.64E-01	6.37E-01	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	chr1p36.21	1563830_a_at	NM_052929 /// XM_001714211 /// XM_934889 /// XM_946265
2.30	2.15	0.15	2.64E-01	6.37E-01	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	chr13q12	204406_at	NM_002019
3.15	2.93	0.23	2.64E-01	6.37E-01	LARP5	La ribonucleoprotein domain family, member 5	chr10p15.3	214216_s_at	NM_015155
2.79	2.61	0.19	2.64E-01	6.37E-01	---	---	---	216675_at	---
6.97	6.70	0.27	2.64E-01	6.37E-01	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	chr5q35.3	206431_x_at	NM_015043 /// NM_198868
6.72	6.52	0.20	2.64E-01	6.38E-01	HMOX1	heme oxygenase (decycling) 1	chr22q12|22q13.1	203665_at	NM_002133
3.81	3.64	0.17	2.64E-01	6.38E-01	LILRA6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	chr19q13.4	208594_x_at	NM_024318
2.36	2.22	0.14	2.64E-01	6.38E-01	---	---	---	239992_at	---
5.28	4.98	0.29	2.64E-01	6.38E-01	hCG_1806964	HCG1806964	chr3q25.1	235173_at	XR_041581 /// XR_041582 /// XR_041583
2.77	2.57	0.20	2.64E-01	6.38E-01	---	---	---	1565810_at	---
7.14	6.79	0.35	2.64E-01	6.38E-01	RYK	RYK receptor-like tyrosine kinase	chr3q22	202853_s_at	NM_001005861 /// NM_002958

2.82	2.65	0.17	2.65E-01	6.38E-01	LYPD6B	LY6/PLAUR domain containing 6B	chr2q23.2	228360_at	NM_177964
7.51	6.96	0.55	2.65E-01	6.38E-01	KLF6	Kruppel-like factor 6	chr10p15	224606_at	NM_001300
2.71	2.56	0.16	2.65E-01	6.38E-01	---	---	---	236585_at	---
2.70	2.52	0.18	2.65E-01	6.38E-01	---	---	---	1563081_at	---
3.03	2.76	0.27	2.65E-01	6.38E-01	SAMD8	sterile alpha motif domain containing 8	chr10q22.2	242062_at	NM_144660
5.59	5.30	0.29	2.65E-01	6.38E-01	AGK	acylglycerol kinase	chr7q34	218568_at	NM_018238
5.83	5.48	0.34	2.65E-01	6.38E-01	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	chr8p12	221539_at	NM_004095
5.37	5.21	0.16	2.65E-01	6.38E-01	---	---	---	244167_at	---
2.74	2.55	0.19	2.65E-01	6.38E-01	---	---	---	1557149_at	---
5.17	4.95	0.22	2.65E-01	6.38E-01	C11orf30	chromosome 11 open reading frame 30	chr11q13.5	222807_at	NM_020193
2.34	2.16	0.18	2.65E-01	6.38E-01	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	chr17q22	1560227_at	NM_182569
12.21	12.07	0.14	2.65E-01	6.38E-01	LOC100128936 /// RPL10A	similar to ribosomal protein L10a /// ribosomal protein L10a	chr3p14.2 /// chr6p21.3-p21.2	229563_s_at	NM_007104 /// XM_001721819 /// XM_001726108 /// XM_001726387
4.53	4.31	0.22	2.65E-01	6.38E-01	APOM	apolipoprotein M	chr6p21.33	214910_s_at	NM_019101
1.87	1.75	0.13	2.65E-01	6.38E-01	CD58	CD58 molecule	chr1p13	216322_at	NM_001779
2.19	2.06	0.12	2.65E-01	6.39E-01	FCRLA	Fc receptor-like A	chr1q23.3	235400_at	NM_032738
3.19	2.85	0.34	2.65E-01	6.39E-01	TUBE1	tubulin, epsilon 1	chr6q21	226181_at	NM_016262
5.50	5.17	0.32	2.65E-01	6.39E-01	SLC30A7	solute carrier family 30 (zinc transporter), member 7	chr1p21.2	226601_at	NM_133496
2.19	2.05	0.14	2.65E-01	6.39E-01	GPR128	G protein-coupled receptor 128	chr3q12.2	1553296_at	NM_032787
3.44	3.25	0.19	2.65E-01	6.39E-01	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	chr16q21-q22.1	1555704_at	NM_001048251 /// NM_144601 /// NM_181553 /// NM_181554
7.78	7.63	0.15	2.65E-01	6.39E-01	H2AFY	H2A histone family, member Y	chr5q31.3-q32	214501_s_at	NM_001040158 /// NM_004893 /// NM_138609 /// NM_138610
4.98	4.82	0.17	2.65E-01	6.39E-01	DUSP8	dual specificity phosphatase 8	chr11p15.5	238594_x_at	NM_004420
2.74	2.58	0.16	2.65E-01	6.39E-01	---	---	---	1560070_at	---
8.33	8.17	0.16	2.65E-01	6.39E-01	CD47	CD47 molecule	chr3q13.1-q13.2	213857_s_at	NM_001025079 /// NM_001777 /// NM_198793
4.51	4.31	0.20	2.66E-01	6.39E-01	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	chr4q34.2	222753_s_at	NM_021928
11.39	11.09	0.29	2.66E-01	6.39E-01	MGP	matrix Gla protein	chr12p13.1-p12.3	202291_s_at	NM_000900
4.10	3.89	0.20	2.66E-01	6.39E-01	---	---	---	1556586_x_at	---
6.21	6.01	0.19	2.66E-01	6.39E-01	MFSD11	major facilitator superfamily domain containing 11	chr17q25	223242_s_at	NM_024311
5.64	5.42	0.21	2.66E-01	6.39E-01	EXDL2	exonuclease 3'-5' domain-like 2	chr14q24.1	218363_at	NM_018199
2.08	1.95	0.13	2.66E-01	6.39E-01	---	---	---	244116_at	---
4.41	3.91	0.50	2.66E-01	6.39E-01	LRP6	low density lipoprotein receptor-related protein 6	chr12p11-p13	225745_at	NM_002336
7.41	7.22	0.19	2.66E-01	6.39E-01	MYO9B	myosin IXB	chr19p13.1	214780_s_at	NM_001130065 /// NM_004145
3.14	2.94	0.21	2.66E-01	6.39E-01	ELA3A	elastase 3A, pancreatic	chr1p36.12	211738_x_at	NM_005747
2.82	2.60	0.22	2.66E-01	6.39E-01	BMS1P5 /// CTGLF1 /// CTGLF6 /// CTGLF7	BMS1 pseudogene 5 /// centaurin, gamma-like family, member 1 /// centaurin, gamma-like family, member 6 /// centaurin, gamma-like family, member 7	chr10q11.21 /// chr10q11.22	238553_at	NM_133446 /// NR_003611 /// XM_001714786 /// XM_001716810
5.78	5.39	0.39	2.67E-01	6.40E-01	FMR1	fragile X mental retardation 1	chrXq27.3	215245_x_at	NM_002024
11.73	11.54	0.19	2.67E-01	6.40E-01	CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2	chr7p11.2	217720_at	NM_016139

6.08	5.80	0.28	2.67E-01	6.40E-01	CASP8	caspase 8, apoptosis-related cysteine peptidase	chr2q33-q34	213373_s_at	NM_001080124 /// NM_001080125 /// NM_001228 /// NM_033355 /// NM_033356 /// NM_033358																				
2.66	2.49	0.17	2.67E-01	6.40E-01	SIM2	single-minded homolog 2 (Drosophila)	chr21q22.2|21q22.13	208157_at	NM_005069 /// NM_009586																				
2.64	2.48	0.16	2.67E-01	6.40E-01	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	chr3p25.3	220244_at	NM_013343 /// NR_024065																				
4.10	3.52	0.58	2.67E-01	6.40E-01	PSPC1	paraspeckle component 1	chr13q12.11	222611_s_at	NM_001042414 /// NR_003272																				
4.71	4.46	0.26	2.67E-01	6.40E-01	ORAI2	ORAI calcium release-activated calcium modulator 2	chr7q22.1	218812_s_at	NM_001126340 /// NM_032831																				
2.15	1.99	0.15	2.67E-01	6.40E-01	HOXD1	homeobox D1	chr2q31.1	205974_at	NM_024501																				
5.69	5.50	0.19	2.67E-01	6.40E-01	OTUD5	OTU domain containing 5	chrXp11.23	233933_s_at	NM_017602																				
5.85	5.54	0.30	2.67E-01	6.40E-01	RNF25	ring finger protein 25	chr2q35	218861_at	NM_022453																				
2.80	2.67	0.14	2.67E-01	6.40E-01	C7orf63	chromosome 7 open reading frame 63	chr7q21.13	1554919_s_at	NM_001039706																				
8.07	7.78	0.28	2.67E-01	6.40E-01	CYB5R1	cytochrome b5 reductase 1	chr1p36.13-q41	202263_at	NM_016243																				
6.29	6.13	0.16	2.67E-01	6.40E-01	TULP3	tubby like protein 3	chr12p13.3	221964_at	NM_003324																				
7.03	6.80	0.23	2.67E-01	6.40E-01	GBA /// GBAP	glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid, pseudogene	chr1q21	209093_s_at	NM_000157 /// NM_001005741 /// NM_001005742 /// NM_001005749 /// NM_001005750 /// NR_002188 /// XR_042183																				
4.12	3.86	0.25	2.67E-01	6.40E-01	ATG4B /// LOC727737	ATG4 autophagy related 4 homolog B (S. cerevisiae) /// similar to APG4 autophagy 4 homolog B	chr2q37.3	204902_s_at	NM_013325 /// NM_178326 /// XM_001126076 /// XM_001126088																				
2.66	2.51	0.15	2.67E-01	6.40E-01	CA12	carbonic anhydrase XII	chr15q22	210735_s_at	NM_001218 /// NM_206925																				
2.92	2.74	0.17	2.67E-01	6.40E-01	LOC100131226	hypothetical protein LOC100131226	chr3p21.31	229636_at	XM_001717891 /// XM_001718630																				
4.95	4.64	0.31	2.67E-01	6.40E-01	BCL2L13	BCL2-like 13 (apoptosis facilitator)	chr22q11.1	223664_x_at	NM_015367																				
3.55	3.38	0.17	2.67E-01	6.40E-01	---	---	---	234834_at	---																				
7.70	7.38	0.32	2.67E-01	6.40E-01	LHFPL2	lipoma HMGIC fusion partner-like 2	chr5q14.1	212658_at	NM_005779																				
5.97	5.70	0.27	2.67E-01	6.40E-01	PDCL	phosducin-like	chr9q12-q13	204448_s_at	NM_005388																				
2.99	2.74	0.24	2.68E-01	6.41E-01	SOX13	SRY (sex determining region Y)-box 13	chr1q32	1569111_at	NM_005686																				
2.16	2.04	0.12	2.68E-01	6.41E-01	---	---	---	231473_at	---																				
6.29	6.10	0.19	2.68E-01	6.41E-01	TK2	thymidine kinase 2, mitochondrial	chr16q22-q23.1	204277_s_at	NM_004614																				
6.44	6.19	0.25	2.68E-01	6.41E-01	SIRPA	signal-regulatory protein alpha	chr20p13	202896_s_at	NM_001040022 /// NM_001040023 /// NM_080792																				
9.96	9.76	0.20	2.68E-01	6.41E-01	EIF3K	eukaryotic translation initiation factor 3, subunit K	chr19q13.2	212716_s_at	NM_013234																				
3.65	3.43	0.22	2.68E-01	6.41E-01	TSNAXIP1	translin-associated factor X interacting protein 1	chr16q22.1	222220_s_at	NM_018430																				
2.95	2.78	0.17	2.68E-01	6.41E-01	ZNF33B	Zinc finger protein 33B	chr10q11.2	1562743_at	NM_006955																				
6.59	6.22	0.37	2.68E-01	6.41E-01	WIPF2	WAS/WASL interacting protein family, member 2	chr17q21.2	212051_at	NM_133264																				
3.90	3.73	0.17	2.68E-01	6.41E-01	---	---	---	217107_at	---																				

3.90	3.55	0.35	2.68E-01	6.41E-01	PLEKHM3	pleckstrin homology domain containing, family M, member 3	chr2q33.3	1560069_at	NM_001080475																				
5.69	5.47	0.22	2.68E-01	6.41E-01	KIAA0415	KIAA0415	chr7p22.2	209912_s_at	NM_014855																				
2.09	1.95	0.14	2.68E-01	6.41E-01	MRPL39	Mitochondrial ribosomal protein L39	chr21q21.3	236910_at	NM_017446 /// NM_080794																				
4.04	3.80	0.24	2.68E-01	6.42E-01	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	chr18q22.3	1562460_at	NM_018235																				
3.81	3.66	0.15	2.68E-01	6.42E-01	FAM160B2	family with sequence similarity 160, member B2	chr8p21.3	222928_s_at	NM_022749																				
2.77	2.59	0.18	2.68E-01	6.42E-01	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	chr1q32.1	1560785_at	NM_001004023 /// NM_003582																				
6.85	6.38	0.47	2.69E-01	6.42E-01	BTBD14A	BTB (POZ) domain containing 14A	chr9q34.3	212993_at	NM_144653																				
10.06	9.87	0.19	2.69E-01	6.42E-01	NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	chr19p13.2	220864_s_at	NM_015965																				
5.34	5.07	0.27	2.69E-01	6.42E-01	LOC100127891	similar to hCG2042508	chr7q32.2	235967_at	XM_001715175 /// XM_001715763 /// XM_001718717																				
11.81	11.65	0.16	2.69E-01	6.42E-01	ACTG1	actin, gamma 1	chr17q25	212363_x_at	NM_001614																				
4.58	4.40	0.18	2.69E-01	6.42E-01	ZNF771	Zinc finger protein 771	chr16p11.2	232561_at	NM_016643 /// XM_001721231 /// XM_001721234																				
3.79	3.63	0.16	2.69E-01	6.42E-01	CPM	carboxypeptidase M	chr12q14.3	243403_x_at	NM_001005502 /// NM_001874 /// NM_198320																				
4.06	3.90	0.16	2.69E-01	6.42E-01	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	chr4q28.2-q31.1	232146_at	NM_002494																				
3.86	3.53	0.33	2.69E-01	6.42E-01	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	chr10q11.21	221578_at	NM_032023																				
3.53	2.80	0.73	2.69E-01	6.42E-01	HIST1H2BG	histone cluster 1, H2bg	chr6p21.3	210387_at	NM_003518																				
8.68	8.48	0.20	2.69E-01	6.42E-01	PRELID1	PRELI domain containing 1	chr5q35.3	223032_x_at	NM_013237																				
2.21	2.08	0.13	2.69E-01	6.42E-01	---	---	---	240924_x_at	---																				
5.65	5.47	0.18	2.69E-01	6.42E-01	LUZP1	leucine zipper protein 1	chr1p36	221831_at	NM_033631																				
5.56	5.39	0.17	2.69E-01	6.42E-01	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	chr3q27-qter	208624_s_at	NM_004953 /// NM_182917 /// NM_198241 /// NM_198242 /// NM_198244																				
2.71	2.56	0.16	2.69E-01	6.42E-01	---	---	---	1562661_at	---																				
3.83	3.33	0.50	2.69E-01	6.42E-01	FGD6	FYVE, RhoGEF and PH domain containing 6	chr12q22	219901_at	NM_018351																				
4.62	4.33	0.29	2.69E-01	6.42E-01	NOLC1	nucleolar and coiled-body phosphoprotein 1	chr10q24.32	211949_s_at	NM_004741																				
2.09	1.93	0.15	2.69E-01	6.42E-01	TBC1D12	TBC1 domain family, member 12	chr10q23.33	1557609_s_at	NM_015188																				
3.93	3.61	0.32	2.69E-01	6.42E-01	DHRS2	dehydrogenase/reductase (SDR family) member 2	chr14q11.2	206463_s_at	NM_005794 /// NM_182908																				
2.12	1.97	0.16	2.69E-01	6.42E-01	---	---	---	241257_at	---																				
7.70	7.45	0.25	2.69E-01	6.42E-01	WBP11	WW domain binding protein 11	chr12p12.3	217822_at	NM_016312																				
3.65	3.45	0.21	2.69E-01	6.42E-01	PVT1	Pvt1 oncogene homolog (mouse)	chr8q24	222087_at	NR_003367																				
2.49	2.30	0.19	2.70E-01	6.43E-01	TBX1	T-box 1	chr22q11.21	211273_s_at	NM_005992 /// NM_080646 /// NM_080647																				
1.93	1.78	0.16	2.70E-01	6.43E-01	---	---	---	244067_x_at	---																				
2.98	2.33	0.65	2.70E-01	6.43E-01	CYorf15B	chromosome Y open reading frame 15B	chrYq11.222	223646_s_at	NM_032576																				
3.32	3.04	0.27	2.70E-01	6.43E-01	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	chr1p36.3	206752_s_at	NM_004402																				
3.27	3.13	0.14	2.70E-01	6.43E-01	ZER1	Zer-1 homolog (C. elegans)	chr9q34.11	230358_at	NM_006336																				
4.70	4.44	0.26	2.70E-01	6.43E-01	RAB11FIP1	RAB11 family interacting protein 1 (class I)	chr8p11.22	219681_s_at	NM_001002233 /// NM_001002814 /// NM_025151																				
2.76	2.63	0.13	2.70E-01	6.43E-01	CNTNAP4	contactin associated protein-like 4	chr16q23.1	232388_at	NM_033401 /// NM_138994																				

2.50	2.38	0.13	2.70E-01	6.43E-01	ADCYAP1	adenylate cyclase activating polypeptide 1 (pituitary)	chr18p11	206281_at	NM_001099733 /// NM_001117
2.26	2.11	0.15	2.70E-01	6.43E-01	---	---	---	242783_at	---
3.20	2.97	0.23	2.70E-01	6.43E-01	---	---	---	244078_at	---
6.67	6.35	0.32	2.70E-01	6.43E-01	AKIRIN1	akirin 1	chr1p34.3	217893_s_at	NM_024595
2.44	2.24	0.20	2.70E-01	6.43E-01	ZCCHC18	zinc finger, CCHC domain containing 18 pseudogene	chrXq22.2	230224_at	XR_016527 /// XR_018173 /// XR_039901
7.26	6.99	0.27	2.70E-01	6.43E-01	IFRD2	interferon-related developmental regulator 2	chr3p21.3	209100_at	NM_006764
2.93	2.61	0.32	2.70E-01	6.43E-01	PLA2G5	phospholipase A2, group V	chr1p36-p34	215870_s_at	NM_000929
9.95	9.47	0.48	2.70E-01	6.43E-01	CXCR4	chemokine (C-X-C motif) receptor 4	chr2q21	217028_at	NM_001008540 /// NM_003467
4.99	4.46	0.53	2.70E-01	6.43E-01	LOC339803	hypothetical protein LOC339803	chr2p16.1	227941_at	---
5.54	5.24	0.30	2.71E-01	6.43E-01	TM7SF3	transmembrane 7 superfamily member 3	chr12q11-q12	217974_at	NM_016551
6.23	6.02	0.20	2.71E-01	6.43E-01	CD99L2	CD99 molecule-like 2	chrXq28	233825_s_at	NM_031462 /// NM_134445 /// NM_134446
3.16	3.03	0.13	2.71E-01	6.43E-01	UNC5C	unc-5 homolog C (C. elegans)	chr4q21-q23	1555342_a_at	NM_003728
2.47	2.26	0.22	2.71E-01	6.43E-01	---	---	---	236204_at	---
2.44	2.30	0.14	2.71E-01	6.44E-01	---	---	---	240415_at	---
6.56	6.26	0.29	2.71E-01	6.44E-01	NAGA	N-acetylgalactosaminidase, alpha-	chr22q13-qter|22q11	202943_s_at	NM_000262
6.12	5.80	0.32	2.71E-01	6.44E-01	NCLN	nicalin homolog (zebrafish)	chr19p13.3	222206_s_at	NM_020170
5.01	4.79	0.22	2.71E-01	6.44E-01	---	---	---	231071_at	---
2.55	2.35	0.20	2.71E-01	6.44E-01	ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18	chr16q23	242823_at	NM_199355
7.85	7.62	0.23	2.71E-01	6.44E-01	SCAMP2	secretory carrier membrane protein 2	chr15q23-q25	218143_s_at	NM_005697
5.87	5.53	0.34	2.71E-01	6.44E-01	BTBD2	BTB (POZ) domain containing 2	chr19p13.3	207722_s_at	NM_017797
4.11	3.73	0.38	2.71E-01	6.44E-01	CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit	chr22q13.1	221631_at	NM_001003406 /// NM_021096
4.14	4.00	0.14	2.71E-01	6.44E-01	KIAA1045	KIAA1045	chr9p13.3	213636_at	NM_015297
5.89	5.36	0.53	2.71E-01	6.44E-01	FMR1	fragile X mental retardation 1	chrXq27.3	203689_s_at	NM_002024
6.54	6.35	0.19	2.71E-01	6.44E-01	NEO1	neogenin homolog 1 (chicken)	chr15q22.3-q23	225270_at	NM_002499
2.28	2.15	0.13	2.71E-01	6.44E-01	---	---	---	244147_at	---
1.98	1.81	0.16	2.71E-01	6.44E-01	ARG1	Arginase, liver	chr6q23	231665_at	NM_000045
5.39	5.13	0.26	2.72E-01	6.44E-01	C17orf48	chromosome 17 open reading frame 48	chr17p13.1	223401_at	NM_020233
2.67	2.52	0.15	2.72E-01	6.44E-01	C21orf49	chromosome 21 open reading frame 49	chr21q22.11	1557782_s_at	XR_017702 /// XR_017893 /// XR_041041
9.20	8.97	0.23	2.72E-01	6.44E-01	CCT3	chaperonin containing TCP1, subunit 3 (gamma)	chr1q23	200910_at	NM_001008800 /// NM_001008883 /// NM_005998
6.60	6.28	0.32	2.72E-01	6.44E-01	AGBL5	ATP/GTP binding protein-like 5	chr2p23.3	231857_s_at	NM_001035507 /// NM_021831
3.93	3.55	0.37	2.72E-01	6.44E-01	---	---	---	244512_at	---
2.46	2.27	0.19	2.72E-01	6.45E-01	---	---	---	238747_at	---
7.99	7.31	0.68	2.72E-01	6.45E-01	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	chr20q11	208937_s_at	NM_002165 /// NM_181353
3.21	3.03	0.18	2.72E-01	6.45E-01	LOC100131088	similar to hCG2045262	---	230940_at	XM_001722420 /// XM_001726071
2.20	2.03	0.17	2.72E-01	6.45E-01	---	---	---	241101_at	---
2.41	2.28	0.13	2.72E-01	6.45E-01	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	chr2q23.3	236477_at	NM_017892
2.67	2.49	0.19	2.72E-01	6.45E-01	---	---	---	1569855_at	---
4.89	4.58	0.31	2.72E-01	6.45E-01	ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	chr7q33-q35	204765_at	NM_005435
3.26	2.99	0.27	2.72E-01	6.45E-01	MED30	mediator complex subunit 30	chr8q24.11	227786_at	NM_080651
8.10	7.88	0.22	2.72E-01	6.45E-01	AUP1	ancient ubiquitous protein 1	chr2p13	220525_s_at	NM_181575
7.22	6.83	0.39	2.72E-01	6.45E-01	GATAD2A	GATA zinc finger domain containing 2A	chr19p13.11	218131_s_at	NM_017660
7.37	7.10	0.27	2.72E-01	6.45E-01	C10orf54	chromosome 10 open reading frame 54	chr10q22.1	225373_at	NM_022153
2.86	2.73	0.13	2.72E-01	6.45E-01	STC2	stanniocalcin 2	chr5q35.2	203438_at	NM_003714
2.30	2.14	0.16	2.72E-01	6.45E-01	RNF17	ring finger protein 17	chr13q12.12	220270_at	NM_031277
6.84	6.53	0.31	2.72E-01	6.45E-01	MGMT	O-6-methylguanine-DNA methyltransferase	chr10q26	204880_at	NM_002412

7.52	7.30	0.22	2.72E-01	6.45E-01	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	chr12p13	203005_at	NM_002342
6.80	6.50	0.30	2.72E-01	6.45E-01	JARID1C	jumonji, AT rich interactive domain 1C	chrXp11.22-p11.21	202383_at	NM_004187
8.93	8.72	0.21	2.72E-01	6.45E-01	SELK	selenoprotein K	chr3p21.31	223070_at	NM_021237
3.50	3.20	0.30	2.72E-01	6.45E-01	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	chr9p21	207039_at	NM_000077 /// NM_058195 /// NM_058197
3.77	3.57	0.20	2.72E-01	6.45E-01	---	---	---	234273_at	---
5.15	4.85	0.30	2.72E-01	6.45E-01	C14orf100	chromosome 14 open reading frame 100	chr14q23.1	223547_at	NM_001098625 /// NM_016475
2.09	1.98	0.12	2.72E-01	6.45E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	216178_x_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376
5.70	5.33	0.37	2.72E-01	6.45E-01	NSMCE4A	non-SMC element 4 homolog A (S. cerevisiae)	chr10q26.13	219067_s_at	NM_017615
6.66	6.43	0.24	2.72E-01	6.45E-01	GBL	G protein beta subunit-like	chr16p13.3	220587_s_at	NM_022372
3.01	2.75	0.26	2.72E-01	6.45E-01	NLRP13	NLR family, pyrin domain containing 13	chr19q13.42	1553525_at	NM_176810
4.56	4.05	0.52	2.73E-01	6.45E-01	RP5-1022P6.2	hypothetical protein KIAA1434	chr20p12.3	230492_s_at	NM_019593
5.23	5.04	0.19	2.73E-01	6.45E-01	WDR61	WD repeat domain 61	chr15q25.1	232075_at	NM_025234
2.96	2.79	0.17	2.73E-01	6.45E-01	MBNL1	muscleblind-like (Drosophila)	chr3q25	233015_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297
5.69	5.29	0.41	2.73E-01	6.45E-01	---	---	---	213848_at	---
2.96	2.46	0.50	2.73E-01	6.45E-01	LOC401629 /// LOC401630	LOC401629 /// LOC401630	chrYq11.221	235942_at	NR_002160 /// NR_002161
4.18	3.97	0.20	2.73E-01	6.45E-01	E2F1	E2F transcription factor 1	chr20q11.2	2028_s_at	NM_005225
2.59	2.38	0.21	2.73E-01	6.45E-01	---	---	---	238785_at	---
6.95	6.58	0.38	2.73E-01	6.46E-01	PLD1	phospholipase D1, phosphatidylcholine-specific	chr3q26	226636_at	NM_001130081 /// NM_002662
4.44	4.19	0.25	2.73E-01	6.46E-01	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	chr10q26.13	205355_at	NM_001609
3.12	2.80	0.32	2.73E-01	6.46E-01	---	---	---	1558742_at	---
7.29	7.07	0.23	2.73E-01	6.46E-01	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	chr11p15.5	212159_x_at	NM_012305
2.30	2.17	0.13	2.73E-01	6.46E-01	---	---	---	1563348_at	---
5.32	5.00	0.32	2.73E-01	6.46E-01	TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	chr6p21.1	229412_at	NM_138572
6.95	6.33	0.62	2.73E-01	6.46E-01	PNN	pinin, desmosome associated protein	chr14q21.1	212036_s_at	NM_002687
6.57	6.40	0.16	2.74E-01	6.46E-01	TCTN3	tectonic family member 3	chr10q23.33	212123_at	NM_015631
3.40	3.16	0.24	2.74E-01	6.46E-01	IL1RL2	interleukin 1 receptor-like 2	chr2q12	208038_at	NM_003854
2.52	2.36	0.16	2.74E-01	6.46E-01	KIAA0513	KIAA0513	chr16q24.1	1554440_at	NM_014732
7.12	6.66	0.46	2.74E-01	6.46E-01	EXOC6B	exocyst complex component 6B	chr2p13.3-p13.2	225900_at	NM_015189
5.92	5.63	0.29	2.74E-01	6.46E-01	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	chr11p13	203947_at	NM_001033505 /// NM_001033506 /// NM_001326
6.72	6.34	0.38	2.74E-01	6.46E-01	IVD	isovaleryl Coenzyme A dehydrogenase	chr15q14-q15	216958_s_at	NM_002225
4.86	4.07	0.78	2.74E-01	6.46E-01	GLS	glutaminase	chr2q32-q34	223079_s_at	NM_014905
4.22	3.88	0.33	2.74E-01	6.46E-01	WWTR1	WW domain containing transcription regulator 1	chr3q23-q24	202134_s_at	NM_015472
2.02	1.89	0.13	2.74E-01	6.46E-01	---	---	---	1559035_a_at	---
4.84	4.48	0.36	2.74E-01	6.46E-01	RP4-691N24.1	ninein-like	chr20p11.22-p11.1	207705_s_at	NM_025176
3.82	3.59	0.22	2.74E-01	6.46E-01	---	---	---	228773_at	---
3.86	3.61	0.24	2.74E-01	6.46E-01	CELP	carboxyl ester lipase pseudogene	chr9q34.3	207412_x_at	NR_001275

7.87	7.46	0.41	2.74E-01	6.46E-01	STOM	stomatin	chr9q34.1	201060_x_at	NM_004099 /// NM_198194																				
4.99	4.63	0.35	2.74E-01	6.46E-01	JMJD4	jumonji domain containing 4	chr1q42.13	218560_s_at	NM_023007																				
5.28	5.07	0.21	2.74E-01	6.46E-01	CYGB	cytoglobin	chr17q25.3	1570410_at	NM_134268																				
4.67	4.35	0.32	2.74E-01	6.46E-01	IRX3	iroquois homeobox 3	chr16q12.2	229638_at	NM_024336																				
3.60	3.45	0.16	2.74E-01	6.46E-01	---	---	---	231110_at	---																				
5.65	5.40	0.25	2.74E-01	6.46E-01	KIAA0999	KIAA0999 protein	chr11q23.3	213034_at	NM_025164																				
2.05	1.93	0.12	2.74E-01	6.46E-01	LOC152586	similar to RIKEN cDNA 4933434I20	chr4q31.1	1569995_at	XM_001720199 /// XM_001720248 /// XM_001725473																				
7.90	7.56	0.34	2.74E-01	6.46E-01	MLF2	myeloid leukemia factor 2	chr12p13	200948_at	NM_005439																				
2.56	2.41	0.15	2.74E-01	6.46E-01	---	---	---	234704_at	---																				
3.02	2.83	0.19	2.74E-01	6.46E-01	ZSCAN10	zinc finger and SCAN domain containing 10	chr16p13.3	1553874_a_at	NM_032805																				
5.34	5.08	0.26	2.74E-01	6.46E-01	FKBPL	FK506 binding protein like	chr6p21.3	219187_at	NM_022110																				
8.17	7.97	0.20	2.74E-01	6.46E-01	APLP2	amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	208702_x_at	NM_001642																				
2.45	2.27	0.18	2.74E-01	6.47E-01	---	---	---	240892_at	---																				
2.41	2.27	0.14	2.74E-01	6.47E-01	---	---	---	1558401_at	---																				
6.45	6.12	0.32	2.74E-01	6.47E-01	SQSTM1	Sequestosome 1	chr5q35	244804_at	NM_003900																				
4.18	3.35	0.84	2.74E-01	6.47E-01	IL8	interleukin 8	chr4q13-q21	202859_x_at	NM_000584																				
2.35	2.23	0.12	2.75E-01	6.47E-01	---	---	---	233792_at	---																				
2.44	2.30	0.14	2.75E-01	6.47E-01	---	---	---	1559976_at	---																				
2.77	2.57	0.20	2.75E-01	6.47E-01	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	chr5p15	210959_s_at	NM_001047																				
6.34	5.94	0.39	2.75E-01	6.47E-01	KHSRP	KH-type splicing regulatory protein	chr19p13.3	212303_x_at	NM_003685																				
3.22	2.91	0.31	2.75E-01	6.47E-01	FAM116B	family with sequence similarity 116, member B	chr22q13.33	229739_s_at	NM_001001794																				
3.35	3.10	0.25	2.75E-01	6.47E-01	BAG5	BCL2-associated athanogene 5	chr14q32.33	230427_s_at	NM_001015048 /// NM_001015049 /// NM_004873																				
3.28	3.13	0.15	2.75E-01	6.47E-01	LOC100131861	hypothetical protein LOC100131861	chr22q13.31	230396_at	XM_001716418 /// XM_001724537 /// XM_001725780																				
4.82	4.60	0.21	2.75E-01	6.47E-01	C10orf125	chromosome 10 open reading frame 125	chr10q26.3	230259_at	NM_001098483 /// NM_198472																				
2.88	2.75	0.13	2.75E-01	6.47E-01	CCDC120	coiled-coil domain containing 120	chrXp11.23	239403_at	NM_033626																				
6.51	6.28	0.23	2.75E-01	6.47E-01	CBFB	core-binding factor, beta subunit	chr16q22.1	202370_s_at	NM_001755 /// NM_022845																				
7.29	6.98	0.31	2.75E-01	6.47E-01	ZFAND6	zinc finger, AN1-type domain 6	chr15q25.1	221613_s_at	NM_019006																				
3.00	2.74	0.26	2.75E-01	6.47E-01	---	---	---	238496_at	---																				
4.41	3.95	0.46	2.75E-01	6.47E-01	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	chr1q32.1	228386_s_at	NM_001031725 /// NM_031306																				
7.77	7.47	0.30	2.75E-01	6.47E-01	PHF15	PHD finger protein 15	chr5q31.1	212660_at	NM_015288																				
2.66	2.49	0.17	2.75E-01	6.47E-01	AFF3	AF4/FMR2 family, member 3	chr2q11.2-q12	243967_at	NM_001025108 /// NM_002285																				
2.94	2.72	0.22	2.75E-01	6.47E-01	OMP	olfactory marker protein	chr11q13.5	221361_at	NM_006189																				
2.74	2.50	0.23	2.75E-01	6.47E-01	LOC652637 /// WHDC1L1	similar to junction-mediating and regulatory protein /// WAS protein homology region 2 domain containing 1-like 1	chr15q11.2	213908_at	NR_003521 /// XM_942188 /// XR_042166																				
2.54	2.43	0.11	2.75E-01	6.47E-01	SH2D4B	SH2 domain containing 4B	chr10q23.1	1563849_at	NM_207372																				
2.05	1.93	0.12	2.75E-01	6.47E-01	---	---	---	237253_at	---																				
4.53	4.08	0.45	2.75E-01	6.47E-01	SHANK3	SH3 and multiple ankyrin repeat domains 3	chr22q13.3	227923_at	NM_001080420																				
2.42	2.26	0.16	2.75E-01	6.47E-01	MC5R	melanocortin 5 receptor	chr18p11.2	208565_at	NM_005913																				
2.35	2.21	0.14	2.75E-01	6.47E-01	CDC20B	cell division cycle 20 homolog B (S. cerevisiae)	chr5q11.2	1553655_at	NM_152623																				
9.49	9.35	0.13	2.75E-01	6.47E-01	PSME1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	chr14q11.2	200814_at	NM_006263 /// NM_176783																				

4.32	4.13	0.19	2.75E-01	6.47E-01	LOC100129015	hypothetical protein LOC100129015	chr9q34.3	225423_x_at	XM_001715056 /// XM_001716341 /// XM_001716632																				
5.92	5.50	0.42	2.75E-01	6.47E-01	STRN4	striatin, calmodulin binding protein 4	chr19q13.2	217903_at	NM_001039877 /// NM_013403																				
5.92	5.51	0.41	2.75E-01	6.47E-01	NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	chr16p13.3	205090_s_at	NM_016256																				
2.34	2.19	0.15	2.76E-01	6.47E-01	---	---	---	1569947_at	---																				
2.42	2.24	0.18	2.76E-01	6.48E-01	---	---	---	1556769_a_at	---																				
3.36	3.21	0.15	2.76E-01	6.48E-01	---	---	---	1564984_at	---																				
5.35	5.01	0.34	2.76E-01	6.48E-01	TSFM	Ts translation elongation factor, mitochondrial	chr12q13-q14	214331_at	NM_005726																				
6.27	5.97	0.30	2.76E-01	6.48E-01	AEBP2	AE binding protein 2	chr12p12.3	225889_at	NM_001114176 /// NM_153207																				
6.95	6.70	0.25	2.76E-01	6.48E-01	L3MBTL2	l(3)mbt-like 2 (Drosophila)	chr22q13.31-q13.33	223205_s_at	NM_031488																				
2.07	1.94	0.13	2.76E-01	6.48E-01	HECTD2	HECT domain containing 2	chr10q23.32	238803_at	NM_173497 /// NM_182765																				
2.78	2.56	0.22	2.76E-01	6.48E-01	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	chr12q13.13	207552_at	NM_001002031 /// NM_005176																				
3.49	3.26	0.22	2.76E-01	6.48E-01	---	---	---	1555681_at	---																				
2.85	2.68	0.17	2.76E-01	6.48E-01	---	---	---	1564407_a_at	---																				
5.85	4.91	0.94	2.76E-01	6.48E-01	SEC14L4	SEC14-like 4 (S. cerevisiae)	chr22q12.2	239492_at	NM_174977																				
4.94	4.71	0.23	2.76E-01	6.48E-01	---	---	---	227009_at	---																				
3.53	3.34	0.19	2.76E-01	6.48E-01	---	---	---	1556971_a_at	---																				
2.85	2.70	0.14	2.76E-01	6.48E-01	---	---	---	1559817_at	---																				
2.04	1.90	0.14	2.76E-01	6.48E-01	---	---	---	1557256_a_at	---																				
7.67	7.31	0.35	2.76E-01	6.48E-01	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	chr16q22.1	225009_at	NM_178818 /// NM_181521																				
5.13	4.61	0.52	2.76E-01	6.48E-01	GM2A	GM2 ganglioside activator	chr5q31.3-q33.1	215891_s_at	NM_000405																				
2.52	2.30	0.22	2.76E-01	6.48E-01	HPS3	Hermansky-Pudlak syndrome 3	chr3q24	231121_at	NM_032383																				
2.50	2.37	0.12	2.76E-01	6.48E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	1566093_at	NM_015313																				
4.41	3.84	0.58	2.76E-01	6.48E-01	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	chr9q31	202490_at	NM_003640																				
6.33	6.13	0.20	2.76E-01	6.48E-01	MED13L	mediator complex subunit 13-like	chr12q24.21	212209_at	NM_015335																				
7.01	6.78	0.23	2.76E-01	6.48E-01	TEX264	testis expressed 264	chr3p21.31	233350_s_at	NM_001129884 /// NM_015926 /// NR_024012																				
7.06	6.82	0.24	2.76E-01	6.48E-01	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	chr5q35.3	212054_x_at	NM_015043 /// NM_198868																				
7.01	6.80	0.21	2.76E-01	6.48E-01	TUSC2	tumor suppressor candidate 2	chr3p21.3	203273_s_at	NM_007275																				
2.28	2.13	0.14	2.77E-01	6.48E-01	---	---	---	1559086_at	---																				
3.38	3.00	0.38	2.77E-01	6.48E-01	KIF21A	kinesin family member 21A	chr12q12	226003_at	NM_017641																				
4.61	4.16	0.45	2.77E-01	6.48E-01	---	---	---	240008_at	---																				
3.63	3.37	0.26	2.77E-01	6.48E-01	HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	chr1p13.1	204515_at	NM_000862																				
3.41	2.73	0.68	2.77E-01	6.48E-01	IL8	interleukin 8	chr4q13-q21	211506_s_at	NM_000584																				
6.31	5.98	0.32	2.77E-01	6.48E-01	C12orf65	chromosome 12 open reading frame 65	chr12q24.31	223477_s_at	NM_152269																				
7.04	6.84	0.20	2.77E-01	6.48E-01	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	chr13q32.2	201911_s_at	NM_001001715 /// NM_005766																				
5.02	4.81	0.21	2.77E-01	6.48E-01	TAPBP	TAP binding protein (tapasin)	chr6p21.3	1555565_s_at	NM_003190 /// NM_172208 /// NM_172209																				
2.56	2.42	0.13	2.77E-01	6.48E-01	PMCHL2	pro-melanin-concentrating hormone-like 2	chr5q13	224422_x_at	NR_003922																				
4.73	4.38	0.35	2.77E-01	6.49E-01	---	---	---	229716_at	---																				
8.86	8.56	0.30	2.77E-01	6.49E-01	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	chr17q23-q24	200603_at	NM_002734 /// NM_212471 /// NM_212472																				

3.29	3.15	0.14	2.77E-01	6.49E-01	LOC653160	Hypothetical protein LOC653160	chr1p34.3	236246_x_at	XM_927678 /// XM_932244 /// XM_941504 /// XM_945233
4.67	4.45	0.22	2.77E-01	6.49E-01	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide	chr6q13-q15	213321_at	NM_000056 /// NM_183050
2.13	2.00	0.14	2.77E-01	6.49E-01	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	chr17q24.2	235335_at	NM_080283
5.97	5.78	0.19	2.77E-01	6.49E-01	LOC390612	hypothetical LOC390612	chr15q25.1	222297_x_at	XR_017663 /// XR_018903 /// XR_038231
2.65	2.32	0.33	2.77E-01	6.49E-01	---	---	---	244811_at	---
3.68	3.53	0.15	2.77E-01	6.49E-01	TPPP	tubulin polymerization promoting protein	chr5p15.3	227643_at	NM_007030
4.03	3.83	0.20	2.77E-01	6.49E-01	PL-5283 /// SLC13A4	PL-5283 protein /// solute carrier family 13 (sodium/sulfate symporters), member 4	chr7q33	224758_at	NM_001130929 /// NM_012450 /// XM_930101 /// XM_935586 /// XM_938850
8.16	7.97	0.19	2.77E-01	6.49E-01	---	---	---	221844_x_at	---
2.22	2.10	0.12	2.77E-01	6.49E-01	PTTG2	pituitary tumor-transforming 2	chr4p12	214557_at	NM_006607
6.41	6.19	0.22	2.77E-01	6.49E-01	RRP1	ribosomal RNA processing 1 homolog (S. cerevisiae)	chr21q22.3	218758_s_at	NM_003683
4.47	4.24	0.23	2.77E-01	6.49E-01	ZNF346	zinc finger protein 346	chr5q35.2	236267_at	NM_012279
4.07	3.86	0.20	2.77E-01	6.49E-01	RNF207	ring finger protein 207	chr1p36.31	233065_at	NM_207396 /// XM_001716213 /// XM_001718203 /// XM_001719665
3.52	3.32	0.19	2.78E-01	6.49E-01	C4orf30	chromosome 4 open reading frame 30	chr4p15.32	219717_at	NM_017741
3.26	3.04	0.22	2.78E-01	6.49E-01	LIFR	leukemia inhibitory factor receptor alpha	chr5p13-p12	205876_at	NM_001127671 /// NM_002310
2.84	2.45	0.40	2.78E-01	6.49E-01	COL11A1	collagen, type XI, alpha 1	chr1p21	204320_at	NM_001854 /// NM_080629 /// NM_080630
6.69	6.53	0.17	2.78E-01	6.49E-01	ZC3HC1	zinc finger, C3HC-type containing 1	chr7q32.2	223163_s_at	NM_016478
2.30	2.12	0.19	2.78E-01	6.49E-01	---	---	---	217181_at	---
8.20	7.90	0.30	2.78E-01	6.49E-01	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	chr7q22.1	201954_at	NM_005720
7.34	7.11	0.23	2.78E-01	6.49E-01	TXNDC15	thioredoxin domain containing 15	chr5q31.1	227873_at	NM_024715
2.12	1.93	0.19	2.78E-01	6.49E-01	---	---	---	1557195_at	---
4.77	4.45	0.32	2.78E-01	6.49E-01	TTC12	tetratricopeptide repeat domain 12	chr11q23.1	219587_at	NM_017868
2.36	2.19	0.17	2.78E-01	6.49E-01	---	---	---	1566505_at	---
7.21	7.09	0.12	2.78E-01	6.49E-01	C20orf43	chromosome 20 open reading frame 43	chr20q13.31	217737_x_at	NM_016407
2.48	2.35	0.13	2.78E-01	6.49E-01	FAM115C	family with sequence similarity 115, member C	chr7q35	1564027_a_at	NM_001130025 /// NM_001130026 /// NM_173678
4.40	3.92	0.48	2.78E-01	6.49E-01	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	chrXp11.23	206756_at	NM_019886
2.14	2.02	0.12	2.78E-01	6.49E-01	---	---	---	1565876_x_at	---
4.37	4.09	0.28	2.78E-01	6.49E-01	TXNRD3	thioredoxin reductase 3	chr3q21.3	221906_at	XM_001129642 /// XM_001130163
3.71	3.58	0.13	2.78E-01	6.49E-01	C12orf47	chromosome 12 open reading frame 47	chr12q24.12	64432_at	NR_015404 /// XR_017874 /// XR_017973
3.08	2.81	0.27	2.78E-01	6.50E-01	---	---	---	238011_at	---

4.49	4.15	0.35	2.78E-01	6.50E-01	RTN1	reticulon 1	chr14q23.1	210222_s_at	NM_021136 /// NM_206852 /// NM_206857																			
6.46	6.24	0.22	2.78E-01	6.50E-01	STK11	serine/threonine kinase 11	chr19p13.3	41657_at	NM_000455																			
2.80	2.11	0.68	2.78E-01	6.50E-01	CRISP2	cysteine-rich secretory protein 2	chr6p21-qter	210262_at	NM_003296																			
2.19	2.06	0.13	2.79E-01	6.50E-01	---	---	---	215940_at	---																			
6.38	6.17	0.22	2.79E-01	6.50E-01	CTBS	chitobiase, di-N-acetyl-	chr1p22	218924_s_at	NM_004388																			
2.68	2.49	0.19	2.79E-01	6.50E-01	C17orf100	chromosome 17 open reading frame 100	chr17p13.2	229071_at	NM_001105520																			
2.19	2.02	0.17	2.79E-01	6.50E-01	BBS9	Bardet-Biedl syndrome 9	chr7p14	216239_at	NM_001033604 /// NM_001033605 /// NM_014451 /// NM_198428																			
6.19	5.85	0.34	2.79E-01	6.50E-01	C13orf37	chromosome 13 open reading frame 37	chr13q22.1	225578_at	NM_001071775																			
7.07	6.82	0.25	2.79E-01	6.50E-01	EFHD2	EF-hand domain family, member D2	chr1p36.21	217992_s_at	NM_024329																			
2.44	2.14	0.30	2.79E-01	6.50E-01	C5orf24	chromosome 5 open reading frame 24	chr5q31.1	1553106_at	NM_152409																			
2.57	2.39	0.18	2.79E-01	6.50E-01	LOC100130744	hypothetical LOC100130744	chr5p15.2	236228_at	XM_001720249 /// XM_001721727 /// XM_001724061																			
7.35	7.14	0.21	2.79E-01	6.50E-01	VGLL4	vestigial like 4 (Drosophila)	chr3p25.2	214004_s_at	NM_001128219 /// NM_001128220 /// NM_001128221 /// NM_014667																			
6.17	5.89	0.28	2.79E-01	6.50E-01	HTF9C	HpaII tiny fragments locus 9C	chr22q11.1-22q13|22q11.21	218475_at	NM_022727 /// NM_182984																			
2.63	2.45	0.19	2.79E-01	6.50E-01	LOC100132767	hypothetical protein LOC100132767	chr16p11.2	1569523_a_at	XM_001720251 /// XM_001725561																			
3.69	3.44	0.25	2.79E-01	6.50E-01	OGG1	8-oxoguanine DNA glycosylase	chr3p26.2	205760_s_at	NM_002542 /// NM_016819 /// NM_016820 /// NM_016821 /// NM_016826 /// NM_016827 /// NM_016828 /// NM_016829																			
3.24	3.03	0.22	2.79E-01	6.51E-01	---	---	---	1569537_at	---																			
2.08	1.96	0.12	2.79E-01	6.51E-01	---	---	---	1566969_at	---																			
7.93	7.63	0.31	2.79E-01	6.51E-01	MTA3	metastasis associated 1 family, member 3	chr2p21	223311_s_at	NM_020744																			
7.35	6.89	0.46	2.79E-01	6.51E-01	CRYZ	crystallin, zeta (quinone reductase)	chr1p31-p22	202950_at	NM_001130042 /// NM_001130043 /// NM_001134759 /// NM_001889																			
6.28	5.94	0.34	2.79E-01	6.51E-01	41525	septin 8	chr5q31	208999_at	NM_001098811 /// NM_001098812 /// NM_001098813 /// NM_015146																			
3.69	3.53	0.17	2.79E-01	6.51E-01	LOC154822	hypothetical LOC154822	chr7q36.3	243261_at	---																			

2.72	2.50	0.22	2.79E-01	6.51E-01	C17orf69	chromosome 17 open reading frame 69	chr17q21.31	1553400_a_at	XR_040436 /// XR_040437 /// XR_040438																				
4.95	4.73	0.22	2.79E-01	6.51E-01	TRIM33	tripartite motif-containing 33	chr1p13.1	212436_at	NM_015906 /// NM_033020																				
2.79	2.57	0.22	2.80E-01	6.51E-01	PTPRO	protein tyrosine phosphatase, receptor type, O	chr12p13.3-p13.2|12p13-p12	208121_s_at	NM_002848 /// NM_030667 /// NM_030668 /// NM_030669 /// NM_030670 /// NM_030671																				
6.60	6.34	0.27	2.80E-01	6.51E-01	C19orf6	chromosome 19 open reading frame 6	chr19p13.3	225247_at	NM_001033026 /// NM_033420																				
8.26	7.69	0.56	2.80E-01	6.51E-01	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	chr6p21.3	213451_x_at	NM_019105 /// NM_032470 /// NR_001284																				
6.41	6.17	0.24	2.80E-01	6.51E-01	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	chr1p22.1	209187_at	NM_001938																				
2.66	2.47	0.19	2.80E-01	6.51E-01	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	chr17p12-p11.2	232262_at	NM_004278																				
3.27	3.13	0.15	2.80E-01	6.51E-01	---	---	---	233428_at	---																				
3.41	3.22	0.19	2.80E-01	6.51E-01	FAM69B	Family with sequence similarity 69, member B	chr9q34.3	229003_x_at	NM_152421																				
3.00	2.82	0.18	2.80E-01	6.51E-01	DDI2	DDI1, DNA-damage inducible 1, homolog 2 (S. cerevisiae)	chr1p36.21	224449_at	NM_032341																				
2.77	2.36	0.41	2.80E-01	6.52E-01	C5orf33	chromosome 5 open reading frame 33	chr5p13.2	229299_at	NM_001085411 /// NM_153013																				
4.89	4.61	0.28	2.80E-01	6.52E-01	SUSD1	sushi domain containing 1	chr9q31.3-q33.1	226264_at	NM_022486																				
7.32	7.08	0.24	2.80E-01	6.52E-01	MRPL52	mitochondrial ribosomal protein L52	chr14q11.2	226241_s_at	NM_178336 /// NM_180982 /// NM_181304 /// NM_181305 /// NM_181306 /// NM_181307																				
11.10	10.91	0.19	2.80E-01	6.52E-01	PFDN5	prefoldin subunit 5	chr12q12	207132_x_at	NM_002624 /// NM_145897																				
2.50	2.31	0.20	2.80E-01	6.52E-01	CR1 /// CR1L	complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1-like	chr1q32 /// chr1q32.1	239205_s_at	NM_000573 /// NM_000651 /// NM_175710																				
3.87	3.68	0.19	2.80E-01	6.52E-01	---	---	---	1566029_at	---																				
2.37	2.23	0.14	2.81E-01	6.52E-01	TRPM3	transient receptor potential cation channel, subfamily M, member 3	chr9q21.11-q21.12	216452_at	NM_001007470 /// NM_001007471 /// NM_020952 /// NM_024971 /// NM_206944 /// NM_206945 /// NM_206946 /// NM_206947 /// NM_206948																				

5.41	5.08	0.33	2.81E-01	6.52E-01	SEC23B	Sec23 homolog B (S. cerevisiae)	chr20p11.23	201582_at	NM_006363 /// NM_032985 /// NM_032986																				
2.91	2.73	0.18	2.81E-01	6.52E-01	hCG_1774568	similar to hCG1774568	chr13q34	220354_at	XM_001715564																				
10.43	10.29	0.14	2.81E-01	6.53E-01	EIF1	eukaryotic translation initiation factor 1	chr17q21.2	212130_x_at	NM_005801																				
6.18	5.88	0.30	2.81E-01	6.53E-01	TNFSF12 /// TNFSF12-TNFSF13 /// TNFSF13	tumor necrosis factor (ligand) superfamily, member 12 /// TNFSF12-TNFSF13 /// tumor necrosis factor (ligand) superfamily, member 13	chr17p13 /// chr17p13.1	211495_x_at	NM_003808 /// NM_003809 /// NM_172087 /// NM_172088 /// NM_172089																				
3.70	3.45	0.25	2.81E-01	6.53E-01	---	---	---	1555461_at	---																				
4.54	4.24	0.29	2.81E-01	6.53E-01	NAV1	neuron navigator 1	chr1q32.3	227584_at	NM_020443																				
3.24	3.06	0.19	2.81E-01	6.53E-01	FLJ35776	Hypothetical LOC649446	chr18p11.31	239421_at	NM_001039796 /// NR_024101																				
4.74	4.57	0.17	2.81E-01	6.53E-01	JMJD5	jumonji domain containing 5	chr16p12.1	220070_at	NM_024773																				
5.62	5.22	0.39	2.81E-01	6.53E-01	DPY19L1	dpy-19-like 1 (C. elegans)	chr7p14.3	212792_at	NM_015283																				
7.21	6.96	0.26	2.81E-01	6.53E-01	SLC41A1	solute carrier family 41, member 1	chr1q32.1	225570_at	NM_173854																				
3.61	3.42	0.19	2.81E-01	6.53E-01	LOC284630	hypothetical protein LOC284630	chr1p36.32	1565729_at	---																				
3.63	3.43	0.21	2.81E-01	6.53E-01	CENTD1	centaurin, delta 1	chr4p14	214102_at	NM_015230 /// NM_139182																				
7.47	7.23	0.23	2.81E-01	6.53E-01	C5orf4	chromosome 5 open reading frame 4	chr5q31-q32	48030_i_at	NM_016348 /// NM_032385																				
5.19	4.88	0.31	2.81E-01	6.53E-01	STK10	serine/threonine kinase 10	chr5q35.1	40420_at	NM_005990																				
2.27	2.14	0.13	2.81E-01	6.53E-01	HRH4	histamine receptor H4	chr18q11.2	221169_s_at	NM_021624																				
3.59	3.30	0.30	2.81E-01	6.53E-01	---	---	---	229754_at	---																				
5.87	5.58	0.29	2.81E-01	6.53E-01	MED23	mediator complex subunit 23	chr6q22.33-q24.1	218846_at	NM_004830 /// NM_015979																				
6.52	6.23	0.29	2.81E-01	6.53E-01	PRMT2	protein arginine methyltransferase 2	chr21q22.3	202098_s_at	NM_001535 /// NM_206962																				
5.32	4.92	0.39	2.81E-01	6.53E-01	AKIRIN1	akirin 1	chr1p34.3	222458_s_at	NM_024595																				
2.33	2.16	0.16	2.81E-01	6.53E-01	JPH1	junctophilin 1	chr8q21	1553533_at	NM_020647																				
7.37	7.06	0.31	2.82E-01	6.53E-01	MGC21874	transcriptional adaptor 2 (ADA2 homolog, yeast)-beta	chr4p16.1	236248_x_at	NM_152293																				
2.69	2.51	0.18	2.82E-01	6.53E-01	---	---	---	216792_at	---																				
2.94	2.79	0.15	2.82E-01	6.53E-01	ZNF143	zinc finger protein 143	chr11p15.4	206428_s_at	NM_003442																				
8.18	7.94	0.24	2.82E-01	6.53E-01	TMEM219	transmembrane protein 219	chr16p11.2	224981_at	NM_001083613 /// NM_194280																				
4.42	4.29	0.13	2.82E-01	6.53E-01	CMIP	C-Maf-inducing protein	chr16q23	243720_at	NM_030629 /// NM_198390																				
3.27	3.05	0.22	2.82E-01	6.53E-01	---	---	---	229117_s_at	---																				
2.40	2.23	0.17	2.82E-01	6.53E-01	LOC389857 /// LOC441495	hypothetical protein /// hypothetical LOC441495	chrXp11.22	236756_at	XM_001717451 /// XM_372214 /// XM_497110 /// XM_938184																				
3.06	2.86	0.19	2.82E-01	6.53E-01	C3orf23	chromosome 3 open reading frame 23	chr3p21.33-p21.32	1555905_a_at	NM_001029839 /// NM_001029840 /// NM_173826																				
4.56	4.32	0.23	2.82E-01	6.53E-01	FAM110A	family with sequence similarity 110, member A	chr20p13	226584_s_at	NM_001042353 /// NM_031424 /// NM_207121																				
2.86	2.69	0.18	2.82E-01	6.53E-01	---	---	---	232118_at	---																				
2.65	2.48	0.17	2.82E-01	6.53E-01	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	chr20p12.1	222765_x_at	NM_016649																				
11.80	11.67	0.13	2.82E-01	6.53E-01	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	chr11q13	200019_s_at	NM_001997																				
2.31	2.18	0.13	2.82E-01	6.53E-01	---	---	---	215347_at	---																				

9.37	9.18	0.18	2.82E-01	6.53E-01	ENO1	enolase 1, (alpha)	chr1p36.3-p36.2	201231_s_at	NM_001428
10.16	9.76	0.40	2.82E-01	6.53E-01	FDX1	ferredoxin 1	chr11q22	203646_at	NM_004109
7.05	6.75	0.30	2.82E-01	6.53E-01	LOC92482	UPF0604 protein	chr10q25.2	213220_at	XM_001716109 /// XM_001725802 /// XM_001725803 /// XM_001725804 /// XM_001726022 /// XM_001726023 /// XM_001726024
5.00	4.83	0.17	2.82E-01	6.53E-01	SLC25A22	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	chr11p15.5	218725_at	NM_024698
2.75	2.35	0.41	2.82E-01	6.53E-01	AMY1A /// AMY1B /// AMY1C /// AMY2A /// AMY2B	amylase, alpha 1A (salivary) /// amylase, alpha 1B (salivary) /// amylase, alpha 1C (salivary) /// amylase, alpha 2A (pancreatic) /// amylase, alpha 2B (pancreatic)	chr1p21	208498_s_at	NM_000699 /// NM_001008218 /// NM_001008219 /// NM_001008221 /// NM_004038 /// NM_020978
2.86	2.71	0.15	2.82E-01	6.53E-01	LOC348120	Hypothetical LOC727899	chr15q11.2	231132_at	---
2.10	1.98	0.13	2.82E-01	6.53E-01	HR44	Hr44 antigen	---	216872_at	---
2.35	2.20	0.15	2.82E-01	6.53E-01	LOC153469	hypothetical protein LOC153469	chr5q32	1561101_at	XM_001720001 /// XM_001723918 /// XM_001724056
4.68	3.88	0.81	2.82E-01	6.53E-01	---	---	---	233127_at	---
7.31	7.03	0.29	2.82E-01	6.53E-01	PERP	PERP, TP53 apoptosis effector	chr6q24	222392_x_at	NM_022121
4.40	4.04	0.36	2.83E-01	6.53E-01	LIX1L	Lix1 homolog (mouse)-like	chr1q21.1	235036_at	NM_153713
6.53	6.05	0.48	2.83E-01	6.53E-01	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	chr1p31	202502_at	NM_000016 /// NM_001127328
6.83	6.50	0.33	2.83E-01	6.53E-01	ARPP-19	cyclic AMP phosphoprotein, 19 kD	chr15q21.2	221482_s_at	NM_006628
3.23	3.00	0.23	2.83E-01	6.53E-01	ARPM1	actin related protein M1	chr3q26.2	223665_at	NM_032487
4.46	4.21	0.25	2.83E-01	6.53E-01	C8orf76	chromosome 8 open reading frame 76	chr8q24.13	225702_at	NM_032847
2.36	2.08	0.29	2.83E-01	6.53E-01	DSEL	dermatan sulfate epimerase-like	chr18q22.1	232825_s_at	NM_032160
3.95	3.76	0.19	2.83E-01	6.54E-01	LOC286359	hypothetical protein LOC286359	chr9q22.33	1563607_x_at	XR_040737 /// XR_040738 /// XR_040739
7.71	7.54	0.16	2.83E-01	6.54E-01	DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	chr1p35.3	212491_s_at	NM_014280
2.03	1.89	0.14	2.83E-01	6.54E-01	FOXR1	forkhead box R1	chr11q23.3	237613_at	NM_181721
6.55	6.09	0.47	2.83E-01	6.54E-01	CXorf15	chromosome X open reading frame 15	chrXp22.2	227520_at	NM_018360
5.59	5.04	0.55	2.83E-01	6.54E-01	KIF16B	kinesin family member 16B	chr20p11.23	232083_at	NM_024704
6.57	5.89	0.68	2.83E-01	6.54E-01	GEM	GTP binding protein overexpressed in skeletal muscle	chr8q13-q21	204472_at	NM_005261 /// NM_181702
7.23	6.88	0.35	2.83E-01	6.54E-01	GAS2L1	growth arrest-specific 2 like 1	chr22q12.2	31874_at	NM_006478 /// NM_152236 /// NM_152237
5.56	5.10	0.46	2.83E-01	6.54E-01	IMPAD1	inositol monophosphatase domain containing 1	chr8q12.1	222654_at	NM_017813
3.02	2.76	0.26	2.83E-01	6.54E-01	BHLHB3	basic helix-loop-helix domain containing, class B, 3	chr12p11.23-p12.1	223185_s_at	NM_030762
6.38	6.03	0.34	2.83E-01	6.54E-01	RYBP	RING1 and YY1 binding protein	chr3p13	201845_s_at	NM_012234
3.87	3.45	0.43	2.83E-01	6.54E-01	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	chr3q26.1	226098_at	NM_020800
4.89	4.68	0.21	2.83E-01	6.54E-01	---	---	---	238904_at	---
2.71	2.54	0.17	2.83E-01	6.54E-01	ASB9	ankyrin repeat and SOCS box-containing 9	---	205673_s_at	NM_001031739 /// NM_024087
6.05	5.88	0.17	2.83E-01	6.54E-01	ZNF259	zinc finger protein 259	chr11q23.3	200054_at	NM_003904

2.37	2.22	0.15	2.83E-01	6.54E-01	BTBD11	BTB (POZ) domain containing 11	chr12q23.3	238692_at	NM_001017523 /// NM_001018072																			
5.34	5.08	0.26	2.83E-01	6.54E-01	HRB	HIV-1 Rev binding protein	chr2q36.3	218092_s_at	NM_004504																			
2.64	2.49	0.15	2.83E-01	6.54E-01	IFNA7	interferon, alpha 7	chr9p22	208259_x_at	NM_021057																			
2.25	2.11	0.14	2.83E-01	6.54E-01	FLJ32063	hypothetical protein LOC150538	chr2q33.1	1553420_at	XR_041743 /// XR_041744 /// XR_041745																			
2.63	2.50	0.13	2.84E-01	6.54E-01	---	---	---	1556460_a_at	---																			
4.09	3.86	0.23	2.84E-01	6.54E-01	APEH	N-acylaminoacyl-peptide hydrolase	chr3p21.31	242015_x_at	NM_001640																			
4.77	4.58	0.19	2.84E-01	6.54E-01	DPP9	dipeptidyl-peptidase 9	chr19p13.3	230018_at	NM_139159																			
1.98	1.85	0.13	2.84E-01	6.54E-01	DMD	Dystrophin	chrXp21.2	234752_x_at	NM_000109 /// NM_004006 /// NM_004007 /// NM_004009 /// NM_004010 /// NM_004011 /// NM_004012 /// NM_004013 /// NM_004014 /// NM_004015 /// NM_004016 /// NM_004017 /// NM_004018 /// NM_004019 /// NM_004020 /// NM_004021 /// NM_004022 /// NM_004023																	
2.94	2.78	0.16	2.84E-01	6.55E-01	TMEM121	transmembrane protein 121	chr14q32.33	222914_s_at	NM_025268																			
7.26	7.05	0.22	2.84E-01	6.55E-01	DHPS	deoxyhypusine synthase	chr19p13.2-p13.1	207831_x_at	NM_001930 /// NM_013406 /// NM_013407																			
2.48	2.34	0.14	2.84E-01	6.55E-01	---	---	---	241015_at	---																			
2.97	2.82	0.15	2.84E-01	6.55E-01	PDPN	podoplanin	chr1p36.21	226658_at	NM_001006624 /// NM_001006625 /// NM_006474 /// NM_198389																			
3.10	2.93	0.17	2.84E-01	6.55E-01	---	---	---	232769_at	---																			
6.93	6.73	0.20	2.84E-01	6.55E-01	GRLF1	glucocorticoid receptor DNA binding factor 1	chr19q13.3	229394_s_at	NM_004491																			
2.27	2.11	0.16	2.84E-01	6.55E-01	---	---	---	1557179_s_at	---																			
6.21	5.98	0.24	2.84E-01	6.55E-01	RNF126	ring finger protein 126	chr19p13.3	223332_x_at	NM_194460																			
2.30	2.16	0.13	2.84E-01	6.55E-01	CCDC138	Coiled-coil domain containing 138	chr2q13	230339_at	NM_144978																			
6.30	5.92	0.38	2.84E-01	6.55E-01	TRIB2	tribbles homolog 2 (Drosophila)	chr2p25.1-p24.3	202479_s_at	NM_021643																			
3.10	2.91	0.19	2.84E-01	6.55E-01	---	---	---	1560862_at	---																			
2.79	2.57	0.23	2.84E-01	6.55E-01	ARMC8	armadillo repeat containing 8	chr3q22.3	1555281_x_at	NM_014154 /// NM_015396 /// NM_213654																			
2.02	1.89	0.12	2.84E-01	6.55E-01	---	---	---	244009_at	---																			

2.28	2.14	0.14	2.84E-01	6.55E-01	---	---	---	243472_at	---																			
2.32	2.15	0.17	2.85E-01	6.55E-01	---	---	---	1563856_at	---																			
2.68	2.52	0.16	2.85E-01	6.55E-01	OSBPL3	oxysterol binding protein-like 3	chr7p15	209626_s_at	NM_015550 /// NM_145320 /// NM_145321 /// NM_145322																			
5.78	5.48	0.29	2.85E-01	6.55E-01	ZNF618	zinc finger protein 618	chr9q32	238444_at	NM_133374																			
5.09	4.79	0.30	2.85E-01	6.55E-01	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	chr14q32.3	217849_s_at	NM_006035																			
5.90	5.67	0.23	2.85E-01	6.55E-01	C17orf90	chromosome 17 open reading frame 90	chr17q25.3	221797_at	NM_001039842																			
3.03	2.84	0.19	2.85E-01	6.55E-01	---	---	---	242434_at	---																			
1.86	1.76	0.11	2.85E-01	6.55E-01	---	---	---	220656_at	---																			
2.41	2.27	0.14	2.85E-01	6.55E-01	KCNIP2	Kv channel interacting protein 2	chr10q24	1555230_a_at	NM_014591 /// NM_173191 /// NM_173192 /// NM_173193 /// NM_173194 /// NM_173195 /// NM_173197																			
2.70	2.54	0.16	2.85E-01	6.55E-01	LMX1A	LIM homeobox transcription factor 1, alpha	chr1q22-q23	1553541_at	NM_001033507 /// NM_177398 /// NM_177399																			
3.08	2.93	0.15	2.85E-01	6.55E-01	LOC553103	hypothetical LOC553103	---	241899_at	---																			
3.78	3.49	0.29	2.85E-01	6.55E-01	---	---	---	230596_at	---																			
3.15	2.93	0.22	2.85E-01	6.55E-01	FAM53A	family with sequence similarity 53, member A	chr4p16.3	1569139_s_at	NM_001013622																			
7.31	7.05	0.26	2.85E-01	6.55E-01	CCDC51	coiled-coil domain containing 51	chr3p21.31	218722_s_at	NM_024661																			
6.69	6.40	0.29	2.85E-01	6.55E-01	GMEB2	glucocorticoid modulatory element binding protein 2	chr20q13.33	44146_at	NM_012384																			
5.25	4.66	0.59	2.85E-01	6.56E-01	OLFM1	olfactomedin 1	chr9q34.3	213131_at	NM_006334 /// NM_014279																			
7.73	7.43	0.31	2.85E-01	6.56E-01	KIAA0515	KIAA0515	chr9q34.13	212068_s_at	NM_013318																			
3.78	3.59	0.19	2.85E-01	6.56E-01	LMO4	LIM domain only 4	chr1p22.3	209204_at	NM_006769																			
2.54	2.34	0.21	2.85E-01	6.56E-01	---	---	---	229896_at	---																			
2.90	2.74	0.16	2.85E-01	6.56E-01	EPB42	erythrocyte membrane protein band 4.2	chr15q15-q21	210746_s_at	NM_000119 /// NM_001114134																			
5.16	4.70	0.46	2.85E-01	6.56E-01	KIAA1274	KIAA1274	chr10q22.1	231887_s_at	NM_014431																			
4.96	4.60	0.36	2.85E-01	6.56E-01	FBXO31	F-box protein 31	chr16q24.2	219785_s_at	NM_024735																			
2.39	2.23	0.16	2.85E-01	6.56E-01	CLRN3	clarin 3	chr10q26.2	229777_at	NM_152311																			
2.14	2.01	0.13	2.85E-01	6.56E-01	---	---	---	1557705_a_at	---																			
4.44	4.07	0.37	2.85E-01	6.56E-01	MSI2	musashi homolog 2 (Drosophila)	chr17q22	1552364_s_at	NM_138962 /// NM_170721																			
3.46	3.30	0.16	2.85E-01	6.56E-01	MARVELD3	MARVEL domain containing 3	chr16q22.3	239350_at	NM_001017967 /// NM_052858																			
5.62	5.30	0.32	2.85E-01	6.56E-01	C20orf112	chromosome 20 open reading frame 112	chr20q11.1-q11.23	225224_at	NM_080616																			
7.24	7.03	0.21	2.85E-01	6.56E-01	HLA-G	major histocompatibility complex, class I, G	chr6p21.3	211530_x_at	NM_002127																			
5.45	5.05	0.40	2.85E-01	6.56E-01	PYY2	peptide YY, 2 (seminalplasmin)	chr17q11	220209_at	NR_003064																			
4.03	3.87	0.16	2.85E-01	6.56E-01	DDX19B	DEAD (Asp-Glu-Ala-As) box polypeptide 19B	chr16q22.1	230974_at	NM_001014449 /// NM_001014451 /// NM_007242																			
3.16	2.96	0.19	2.85E-01	6.56E-01	CEP135	centrosomal protein 135kDa	chr4q12	206003_at	NM_025009																			
4.66	4.39	0.27	2.85E-01	6.56E-01	KRT80	keratin 80	chr12q13.13	231849_at	NM_001081492 /// NM_182507																			
2.88	2.72	0.16	2.86E-01	6.56E-01	---	---	---	233726_at	---																			
2.21	2.08	0.13	2.86E-01	6.56E-01	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	chr4q32.3	1559585_at	NM_001012967																			

2.97	2.76	0.21	2.86E-01	6.56E-01	LOC100128946	Hypothetical protein LOC100128946	chr22q13.32	1557588_at	XM_001719910 /// XM_001725064 /// XM_001726053																			
7.35	7.05	0.30	2.86E-01	6.56E-01	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	chr10q21	224654_at	NM_004728																			
4.89	4.44	0.45	2.86E-01	6.56E-01	CHD1	chromodomain helicase DNA binding protein 1	chr5q15-q21	235791_x_at	NM_001270																			
3.10	2.81	0.28	2.86E-01	6.56E-01	TARP	TCR gamma alternate reading frame protein	chr7p15-p14	209813_x_at	NM_001003799 /// NM_001003806																			
4.49	4.08	0.41	2.86E-01	6.56E-01	RASSF5	Ras association (RalGDS/AF-6) domain family member 5	chr1q32.1	1554834_a_at	NM_182663 /// NM_182664 /// NM_182665																			
6.15	5.65	0.50	2.86E-01	6.56E-01	KIAA1530	KIAA1530	chr4p16.3	233893_s_at	NM_020894 /// XM_001720077																			
5.67	5.45	0.21	2.86E-01	6.56E-01	CRKRS	Cdc2-related kinase, arginine/serine-rich	chr17q12	225691_at	NM_015083 /// NM_016507																			
2.20	2.05	0.14	2.86E-01	6.56E-01	GSG1	germ cell associated 1	chr12p13.1	241553_at	NM_001080554 /// NM_001080555 /// NM_031289 /// NM_153823																			
2.41	2.25	0.16	2.86E-01	6.56E-01	---	---	---	1566986_at	---																			
6.95	6.70	0.25	2.86E-01	6.56E-01	INTS10	integrator complex subunit 10	chr8p21.3	229632_s_at	NM_018142																			
2.54	2.35	0.18	2.86E-01	6.56E-01	ARHGAP28	Rho GTPase activating protein 28	chr18p11.31	220381_at	NM_001010000 /// NM_030672																			
2.77	2.63	0.14	2.86E-01	6.56E-01	ZNF81	zinc finger protein 81	chrXp11.23	1561039_a_at	NM_007137																			
5.35	5.09	0.26	2.86E-01	6.56E-01	RPAP1	RNA polymerase II associated protein 1	chr15q15.1	218441_s_at	NM_015540																			
2.64	2.50	0.14	2.86E-01	6.56E-01	DMRT2	doublesex and mab-3 related transcription factor 2	chr9p24.3	223986_x_at	NM_001130865 /// NM_006557 /// NM_181872																			
2.92	2.71	0.20	2.86E-01	6.56E-01	BCL2L11	BCL2-like 11 (apoptosis facilitator)	chr2q13	222343_at	NM_006538 /// NM_138621 /// NM_207002																			
6.04	5.68	0.36	2.86E-01	6.56E-01	GM2A	GM2 ganglioside activator	chr5q31.3-q33.1	33646_g_at	NM_000405																			
3.58	3.34	0.24	2.86E-01	6.56E-01	RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)	chr19q13.42	227360_at	NM_138412																			
2.97	2.76	0.22	2.86E-01	6.56E-01	NHLRC2	NHL repeat containing 2	chr10q25.3	244320_at	NM_198514																			
6.80	6.48	0.32	2.86E-01	6.56E-01	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	chr12q13-q14	209518_at	NM_003076 /// NM_139071																			
3.58	3.27	0.31	2.86E-01	6.56E-01	RAB28	RAB28, member RAS oncogene family	chr4p15.33	209084_s_at	NM_001017979 /// NM_004249																			
7.60	7.33	0.27	2.86E-01	6.56E-01	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	chr1p33-p32.3	224729_s_at	NM_001042546 /// NM_022745																			
2.23	2.11	0.12	2.86E-01	6.56E-01	BCAS1	Breast carcinoma amplified sequence 1	chr20q13.2	234780_at	NM_003657																			
10.35	10.13	0.22	2.86E-01	6.57E-01	TPI1	triosephosphate isomerase 1	chr12p13	200822_x_at	NM_000365																			
3.71	3.49	0.22	2.86E-01	6.57E-01	AKIRIN2	Akirin 2	chr6q15	213810_s_at	NM_018064																			
3.32	3.16	0.16	2.87E-01	6.57E-01	---	---	---	1559522_at	---																			
2.42	2.25	0.17	2.87E-01	6.57E-01	---	---	---	1559259_at	---																			
5.24	4.89	0.35	2.87E-01	6.57E-01	FAM86B1	family with sequence similarity 86, member B1	chr8p23.1	65585_at	NM_001083537 /// NR_003494																			
6.70	6.49	0.22	2.87E-01	6.57E-01	DSCR3	Down syndrome critical region gene 3	chr21q22.2	203635_at	NM_006052																			
10.72	10.56	0.16	2.87E-01	6.57E-01	SNX3	sorting nexin 3	chr6q21	210648_x_at	NM_003795																			
3.45	3.26	0.18	2.87E-01	6.57E-01	L3MBTL	l(3)mbt-like (Drosophila)	chr20q13.12	216077_s_at	NM_015478 /// NM_032107																			
3.03	2.87	0.15	2.87E-01	6.57E-01	KCTD7	potassium channel tetramerisation domain containing 7	chr7q11.21	1553717_at	NM_153033																			
6.02	5.53	0.49	2.87E-01	6.57E-01	---	---	---	240135_x_at	---																			
2.51	2.38	0.12	2.87E-01	6.57E-01	SYNJ2	synaptojanin 2	chr6q25.3	240257_at	NM_003898																			
2.28	2.14	0.14	2.87E-01	6.57E-01	SMPX	small muscle protein, X-linked	chrXp22.1	219772_s_at	NM_014332																			

3.82	3.56	0.26	2.87E-01	6.57E-01	---	---	---	1555845_at	---
2.79	2.65	0.14	2.87E-01	6.57E-01	CFDP1	Craniofacial development protein 1	chr16q22.2-q22.3	236588_at	NM_006324
2.25	2.14	0.11	2.87E-01	6.57E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	234402_at	---
2.68	2.48	0.20	2.87E-01	6.57E-01	MYT1	myelin transcription factor 1	chr20q13.33	210341_at	NM_004535
2.25	2.10	0.14	2.87E-01	6.57E-01	---	---	---	1561867_at	---
2.25	2.12	0.13	2.87E-01	6.57E-01	C14orf91	chromosome 14 open reading frame 91	chr14q22.1-q23.3	1570162_at	---
4.61	4.43	0.18	2.87E-01	6.57E-01	TSPYL1	TSPY-like 1	chr6q22-q23	1560648_s_at	NM_003309
2.27	2.13	0.14	2.87E-01	6.57E-01	---	---	---	239340_at	---
4.46	4.18	0.27	2.87E-01	6.57E-01	WDR5	WD repeat domain 5	chr9q34	223308_s_at	NM_017588 /// NM_052821
4.29	3.92	0.37	2.87E-01	6.57E-01	ADAMTSL1	ADAMTS-like 1	chr9p22.2-p22.1	239909_at	NM_001040272 /// NM_052866
7.64	7.29	0.35	2.87E-01	6.57E-01	VISA	virus-induced signaling adapter	chr20p13	226495_at	NM_020746
2.72	2.53	0.19	2.87E-01	6.57E-01	CNTLN	centlein, centrosomal protein	chr9p22.2	239989_at	NM_001114395 /// NM_017738
6.14	5.81	0.32	2.87E-01	6.57E-01	PBX2	pre-B-cell leukemia homeobox 2	chr6p21.3	202875_s_at	NM_002586
3.19	3.00	0.19	2.87E-01	6.57E-01	NFKBID	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	chr19q13.12	1553042_a_at	NM_139239
3.27	3.07	0.20	2.87E-01	6.57E-01	TCTE3	t-complex-associated-testis-expressed 3	chr6q27	1554400_at	NM_174910
4.36	4.18	0.18	2.87E-01	6.57E-01	SOCS3	suppressor of cytokine signaling 3	chr17q25.3	206360_s_at	NM_003955
2.18	2.03	0.14	2.87E-01	6.57E-01	---	---	---	244451_x_at	---
2.54	2.37	0.17	2.87E-01	6.57E-01	ZNF540	Zinc finger protein 540	chr19q13.12	229328_at	NM_152606
2.06	1.95	0.11	2.87E-01	6.57E-01	C9orf93	chromosome 9 open reading frame 93	chr9p22.3	236945_at	NM_173550
2.33	2.14	0.19	2.88E-01	6.57E-01	ZNF280C	zinc finger protein 280C	chrXq25	235520_at	NM_017666
6.49	6.10	0.39	2.88E-01	6.57E-01	PCTK1	PCTAIRE protein kinase 1	chrXp11.3-p11.23	207239_s_at	NM_006201 /// NM_033018
5.61	5.37	0.24	2.88E-01	6.57E-01	---	---	---	236671_at	---
2.77	2.54	0.23	2.88E-01	6.57E-01	---	---	---	236106_at	---
2.55	2.35	0.20	2.88E-01	6.57E-01	CD109	CD109 molecule	chr6q13	239719_at	NM_133493
4.60	4.00	0.59	2.88E-01	6.57E-01	---	---	---	236190_at	---
6.56	6.34	0.22	2.88E-01	6.57E-01	MAX	MYC associated factor X	chr14q23	210734_x_at	NM_002382 /// NM_145112 /// NM_145113 /// NM_145114 /// NM_145116 /// NM_197957
4.87	4.51	0.37	2.88E-01	6.57E-01	---	---	---	230894_s_at	---
2.50	2.34	0.15	2.88E-01	6.57E-01	C12orf65	chromosome 12 open reading frame 65	chr12q24.31	232650_at	NM_152269
8.04	7.68	0.37	2.88E-01	6.57E-01	C16orf14	chromosome 16 open reading frame 14	chr16p13.3	1553715_s_at	NM_138418
4.34	4.18	0.16	2.88E-01	6.57E-01	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	chr5q31.2	227169_at	NM_152686
2.14	2.01	0.13	2.88E-01	6.58E-01	---	---	---	1563371_at	---
3.15	3.01	0.14	2.88E-01	6.58E-01	KIAA0484	hypothetical LOC57240	---	216000_at	---
2.70	2.55	0.15	2.88E-01	6.58E-01	STC1	stanniocalcin 1	chr8p21-p11.2	204596_s_at	NM_003155
2.79	2.59	0.19	2.88E-01	6.58E-01	EZH2	enhancer of zeste homolog 2 (Drosophila)	chr7q35-q36	203358_s_at	NM_004456 /// NM_152998
3.62	3.34	0.28	2.88E-01	6.58E-01	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	chr14q12-q13	217986_s_at	NM_013448 /// NM_182648
2.24	2.10	0.14	2.88E-01	6.58E-01	---	---	---	1570385_at	---
7.97	7.50	0.46	2.88E-01	6.58E-01	PORCN	porcupine homolog (Drosophila)	chrXp11.23	219483_s_at	NM_022825 /// NM_203473 /// NM_203474 /// NM_203475 /// NM_203476
2.38	2.22	0.16	2.88E-01	6.58E-01	NCR2	natural cytotoxicity triggering receptor 2	chr6p21.1	221075_s_at	NM_004828
3.20	3.08	0.12	2.88E-01	6.58E-01	SPPL2B	signal peptide peptidase-like 2B	chr19p13.3	210693_at	NM_001077238 /// NM_152988
1.95	1.83	0.12	2.88E-01	6.58E-01	LOC283666	Hypothetical LOC283666	chr15q21.3	241760_x_at	---
3.23	3.04	0.20	2.89E-01	6.58E-01	---	---	---	235217_at	---
5.10	4.80	0.30	2.89E-01	6.58E-01	TSSC4	tumor suppressing subtransferable candidate 4	chr11p15.5	218612_s_at	NM_005706

2.24	2.08	0.16	2.89E-01	6.58E-01	LOC730200	Hypothetical LOC730200	chr2p14	233172_at	XM_001132901 /// XM_001133006 /// XM_001719237																			
2.62	2.39	0.23	2.89E-01	6.58E-01	SLC44A5	solute carrier family 44, member 5	chr1p31.1	1569112_at	NM_001130058 /// NM_152697																			
3.17	2.95	0.22	2.89E-01	6.58E-01	ZNF839	zinc finger protein 839	chr14q32.31	219086_at	NM_018335																			
2.78	2.58	0.20	2.89E-01	6.58E-01	ZNF527	zinc finger protein 527	chr19q13.1	1570238_at	NM_032453																			
5.72	5.51	0.21	2.89E-01	6.58E-01	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	chrXq11.1	203264_s_at	NM_015185																			
2.25	2.07	0.18	2.89E-01	6.58E-01	STOX2	storkhead box 2	chr4q35.1	231969_at	NM_020225																			
3.47	3.23	0.25	2.89E-01	6.58E-01	MRPL35	mitochondrial ribosomal protein L35	chr2p11.2	225255_at	NM_016622 /// NM_145644																			
2.59	2.40	0.19	2.89E-01	6.58E-01	TIGD7	tigger transposable element derived 7	chr16p13.3	238793_at	NM_033208																			
7.36	7.07	0.29	2.89E-01	6.58E-01	CGNL1	cingulin-like 1	chr15q21.3	225817_at	NM_032866																			
3.37	3.19	0.18	2.89E-01	6.58E-01	GRB7	growth factor receptor-bound protein 7	chr17q12	210761_s_at	NM_001030002 /// NM_005310																			
5.86	5.58	0.28	2.89E-01	6.58E-01	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	chr8q12.1	222701_s_at	NM_001011667 /// NM_001011668 /// NM_001011669 /// NM_001011670 /// NM_001011671 /// NM_024300																			
4.26	3.94	0.31	2.89E-01	6.58E-01	KIAA1632	KIAA1632	chr18q12.3-q21.1	227638_at	NM_020964																			
7.63	7.31	0.32	2.89E-01	6.58E-01	IRF2BP2	interferon regulatory factor 2 binding protein 2	chr1q42.3	224571_at	NM_001077397 /// NM_182972																			
2.18	2.06	0.12	2.89E-01	6.58E-01	---	---	---	242754_at	---																			
2.82	2.29	0.52	2.89E-01	6.58E-01	CD69	CD69 molecule	chr12p13-p12	209795_at	NM_001781																			
4.19	3.73	0.46	2.89E-01	6.58E-01	TRIM52	tripartite motif-containing 52	chr5q35.3	221897_at	NM_032765																			
2.39	2.22	0.17	2.89E-01	6.58E-01	LOC644215	Hypothetical LOC644215	chr10q24.1	1566082_at	XM_927403 /// XM_938015																			
8.23	7.72	0.51	2.89E-01	6.58E-01	PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	chr10q23-q24	204284_at	NM_005398																			
2.33	2.15	0.18	2.89E-01	6.59E-01	---	---	---	241654_at	---																			
2.85	2.64	0.21	2.89E-01	6.59E-01	DLGAP1	discs, large (Drosophila) homolog-associated protein 1	chr18p11.3	206490_at	NM_001003809 /// NM_004746																			
6.81	6.41	0.41	2.89E-01	6.59E-01	RHOBTB1	Rho-related BTB domain containing 1	chr10q21.2	212651_at	NM_001032380 /// NM_014836 /// NM_198225																			
2.38	2.24	0.14	2.90E-01	6.59E-01	NDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	chr16p13.11	227843_at	NM_017668																			
2.74	2.57	0.17	2.90E-01	6.59E-01	MDM1	Mdm1 nuclear protein homolog (mouse)	chr12q15	220397_at	NM_017440 /// NM_020128																			
3.16	2.93	0.23	2.90E-01	6.59E-01	B9D1	B9 protein domain 1	chr17p11.2	210535_at	NM_015681																			
4.00	3.86	0.14	2.90E-01	6.59E-01	KIAA1257 /// LOC100132731	KIAA1257 /// hypothetical protein LOC100132731	chr3q21.3	1557601_s_at	NM_020741 /// XM_001720345 /// XM_001723583 /// XM_001724331																			
4.83	4.53	0.30	2.90E-01	6.59E-01	WDR20	WD repeat domain 20	chr14q32.31	227693_at	NM_144574 /// NM_181291 /// NM_181302 /// NM_181308																			
2.12	1.97	0.15	2.90E-01	6.59E-01	---	---	---	241806_at	---																			
3.22	3.04	0.19	2.90E-01	6.59E-01	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	chr7q22.1	212668_at	NM_020429 /// NM_181349																			

4.36	4.14	0.22	2.90E-01	6.59E-01	IRAK1	interleukin-1 receptor-associated kinase 1	chrXq28	1555784_s_at	NM_001025242 /// NM_001025243 /// NM_001569																				
3.65	3.50	0.15	2.90E-01	6.59E-01	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	chr10q24.31	1568598_at	NM_030929																				
5.42	5.22	0.20	2.90E-01	6.59E-01	SLC35E1	solute carrier family 35, member E1	chr19p13.11	79005_at	NM_024881																				
6.23	5.94	0.29	2.90E-01	6.59E-01	CIZ1	CDKN1A interacting zinc finger protein 1	chr9q34.1	213977_s_at	NM_001131015 /// NM_001131016 /// NM_001131017 /// NM_001131018 /// NM_012127																				
2.59	2.41	0.19	2.90E-01	6.59E-01	LOC728011	hypothetical LOC728011	chr10q26.13	1565805_at	XM_001126352 /// XM_001131796 /// XM_001717016																				
3.28	2.96	0.32	2.90E-01	6.59E-01	LOC375196	hypothetical protein LOC375196	chr2p22.3	1556244_s_at	---																				
2.66	2.44	0.22	2.90E-01	6.59E-01	SIX3	SIX homeobox 3	chr2p16-p21	206634_at	NM_005413																				
2.79	2.64	0.15	2.90E-01	6.59E-01	LOC728805	hypothetical protein LOC728805	chr20q13.2	1561472_at	XR_041740 /// XR_041741 /// XR_041742																				
5.04	4.84	0.20	2.90E-01	6.59E-01	KLF3	Kruppel-like factor 3 (basic)	chr4p14	222913_at	NM_016531																				
7.33	7.09	0.24	2.90E-01	6.59E-01	MRPL21	mitochondrial ribosomal protein L21	chr11q13.2	225315_at	NM_181514 /// NM_181515																				
2.96	2.70	0.26	2.90E-01	6.59E-01	MASTL	microtubule associated serine/threonine kinase-like	chr10p12.1	228468_at	NM_032844																				
5.99	5.80	0.19	2.90E-01	6.59E-01	FAM120B	family with sequence similarity 120B	chr6q27	227895_at	NM_032448																				
6.68	6.46	0.22	2.90E-01	6.59E-01	USP19	ubiquitin specific peptidase 19	chr3p21.31	226357_at	NM_006677																				
3.10	2.84	0.26	2.90E-01	6.59E-01	CDADC1	cytidine and dCMP deaminase domain containing 1	chr13q14.2	221015_s_at	NM_030911																				
7.53	7.30	0.24	2.90E-01	6.59E-01	LRRC8A	leucine rich repeat containing 8 family, member A	chr9q34.11	224624_at	NM_001127244 /// NM_001127245 /// NM_019594																				
5.45	5.04	0.40	2.91E-01	6.59E-01	FHL1	four and a half LIM domains 1	chrXq26	201539_s_at	NM_001449																				
8.83	8.70	0.13	2.91E-01	6.59E-01	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	chr22q13.2-q13.31	202001_s_at	NM_002490																				
2.30	2.18	0.13	2.91E-01	6.59E-01	CREB5	cAMP responsive element binding protein 5	chr7p15.1	205931_s_at	NM_001011666 /// NM_004904 /// NM_182898 /// NM_182899																				
8.28	8.05	0.23	2.91E-01	6.59E-01	ACP1	acid phosphatase 1, soluble	chr2p25	201630_s_at	NM_001040649 /// NM_004300 /// NM_007099 /// NR_024080																				
3.30	3.09	0.21	2.91E-01	6.59E-01	DDX11 /// DDX12	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) /// DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 (CHL1-like helicase homolog, S. cerevisiae)	chr12p11 /// chr12p13.31	232816_s_at	NM_004399 /// NM_030653 /// NM_152438 /// XM_001716130 /// XM_495908 /// XM_931833																				
2.64	2.27	0.37	2.91E-01	6.59E-01	ZMAT1	zinc finger, matrin type 1	chrXq21	226344_at	NM_001011657 /// NM_032441																				

4.25	4.05	0.20	2.91E-01	6.59E-01	ANK1	ankyrin 1, erythrocytic	chr8p11.1	208352_x_at	NM_000037 /// NM_020475 /// NM_020476 /// NM_020477 /// NM_020478 /// NM_020480																				
2.35	2.16	0.18	2.91E-01	6.60E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	1555022_at	NM_002926 /// NM_198227 /// NM_198229																				
3.05	2.81	0.24	2.91E-01	6.60E-01	OBFC1	Oligonucleotide/oligosaccharide-binding fold containing 1	chr10q24.33	228781_at	NM_024928																				
2.44	2.32	0.12	2.91E-01	6.60E-01	ERGIC3	ERGIC and golgi 3	chr20pter-q12	215257_at	NM_015966 /// NM_198398																				
3.24	3.03	0.21	2.91E-01	6.60E-01	C20orf19	Chromosome 20 open reading frame 19	chr20pter-q11.23	228290_at	NM_018474																				
2.54	2.37	0.17	2.91E-01	6.60E-01	C13orf18 /// LOC728970	chromosome 13 open reading frame 18 /// hypothetical LOC728970	chr13q14.12 /// chr13q14.13	44790_s_at	NM_025113 /// XM_001132115 /// XM_001133896 /// XM_001720155																				
2.45	2.30	0.15	2.91E-01	6.60E-01	BTF3L1	basic transcription factor 3, like 1 pseudogene	chr13q22	208529_at	---																				
3.37	3.16	0.21	2.91E-01	6.60E-01	FCF1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	chr14q24.3	219927_at	NM_015962																				
3.00	2.77	0.24	2.91E-01	6.60E-01	LOC285943	Hypothetical protein LOC285943	chr7p15.2	242528_at	XR_040113 /// XR_040114 /// XR_040115 /// XR_040116																				
6.24	6.03	0.22	2.91E-01	6.60E-01	RHOD	ras homolog gene family, member D	chr11q14.3	31846_at	NM_014578																				
10.32	9.74	0.58	2.91E-01	6.60E-01	ZFAND5	zinc finger, AN1-type domain 5	chr9q13-q21	210275_s_at	NM_001102420 /// NM_001102421 /// NM_006007																				
6.58	6.35	0.23	2.91E-01	6.60E-01	LOC728944 /// THAP4	similar to THAP domain-containing protein 4 /// THAP domain containing 4	chr2q37.3	224057_s_at	NM_015963 /// XM_001128859																				
7.05	6.80	0.25	2.91E-01	6.60E-01	C18orf32	chromosome 18 open reading frame 32	chr18q21.1	224957_at	NM_001035005																				
4.67	4.50	0.17	2.91E-01	6.60E-01	ERN2	endoplasmic reticulum to nucleus signaling 2	chr16p12.2	223910_at	NM_033266																				
2.77	2.59	0.18	2.91E-01	6.60E-01	ETS2	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	chr21q22.3|21q22.2	241193_at	NM_005239																				
2.28	2.12	0.17	2.91E-01	6.60E-01	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	chr8q22	1564642_at	NM_004349 /// NM_175634 /// NM_175635 /// NM_175636																				
4.25	3.96	0.29	2.91E-01	6.60E-01	MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	chr1q21	214057_at	NM_021960 /// NM_182763																				
2.56	2.41	0.16	2.91E-01	6.60E-01	---	---	---	237728_at	---																				
3.93	3.49	0.44	2.91E-01	6.60E-01	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	chr7q36.3	1555830_s_at	NM_020728																				
4.95	4.65	0.30	2.92E-01	6.60E-01	XRN1	5'-3' exoribonuclease 1	chr3q23	225814_at	NM_001042604 /// NM_019001																				
2.39	2.26	0.13	2.92E-01	6.60E-01	---	---	---	237022_at	---																				
6.02	5.80	0.23	2.92E-01	6.60E-01	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	chr1q21.3	212541_at	NM_025207 /// NM_201398																				
5.09	4.87	0.21	2.92E-01	6.60E-01	CD5	CD5 molecule	chr11q13	206485_at	NM_014207																				

6.14	5.83	0.31	2.92E-01	6.60E-01	ANGEL1	angel homolog 1 (Drosophila)	chr14q24.3	213099_at	NM_015305
4.10	3.88	0.22	2.92E-01	6.60E-01	NRF1	nuclear respiratory factor 1	chr7q32	211280_s_at	NM_001040110 /// NM_005011
11.40	10.58	0.82	2.92E-01	6.60E-01	HBB	hemoglobin, beta	chr11p15.5	209116_x_at	NM_000518
6.33	6.08	0.26	2.92E-01	6.60E-01	PCSK7	proprotein convertase subtilisin/kexin type 7	chr11q23-q24	203118_at	NM_004716
4.84	4.58	0.26	2.92E-01	6.60E-01	PCIF1	PDX1 C-terminal inhibiting factor 1	chr20q13.12	222045_s_at	NM_022104
2.76	2.56	0.20	2.92E-01	6.60E-01	---	---	---	1563345_at	---
5.37	5.11	0.27	2.92E-01	6.60E-01	SECISBP2	SECIS binding protein 2	chr9q22.2	218265_at	NM_024077
2.65	2.54	0.11	2.92E-01	6.60E-01	---	---	---	1560129_at	---
5.80	5.41	0.39	2.92E-01	6.60E-01	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	chr1q21	211071_s_at	NM_006818
7.28	6.89	0.39	2.92E-01	6.60E-01	SLC25A29	solute carrier family 25, member 29	chr14q32.2	225306_s_at	NM_001039355
2.99	2.82	0.17	2.92E-01	6.60E-01	RECQL5	RecQ protein-like 5	chr17q25.2-q25.3	211468_s_at	NM_001003715 /// NM_001003716 /// NM_004259
2.62	2.35	0.26	2.92E-01	6.60E-01	LINS1	lines homolog 1 (Drosophila)	chr15q26.3	220121_at	NM_001040614 /// NM_001040615 /// NM_001040616 /// NM_018148
4.73	4.53	0.20	2.92E-01	6.60E-01	UGT1A1 /// UGT1A10 /// UGT1A4 /// UGT1A6 /// UGT1A8 /// UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 family, polypeptide A4 /// UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A8 /// UDP glucuronosyltransferase 1 family, polypeptide A9	chr2q37	207126_x_at	NM_000463 /// NM_001072 /// NM_007120 /// NM_019075 /// NM_019076 /// NM_021027 /// NM_205862
2.27	2.12	0.14	2.92E-01	6.60E-01	LOC100093698	unknown transcript	---	216543_at	---
4.55	4.38	0.18	2.92E-01	6.60E-01	RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	chr12q13-q14	210106_at	NM_002905
5.37	5.14	0.23	2.92E-01	6.60E-01	HEXIM2	Hexamthylene bis-acetamide inducible 2	chr17q21.31	243796_at	NM_144608
2.82	2.68	0.14	2.92E-01	6.60E-01	TIMM22	Translocase of inner mitochondrial membrane 22 homolog (yeast)	chr17p13	231400_s_at	NM_013337
5.39	5.05	0.34	2.92E-01	6.61E-01	MPV17L	MPV17 mitochondrial membrane protein-like	chr16p13.11	1559167_x_at	NM_001128423 /// NM_173803
3.41	3.15	0.26	2.92E-01	6.61E-01	HOOK3	hook homolog 3 (Drosophila)	chr8p11.21	224359_s_at	NM_032410
7.32	7.04	0.27	2.92E-01	6.61E-01	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	chr5q35.3	212052_s_at	NM_015043 /// NM_198868
2.68	2.51	0.18	2.92E-01	6.61E-01	ZNF569	zinc finger protein 569	chr19q13.12	1569366_a_at	NM_152484
6.61	6.33	0.28	2.93E-01	6.61E-01	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	chr9p21	209644_x_at	NM_000077 /// NM_058195 /// NM_058197
2.24	2.06	0.18	2.93E-01	6.61E-01	---	---	---	243949_at	---
2.24	2.09	0.15	2.93E-01	6.61E-01	RARS2	arginyl-tRNA synthetase 2, mitochondrial	chr6q16.1	207472_at	NM_020320
2.40	2.21	0.18	2.93E-01	6.61E-01	---	---	---	1560968_at	---
2.12	2.01	0.12	2.93E-01	6.61E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	1565868_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392
2.18	2.06	0.11	2.93E-01	6.61E-01	---	---	---	224363_at	---
3.70	3.58	0.13	2.93E-01	6.61E-01	---	---	---	1560480_at	---

8.10	7.91	0.20	2.93E-01	6.61E-01	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	chr17q21.31	208991_at	NM_003150 /// NM_139276 /// NM_213662																				
2.59	2.42	0.17	2.93E-01	6.61E-01	FAM151A	family with sequence similarity 151, member A	---	1554668_a_at	NM_176782																				
2.66	2.53	0.13	2.93E-01	6.61E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	1554969_x_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891																				
2.97	2.83	0.15	2.93E-01	6.61E-01	FGFR1	fibroblast growth factor receptor 1	chr8p11.2-p11.1	207822_at	NM_015850 /// NM_023105 /// NM_023106 /// NM_023107 /// NM_023108 /// NM_023110 /// NM_023111																				
7.36	7.11	0.25	2.93E-01	6.61E-01	TMED7	transmembrane emp24 protein transport domain containing 7	chr5q22.3	209404_s_at	NM_181836																				
2.36	2.17	0.19	2.93E-01	6.61E-01	---	---	---	1560924_at	---																				
12.88	12.77	0.11	2.93E-01	6.61E-01	LOC100130553 /// RPS18	hypothetical protein LOC100130553 /// ribosomal protein S18	chr6p21.3	201049_s_at	NM_022551 /// XM_001713658																				
3.69	3.47	0.21	2.93E-01	6.61E-01	---	---	---	239912_at	---																				
2.12	1.97	0.15	2.93E-01	6.61E-01	C5orf49	chromosome 5 open reading frame 49	chr5p15.31	239722_at	NM_001089584																				
4.49	4.10	0.38	2.93E-01	6.61E-01	---	---	---	228907_at	---																				
3.10	2.91	0.19	2.93E-01	6.61E-01	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	chr15q15.1	205024_s_at	NM_002875 /// NM_133487																				
2.24	1.98	0.26	2.93E-01	6.61E-01	AHI1	Abelson helper integration site 1	chr6q23.3	232461_at	NM_017651																				
2.80	2.56	0.24	2.93E-01	6.61E-01	MRPS15	mitochondrial ribosomal protein S15	chr1p35-p34.1	223292_s_at	NM_031280																				
2.19	2.07	0.13	2.93E-01	6.61E-01	REG4	regenerating islet-derived family, member 4	chr1p13.1-p12	238984_at	NM_032044																				
8.41	8.11	0.30	2.93E-01	6.61E-01	NEU1	sialidase 1 (lysosomal sialidase)	chr6p21.3	208926_at	NM_000434																				
2.11	1.99	0.11	2.93E-01	6.62E-01	---	---	---	1556622_s_at	---																				
7.37	7.02	0.34	2.94E-01	6.62E-01	NOLC1	nucleolar and coiled-body phosphoprotein 1	chr10q24.32	211951_at	NM_004741																				
2.35	2.20	0.14	2.94E-01	6.62E-01	LOC100127940	hypothetical LOC100127940	chr7p22.3	1564299_at	XM_001714084 /// XM_001720481																				
5.72	4.65	1.07	2.94E-01	6.62E-01	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	chr7q21.1	214234_s_at	NM_000777																				
3.00	2.79	0.21	2.94E-01	6.62E-01	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	chr6p22.2-p22.3	203609_s_at	NM_001080 /// NM_170740																				
2.50	2.38	0.12	2.94E-01	6.62E-01	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2	chr12q24.31	1555114_at	NM_012463																				
2.39	2.24	0.16	2.94E-01	6.62E-01	---	---	---	241421_at	---																				
4.88	4.56	0.32	2.94E-01	6.62E-01	CTSZ	cathepsin Z	chr20q13	210042_s_at	NM_001336																				
3.21	3.04	0.18	2.94E-01	6.62E-01	ARHGAP19	Rho GTPase activating protein 19	chr10q24.1	37577_at	NM_032900																				
5.44	5.24	0.20	2.94E-01	6.62E-01	NOL9	nucleolar protein 9	chr1p36.31	1554084_a_at	NM_024654																				
7.87	7.64	0.23	2.94E-01	6.62E-01	WIPI2	WD repeat domain, phosphoinositide interacting 2	chr7p22.1	204710_s_at	NM_001033518 /// NM_001033519 /// NM_001033520 /// NM_015610 /// NM_016003																				
2.29	2.11	0.18	2.94E-01	6.62E-01	---	---	---	235511_at	---																				
5.20	4.90	0.30	2.94E-01	6.62E-01	MICAL1	microtubule associated monoxygenase, calponin and LIM domain containing 1	chr6q21	218376_s_at	NM_022765																				
2.54	2.37	0.17	2.94E-01	6.62E-01	LOC440288	similar to FLJ16518 protein	chr15q24.1	239792_at	XM_001714156 /// XM_001714173 /// XM_001719502																				

3.26	2.94	0.31	2.94E-01	6.62E-01	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	chr18q21	208309_s_at	NM_006785 /// NM_173844																				
2.21	2.06	0.15	2.94E-01	6.62E-01	AJAP1	adherens junctions associated protein 1	chr1p36.32	215790_at	NM_001042478 /// NM_018836																				
4.71	4.16	0.54	2.94E-01	6.62E-01	SOX9	SRY (sex determining region Y)-box 9	chr17q24.3-q25.1	202936_s_at	NM_000346																				
1.92	1.81	0.12	2.94E-01	6.62E-01	---	---	---	1559213_at	---																				
2.57	2.44	0.13	2.94E-01	6.62E-01	KCNIP1	Kv channel interacting protein 1	chr5q35.1	221307_at	NM_001034837 /// NM_001034838 /// NM_014592																				
6.49	6.15	0.33	2.94E-01	6.62E-01	KLF3	Kruppel-like factor 3 (basic)	chr4p14	225133_at	NM_016531																				
2.10	1.86	0.23	2.94E-01	6.62E-01	ZMYM5	zinc finger, MYM-type 5	chr13q12	206744_s_at	NM_001039649 /// NM_001039650																				
6.79	6.60	0.19	2.94E-01	6.62E-01	CHD8	chromodomain helicase DNA binding protein 8	chr14q11.2	212571_at	NM_020920																				
2.33	2.19	0.13	2.94E-01	6.62E-01	BNIPL	BCL2/adenovirus E1B 19kD interacting protein like	chr1q21.2	236534_at	NM_138278																				
4.17	3.46	0.71	2.94E-01	6.62E-01	---	---	---	231828_at	---																				
5.13	4.82	0.31	2.94E-01	6.62E-01	PPL	periplakin	chr16p13.3	203407_at	NM_002705																				
2.70	2.54	0.16	2.95E-01	6.62E-01	CRX	cone-rod homeobox	chr19q13.3	231742_at	NM_000554																				
7.21	6.97	0.24	2.95E-01	6.63E-01	KAT5	K(lysine) acetyltransferase 5	chr11q13	206689_x_at	NM_006388 /// NM_182709 /// NM_182710																				
5.53	5.34	0.19	2.95E-01	6.63E-01	GRK6	G protein-coupled receptor kinase 6	chr5q35	202849_x_at	NM_001004105 /// NM_001004106 /// NM_002082																				
3.33	2.98	0.34	2.95E-01	6.63E-01	ZNF673	zinc finger family member 673	chrXp11.3	206583_at	NM_001129898 /// NM_001129899 /// NM_001129900 /// NM_017776																				
4.86	4.52	0.34	2.95E-01	6.63E-01	TOPBP1	topoisomerase (DNA) II binding protein 1	chr3q22.1	202633_at	NM_007027																				
3.81	3.57	0.25	2.95E-01	6.63E-01	BTRC	beta-transducin repeat containing	chr10q24.32	204901_at	NM_003939 /// NM_033637																				
3.28	2.78	0.50	2.95E-01	6.63E-01	RGS4	regulator of G-protein signaling 4	chr1q23.3	204338_s_at	NM_001102445 /// NM_001113380 /// NM_001113381 /// NM_005613																				
6.98	6.79	0.19	2.95E-01	6.63E-01	MRPL28	mitochondrial ribosomal protein L28	chr16p13.3	204599_s_at	NM_006428																				
4.04	3.83	0.21	2.95E-01	6.63E-01	---	---	---	231036_at	---																				
6.19	5.86	0.33	2.95E-01	6.63E-01	GPN3	GPN-loop GTPase 3	chr12q24.11	218461_at	NM_016301																				
8.95	8.77	0.18	2.95E-01	6.63E-01	C3orf10	chromosome 3 open reading frame 10	chr3p25.3	224575_at	NM_018462																				
2.05	1.91	0.13	2.95E-01	6.63E-01	C8orf8	chromosome 8 open reading frame 8	chr8p23-p22	1565424_at	---																				
5.86	5.65	0.20	2.95E-01	6.63E-01	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	chr12q24.13	219111_s_at	NM_001111322 /// NM_024072																				
3.35	2.63	0.72	2.95E-01	6.63E-01	LOC348174	secretory protein LOC348174	chr16q22.1	230022_at	NM_182619																				
2.54	2.34	0.21	2.95E-01	6.63E-01	---	---	---	232413_at	---																				
5.19	4.90	0.29	2.95E-01	6.63E-01	---	---	---	235926_at	---																				
4.92	4.71	0.21	2.95E-01	6.63E-01	C9orf140	chromosome 9 open reading frame 140	chr9q34.3	225777_at	NM_178448																				
7.50	7.13	0.37	2.96E-01	6.64E-01	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3	chr22q13.2-q13.3	202211_at	NM_014570																				
3.14	2.97	0.17	2.96E-01	6.64E-01	ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	chr16p12.1	205444_at	NM_004320 /// NM_173201																				
7.53	7.41	0.12	2.96E-01	6.64E-01	VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	chr20q13.33	202550_s_at	NM_004738																				
4.49	4.06	0.43	2.96E-01	6.64E-01	BDH1	3-hydroxybutyrate dehydrogenase, type 1	chr3q29	211715_s_at	NM_004051 /// NM_203314 /// NM_203315																				

6.09	5.58	0.51	2.96E-01	6.64E-01	LSR	lipolysis stimulated lipoprotein receptor	chr19q13.12	208190_s_at	NM_015925 /// NM_205834 /// NM_205835																				
6.67	6.41	0.26	2.96E-01	6.64E-01	MECR	mitochondrial trans-2-enoyl-CoA reductase	chr1p36.1-p35.1	218664_at	NM_001024732 /// NM_016011																				
3.33	3.10	0.23	2.96E-01	6.64E-01	RAD54B	RAD54 homolog B (S. cerevisiae)	chr8q21.3-q22	219494_at	NM_012415																				
4.63	4.39	0.23	2.96E-01	6.64E-01	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	chr2q13	233341_s_at	NM_019014																				
5.48	5.20	0.28	2.96E-01	6.64E-01	---	---	---	237568_at	---																				
4.72	4.51	0.21	2.96E-01	6.64E-01	SYTL3	synaptotagmin-like 3	chr6q25.3	238423_at	NM_001009991																				
5.08	4.87	0.21	2.96E-01	6.64E-01	MYO5A	myosin VA (heavy chain 12, myoxin)	chr15q21	227761_at	NM_000259																				
11.04	10.26	0.78	2.96E-01	6.64E-01	HBB	hemoglobin, beta	chr11p15.5	217232_x_at	NM_000518																				
8.23	8.07	0.17	2.96E-01	6.64E-01	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	chr12p13.3	208969_at	NM_005002																				
2.31	2.14	0.17	2.96E-01	6.64E-01	---	---	---	1565557_at	---																				
6.42	5.89	0.53	2.96E-01	6.64E-01	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	chr4q13-q21	1554678_s_at	NM_031372 /// NR_003249																				
2.82	2.62	0.21	2.96E-01	6.64E-01	KIAA1107	KIAA1107	chr1p22.1	214098_at	NM_015237 /// XM_034086 /// XM_937137																				
4.09	3.85	0.24	2.96E-01	6.64E-01	TRAPPC10	trafficking protein particle complex 10	chr21q22.3	208184_s_at	NM_001001723 /// NM_003274																				
9.89	9.71	0.17	2.96E-01	6.64E-01	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	chr1q21	202244_at	NM_002796																				
2.86	2.63	0.24	2.96E-01	6.64E-01	HOXA2	homeobox A2	chr7p15-p14	214457_at	NM_006735																				
3.00	2.75	0.26	2.96E-01	6.64E-01	BFSP1	beaded filament structural protein 1, filensin	chr20p11.23-p12.1	206746_at	NM_001195																				
2.58	2.36	0.22	2.96E-01	6.64E-01	RUFY2	RUN and FYVE domain containing 2	chr10q21.3	233192_s_at	NM_001042417 /// NM_017987																				
2.62	2.47	0.15	2.96E-01	6.64E-01	LOC730496	hypothetical protein LOC730496	---	243021_at	XM_001126091																				
2.26	2.04	0.22	2.96E-01	6.64E-01	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	chr15q21.1	240863_at	NM_000103 /// NM_031226																				
2.67	2.48	0.19	2.96E-01	6.64E-01	HELB	helicase (DNA) B	chr12q14.3	1570200_at	NM_033647																				
8.50	8.26	0.24	2.96E-01	6.64E-01	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	chr1p33-p32	201900_s_at	NM_006066 /// NM_153326																				
2.51	2.33	0.18	2.96E-01	6.64E-01	TTTY10	testis-specific transcript, Y-linked 10	chrYq11.221	224293_at	NR_001542																				
6.01	5.75	0.26	2.97E-01	6.64E-01	SLC39A1	solute carrier family 39 (zinc transporter), member 1	chr1q21	217778_at	NM_014437																				
6.60	6.37	0.23	2.97E-01	6.64E-01	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	chr1p36.1-p35	209453_at	NM_003047																				
3.54	3.18	0.36	2.97E-01	6.64E-01	LYST	lysosomal trafficking regulator	chr1q42.1-q42.2	203518_at	NM_000081																				
5.20	4.84	0.37	2.97E-01	6.64E-01	NCDN	neurochondrin	chr1p34.3	209556_at	NM_001014839 /// NM_001014841 /// NM_014284																				
6.69	6.42	0.27	2.97E-01	6.64E-01	ZNF629	zinc finger protein 629	chr16p11.2	213196_at	NM_001080417																				
2.39	2.25	0.14	2.97E-01	6.64E-01	---	---	---	1554194_at	---																				
2.37	2.18	0.19	2.97E-01	6.64E-01	CECR9	cat eye syndrome chromosome region, candidate 9	---	1567687_at	---																				
2.82	2.52	0.30	2.97E-01	6.64E-01	ZNF320	zinc finger protein 320	chr19q13.41	229614_at	NM_207333																				
2.43	2.28	0.15	2.97E-01	6.64E-01	---	---	---	234056_at	---																				
8.28	8.07	0.20	2.97E-01	6.65E-01	C20orf116	chromosome 20 open reading frame 116	chr20p13	218159_at	NM_023935																				
5.40	4.62	0.79	2.97E-01	6.65E-01	SF1	splicing factor 1	chr11q13	210172_at	NM_004630 /// NM_201995 /// NM_201997 /// NM_201998																				
2.07	1.93	0.14	2.97E-01	6.65E-01	CHDH	choline dehydrogenase	chr3p21.1	1559590_at	NM_018397																				
4.13	3.70	0.42	2.98E-01	6.65E-01	CALN1	calneuron 1	chr7q11	1555168_a_at	NM_001017440 /// NM_031468																				
2.96	2.70	0.26	2.98E-01	6.65E-01	FAM84A	family with sequence similarity 84, member A	chr2p24.3	234331_s_at	NM_145175																				
6.33	5.84	0.49	2.98E-01	6.65E-01	XYLT1	xylosyltransferase I	chr16p12.3	213725_x_at	NM_022166																				
3.15	2.96	0.19	2.98E-01	6.65E-01	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	chr2q37.1	232337_at	NM_145236																				

6.25	5.99	0.25	2.98E-01	6.65E-01	IRF2BP1	interferon regulatory factor 2 binding protein 1	chr19q13.32	213771_at	NM_015649
2.92	2.61	0.31	2.98E-01	6.65E-01	---	---	---	235612_at	---
6.57	6.36	0.21	2.98E-01	6.65E-01	E2F4	E2F transcription factor 4, p107/p130-binding	chr16q21-q22	38707_r_at	NM_001950
3.05	2.81	0.24	2.98E-01	6.65E-01	FCHSD1	FCH and double SH3 domains 1	chr5q31.3	226698_at	NM_033449
2.46	2.29	0.16	2.98E-01	6.65E-01	ICOS	inducible T-cell co-stimulator	chr2q33	210439_at	NM_012092
2.88	2.64	0.23	2.98E-01	6.65E-01	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	chr12q21.3	212930_at	NM_001001323 /// NM_001682
5.30	5.14	0.16	2.98E-01	6.65E-01	---	---	---	241927_x_at	---
4.61	4.20	0.41	2.98E-01	6.65E-01	GSTM4	glutathione S-transferase M4	chr1p13.3	210912_x_at	NM_000850 /// NM_147148
5.57	5.22	0.35	2.98E-01	6.65E-01	KTI12	KTI12 homolog, chromatin associated (S. cerevisiae)	chr1p32.3	225642_at	NM_138417
2.87	2.52	0.35	2.98E-01	6.65E-01	ELA2A /// RP11-265F14.2	elastase 2A /// elastase 2B	chr1p36.21	206446_s_at	NM_015849 /// NM_033440
3.11	2.87	0.24	2.98E-01	6.65E-01	KLHDC4	kelch domain containing 4	chr16q24.3	229035_s_at	NM_017566
6.10	5.88	0.22	2.98E-01	6.65E-01	PEX11G	peroxisomal biogenesis factor 11 gamma	chr19p13.2	244126_at	NM_080662
2.22	2.06	0.16	2.98E-01	6.65E-01	FMNL2	Formin-like 2	chr2q23.3	235881_at	NM_052905
3.73	3.45	0.28	2.98E-01	6.65E-01	---	---	---	230659_at	---
2.50	2.35	0.15	2.98E-01	6.65E-01	TRSPAP1	tRNA selenocysteine associated protein 1	chr1p35.3	223965_at	NM_017846 /// NR_003109
2.99	2.79	0.20	2.98E-01	6.65E-01	---	---	---	230935_at	---
3.73	3.46	0.27	2.98E-01	6.65E-01	NHSL1	NHS-like 1	chr6q23.3	231034_s_at	XM_001723403 /// XM_496826 /// XM_941807
6.08	5.12	0.95	2.98E-01	6.65E-01	WBSCR17	Williams-Beuren syndrome chromosome region 17	chr7q11.23	227434_at	NM_022479
4.34	4.09	0.25	2.98E-01	6.65E-01	STOML1	stomatin (EPB72)-like 1	chr15q24-q25	1556320_at	NM_004809
5.09	4.89	0.20	2.98E-01	6.65E-01	---	---	---	225318_at	---
2.14	2.03	0.11	2.98E-01	6.65E-01	---	---	---	1558406_a_at	---
7.51	7.28	0.23	2.98E-01	6.65E-01	GCSH /// LOC730107	glycine cleavage system protein H (aminomethyl carrier) /// similar to Glycine cleavage system H protein, mitochondrial	chr16q23.2 /// chr1q24.2	213129_s_at	NM_004483 /// XM_001134369 /// XM_001721064
3.10	2.93	0.17	2.98E-01	6.65E-01	LCE3D	late cornified envelope 3D	chr1q21	224328_s_at	NM_032563
4.20	3.91	0.29	2.98E-01	6.65E-01	PYCRL	pyrroline-5-carboxylate reductase-like	chr8q24.3	218944_at	NM_023078
2.95	2.73	0.22	2.98E-01	6.65E-01	TBC1D22B	TBC1 domain family, member 22B	chr6p21.2	216549_s_at	NM_017772
3.53	3.32	0.21	2.99E-01	6.65E-01	LBP	lipopolysaccharide binding protein	chr20q11.23-q12	211652_s_at	NM_004139
7.00	6.63	0.38	2.99E-01	6.65E-01	CCND1	cyclin D1	chr11q13	208712_at	NM_053056
2.78	2.53	0.25	2.99E-01	6.65E-01	CMTM2	CKLF-like MARVEL transmembrane domain containing 2	chr16q21	229967_at	NM_144673
3.46	3.01	0.45	2.99E-01	6.66E-01	HOMER1	homer homolog 1 (Drosophila)	chr5q14.2	213793_s_at	NM_004272
2.77	2.64	0.13	2.99E-01	6.66E-01	---	---	---	220820_at	---
2.95	2.80	0.15	2.99E-01	6.66E-01	---	---	---	215403_at	---
2.66	2.52	0.14	2.99E-01	6.66E-01	SPAG6	sperm associated antigen 6	chr10p12.2	210032_s_at	NM_012443 /// NM_172242
2.14	2.03	0.11	2.99E-01	6.66E-01	LOC729178	hypothetical protein LOC729178	chr6q24.3	1557890_at	XR_041025 /// XR_041026 /// XR_041027
6.24	5.89	0.35	2.99E-01	6.66E-01	RBPMS	RNA binding protein with multiple splicing	chr8p12-p11	207836_s_at	NM_001008710 /// NM_001008711 /// NM_001008712 /// NM_006867
9.24	9.01	0.23	2.99E-01	6.66E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	210638_s_at	NM_012347 /// NM_033480 /// NM_033481
2.55	2.39	0.16	2.99E-01	6.66E-01	KIAA1432	KIAA1432	chr9p24.1	223826_s_at	NM_020829
2.18	2.04	0.14	2.99E-01	6.66E-01	---	---	---	1566698_at	---
2.75	2.62	0.13	2.99E-01	6.66E-01	---	---	---	240126_x_at	---
4.70	4.41	0.29	2.99E-01	6.66E-01	TMEM39B	transmembrane protein 39B	chr1p35.1	218770_s_at	NM_018056
2.74	2.50	0.25	2.99E-01	6.66E-01	---	---	---	236113_at	---
3.00	2.76	0.23	2.99E-01	6.66E-01	---	---	---	238415_at	---
3.06	2.83	0.23	2.99E-01	6.66E-01	---	---	---	244516_at	---

6.43	6.18	0.25	2.99E-01	6.66E-01	C6orf204	Chromosome 6 open reading frame 204	chr6q22	228007_at	NM_001042475 /// NM_206921
2.59	2.46	0.13	2.99E-01	6.66E-01	---	---	---	1562989_at	---
11.27	11.17	0.11	2.99E-01	6.66E-01	TPT1	tumor protein, translationally-controlled 1	chr13q12-q14	214327_x_at	NM_003295
2.24	2.07	0.18	2.99E-01	6.66E-01	TCP11L1	t-complex 11 (mouse)-like 1	chr11p13	233472_at	NM_018393
5.36	4.92	0.45	2.99E-01	6.66E-01	---	---	---	231169_at	---
5.22	4.79	0.43	3.00E-01	6.66E-01	---	---	---	228740_at	---
3.35	3.15	0.20	3.00E-01	6.66E-01	LOC730631	Hypothetical LOC730631	chr1q21.2	238529_at	XM_001715137 /// XM_001720519 /// XM_001723714
2.37	2.14	0.23	3.00E-01	6.67E-01	---	---	---	1559535_s_at	---
6.34	6.00	0.34	3.00E-01	6.67E-01	---	---	---	232058_at	---
2.10	1.97	0.13	3.00E-01	6.67E-01	---	---	---	238483_at	---
2.67	2.50	0.17	3.00E-01	6.67E-01	C10orf44	Chromosome 10 open reading frame 44	---	1562812_at	---
4.43	4.11	0.32	3.00E-01	6.67E-01	GAS7	growth arrest-specific 7	chr17p13.1	211067_s_at	NM_001130831 /// NM_003644 /// NM_201432 /// NM_201433
4.86	4.42	0.44	3.00E-01	6.67E-01	FHL1	four and a half LIM domains 1	chrXq26	210298_x_at	NM_001449
2.45	2.25	0.20	3.00E-01	6.67E-01	C14orf108	chromosome 14 open reading frame 108	chr14q23.1	1555448_at	NM_018229
5.34	4.97	0.37	3.00E-01	6.67E-01	MYCBP	c-myc binding protein	chr1p33-p32.2	203359_s_at	NM_012333
3.88	3.56	0.31	3.00E-01	6.67E-01	OBSL1	obscurin-like 1	chr2q35	213946_s_at	NM_015311
3.58	3.44	0.14	3.00E-01	6.67E-01	DEFA4	defensin, alpha 4, corticostatin	chr8p23	207269_at	NM_001925
3.74	3.61	0.13	3.00E-01	6.67E-01	FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	chr8p12	239020_at	NM_032664
3.23	3.07	0.16	3.00E-01	6.67E-01	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	chr19p13.3	209807_s_at	NM_002501
2.71	2.54	0.18	3.00E-01	6.67E-01	---	---	---	241307_at	---
2.06	1.94	0.11	3.00E-01	6.67E-01	TNPO1	Transportin 1	chr5q13.2	1557278_s_at	NM_002270 /// NM_153188
2.14	2.03	0.11	3.00E-01	6.67E-01	OPRM1	opioid receptor, mu 1	chr6q24-q25	207989_at	NM_000914 /// NM_001008503 /// NM_001008504 /// NM_001008505
4.65	4.49	0.15	3.00E-01	6.67E-01	---	---	---	233307_x_at	---
2.35	2.19	0.16	3.00E-01	6.67E-01	---	---	---	233445_at	---
4.37	4.22	0.16	3.00E-01	6.67E-01	FAM118A	family with sequence similarity 118, member A	chr22q13	226475_at	NM_001104595 /// NM_017911
2.10	1.99	0.11	3.00E-01	6.67E-01	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	chr7q31.3	204469_at	NM_002851
7.00	6.77	0.22	3.01E-01	6.67E-01	WDR81	WD repeat domain 81	chr17p13.3	226738_at	NM_152348
5.99	5.38	0.61	3.01E-01	6.67E-01	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	chr6q27	212912_at	NM_001006932 /// NM_021135
5.52	5.18	0.34	3.01E-01	6.67E-01	EIF3B	eukaryotic translation initiation factor 3, subunit B	chr7p22.2	236274_at	NM_001037283 /// NM_003751
4.47	4.23	0.23	3.01E-01	6.67E-01	TARSL2	threonyl-tRNA synthetase-like 2	chr15q26.3	227611_at	NM_152334
4.95	4.55	0.40	3.01E-01	6.67E-01	NFASC	neurofascin homolog (chicken)	chr1q32.1	213438_at	NM_015090
3.60	3.15	0.45	3.01E-01	6.67E-01	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	chr4p16	205466_s_at	NM_005114
5.53	5.25	0.27	3.01E-01	6.67E-01	FAM108B1	family with sequence similarity 108, member B1	chr9q21.13	227551_at	NM_001025780 /// NM_016014
3.20	2.97	0.23	3.01E-01	6.67E-01	ZNF619	zinc finger protein 619	chr3p22.1	1552836_at	NM_173656
5.45	5.20	0.25	3.01E-01	6.67E-01	LOC400236	hypothetical LOC400236	chr14q32.11	227887_at	XM_001715158 /// XM_378472 /// XM_944198
7.54	7.35	0.19	3.01E-01	6.67E-01	RAB35	RAB35, member RAS oncogene family	chr12q24.31	221819_at	NM_006861
2.95	2.81	0.14	3.01E-01	6.68E-01	ITLN1	intelectin 1 (galactofuranose binding)	chr1q22-q23.5	223597_at	NM_017625
7.93	7.51	0.42	3.01E-01	6.68E-01	ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	chr2q31-q32	202351_at	NM_002210
3.77	3.63	0.15	3.01E-01	6.68E-01	RNF5	ring finger protein 5	chr6p21.3	216018_at	NM_006913
3.48	3.30	0.18	3.01E-01	6.68E-01	C20orf62	chromosome 20 open reading frame 62	chr20q13.12	1570328_s_at	NM_178476

2.98	2.77	0.21	3.01E-01	6.68E-01	FLJ90757	hypothetical protein LOC440465	chr17q25.3	1566557_at	XR_017883 /// XR_017982 /// XR_040055																				
4.04	3.83	0.21	3.01E-01	6.68E-01	DHRSX	dehydrogenase/reductase (SDR family) X-linked	chrXp22.33; Yp11.2	238053_at	NM_145177																				
4.23	4.01	0.22	3.02E-01	6.68E-01	PWWP2A	PWWP domain containing 2A	chr5q33.3	226720_at	NM_001130864 /// NM_052927																				
2.24	2.12	0.12	3.02E-01	6.68E-01	---	---	---	1554403_a_at	---																				
2.70	2.48	0.21	3.02E-01	6.68E-01	C20orf82	chromosome 20 open reading frame 82	chr20p12.1	235182_at	NM_080826																				
5.41	5.27	0.14	3.02E-01	6.68E-01	FAHD1	fumarylacetoacetate hydrolase domain containing 1	chr16p13.3	226767_s_at	NM_001018104 /// NM_031208																				
5.34	5.07	0.26	3.02E-01	6.68E-01	RASA3	RAS p21 protein activator 3	chr13q34	225562_at	NM_007368																				
2.16	2.05	0.12	3.02E-01	6.68E-01	LOC285501	hypothetical protein LOC285501	chr4q34.3	1561566_at	NM_001085490																				
10.15	10.03	0.11	3.02E-01	6.69E-01	TBCA	tubulin folding cofactor A	chr5q14.1	203667_at	NM_004607																				
5.47	5.28	0.19	3.02E-01	6.69E-01	GMEB1	glucocorticoid modulatory element binding protein 1	chr1p35.3	220938_s_at	NM_006582 /// NM_024482																				
4.33	4.06	0.27	3.02E-01	6.69E-01	---	---	---	235058_at	---																				
2.88	2.72	0.15	3.02E-01	6.69E-01	MORN3	MORN repeat containing 3	chr12q24.31	237211_x_at	NM_173855																				
2.84	2.63	0.21	3.02E-01	6.69E-01	INADL	InaD-like (Drosophila)	chr1p31.3	232041_at	NM_176877																				
2.05	1.93	0.12	3.02E-01	6.69E-01	RFX4	regulatory factor X, 4 (influences HLA class II expression)	chr12q24	223673_at	NM_002920 /// NM_032491 /// NM_213594																				
3.39	3.22	0.17	3.02E-01	6.69E-01	WNK3	WNK lysine deficient protein kinase 3	chrXp11.23-p11.21	1555248_a_at	NM_001002838 /// NM_020922																				
4.72	4.41	0.30	3.02E-01	6.69E-01	LRSAM1	leucine rich repeat and sterile alpha motif containing 1	chr9q33.3-q34.11	227675_at	NM_001005373 /// NM_001005374 /// NM_138361																				
2.69	2.53	0.16	3.02E-01	6.69E-01	CRP	C-reactive protein, pentraxin-related	chr1q21-q23	205753_at	NM_000567																				
7.67	7.40	0.27	3.02E-01	6.69E-01	EGLN2	egl nine homolog 2 (C. elegans)	chr19q13.2	220956_s_at	NM_053046 /// NM_080732																				
3.79	3.54	0.25	3.02E-01	6.69E-01	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	chr15q22	212769_at	NM_001105192 /// NM_005078 /// NM_020908																				
3.54	3.37	0.18	3.02E-01	6.69E-01	---	---	---	238637_at	---																				
8.25	8.10	0.15	3.02E-01	6.69E-01	BRP44L	brain protein 44-like	chr6q27	218024_at	NM_016098																				
2.03	1.89	0.13	3.03E-01	6.69E-01	C7orf45	chromosome 7 open reading frame 45	chr7q32.2	1553329_at	NM_145268																				
5.83	5.29	0.54	3.03E-01	6.69E-01	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	chr9p21.3	244050_at	NM_001010915																				
4.23	3.60	0.63	3.03E-01	6.69E-01	C9orf72	chromosome 9 open reading frame 72	chr9p21.2	225919_s_at	NM_018325 /// NM_145005																				
3.57	3.16	0.40	3.03E-01	6.69E-01	SNHG9	small nucleolar RNA host gene 9 (non-protein coding)	chr16p13.3	228645_at	NR_003142																				
3.00	2.62	0.38	3.03E-01	6.69E-01	---	---	---	229041_s_at	---																				
2.45	2.32	0.13	3.03E-01	6.69E-01	FLJ44054	hypothetical protein LOC643365	chr13q34	1570447_at	XM_001721556 /// XM_001721577 /// XM_001722970																				
4.51	4.21	0.31	3.03E-01	6.69E-01	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	chr12q24.31	219246_s_at	NM_024623																				
2.12	1.98	0.13	3.03E-01	6.69E-01	---	---	---	1565192_at	---																				
2.47	2.34	0.13	3.03E-01	6.70E-01	PKD2L2	polycystic kidney disease 2-like 2	chr5q31	221118_at	NM_014386																				
2.25	2.06	0.19	3.03E-01	6.70E-01	LOC285547	hypothetical protein LOC285547	chr4p15.33	1562683_a_at	---																				
3.33	3.15	0.18	3.03E-01	6.70E-01	GADD45GIP1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	chr19p13.13	212889_x_at	NM_052850																				
2.16	2.01	0.14	3.03E-01	6.70E-01	---	---	---	221038_at	---																				
2.49	2.31	0.18	3.03E-01	6.70E-01	---	---	---	241236_at	---																				
2.71	2.55	0.16	3.04E-01	6.70E-01	HSPB3	heat shock 27kDa protein 3	chr5q11.2	206375_s_at	NM_006308																				
3.57	3.42	0.16	3.04E-01	6.70E-01	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	chr16q22.1	219695_at	NM_018667																				

2.07	1.89	0.18	3.04E-01	6.70E-01	PITX2	paired-like homeodomain 2	chr4q25-q27	207558_s_at	NM_000325 /// NM_153426 /// NM_153427
5.79	5.58	0.21	3.04E-01	6.70E-01	THEM4	thioesterase superfamily member 4	chr1q21	1553118_at	NM_053055
3.96	3.72	0.24	3.04E-01	6.70E-01	HK3	hexokinase 3 (white cell)	chr5q35.2	205936_s_at	NM_002115
6.66	6.20	0.45	3.04E-01	6.70E-01	HACL1	2-hydroxyacyl-CoA lyase 1	chr3p24.3	223211_at	NM_012260
3.18	3.00	0.19	3.04E-01	6.70E-01	RHBDL3	rhomboid, veinlet-like 3 (Drosophila)	chr17q11.2	233409_at	NM_138328
7.06	6.80	0.26	3.04E-01	6.70E-01	DUSP6	dual specificity phosphatase 6	chr12q22-q23	208891_at	NM_001946 /// NM_022652
6.32	5.80	0.52	3.04E-01	6.70E-01	TSPYL5	TSPY-like 5	chr8q22.1	213122_at	NM_033512
6.94	6.73	0.21	3.04E-01	6.70E-01	HARS2	histidyl-tRNA synthetase 2, mitochondrial (putative)	chr5q31.3	209252_at	NM_012208
2.47	2.14	0.33	3.04E-01	6.70E-01	LOC100130829 /// ZFX /// ZFY	hypothetical protein LOC100130829 /// zinc finger protein, X-linked /// zinc finger protein, Y-linked	chrXp21.3 /// chrYp11.3	207247_s_at	NM_003410 /// NM_003411 /// XM_001713692
2.33	2.21	0.12	3.04E-01	6.70E-01	PTCH1	patched homolog 1 (Drosophila)	chr9q22.3	1555520_at	NM_000264 /// NM_001083602 /// NM_001083603 /// NM_001083604 /// NM_001083605 /// NM_001083606 /// NM_001083607
8.07	7.60	0.47	3.04E-01	6.70E-01	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	chr17q21	204894_s_at	NM_003734
2.42	2.30	0.12	3.04E-01	6.70E-01	LOC387895	hypothetical gene supported by BC040060	chr12q24.32	1560573_at	XM_373553 /// XM_945559
4.61	4.38	0.23	3.04E-01	6.70E-01	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	chr19p13.2-p13.11	208947_s_at	NM_002911
2.48	2.29	0.19	3.04E-01	6.70E-01	---	---	---	1565803_at	---
5.27	5.08	0.20	3.04E-01	6.70E-01	---	---	---	229338_at	---
2.48	2.31	0.17	3.04E-01	6.70E-01	RFX3	regulatory factor X, 3 (influences HLA class II expression)	chr9p24.2	207234_at	NM_002919 /// NM_134428
2.17	2.05	0.12	3.04E-01	6.70E-01	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	1570342_at	NM_005385
6.33	5.80	0.53	3.04E-01	6.70E-01	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	chrXp22.2-p22.1	203843_at	NM_004586
5.54	5.35	0.19	3.04E-01	6.70E-01	FAM48A	family with sequence similarity 48, member A	chr13q13.3	220408_x_at	NM_001014286 /// NM_017569
2.82	2.50	0.32	3.04E-01	6.70E-01	---	---	---	1556942_at	---
5.63	5.20	0.43	3.04E-01	6.70E-01	SYPL2	synaptophysin-like 2	chr1p13.3	230611_at	NM_001040709
6.82	6.56	0.25	3.05E-01	6.70E-01	CARD6	caspase recruitment domain family, member 6	chr5p13.1	224414_s_at	NM_032587
1.96	1.86	0.10	3.05E-01	6.71E-01	---	---	---	236637_at	---
5.83	5.57	0.26	3.05E-01	6.71E-01	HCCA2	HCCA2 protein	chr11p15.5	223353_at	NM_053005
6.10	5.82	0.29	3.05E-01	6.71E-01	EML3	echinoderm microtubule associated protein like 3	chr11q12.3	212969_x_at	NM_153265
2.45	2.29	0.16	3.05E-01	6.71E-01	---	---	---	237277_at	---
4.36	4.18	0.18	3.05E-01	6.71E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	204991_s_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833

2.53	2.39	0.14	3.05E-01	6.71E-01	TMEM107	transmembrane protein 107	chr17p13.1	235490_at	NM_032354 /// NM_183065
5.79	5.32	0.47	3.05E-01	6.71E-01	---	---	---	227554_at	---
8.59	8.33	0.26	3.05E-01	6.71E-01	TUSC3	tumor suppressor candidate 3	chr8p22	209228_x_at	NM_006765 /// NM_178234
4.08	3.91	0.17	3.05E-01	6.71E-01	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	chr1p13.2	219490_s_at	NM_022836
7.24	7.01	0.23	3.05E-01	6.71E-01	LSM6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr4q31.22	205036_at	NM_007080
2.44	2.27	0.18	3.05E-01	6.71E-01	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	chr10q22-q23	1564318_at	NM_007055
2.98	2.78	0.20	3.05E-01	6.71E-01	TTC28	tetratricopeptide repeat domain 28	chr22q12.1	234004_at	XM_001726330 /// XM_929318 /// XM_939083
3.24	3.07	0.17	3.05E-01	6.71E-01	---	---	---	1562729_at	---
6.83	6.68	0.15	3.05E-01	6.71E-01	STK4	serine/threonine kinase 4	chr20q11.2-q13.2	225364_at	NM_006282
2.12	1.99	0.13	3.05E-01	6.71E-01	---	---	---	1563536_at	---
2.44	2.31	0.13	3.05E-01	6.71E-01	ORC1L	origin recognition complex, subunit 1-like (yeast)	chr1p32	205085_at	NM_004153
6.47	6.16	0.31	3.06E-01	6.71E-01	NOLC1	nucleolar and coiled-body phosphoprotein 1	chr10q24.32	205895_s_at	NM_004741
2.93	2.77	0.16	3.06E-01	6.71E-01	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	chr16p11.2	1565716_at	NM_004960
2.63	2.38	0.26	3.06E-01	6.71E-01	LOC641767	hypothetical protein LOC641767	---	238921_at	XM_935535
2.09	1.97	0.12	3.06E-01	6.71E-01	TLK1	Tousled-like kinase 1	chr2q31.1	241643_at	NM_012290
2.12	1.98	0.13	3.06E-01	6.71E-01	BCL10	B-cell CLL/lymphoma 10	chr1p22	1557257_at	NM_003921
2.94	2.68	0.25	3.06E-01	6.71E-01	---	---	---	239399_at	---
2.72	2.54	0.17	3.06E-01	6.71E-01	LOC283674	hypothetical protein LOC283674	chr15q22.32	1566839_at	---
4.44	4.09	0.35	3.06E-01	6.71E-01	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	chr22q12.2	205266_at	NM_002309
2.33	2.13	0.19	3.06E-01	6.72E-01	SCLT1	sodium channel and clathrin linker 1	chr4q28.2	1569190_at	NM_144643
2.71	2.58	0.14	3.06E-01	6.72E-01	GHRH	growth hormone releasing hormone	chr20q11.2	214524_at	NM_021081
5.83	5.61	0.22	3.06E-01	6.72E-01	CCDC128	coiled-coil domain containing 128	chr2p16.3	1553955_at	NM_152994
10.08	9.81	0.27	3.06E-01	6.72E-01	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	chr2q33.3	1555037_a_at	NM_005896
4.47	4.01	0.45	3.06E-01	6.72E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	35147_at	NM_001112732 /// NM_024979
2.89	2.76	0.14	3.06E-01	6.72E-01	---	---	---	1562478_at	---
3.27	3.05	0.22	3.06E-01	6.72E-01	HRBL	HIV-1 Rev binding protein-like	chr7q22.1	1554618_at	NM_006076
2.19	2.04	0.15	3.06E-01	6.72E-01	---	---	---	241265_x_at	---
6.30	6.03	0.26	3.06E-01	6.72E-01	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	chr5q11-q14	210802_s_at	NM_014473
3.86	3.58	0.28	3.06E-01	6.72E-01	RP5-1000E10.4	suppressor of IKK epsilon	chr1p13.2	228026_at	NM_001102396 /// NM_025073
5.18	4.70	0.48	3.06E-01	6.72E-01	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	chr12p11.23-p11.22	203735_x_at	NM_003622 /// NM_177444
4.39	3.71	0.68	3.06E-01	6.72E-01	RC3H1	ring finger and CCCH-type zinc finger domains 1	chr1q25.1	228996_at	NM_172071
2.20	2.03	0.17	3.06E-01	6.72E-01	LOC285943	hypothetical protein LOC285943	chr7p15.2	1562640_at	XR_040113 /// XR_040114 /// XR_040115 /// XR_040116
3.58	3.36	0.22	3.07E-01	6.72E-01	HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	chr5p12	1562563_at	NM_021072
3.03	2.86	0.17	3.07E-01	6.72E-01	MAPT	microtubule-associated protein tau	chr17q21.1	206401_s_at	NM_001123066 /// NM_001123067 /// NM_005910 /// NM_016834 /// NM_016835 /// NM_016841
2.72	2.58	0.13	3.07E-01	6.72E-01	AMBRA1	autophagy/beclin-1 regulator 1	chr11p11.2	234237_s_at	NM_017749
4.35	4.18	0.18	3.07E-01	6.72E-01	FZD5	frizzled homolog 5 (Drosophila)	chr2q33-q34	206136_at	NM_003468
2.40	2.22	0.19	3.07E-01	6.72E-01	LOC339894	hypothetical protein LOC339894	chr3q25.31	1561723_at	---
6.83	6.51	0.32	3.07E-01	6.72E-01	---	---	---	227476_at	---
7.10	6.86	0.25	3.07E-01	6.73E-01	FOXJ3	forkhead box J3	chr1pter-q31.3	206015_s_at	NM_014947
3.36	3.13	0.22	3.07E-01	6.73E-01	---	---	---	1559929_at	---

3.61	3.40	0.21	3.07E-01	6.73E-01	ORC5L	origin recognition complex, subunit 5-like (yeast)	chr7q22.1	211212_s_at	NM_002553 /// NM_181747																			
2.49	2.35	0.14	3.07E-01	6.73E-01	LOC285768	hypothetical protein LOC285768	chr6p25.3	1557618_at	XM_379386 /// XM_943096																			
2.31	2.15	0.17	3.07E-01	6.73E-01	SYNPR	synaptoporin	chr3p14.2	230303_at	NM_001130003 /// NM_144642																			
4.44	4.20	0.24	3.07E-01	6.73E-01	C21orf45	chromosome 21 open reading frame 45	chr21q22.11	228597_at	NM_018944																			
6.01	5.84	0.17	3.07E-01	6.73E-01	CCDC97	coiled-coil domain containing 97	chr19q13.2	225254_at	NM_052848																			
5.11	4.77	0.34	3.07E-01	6.73E-01	CCDC91	coiled-coil domain containing 91	chr12p11.22	218545_at	NM_018318																			
4.37	4.08	0.29	3.07E-01	6.73E-01	KPNA5	karyopherin alpha 5 (importin alpha 6)	chr6q22.2	229317_at	NM_002269																			
7.49	7.28	0.21	3.07E-01	6.73E-01	C14orf159	chromosome 14 open reading frame 159	chr14q32.12	218298_s_at	NM_001102366 /// NM_001102367 /// NM_001102368 /// NM_001102369 /// NM_024952																			
3.72	3.50	0.22	3.07E-01	6.73E-01	RPUSD3	RNA pseudouridylate synthase domain containing 3	chr3p25.3	1561329_s_at	NM_173659																			
4.40	4.22	0.18	3.08E-01	6.73E-01	TSFM	Ts translation elongation factor, mitochondrial	chr12q13-q14	214332_s_at	NM_005726																			
2.29	2.07	0.22	3.08E-01	6.73E-01	FAM76B	family with sequence similarity 76, member B	chr11q21	1553749_at	NM_144664																			
7.61	7.36	0.25	3.08E-01	6.73E-01	DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	chr16p13.3	219664_s_at	NM_020664																			
5.97	5.81	0.16	3.08E-01	6.73E-01	POFUT1	protein O-fucosyltransferase 1	chr20q11	212349_at	NM_015352 /// NM_172236																			
7.87	7.64	0.23	3.08E-01	6.73E-01	C16orf13	chromosome 16 open reading frame 13	chr16p13.3	227378_x_at	NM_001040160 /// NM_001040161 /// NM_001040162 /// NM_001040165 /// NM_032366																			
2.44	2.29	0.15	3.08E-01	6.73E-01	LOC100130068	hypothetical protein LOC100130068	chr16q24.2	1556616_a_at	XM_001716878 /// XM_001725697 /// XM_001726892																			
2.51	2.32	0.19	3.08E-01	6.73E-01	SLC23A3	solute carrier family 23 (nucleobase transporters), member 3	chr2q35	1553265_at	NM_144712																			
6.15	5.93	0.23	3.08E-01	6.73E-01	COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)	chr6q16.3	221227_x_at	NM_017421																			
5.49	5.29	0.20	3.08E-01	6.74E-01	TCHP	trichoplein, keratin filament binding	chr12q24.11	223455_at	NM_032300																			
5.23	5.02	0.21	3.08E-01	6.74E-01	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	chr16q24.3	201195_s_at	NM_003486																			
5.11	4.66	0.45	3.08E-01	6.74E-01	BTAF1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)	chr10q22-q23	209430_at	NM_003972																			
2.10	1.98	0.12	3.08E-01	6.74E-01	---	---	---	1560987_a_at	---																			
2.45	2.29	0.16	3.08E-01	6.74E-01	---	---	---	233189_at	---																			
10.70	10.52	0.18	3.08E-01	6.74E-01	PFDN5	prefoldin subunit 5	chr12q12	210908_s_at	NM_002624 /// NM_145897																			
3.85	3.70	0.15	3.09E-01	6.74E-01	KIAA0999	KIAA0999 protein	chr11q23.3	204156_at	NM_025164																			
3.04	2.78	0.26	3.09E-01	6.74E-01	LOC727770	similar to ankyrin repeat domain 20 family, member A1	chr1q12	237737_at	XR_037208																			
2.30	2.15	0.16	3.09E-01	6.74E-01	RHCE /// RHD	Rh blood group, CcEe antigens /// Rh blood group, D antigen	chr1p36.11	210429_at	NM_001127691 /// NM_016124 /// NM_020485 /// NM_138616 /// NM_138617 /// NM_138618																			
6.04	5.89	0.15	3.09E-01	6.74E-01	---	---	---	226546_at	---																			
3.64	3.31	0.33	3.09E-01	6.74E-01	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	chr1p36.22	219677_at	NM_025106																			
4.63	4.26	0.37	3.09E-01	6.74E-01	TRMT11	tRNA methyltransferase 11 homolog (S. cerevisiae)	chr6q11.1-q22.33	218877_s_at	NM_001031712																			

6.93	6.59	0.34	3.09E-01	6.74E-01	RGS19	regulator of G-protein signaling 19	chr20q13.33	204336_s_at	NM_001039467 /// NM_005873																				
3.02	2.84	0.18	3.09E-01	6.75E-01	FAM170A	family with sequence similarity 170, member A	chr5q23.1	1562906_at	NM_182761																				
2.21	2.08	0.13	3.09E-01	6.75E-01	---	---	---	243873_at	---																				
3.91	3.78	0.14	3.09E-01	6.75E-01	GAL3ST1	galactose-3-O-sulfotransferase 1	chr22q12.2	205670_at	NM_004861																				
11.10	10.92	0.17	3.09E-01	6.75E-01	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	chr12q24.2|12q24.2	200925_at	NM_004373																				
2.89	2.73	0.16	3.09E-01	6.75E-01	PRKCB	Protein kinase C, beta	chr16p11.2	228795_at	NM_002738 /// NM_212535																				
3.27	3.12	0.16	3.09E-01	6.75E-01	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	chr22q13.2-q13.31	215308_at	NM_001469																				
2.41	2.30	0.11	3.09E-01	6.75E-01	ZNF573	zinc finger protein 573	chr19q13.12	1556513_at	NM_152360																				
5.57	5.30	0.26	3.09E-01	6.75E-01	EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)	chr16p12.1	227374_at	NM_001083614 /// NR_003501																				
6.46	6.12	0.34	3.09E-01	6.75E-01	SGSM3	small G protein signaling modulator 3	chr22q13.1-q13.2	214779_s_at	NM_015705																				
4.07	3.87	0.20	3.10E-01	6.75E-01	XAB2	XPA binding protein 2	chr19p13.2	218110_at	NM_020196																				
4.62	4.46	0.16	3.10E-01	6.75E-01	LOC374569	Similar to Lysophospholipase	chr14q32.33	1557225_at	NM_001080464																				
4.80	4.57	0.23	3.10E-01	6.75E-01	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)	chr19p13.13	210585_s_at	NM_013433																				
2.41	2.29	0.12	3.10E-01	6.75E-01	ZBTB7A	zinc finger and BTB domain containing 7A	chr19p13.3	213303_x_at	NM_015898																				
5.24	5.09	0.15	3.10E-01	6.75E-01	---	---	---	242997_at	---																				
2.12	2.00	0.12	3.10E-01	6.75E-01	CASC2	cancer susceptibility candidate 2	chr10q26.11	1564372_s_at	XR_041332 /// XR_041333 /// XR_041334																				
4.76	4.41	0.36	3.10E-01	6.75E-01	KAT2B	K(lysine) acetyltransferase 2B	chr3p24	203845_at	NM_003884																				
2.53	2.39	0.14	3.10E-01	6.75E-01	IRAK3	interleukin-1 receptor-associated kinase 3	chr12q14.3	220034_at	NM_007199																				
4.15	4.01	0.13	3.10E-01	6.75E-01	HIRIP3	HIRA interacting protein 3	chr16p11.2	229697_at	NM_003609																				
3.17	3.01	0.16	3.10E-01	6.75E-01	CDKN2D	Cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	chr19p13	213586_at	NM_001800 /// NM_079421																				
2.63	2.45	0.18	3.10E-01	6.75E-01	LOC100130940	similar to LOC100126053 protein	---	231589_at	XR_042498 /// XR_042504																				
3.24	3.00	0.24	3.10E-01	6.75E-01	KCTD6	potassium channel tetramerisation domain containing 6	chr3p14.3	238001_at	NM_001128214 /// NM_153331																				
6.42	6.15	0.27	3.10E-01	6.75E-01	RAD1	RAD1 homolog (S. pombe)	chr5p13.2	204460_s_at	NM_002853 /// NM_133377																				
2.35	2.22	0.13	3.10E-01	6.75E-01	LOC339166	hypothetical protein LOC339166	chr17p13.3-p13.2	1560455_at	---																				
4.93	4.65	0.28	3.10E-01	6.75E-01	PXMP4	peroxisomal membrane protein 4, 24kDa	chr20q11.22	238746_at	NM_007238 /// NM_183397																				
3.84	3.69	0.15	3.10E-01	6.75E-01	---	---	---	221120_at	---																				
5.47	5.20	0.28	3.10E-01	6.75E-01	---	---	---	229303_at	---																				
7.98	7.75	0.23	3.10E-01	6.75E-01	TNS1	tensin 1	chr2q35-q36	221747_at	NM_022648																				
4.88	4.42	0.45	3.10E-01	6.76E-01	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	chr12p11	208149_x_at	NM_004399 /// NM_030653 /// NM_152438																				
2.59	2.43	0.16	3.10E-01	6.76E-01	---	---	---	234822_at	---																				
5.32	5.00	0.32	3.10E-01	6.76E-01	C18orf25	chromosome 18 open reading frame 25	chr18q21.1	226406_at	NM_001008239 /// NM_145055																				
3.48	3.33	0.15	3.10E-01	6.76E-01	PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta	chr4p16.3	210304_at	NM_000283																				
4.06	3.55	0.52	3.10E-01	6.76E-01	MGC13057	hypothetical protein MGC13057	chr2q32.2	223754_at	NM_001042519 /// NM_001042520 /// NM_001042521 /// NM_032321																				
5.90	5.68	0.21	3.11E-01	6.76E-01	DEF8	differentially expressed in FDCP 8 homolog (mouse)	chr16q24.3	219646_at	NM_017702 /// NM_207514																				
8.57	8.37	0.19	3.11E-01	6.76E-01	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	chr16q21	200708_at	NM_002080																				
8.79	8.49	0.30	3.11E-01	6.76E-01	PLXNB2	plexin B2	chr22q13.33	208890_s_at	NM_012401																				
2.52	2.36	0.16	3.11E-01	6.76E-01	HBBP1	hemoglobin, beta pseudogene 1	chr11p15.5	216063_at	NR_001589																				

6.10	5.81	0.29	3.11E-01	6.76E-01	FBXL19	F-box and leucine-rich repeat protein 19	chr16p11.2	228277_at	NM_001099784																				
2.14	2.03	0.11	3.11E-01	6.76E-01	LOC284067	hypothetical LOC284067	chr17q21.31	231453_at	XM_001722064 /// XM_208990 /// XM_937761																				
2.86	2.74	0.12	3.11E-01	6.76E-01	---	---	---	242104_at	---																				
5.29	4.60	0.69	3.11E-01	6.76E-01	BCO2	beta-carotene oxygenase 2	chr11q22.3-q23.1	232449_at	NM_001037290 /// NM_031938																				
5.24	5.02	0.22	3.11E-01	6.76E-01	C17orf69	chromosome 17 open reading frame 69	chr17q21.31	1553399_a_at	XR_040436 /// XR_040437 /// XR_040438																				
6.79	6.54	0.25	3.11E-01	6.76E-01	CLN3	ceroid-lipofuscinosis, neuronal 3	chr16p12.1	210859_x_at	NM_000086 /// NM_001042432																				
3.92	3.73	0.20	3.11E-01	6.76E-01	SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	chr2pter-p25.1	201838_s_at	NM_014860																				
2.60	2.45	0.14	3.11E-01	6.76E-01	---	---	---	1565892_at	---																				
2.91	2.70	0.22	3.11E-01	6.76E-01	ZNF341	zinc finger protein 341	chr20q11.22	240449_at	NM_032819																				
2.93	2.68	0.25	3.11E-01	6.76E-01	---	---	---	228273_at	---																				
7.85	7.64	0.21	3.11E-01	6.76E-01	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	chr7p22.1	200698_at	NM_001100603 /// NM_006854																				
6.26	5.91	0.35	3.11E-01	6.76E-01	MGC3032	hypothetical protein MGC3032	chr11q13	218641_at	XM_001715390 /// XM_933539 /// XM_944529																				
6.47	6.19	0.28	3.11E-01	6.76E-01	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	chr16p13.1	202804_at	NM_004996 /// NM_019862 /// NM_019898 /// NM_019899 /// NM_019900																				
2.14	2.01	0.13	3.11E-01	6.76E-01	---	---	---	244873_s_at	---																				
7.66	7.45	0.22	3.11E-01	6.76E-01	---	---	---	216484_x_at	---																				
4.92	4.60	0.32	3.11E-01	6.76E-01	---	---	---	223408_s_at	---																				
1.92	1.82	0.10	3.11E-01	6.76E-01	ICK	intestinal cell (MAK-like) kinase	chr6p12.3-p11.2	1552837_at	NM_014920 /// NM_016513																				
7.95	7.72	0.23	3.11E-01	6.76E-01	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	chr1p34.3	201586_s_at	NM_005066																				
4.68	4.17	0.51	3.12E-01	6.76E-01	SETD6	SET domain containing 6	chr16q21	219751_at	NM_024860																				
2.04	1.93	0.12	3.12E-01	6.77E-01	IQCH	IQ motif containing H	chr15q23	224165_s_at	NM_001031715 /// NM_022784																				
4.28	3.95	0.34	3.12E-01	6.77E-01	NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	chr14q32.12	243630_at	NM_004545																				
6.52	5.89	0.63	3.12E-01	6.77E-01	ANGPTL1	angiopoietin-like 1	chr1q25.2	231773_at	NM_004673																				
2.92	2.78	0.14	3.12E-01	6.77E-01	---	---	---	1564336_at	---																				
2.28	2.15	0.13	3.12E-01	6.77E-01	PAX8	paired box 8	chr2q12-q14	214528_s_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992																				
5.94	5.66	0.28	3.12E-01	6.77E-01	SMYD5	SMYD family member 5	chr2p13.2	209516_at	NM_006062																				
4.81	4.42	0.39	3.12E-01	6.77E-01	AMACR /// C1QTNF3	alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein 3	chr5p13	209425_at	NM_014324 /// NM_030945 /// NM_181435 /// NM_203382																				
2.45	2.30	0.15	3.12E-01	6.77E-01	---	---	---	1566868_at	---																				
2.20	2.09	0.11	3.12E-01	6.77E-01	---	---	---	1569459_a_at	---																				

4.59	4.39	0.20	3.12E-01	6.77E-01	NRP2	neuropilin 2	chr2q33.3	214632_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279																				
2.33	2.20	0.13	3.12E-01	6.77E-01	AGBL2	ATP/GTP binding protein-like 2	chr11p11.2	220390_at	NM_024783																				
7.26	7.06	0.20	3.12E-01	6.77E-01	NSL1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	chr1q41	209484_s_at	NM_001042549 /// NM_015471																				
2.90	2.67	0.23	3.12E-01	6.77E-01	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	chr21q22.1|21q22.11	210005_at	NM_000819 /// NM_175085																				
7.80	7.37	0.43	3.12E-01	6.77E-01	SLC35F5	solute carrier family 35, member F5	chr2q14.1	225872_at	NM_025181																				
7.38	7.19	0.19	3.12E-01	6.77E-01	DNAJC30	DnaJ (Hsp40) homolog, subfamily C, member 30	chr7q11.23	223367_at	NM_032317																				
10.73	10.56	0.17	3.12E-01	6.77E-01	TUBA1B	tubulin, alpha 1b	chr12q13.12	211072_x_at	NM_006082																				
2.31	2.20	0.11	3.12E-01	6.77E-01	SERP2	Stress-associated endoplasmic reticulum protein family member 2	chr13q14.11	240668_s_at	NM_001010897																				
7.36	7.11	0.25	3.12E-01	6.77E-01	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	chr12q24.13	218749_s_at	NM_024959																				
1.99	1.87	0.12	3.12E-01	6.77E-01	BCORL2	BCL6 co-repressor-like 2	chrYq11.222	1562313_at	NR_002923																				
3.59	3.28	0.31	3.12E-01	6.77E-01	CHKB /// CPT1B	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	chr22q13.33	210070_s_at	NM_004377 /// NM_005198 /// NM_152245 /// NM_152246 /// NM_152247 /// NM_152253																				
2.51	2.36	0.15	3.12E-01	6.77E-01	SIM1	single-minded homolog 1 (Drosophila)	chr6q16.3-q21	1552796_a_at	NM_005068																				
3.53	3.22	0.32	3.12E-01	6.77E-01	C7orf64	chromosome 7 open reading frame 64	chr7q21.2	221596_s_at	NM_032120																				
6.38	5.54	0.84	3.12E-01	6.77E-01	KCNK2	potassium channel, subfamily K, member 2	chr1q41	210261_at	NM_001017424 /// NM_001017425 /// NM_014217																				
2.31	2.17	0.15	3.12E-01	6.77E-01	C21orf37	chromosome 21 open reading frame 37	chr21q21.1	240801_at	NM_001005521																				
3.73	3.43	0.30	3.12E-01	6.77E-01	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	chr3p14	211596_s_at	NM_015541																				
5.22	4.97	0.26	3.12E-01	6.77E-01	USP19	ubiquitin specific peptidase 19	chr3p21.31	214674_at	NM_006677																				
2.05	1.93	0.11	3.12E-01	6.77E-01	---	---	---	237246_at	---																				
3.55	3.29	0.26	3.13E-01	6.77E-01	LOC145786	Hypothetical protein LOC145786	chr15q21.1	229073_at	---																				
6.50	6.31	0.19	3.13E-01	6.77E-01	SNX19	sorting nexin 19	chr11q25	202358_s_at	NM_014758																				
5.19	4.81	0.38	3.13E-01	6.77E-01	IQCG	IQ motif containing G	chr3q29	221185_s_at	NM_001134435 /// NM_032263																				
4.16	4.04	0.12	3.13E-01	6.77E-01	---	---	---	233601_at	---																				
8.77	8.43	0.33	3.13E-01	6.77E-01	NME4	non-metastatic cells 4, protein expressed in	chr16p13.3	212739_s_at	NM_005009																				
2.83	2.48	0.34	3.13E-01	6.77E-01	CHM	choroideremia (Rab escort protein 1)	chrXq21.2	207099_s_at	NM_000390																				
3.02	2.88	0.15	3.13E-01	6.77E-01	LOC257358	hypothetical protein LOC257358	chr5q35.1	1559489_a_at	XR_017851 /// XR_017954 /// XR_040392																				
4.22	4.04	0.18	3.13E-01	6.77E-01	GINS3	GINS complex subunit 3 (Psf3 homolog)	chr16q21	45633_at	NM_001126129 /// NM_001126130 /// NM_022770																				
3.41	3.20	0.21	3.13E-01	6.77E-01	SIGLEC5	sialic acid binding Ig-like lectin 5	chr19q13.3	220000_at	NM_003830																				
5.33	5.04	0.29	3.13E-01	6.77E-01	CC2D1A	coiled-coil and C2 domain containing 1A	chr19p13.12	58994_at	NM_017721																				
2.81	2.65	0.16	3.13E-01	6.77E-01	SYT15	synaptotagmin XV	chr10q11.1	1560879_a_at	NM_031912 /// NM_181519 /// XM_001720092																				

5.98	5.77	0.20	3.13E-01	6.78E-01	CTCFL /// HMG1L1 /// HMGB1 /// LOC100130561 /// LOC100132863	CCCTC-binding factor (zinc finger protein)-like /// high-mobility group (nonhistone chromosomal) protein 1-like 1 /// high-mobility group box 1 /// similar to high-mobility group (nonhistone chromosomal) protein 1-like 10 /// similar to hCG26831	chr13q12 /// chr20q13.31 /// chr20q13.32 /// chr22q12.1 /// chr9q33.2	216508_x_at	NM_001008735 /// NM_002128 /// NM_080618 /// XM_001720622 /// XM_001723188 /// XM_001723189 /// XM_001726254 /// XM_001726255 /// XR_036905 /// XR_038235 /// XR_039604																			
5.72	5.25	0.46	3.13E-01	6.78E-01	CAB39L	calcium binding protein 39-like	chr13q14.2-q14.3	221003_s_at	NM_001079670 /// NM_030925																				
5.97	5.72	0.25	3.13E-01	6.78E-01	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	chr9p12	222618_at	NM_018225																				
2.52	2.37	0.15	3.13E-01	6.78E-01	---	---	---	231343_at	---																				
6.99	6.70	0.28	3.14E-01	6.78E-01	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	chr14q24.3	221588_x_at	NM_005589																				
6.12	5.93	0.19	3.14E-01	6.78E-01	NOC2L	nucleolar complex associated 2 homolog (S. cerevisiae)	chr1p36.33	202115_s_at	NM_015658																				
2.42	2.25	0.17	3.14E-01	6.78E-01	---	---	---	242577_at	---																				
2.42	2.32	0.10	3.14E-01	6.78E-01	LOC284530	hypothetical protein LOC284530	chr1p36.13	1556638_at	---																				
2.44	2.34	0.10	3.14E-01	6.78E-01	SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1	chr1q23-q25.1	1554491_a_at	NM_000488																				
8.74	8.63	0.11	3.14E-01	6.78E-01	EIF4H	eukaryotic translation initiation factor 4H	chr7q11.23	206621_s_at	NM_022170 /// NM_031992																				
5.83	5.58	0.25	3.14E-01	6.78E-01	NLGN2	neuroligin 2	chr17p13.1	226288_s_at	NM_020795																				
3.54	3.38	0.16	3.14E-01	6.78E-01	---	---	---	1556195_a_at	---																				
7.05	6.49	0.56	3.14E-01	6.78E-01	LXN	latexin	chr3q25.32	218729_at	NM_020169																				
2.33	2.20	0.13	3.14E-01	6.78E-01	---	---	---	1564701_at	---																				
3.68	3.44	0.24	3.14E-01	6.78E-01	FLJ10357	hypothetical protein FLJ10357	chr14q11.2	241627_x_at	NM_018071																				
5.14	4.94	0.20	3.14E-01	6.78E-01	ZXDC	ZXD family zinc finger C	chr3q21.2	225964_at	NM_001040653 /// NM_025112																				
2.17	2.05	0.12	3.14E-01	6.78E-01	SALL3	Sal-like 3 (Drosophila)	chr18q23	243672_at	NM_171999																				
2.53	2.39	0.13	3.14E-01	6.78E-01	ACCN3	amiloride-sensitive cation channel 3	chr7q35	207561_s_at	NM_004769 /// NM_020321 /// NM_020322																				
2.86	2.72	0.14	3.14E-01	6.78E-01	TTC21A	tetratricopeptide repeat domain 21A	chr3p22.2	232308_at	NM_001105513 /// NM_145755																				
6.73	6.45	0.28	3.14E-01	6.78E-01	FBXO38	F-box protein 38	chr5q33.1	224369_s_at	NM_030793 /// NM_205836																				
6.06	5.66	0.40	3.14E-01	6.78E-01	MTA1	metastasis associated 1	chr14q32.3	211783_s_at	NM_004689																				
6.54	6.34	0.20	3.14E-01	6.78E-01	TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 associated protein	chr20q11.22	212059_s_at	NM_015638 /// NM_199368																				
7.65	7.44	0.21	3.14E-01	6.78E-01	BOLA2 /// BOLA2B	bolA homolog 2 (E. coli) /// bolA homolog 2B (E. coli)	chr16p11.2	209836_x_at	NM_001031827 /// NM_001039182																				
6.32	6.15	0.17	3.14E-01	6.78E-01	PJA1	praja 1	chrXq13.1	218667_at	NM_001032396 /// NM_022368 /// NM_145119																				
2.77	2.64	0.13	3.14E-01	6.78E-01	C17orf47	chromosome 17 open reading frame 47	chr17q22	1554662_at	NM_001038704																				
6.04	5.80	0.24	3.14E-01	6.78E-01	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	chr2q21.1	203555_at	NM_014369																				
2.83	2.62	0.21	3.14E-01	6.78E-01	---	---	---	1563104_at	---																				
8.63	8.48	0.15	3.14E-01	6.78E-01	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	chr4p16.3	207335_x_at	NM_007100																				

5.40	5.08	0.32	3.14E-01	6.78E-01	SRI	sorcin	chr7q21.1	208920_at	NM_003130 /// NM_198901																			
1.90	1.78	0.12	3.14E-01	6.78E-01	ALDOB	aldolase B, fructose-bisphosphate	chr9q21.3-q22.2	204704_s_at	NM_000035																			
3.99	3.66	0.33	3.15E-01	6.79E-01	JAM3	junctional adhesion molecule 3	chr11q25	231720_s_at	NM_032801																			
7.54	7.36	0.18	3.15E-01	6.79E-01	CHID1	chitinase domain containing 1	chr11p15.5	223061_at	NM_023947																			
9.49	8.81	0.68	3.15E-01	6.79E-01	VCAN	versican	chr5q14.3	204620_s_at	NM_001126336 /// NM_004385																			
3.32	3.20	0.12	3.15E-01	6.79E-01	FLJ40288	hypothetical protein FLJ40288	chr7q32.3	237659_at	XR_040153 /// XR_040154 /// XR_040155 /// XR_040156																			
2.67	2.47	0.20	3.15E-01	6.79E-01	---	---	---	240673_at	---																			
2.38	2.24	0.14	3.15E-01	6.79E-01	---	---	---	1570326_at	---																			
1.97	1.87	0.10	3.15E-01	6.79E-01	---	---	---	243784_s_at	---																			
5.35	4.96	0.38	3.15E-01	6.79E-01	C1orf9	chromosome 1 open reading frame 9	chr1q24	203429_s_at	NM_014283 /// NM_016227																			
3.41	3.24	0.17	3.15E-01	6.79E-01	---	---	---	237419_at	---																			
4.32	4.08	0.24	3.15E-01	6.79E-01	COLQ	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	chr3p25	206073_at	NM_005677 /// NM_080538 /// NM_080539 /// NM_080541 /// NM_080544																			
2.38	2.22	0.17	3.15E-01	6.79E-01	STAMBPL1	STAM binding protein-like 1	chr10q23.31	231891_at	NM_020799																			
2.50	2.30	0.21	3.15E-01	6.79E-01	ANAPC11	APC11 anaphase promoting complex subunit 11	chr17q25.3	224010_at	NM_001002244 /// NM_001002245 /// NM_001002246 /// NM_001002247 /// NM_001002248 /// NM_001002249 /// NM_016476																			
3.09	2.86	0.22	3.15E-01	6.79E-01	LOC440288	similar to FLJ16518 protein	chr15q24.1	238511_at	XM_001714156 /// XM_001714173 /// XM_001719502																			
4.20	3.93	0.27	3.15E-01	6.79E-01	---	---	---	243554_at	---																			
6.94	6.58	0.36	3.15E-01	6.79E-01	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	chr1q23	1554899_s_at	NM_004106																			
2.04	1.92	0.12	3.15E-01	6.79E-01	---	---	---	1569988_at	---																			
3.00	2.80	0.19	3.15E-01	6.79E-01	LOC440335	hypothetical gene supported by BC022385; BC035868; BC048326	chr16p13.3	229599_at	XM_001722191 /// XM_935391 /// XM_945742																			
8.96	8.80	0.17	3.15E-01	6.79E-01	GTF3A	general transcription factor IIIA	chr13q12.3-q13.1	215091_s_at	NM_002097 /// XM_001715623 /// XM_001716951 /// XM_001717641																			
4.90	4.73	0.17	3.16E-01	6.79E-01	MLKL	mixed lineage kinase domain-like	chr16q22.3	238025_at	NM_152649																			
5.52	5.22	0.30	3.16E-01	6.79E-01	C7orf27	chromosome 7 open reading frame 27	chr7p22.2	225437_s_at	NM_152743																			
5.17	4.47	0.69	3.16E-01	6.79E-01	GRB14	growth factor receptor-bound protein 14	chr2q22-q24	206204_at	NM_004490																			
2.86	2.70	0.15	3.16E-01	6.79E-01	CLDN16	claudin 16	chr3q28	220332_at	NM_006580																			
3.30	3.11	0.19	3.16E-01	6.79E-01	GAL3ST3	galactose-3-O-sulfotransferase 3	chr11q13.1	1553257_at	NM_033036																			
9.52	9.39	0.13	3.16E-01	6.79E-01	DAD1	defender against cell death 1	chr14q11-q12	200046_at	NM_001344																			

2.12	1.99	0.14	3.16E-01	6.79E-01	PLEKHA5	pleckstrin homology domain containing, family A member 5	chr12p12	233040_at	NM_019012
3.41	3.26	0.15	3.16E-01	6.79E-01	ERN1	endoplasmic reticulum to nucleus signaling 1	chr17q24.2	207061_at	NM_001433
7.97	7.65	0.31	3.16E-01	6.79E-01	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)	chr19p13.13	221507_at	NM_013433
5.47	5.14	0.33	3.16E-01	6.79E-01	BMS1P5	BMS1 pseudogene 5	chr10q11.22	231106_at	NR_003611
6.62	6.34	0.28	3.16E-01	6.79E-01	C21orf57	chromosome 21 open reading frame 57	chr21q22.3	227421_at	NM_001006114 /// NM_058181
2.09	1.98	0.11	3.16E-01	6.79E-01	IQCH	IQ motif containing H	chr15q23	1569611_a_at	NM_001031715 /// NM_022784
3.88	3.73	0.15	3.16E-01	6.79E-01	IGFN1	immunoglobulin-like and fibronectin type III domain containing 1	chr1q32.1	229275_at	NM_178275
5.41	5.19	0.22	3.16E-01	6.79E-01	ZNF16	zinc finger protein 16	chr8q24	219548_at	NM_001029976 /// NM_006958
6.93	6.65	0.28	3.16E-01	6.79E-01	TJAP1	tight junction associated protein 1 (peripheral)	chr6p21.1	221857_s_at	NM_080604
2.92	2.79	0.13	3.16E-01	6.79E-01	---	---	---	236425_at	---
5.44	4.89	0.54	3.16E-01	6.79E-01	---	---	---	229483_at	---
8.25	7.96	0.28	3.16E-01	6.79E-01	CYBA	cytochrome b-245, alpha polypeptide	chr16q24	203028_s_at	NM_000101
2.81	2.61	0.20	3.16E-01	6.79E-01	LOC146443	hypothetical protein LOC146443	chr16p13.3	1562930_at	---
6.49	5.94	0.54	3.16E-01	6.79E-01	KIF5C	kinesin family member 5C	chr2q23.1	203129_s_at	NM_004522
6.86	6.59	0.27	3.16E-01	6.79E-01	SNX33	sorting nexin 33	chr15q24.2	227151_at	NM_153271
5.29	5.08	0.20	3.17E-01	6.80E-01	RASSF7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	chr11p15.5	204927_at	NM_003475
1.96	1.83	0.13	3.17E-01	6.80E-01	ZRANB2	zinc finger, RAN-binding domain containing 2	chr1p31	241345_at	NM_005455 /// NM_203350
2.40	2.24	0.16	3.17E-01	6.80E-01	NAP1L4	Nucleosome assembly protein 1-like 4	chr11p15.5	236188_s_at	NM_005969
3.08	2.94	0.14	3.17E-01	6.80E-01	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	chr22q13.2-q13.31	230443_at	NM_001003796 /// NM_005008
5.14	4.81	0.33	3.17E-01	6.80E-01	MED22	mediator complex subunit 22	chr9q34.2	206593_s_at	NM_133640 /// NM_181491
6.56	6.37	0.19	3.17E-01	6.80E-01	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	chr18p11	202486_at	NM_006796
4.08	3.88	0.20	3.17E-01	6.80E-01	COL6A1	collagen, type VI, alpha 1	chr21q22.3	212940_at	NM_001848
4.55	4.24	0.31	3.17E-01	6.80E-01	TATDN3	TatD DNase domain containing 3	chr1q32.3	235069_at	NM_001042552 /// NM_001042553
6.59	6.21	0.38	3.17E-01	6.80E-01	FAM117B	family with sequence similarity 117, member B	chr2q33.1	226431_at	NM_173511
2.35	2.19	0.16	3.17E-01	6.80E-01	---	---	---	234640_x_at	---
3.68	3.53	0.14	3.17E-01	6.80E-01	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	chr6q27	214939_x_at	NM_001040000 /// NM_001040001 /// NM_005936
2.91	2.73	0.18	3.17E-01	6.80E-01	---	---	---	231171_at	---
6.36	6.10	0.27	3.17E-01	6.80E-01	PAFAH1B3	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 29kDa	chr19q13.1	203228_at	NM_002573
11.88	11.74	0.15	3.17E-01	6.80E-01	RPL12	ribosomal protein L12	chr9q34	214271_x_at	NM_000976
6.27	5.66	0.62	3.17E-01	6.80E-01	FRMD6	FERM domain containing 6	chr14q22.1	225481_at	NM_001042481 /// NM_152330
3.90	3.66	0.24	3.17E-01	6.80E-01	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	chr22q13.1	203901_at	NM_006116 /// NM_153497
2.44	2.32	0.12	3.17E-01	6.80E-01	---	---	---	241116_at	---
4.33	4.12	0.21	3.17E-01	6.80E-01	TP53	tumor protein p53	chr17p13.1	211300_s_at	NM_000546 /// NM_001126112 /// NM_001126113 /// NM_001126114 /// NM_001126115 /// NM_001126116 /// NM_001126117
2.71	2.52	0.19	3.17E-01	6.80E-01	LOC650392	Hypothetical protein LOC650392	---	1569872_a_at	XM_944170
2.64	2.46	0.18	3.17E-01	6.80E-01	ACTN2	actinin, alpha 2	chr1q42-q43	203864_s_at	NM_001103
2.12	2.02	0.10	3.17E-01	6.80E-01	GABRB1	gamma-aminobutyric acid (GABA) A receptor, beta 1	chr4p12	207010_at	NM_000812
2.08	1.97	0.11	3.18E-01	6.80E-01	SLC7A13	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13	chr8q21.3	238287_at	NM_138817

2.33	2.21	0.13	3.18E-01	6.80E-01	MYH16	myosin, heavy chain 16 pseudogene	chr7q22.1	1564072_at	NR_002147
2.87	2.70	0.16	3.18E-01	6.80E-01	KIAA1833	hypothetical protein KIAA1833	chr8q24.3	230361_at	NM_001099280 /// NM_001099281 /// NM_032450
5.70	5.01	0.68	3.18E-01	6.80E-01	---	---	---	243416_at	---
3.93	3.74	0.19	3.18E-01	6.80E-01	ARL3	ADP-ribosylation factor-like 3	chr10q23.3	1568590_at	NM_004311
5.07	4.88	0.19	3.18E-01	6.80E-01	BCORL1	BCL6 co-repressor-like 1	chrXq25-q26.1	219444_at	NM_021946
4.44	4.24	0.20	3.18E-01	6.80E-01	---	---	---	244411_at	---
7.01	6.79	0.22	3.18E-01	6.80E-01	TBC1D10A	TBC1 domain family, member 10A	chr22q12.1-qter	226133_s_at	NM_031937
2.30	2.16	0.14	3.18E-01	6.80E-01	---	---	---	1562787_at	---
2.21	2.10	0.11	3.18E-01	6.80E-01	LOC400986	Protein immuno-reactive with anti-PTH polyclonal antibodies	chr2q11.2	1555898_at	XM_001714165 /// XM_001714685 /// XM_001717763
7.71	6.83	0.88	3.18E-01	6.80E-01	NFIL3	nuclear factor, interleukin 3 regulated	chr9q22	203574_at	NM_005384
5.84	5.70	0.15	3.18E-01	6.80E-01	NADK	NAD kinase	chr1p36.33-p36.21	215159_s_at	NM_023018
6.08	5.78	0.30	3.18E-01	6.80E-01	CCDC117	coiled-coil domain containing 117	chr22q12.1	225644_at	NM_173510
5.63	5.43	0.19	3.18E-01	6.80E-01	CRKRS	Cdc2-related kinase, arginine/serine-rich	chr17q12	225690_at	NM_015083 /// NM_016507
4.71	4.38	0.33	3.18E-01	6.80E-01	SBK1	SH3-binding domain kinase 1	chr16p11.2	226548_at	NM_001024401
6.56	6.37	0.19	3.18E-01	6.80E-01	NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	chr19q13.1	214062_x_at	NM_001001716 /// NM_002503
5.02	4.78	0.24	3.18E-01	6.81E-01	ZNF785	zinc finger protein 785	chr16p11.2	242272_at	NM_152458
3.04	2.83	0.21	3.18E-01	6.81E-01	EFS	embryonal Fyn-associated substrate	chr14q11.2-q12	204400_at	NM_005864 /// NM_032459
2.15	2.01	0.14	3.18E-01	6.81E-01	---	---	---	1559724_at	---
5.92	5.72	0.20	3.18E-01	6.81E-01	PTPRA	protein tyrosine phosphatase, receptor type, A	chr20p13	213795_s_at	NM_002836 /// NM_080840 /// NM_080841
3.06	2.89	0.17	3.19E-01	6.81E-01	GHRHR	growth hormone releasing hormone receptor	chr7p14	207825_s_at	NM_000823 /// NM_001009824
2.16	2.01	0.15	3.19E-01	6.81E-01	LOC100169752	hypothetical LOC100169752	chr10q	1556133_s_at	NR_023362
6.26	6.04	0.22	3.19E-01	6.81E-01	---	---	---	229898_at	---
4.09	3.83	0.27	3.19E-01	6.81E-01	---	---	---	243691_at	---
11.14	10.85	0.30	3.19E-01	6.81E-01	CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1	chr8q21	214610_at	NM_000497 /// NM_001026213
4.02	3.76	0.26	3.19E-01	6.81E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	214700_x_at	NM_018151
3.73	3.46	0.28	3.19E-01	6.81E-01	---	---	---	217164_at	---
3.49	3.34	0.15	3.19E-01	6.81E-01	FLJ30064	hypothetical protein LOC644975	chr7q21.3	239821_at	NM_001039906
1.99	1.88	0.10	3.19E-01	6.81E-01	IQCF3	IQ motif containing F3	chr3p21.1	236870_at	NM_001085479
3.50	3.13	0.38	3.19E-01	6.81E-01	LOC100130224 /// UTY	hypothetical protein LOC100130224 /// ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	chrYq11	208067_x_at	NM_007125 /// NM_182659 /// NM_182660 /// XM_001713700 /// XM_001713765 /// XM_001713766
7.74	7.44	0.30	3.19E-01	6.81E-01	SPTBN1	spectrin, beta, non-erythrocytic 1	chr2p21	226342_at	NM_003128 /// NM_178313
2.22	2.07	0.16	3.19E-01	6.81E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	1555719_a_at	NM_033364
6.72	6.20	0.52	3.19E-01	6.81E-01	ARRDC3	arrestin domain containing 3	chr5q14.3	224797_at	NM_020801
7.32	6.97	0.35	3.19E-01	6.81E-01	LYPLA1	lysophospholipase I	chr8q11.23	212449_s_at	NM_006330

4.37	4.21	0.16	3.19E-01	6.81E-01	LOC100129380	Hypothetical protein LOC100129380	chr12q24.31	236722_at	XM_001719293 /// XM_001721567 /// XM_001726734																			
2.16	2.03	0.12	3.19E-01	6.81E-01	ACSL6	acyl-CoA synthetase long-chain family member 6	chr5q31	223918_at	NM_001009185 /// NM_015256																			
2.98	2.84	0.14	3.19E-01	6.81E-01	LOC100131928	Hypothetical protein LOC100131928	chr12q24.32	231440_at	XM_001714264 /// XM_001715300 /// XM_001719195																			
3.30	3.16	0.15	3.20E-01	6.81E-01	PRAP1	proline-rich acidic protein 1	chr10q26.3	243669_s_at	NM_145202																			
4.02	3.85	0.17	3.20E-01	6.81E-01	T	T, brachyury homolog (mouse)	chr6q27	206524_at	NM_003181																			
2.90	2.67	0.23	3.20E-01	6.81E-01	---	---	---	240810_at	---																			
4.09	3.67	0.42	3.20E-01	6.81E-01	---	---	---	242888_at	---																			
2.15	2.04	0.11	3.20E-01	6.81E-01	---	---	---	1560690_at	---																			
4.03	3.51	0.51	3.20E-01	6.82E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	244194_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723																			
3.17	2.78	0.40	3.20E-01	6.82E-01	ATF1	activating transcription factor 1	chr12q13	1558233_s_at	NM_005171																			
2.92	2.77	0.14	3.20E-01	6.82E-01	CECR2	cat eye syndrome chromosome region, candidate 2	chr22q11.2	223729_at	NM_031413																			
2.35	2.16	0.19	3.20E-01	6.82E-01	SARS	Seryl-tRNA synthetase	chr1p13.3-p13.1	237689_at	NM_006513																			
3.54	3.35	0.19	3.20E-01	6.82E-01	TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	chr6p21.1	1556178_x_at	NM_138572																			
4.58	4.24	0.35	3.20E-01	6.82E-01	---	---	---	240277_at	---																			
2.67	2.53	0.14	3.20E-01	6.82E-01	GPR75	G protein-coupled receptor 75	chr2p16	220481_at	NM_006794																			
2.19	2.04	0.15	3.20E-01	6.82E-01	---	---	---	1568844_at	---																			
5.34	5.13	0.21	3.20E-01	6.82E-01	SLC37A3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	chr7q34	223304_at	NM_032295 /// NM_207113																			
6.95	6.62	0.34	3.20E-01	6.82E-01	CECR1	cat eye syndrome chromosome region, candidate 1	chr22q11.2	219505_at	NM_017424 /// NM_177405																			
4.07	3.89	0.18	3.20E-01	6.82E-01	DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	chrXq13.1	212728_at	NM_020730 /// NM_021120																			
6.59	6.45	0.14	3.20E-01	6.82E-01	TARS2	threonyl-tRNA synthetase 2, mitochondrial (putative)	chr1q21.2	221189_s_at	NM_025150																			
4.43	4.09	0.34	3.20E-01	6.82E-01	MDH1	Malate dehydrogenase 1, NAD (soluble)	chr2p13.3	235374_at	NM_005917																			
2.02	1.87	0.15	3.20E-01	6.82E-01	IDS	iduronate 2-sulfatase	chrXq28	1556026_at	NM_000202 /// NM_006123																			
2.52	2.37	0.15	3.20E-01	6.82E-01	NOD2	nucleotide-binding oligomerization domain containing 2	chr16q21	220066_at	NM_022162																			
5.49	5.20	0.29	3.20E-01	6.82E-01	BANP	BTG3 associated nuclear protein	chr16q24.2-q24.3	233186_s_at	NM_017869 /// NM_079837 /// XM_001718410																			
3.42	3.16	0.26	3.20E-01	6.82E-01	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	chr17q21.1	210320_s_at	NM_007010 /// NM_152300																			
6.94	6.63	0.32	3.20E-01	6.82E-01	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	chr2q31.2	209139_s_at	NM_003690																			
3.50	3.26	0.24	3.20E-01	6.82E-01	C20orf57 /// DUSP15	chromosome 20 open reading frame 57 /// dual specificity phosphatase 15	chr20q11.21	234829_at	NM_001012644 /// NM_080611 /// NM_177991																			
4.52	4.27	0.25	3.20E-01	6.82E-01	MYO5B	myosin VB	chr18q21	225301_s_at	NM_001080467																			
2.96	2.79	0.17	3.21E-01	6.82E-01	STAB1	stabilin 1	chr3p21.1	1555320_a_at	NM_015136																			
5.99	5.78	0.22	3.21E-01	6.82E-01	MCRS1	microspherule protein 1	chr12q13.12	202556_s_at	NM_001012300 /// NM_006337																			
2.37	2.19	0.17	3.21E-01	6.82E-01	MGC4473	hypothetical LOC79100	chr1q23.3	224020_at	---																			

3.69	3.42	0.27	3.21E-01	6.82E-01	LOC100129500	hypothetical protein LOC100129500	chr19q13.32	212883_at	XM_001722911 /// XM_001722946 /// XM_001724653 /// XM_001724655																				
6.26	5.88	0.38	3.21E-01	6.82E-01	KITLG	KIT ligand	chr12q22	226534_at	NM_000899 /// NM_003994																				
3.31	3.20	0.11	3.21E-01	6.82E-01	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	chr10q24.1	1559127_x_at	NM_015179																				
5.65	5.28	0.37	3.21E-01	6.82E-01	FAM49A	family with sequence similarity 49, member A	chr2p24.3	208092_s_at	NM_030797																				
6.01	5.83	0.17	3.21E-01	6.82E-01	PRMT2	protein arginine methyltransferase 2	chr21q22.3	221564_at	NM_001535 /// NM_206962																				
3.34	3.12	0.21	3.21E-01	6.82E-01	LCK	lymphocyte-specific protein tyrosine kinase	chr1p34.3	204890_s_at	NM_001042771 /// NM_005356																				
5.01	4.67	0.34	3.21E-01	6.82E-01	INVS	inversin	chr9q31	210114_at	NM_014425 /// NM_183245																				
10.39	10.24	0.15	3.21E-01	6.83E-01	UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	chr19q12-q13.1	208909_at	NM_006003																				
2.78	2.62	0.15	3.21E-01	6.83E-01	NPHP1	nephronophthisis 1 (juvenile)	chr2q13	238843_at	NM_000272 /// NM_001128178 /// NM_001128179 /// NM_207181																				
6.49	6.12	0.36	3.21E-01	6.83E-01	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	chr10q22.1	32094_at	NM_004273																				
2.28	2.15	0.13	3.21E-01	6.83E-01	---	---	---	231980_at	---																				
4.77	4.44	0.33	3.21E-01	6.83E-01	KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	chr11q22.3	225128_at	NM_153705																				
2.53	2.41	0.12	3.21E-01	6.83E-01	---	---	---	243191_at	---																				
6.69	6.49	0.20	3.21E-01	6.83E-01	C11orf49	chromosome 11 open reading frame 49	chr11p11.2	203257_s_at	NM_001003676 /// NM_001003677 /// NM_001003678 /// NM_024113																				
2.70	2.55	0.15	3.21E-01	6.83E-01	LOC285796	hypothetical protein LOC285796	chr6q26	1561373_at	---																				
2.45	2.34	0.12	3.21E-01	6.83E-01	---	---	---	1569492_at	---																				
3.32	3.13	0.19	3.21E-01	6.83E-01	MCPH1	microcephalin 1	chr8p23.1	219592_at	NM_024596																				
6.95	6.74	0.21	3.21E-01	6.83E-01	STX18	syntaxin 18	chr4p16.2	218763_at	NM_016930																				
4.17	4.00	0.17	3.21E-01	6.83E-01	FBXO32	F-box protein 32	chr8q24.13	225803_at	NM_058229 /// NM_148177																				
2.24	2.12	0.12	3.21E-01	6.83E-01	---	---	---	1564628_at	---																				
2.61	2.45	0.17	3.21E-01	6.83E-01	PTN	pleiotrophin	chr7q33-q34	209465_x_at	NM_002825																				
4.32	4.04	0.28	3.21E-01	6.83E-01	EVC	Ellis van Creveld syndrome	chr4p16	219432_at	NM_153717																				
4.09	3.87	0.22	3.22E-01	6.83E-01	FKBP11	FK506 binding protein 11, 19 kDa	chr12q13.12	228308_at	NM_016594																				
2.38	2.24	0.14	3.22E-01	6.83E-01	---	---	---	231007_at	---																				
2.96	2.78	0.18	3.22E-01	6.83E-01	---	---	---	228858_at	---																				
2.41	2.29	0.12	3.22E-01	6.83E-01	---	---	---	1567009_at	---																				
2.48	2.35	0.13	3.22E-01	6.83E-01	RPP30	ribonuclease P/MRP 30kDa subunit	chr10q23.31	1556063_s_at	NM_001104546 /// NM_006413																				

4.55	4.38	0.17	3.22E-01	6.83E-01	COL13A1	collagen, type XIII, alpha 1	chr10q22	211809_x_at	NM_001130103 /// NM_005203 /// NM_080798 /// NM_080799 /// NM_080800 /// NM_080801 /// NM_080802 /// NM_080803 /// NM_080804 /// NM_080805 /// NM_080806 /// NM_080807 /// NM_080808 /// NM_080809 /// NM_080810 /// NM_080811 /// NM_080812 /// NM_080813 /// NM_080814 /// NM_080815																			
3.37	2.99	0.37	3.22E-01	6.83E-01	---	---	---	227492_at	---																				
7.23	6.89	0.34	3.22E-01	6.83E-01	GATAD2A	GATA zinc finger domain containing 2A	chr19p13.11	234294_x_at	NM_017660																				
2.37	2.25	0.11	3.22E-01	6.83E-01	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	chr21q22.11	234315_at	NM_001011545 /// NM_001186 /// NM_206866																				
6.31	5.98	0.33	3.22E-01	6.83E-01	PLEKHA3	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	chr2q31.2	223370_at	NM_019091																				
4.68	4.49	0.20	3.22E-01	6.83E-01	MYO9B	myosin IXB	chr19p13.1	217297_s_at	NM_001130065 /// NM_004145																				
2.13	2.02	0.12	3.22E-01	6.83E-01	---	---	---	244380_at	---																				
2.45	2.32	0.13	3.22E-01	6.83E-01	---	---	---	243466_at	---																				
5.40	5.18	0.22	3.22E-01	6.83E-01	NPAT	nuclear protein, ataxia-telangiectasia locus	chr11q22-q23	209798_at	NM_002519																				
2.18	2.06	0.11	3.22E-01	6.83E-01	---	---	---	242993_at	---																				
6.65	6.29	0.36	3.22E-01	6.83E-01	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	chr2p22.1	201129_at	NM_001031684																				
5.60	5.41	0.19	3.22E-01	6.83E-01	C12orf49	chromosome 12 open reading frame 49	chr12q24.22	222767_s_at	NM_024738																				
2.02	1.90	0.12	3.22E-01	6.83E-01	---	---	---	242613_at	---																				
2.26	2.14	0.13	3.22E-01	6.84E-01	TRPC7	transient receptor potential cation channel, subfamily C, member 7	chr5q31.2	208589_at	NM_020389																				
13.27	13.18	0.09	3.23E-01	6.84E-01	RPL41	ribosomal protein L41	chr12q13	201492_s_at	NM_001035267 /// NM_021104																				
4.35	4.03	0.32	3.23E-01	6.84E-01	MFSD8	Major facilitator superfamily domain containing 8	chr4q28.1-q28.2	228282_at	NM_152778																				
2.86	2.63	0.23	3.23E-01	6.84E-01	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	chr12q24.31-q24.32	209334_s_at	NM_002813																				
9.47	9.25	0.21	3.23E-01	6.84E-01	TUFM	Tu translation elongation factor, mitochondrial	chr16p11.2	201113_at	NM_003321																				
5.29	4.96	0.33	3.23E-01	6.84E-01	PTPRJ	protein tyrosine phosphatase, receptor type, J	chr11p11.2	227396_at	NM_001098503 /// NM_002843																				
7.34	7.10	0.25	3.23E-01	6.84E-01	C19orf60	chromosome 19 open reading frame 60	chr19p13.11	51200_at	NM_001100418 /// NM_001100419																				

3.43	3.23	0.20	3.23E-01	6.84E-01	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	chr2q32.3	233085_s_at	NM_001031716
2.17	2.03	0.13	3.23E-01	6.84E-01	KIF27	kinesin family member 27	chr9q21.32	232514_at	NM_017576
4.03	3.81	0.23	3.23E-01	6.84E-01	---	---	---	1557816_a_at	---
5.76	5.54	0.22	3.23E-01	6.84E-01	---	---	---	1570266_x_at	---
3.68	3.58	0.10	3.23E-01	6.84E-01	---	---	---	1558670_at	---
7.63	7.36	0.27	3.23E-01	6.84E-01	CSDC2	cold shock domain containing C2, RNA binding	chr22q13.2-q13.31	209981_at	NM_014460
4.21	3.98	0.23	3.23E-01	6.84E-01	MRPL12	Mitochondrial ribosomal protein L12	chr17q25	229165_at	NM_002949
2.41	2.26	0.15	3.24E-01	6.84E-01	---	---	---	241888_at	---
2.71	2.53	0.19	3.24E-01	6.84E-01	SH3RF2	SH3 domain containing ring finger 2	chr5q32	243582_at	NM_152550
2.21	2.10	0.11	3.24E-01	6.85E-01	CLDND1	claudin domain containing 1	chr3q12.1	239146_at	NM_001040181 /// NM_001040182 /// NM_001040183 /// NM_001040199 /// NM_001040200 /// NM_019895
5.75	5.39	0.36	3.24E-01	6.85E-01	GSPT1	G1 to S phase transition 1	chr16p13.1	240452_at	NM_001130006 /// NM_001130007 /// NM_002094
3.56	3.36	0.20	3.24E-01	6.85E-01	PSMG1	Proteasome (prosome, macropain) assembly chaperone 1	chr21q22.3	238890_at	NM_003720 /// NM_203433
2.70	2.55	0.15	3.24E-01	6.85E-01	XYLB	xylulokinase homolog (H. influenzae)	chr3p22-p21.3	208318_s_at	NM_005108
5.14	4.88	0.26	3.24E-01	6.85E-01	---	---	---	238610_s_at	---
2.69	2.45	0.25	3.24E-01	6.85E-01	---	---	---	242895_x_at	---
3.13	2.95	0.18	3.24E-01	6.85E-01	CCDC149	coiled-coil domain containing 149	chr4p15.2	1553840_a_at	NM_001130726 /// NM_173463
2.38	2.25	0.12	3.24E-01	6.85E-01	CCDC34	coiled-coil domain containing 34	chr11p14.1	1553666_at	NM_030771 /// NM_080654
3.27	3.01	0.27	3.24E-01	6.85E-01	PTEN	phosphatase and tensin homolog	chr10q23.3	233314_at	NM_000314
2.85	2.63	0.22	3.24E-01	6.85E-01	---	---	---	232571_at	---
2.61	2.22	0.39	3.24E-01	6.85E-01	LOC645323	hypothetical LOC645323	chr5q14.3	230272_at	XR_041118 /// XR_041119 /// XR_041120
6.51	6.30	0.22	3.24E-01	6.85E-01	FLJ35348	FLJ35348	chr9q34	213788_s_at	XR_041460 /// XR_041461 /// XR_041462
3.03	2.87	0.15	3.25E-01	6.85E-01	ZFYVE16	zinc finger, FYVE domain containing 16	chr5q14	1555982_at	NM_001105251 /// NM_014733
2.78	2.65	0.13	3.25E-01	6.85E-01	KIAA0226	KIAA0226	chr3q29	1560138_at	NM_014687
6.38	5.98	0.40	3.25E-01	6.85E-01	DKFZP434B0335	DKFZP434B0335 protein	chr7q21.3	227580_s_at	NM_015395
2.62	2.49	0.13	3.25E-01	6.85E-01	CATSPER3	cation channel, sperm associated 3	chr5q31.1	230981_at	NM_178019
4.64	4.41	0.23	3.25E-01	6.85E-01	LIN52	lin-52 homolog (C. elegans)	chr14q24.3	228583_at	NM_001024674
2.20	2.03	0.17	3.25E-01	6.85E-01	---	---	---	236035_at	---
2.47	2.27	0.20	3.25E-01	6.85E-01	---	---	---	1561531_at	---
4.29	4.01	0.28	3.25E-01	6.85E-01	MAP6	microtubule-associated protein 6	chr11q13.5	228448_at	NM_033063 /// NM_207577
5.36	5.04	0.32	3.25E-01	6.85E-01	MBD6	methyl-CpG binding domain protein 6	---	227832_at	NM_052897
6.59	6.30	0.29	3.25E-01	6.86E-01	SF3B4	splicing factor 3b, subunit 4, 49kDa	chr1q12-q21	209044_x_at	NM_005850
8.01	7.79	0.22	3.25E-01	6.86E-01	GLTP	glycolipid transfer protein	chr12q24.11	226177_at	NM_016433
6.89	6.72	0.17	3.25E-01	6.86E-01	C9orf7	chromosome 9 open reading frame 7	chr9q34	61874_at	NM_017586
2.71	2.41	0.29	3.25E-01	6.86E-01	---	---	---	236081_at	---
7.02	6.77	0.25	3.25E-01	6.86E-01	C16orf63	chromosome 16 open reading frame 63	chr16p13.11	225087_at	NM_144600
4.54	4.17	0.37	3.25E-01	6.86E-01	HISPPD1	histidine acid phosphatase domain containing 1	chr5q21.1	203253_s_at	NM_015216
3.77	3.62	0.14	3.25E-01	6.86E-01	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	chr12p12.1	1559204_x_at	NM_004985 /// NM_033360

3.88	3.70	0.18	3.25E-01	6.86E-01	LOC390595	similar to ubiquitin-associated protein 1 (predicted)	chr15q22.31	232663_s_at	XM_001718742 /// XM_372574 /// XM_940509																				
2.04	1.94	0.10	3.25E-01	6.86E-01	---	---	---	1558842_at	---																				
2.23	2.09	0.14	3.25E-01	6.86E-01	MIRHG1	microRNA host gene 1 (non-protein coding)	chr13q31.3	232291_at	XR_042147 /// XR_042176 /// XR_042177																				
5.92	5.76	0.17	3.25E-01	6.86E-01	LYPLA2P1	lysophospholipase II pseudogene 1	chr6p21.32	216606_x_at	NR_001444																				
2.31	2.19	0.13	3.25E-01	6.86E-01	FCRL2	Fc receptor-like 2	chr1q21	224192_at	NM_030764 /// NM_138738																				
7.60	7.38	0.22	3.26E-01	6.86E-01	GPR108	G protein-coupled receptor 108	chr19p13.3	225058_at	NM_001080452 /// NM_020171																				
6.49	6.26	0.23	3.26E-01	6.86E-01	EEF2K	eukaryotic elongation factor-2 kinase	chr16p12.1	225545_at	NM_013302																				
2.04	1.91	0.13	3.26E-01	6.86E-01	IBSP	integrin-binding sialoprotein	chr4q21-q25	236028_at	NM_004967																				
4.15	3.97	0.18	3.26E-01	6.86E-01	LOC151146	hypothetical protein LOC151146	chr2q14.2	227604_at	---																				
9.68	9.44	0.23	3.26E-01	6.86E-01	WBP5	WW domain binding protein 5	chrXq22.1-q22.2	217975_at	NM_001006612 /// NM_001006613 /// NM_001006614 /// NM_016303																				
10.21	10.09	0.12	3.26E-01	6.86E-01	C1orf43	chromosome 1 open reading frame 43	chr1q21.2	223034_s_at	NM_001098616 /// NM_015449 /// NM_138740																				
4.74	4.47	0.27	3.26E-01	6.87E-01	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	chr12q23.2	212959_s_at	NM_024312																				
3.79	3.41	0.38	3.26E-01	6.87E-01	KIAA1543	KIAA1543	chr19p13.3-p13.2	1568617_a_at	NM_001080429 /// NM_020902																				
2.04	1.91	0.12	3.26E-01	6.87E-01	---	---	---	1559133_at	---																				
2.20	2.07	0.13	3.26E-01	6.87E-01	---	---	---	1563523_at	---																				
5.11	4.83	0.27	3.26E-01	6.87E-01	KATNAL1	katanin p60 subunit A-like 1	chr13q12.3	227713_at	NM_001014380 /// NM_032116																				
2.66	2.52	0.14	3.26E-01	6.87E-01	---	---	---	231334_at	---																				
2.79	2.62	0.17	3.26E-01	6.87E-01	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	chr7q21.1	211440_x_at	NM_022820 /// NM_057095 /// NM_057096																				
6.11	5.86	0.25	3.26E-01	6.87E-01	KIAA0652	KIAA0652	chr11p11.2	203363_s_at	NM_014741																				
6.29	6.16	0.14	3.26E-01	6.87E-01	---	---	---	1569200_at	---																				
3.90	3.73	0.16	3.27E-01	6.87E-01	RAB28	RAB28, member RAS oncogene family	chr4p15.33	207495_at	NM_001017979 /// NM_004249																				
2.78	2.60	0.18	3.27E-01	6.87E-01	QPCTL	glutaminyl-peptide cyclotransferase-like	chr19q13.32	220438_at	NM_017659																				
6.99	6.63	0.36	3.27E-01	6.87E-01	CD97	CD97 molecule	chr19p13	202910_s_at	NM_001025160 /// NM_001784 /// NM_078481																				
3.95	3.70	0.26	3.27E-01	6.87E-01	SERHL /// SERHL2	serine hydrolase-like /// serine hydrolase-like 2	chr22q13 /// chr22q13.2-q13.31	214243_s_at	NM_014509 /// NM_170694 /// XM_001719595																				
2.48	2.30	0.18	3.27E-01	6.87E-01	SHANK2	SH3 and multiple ankyrin repeat domains 2	chr11q13.3	1564377_at	NM_012309 /// NM_133266																				
3.20	3.03	0.18	3.27E-01	6.87E-01	WDR21A	WD repeat domain 21A	chr14q24.3	214758_at	NM_015604 /// NM_181340 /// NM_181341																				
5.13	4.98	0.15	3.27E-01	6.87E-01	C10orf76	chromosome 10 open reading frame 76	chr10q24.32	55662_at	NM_024541																				

5.51	5.22	0.29	3.27E-01	6.87E-01	FUBP3	far upstream element (FUSE) binding protein 3	chr9q34.11-q34.12	212824_at	NM_003934
2.21	2.09	0.12	3.27E-01	6.87E-01	---	---	---	216406_at	---
2.30	2.18	0.12	3.27E-01	6.87E-01	IFNA10	interferon, alpha 10	chr9p22	208261_x_at	NM_002171
3.65	3.40	0.24	3.27E-01	6.87E-01	---	---	---	236104_at	---
3.39	3.23	0.16	3.27E-01	6.87E-01	---	---	---	230689_at	---
4.10	3.84	0.26	3.27E-01	6.87E-01	ETNK1	ethanolamine kinase 1	chr12p12.1	222262_s_at	NM_001039481 /// NM_018638
4.10	3.88	0.23	3.27E-01	6.87E-01	PVR	poliovirus receptor	chr19q13.2	214443_at	NM_006505
3.16	3.01	0.16	3.27E-01	6.87E-01	---	---	---	1556240_at	---
2.40	2.29	0.11	3.27E-01	6.87E-01	---	---	---	243308_at	---
2.25	2.13	0.12	3.27E-01	6.87E-01	---	---	---	1563174_at	---
3.03	2.85	0.18	3.27E-01	6.87E-01	---	---	---	239405_at	---
7.07	6.86	0.21	3.27E-01	6.88E-01	RILPL2	Rab interacting lysosomal protein-like 2	chr12q24.31	227983_at	NM_145058
2.63	2.47	0.16	3.27E-01	6.88E-01	FER1L5	fer-1-like 5 (C. elegans)	chr2q11.2	233353_at	NM_001077400 /// NM_001113382
2.22	2.04	0.18	3.27E-01	6.88E-01	TGFB2	transforming growth factor, beta 2	chr1q41	209908_s_at	NM_003238
6.78	6.41	0.37	3.27E-01	6.88E-01	CALR	calreticulin	chr19p13.3-p13.2	214315_x_at	NM_004343
4.55	4.40	0.16	3.27E-01	6.88E-01	ANKRD24	ankyrin repeat domain 24	chr19p13.3	233895_at	NM_133475
3.37	3.14	0.23	3.27E-01	6.88E-01	CCBL2 /// LOC100131735 /// RBMX	cysteine conjugate-beta lyase 2 /// similar to RNA binding motif protein, X-linked /// RNA binding motif protein, X-linked	chr1p22.2 /// chrXq26.3	1556336_at	NM_001008661 /// NM_001008662 /// NM_002139 /// NM_019610 /// XR_038716 /// XR_039081
2.30	2.17	0.13	3.27E-01	6.88E-01	---	---	---	1564074_at	---
3.83	3.70	0.14	3.28E-01	6.88E-01	ACY3	aspartoacylase (aminocyclase) 3	chr11q13.2	1554974_at	NM_080658
3.61	2.93	0.68	3.28E-01	6.88E-01	CYCS	cytochrome c, somatic	chr7p15.2	244546_at	NM_018947
1.88	1.77	0.11	3.28E-01	6.88E-01	LOC340184	hypothetical protein LOC340184	chr6p24.1	1563589_at	---
2.90	2.74	0.16	3.28E-01	6.88E-01	---	---	---	216429_at	---
2.22	2.05	0.17	3.28E-01	6.88E-01	DEPDC1	DEP domain containing 1	chr1p31.2	220295_x_at	NM_001114120 /// NM_017779
3.19	3.03	0.16	3.28E-01	6.88E-01	YTHDC2	YTH domain containing 2	chr5q22.2	205835_s_at	NM_022828
3.14	2.95	0.19	3.28E-01	6.88E-01	FLJ13439	hypothetical gene supported by AK023501	chr11p15.1	233077_at	---
3.04	2.88	0.16	3.28E-01	6.88E-01	---	---	---	234609_at	---
3.63	3.43	0.19	3.28E-01	6.88E-01	CDCA7L	cell division cycle associated 7-like	chr7p15.3	225081_s_at	NM_001127370 /// NM_001127371 /// NM_018719
2.27	2.12	0.15	3.28E-01	6.88E-01	---	---	---	241126_at	---
3.14	2.96	0.18	3.28E-01	6.88E-01	---	---	---	1558719_s_at	---
4.31	4.01	0.30	3.28E-01	6.88E-01	C10orf47	chromosome 10 open reading frame 47	chr10p14	229801_at	NM_153256
2.15	1.99	0.16	3.28E-01	6.88E-01	DEFB114	defensin, beta 114	chr6p21	1567878_at	NM_001037499
7.04	6.81	0.23	3.28E-01	6.88E-01	LRWD1	leucine-rich repeats and WD repeat domain containing 1	chr7q22.1	225680_at	NM_152892
5.51	5.00	0.51	3.28E-01	6.88E-01	SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	chr20q13.1	221024_s_at	NM_030777
2.92	2.68	0.24	3.28E-01	6.88E-01	---	---	---	241631_at	---
5.62	5.42	0.19	3.28E-01	6.88E-01	CCDC23	coiled-coil domain containing 23	chr1p34.2	226723_at	NM_199342
5.48	5.08	0.40	3.28E-01	6.88E-01	PROCR	protein C receptor, endothelial (EPCR)	chr20q11.2	203650_at	NM_006404
2.79	2.66	0.14	3.28E-01	6.88E-01	---	---	---	216816_at	---
2.38	2.27	0.12	3.28E-01	6.88E-01	---	---	---	241170_at	---
3.82	3.63	0.19	3.29E-01	6.88E-01	FCHSD1	FCH and double SH3 domains 1	chr5q31.3	226699_at	NM_033449
4.12	3.94	0.18	3.29E-01	6.88E-01	---	---	---	241993_x_at	---
2.12	1.99	0.13	3.29E-01	6.88E-01	LRRC41	leucine rich repeat containing 41	chr1p33	1558983_at	NM_006369
2.39	2.17	0.22	3.29E-01	6.88E-01	RIT1	Ras-like without CAAX 1	chr1q22	236223_s_at	NM_006912
5.57	5.24	0.33	3.29E-01	6.88E-01	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	chr8p21.3	204076_at	NM_001128930 /// NM_004901
7.90	7.68	0.22	3.29E-01	6.89E-01	RAB5A	RAB5A, member RAS oncogene family	chr3p24-p22	209089_at	NM_004162
8.43	8.11	0.32	3.29E-01	6.89E-01	APP	amyloid beta (A4) precursor protein	chr21q21.2|21q21.3	200602_at	NM_000484 /// NM_201413 /// NM_201414

4.42	4.22	0.21	3.29E-01	6.89E-01	CRIM2	cysteine rich BMP regulator 2 (chordin-like)	chr7q32.1	1557621_at	XM_001128429 /// XM_001715223 /// XM_001715714																				
2.79	2.64	0.15	3.29E-01	6.89E-01	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	chr17p11.2	1557986_s_at	NM_144775																				
2.54	2.38	0.16	3.29E-01	6.89E-01	---	---	---	207915_at	---																				
6.50	5.81	0.69	3.29E-01	6.89E-01	---	---	---	1559910_at	---																				
2.40	2.26	0.14	3.30E-01	6.89E-01	AGMAT	agmatine ureohydrolase (agmatinase)	chr1p36.21	219792_at	NM_024758																				
3.78	3.55	0.23	3.30E-01	6.89E-01	---	---	---	244397_at	---																				
5.84	5.51	0.33	3.30E-01	6.89E-01	C7orf50	chromosome 7 open reading frame 50	chr7p22.3	224478_s_at	NM_001134395 /// NM_001134396 /// NM_032350																				
5.36	5.13	0.23	3.30E-01	6.89E-01	OPA3	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	chr19q13.32	229624_at	NM_001017989 /// NM_025136																				
2.88	2.62	0.26	3.30E-01	6.89E-01	PNN	pinin, desmosome associated protein	chr14q21.1	1567213_at	NM_002687																				
4.47	4.25	0.22	3.30E-01	6.89E-01	ARGLU1	arginine and glutamate rich 1	chr13q33.3	222508_s_at	NM_018011																				
2.25	2.11	0.14	3.30E-01	6.89E-01	---	---	---	239830_at	---																				
4.51	4.31	0.20	3.30E-01	6.89E-01	UGT1A1 /// UGT1A10 /// UGT1A4 /// UGT1A6 /// UGT1A8 /// UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 family, polypeptide A4 /// UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A8 /// UDP glucuronosyltransferase 1 family, polypeptide A9	chr2q37	204532_x_at	NM_000463 /// NM_001072 /// NM_007120 /// NM_019075 /// NM_019076 /// NM_021027 /// NM_205862																				
12.19	12.07	0.12	3.30E-01	6.89E-01	RPL37	ribosomal protein L37	chr5p13	200092_s_at	NM_000997																				
3.26	3.09	0.17	3.30E-01	6.89E-01	MGC10981	hypothetical protein MGC10981	chr4p16.1	223779_at	XR_040178 /// XR_040179 /// XR_040180																				
5.01	4.80	0.20	3.30E-01	6.89E-01	WDR79	WD repeat domain 79	chr17p13.1	220258_s_at	NM_018081																				
7.63	7.45	0.18	3.30E-01	6.89E-01	ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	chr5q35.1-q35.2	223847_s_at	NM_001031711 /// NM_020462																				
3.24	3.00	0.24	3.30E-01	6.89E-01	LOC643406	hypothetical protein LOC643406	chr20p12.3	243402_at	XM_001723623 /// XM_001725180 /// XM_001725203																				
3.95	3.68	0.27	3.30E-01	6.90E-01	PGA3 /// PGA4 /// PGA5	pepsinogen 3, group I (pepsinogen A) /// pepsinogen 4, group I (pepsinogen A) /// pepsinogen 5, group I (pepsinogen A)	chr11q12.2 /// chr11q13	213265_at	NM_001079807 /// NM_001079808 /// NM_014224																				
3.15	2.92	0.22	3.30E-01	6.90E-01	CPA2	carboxypeptidase A2 (pancreatic)	chr7q32	206212_at	NM_001869																				
3.80	3.47	0.34	3.30E-01	6.90E-01	METTL10	methyltransferase like 10	chr10q26.13	226631_at	NM_212554																				
3.78	3.51	0.26	3.30E-01	6.90E-01	PRDM2	PR domain containing 2, with ZNF domain	chr1p36.21	205277_at	NM_001007257 /// NM_012231 /// NM_015866																				
7.69	7.17	0.53	3.30E-01	6.90E-01	LRRN3	leucine rich repeat neuronal 3	chr7q31.1	209841_s_at	NM_001099658 /// NM_001099660 /// NM_018334																				
9.21	8.89	0.32	3.31E-01	6.90E-01	MKNK2	MAP kinase interacting serine/threonine kinase 2	chr19p13.3	218205_s_at	NM_017572 /// NM_199054																				
2.76	2.58	0.18	3.31E-01	6.90E-01	---	---	---	1570123_at	---																				
5.31	5.15	0.16	3.31E-01	6.90E-01	CRKRS	Cdc2-related kinase, arginine/serine-rich	chr17q12	219226_at	NM_015083 /// NM_016507																				

2.43	2.32	0.10	3.31E-01	6.90E-01	TNP2	transition protein 2 (during histone to protamine replacement)	chr16p13.13	207736_s_at	NM_005425																				
5.34	4.99	0.35	3.31E-01	6.90E-01	AHDC1	AT hook, DNA binding motif, containing 1	chr1p36.13	205002_at	NM_001029882																				
2.92	2.81	0.11	3.31E-01	6.90E-01	PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	chr11q12	211743_s_at	NM_002728																				
6.89	6.65	0.24	3.31E-01	6.90E-01	PIGY	phosphatidylinositol glycan anchor biosynthesis, class Y	chr4q22.1	224661_at	NM_001042616 /// NM_032906																				
2.80	2.66	0.14	3.31E-01	6.90E-01	COL27A1	Collagen, type XXVII, alpha 1	chr9q32	1564008_at	NM_032888																				
8.66	8.48	0.18	3.31E-01	6.90E-01	PFKM	phosphofructokinase, muscle	chr12q13.3	210976_s_at	NM_000289																				
3.97	3.75	0.22	3.31E-01	6.90E-01	TNFRSF4	tumor necrosis factor receptor superfamily, member 4	chr1p36	214228_x_at	NM_003327																				
5.01	4.24	0.77	3.31E-01	6.90E-01	SCN4B	sodium channel, voltage-gated, type IV, beta	chr11q23.3	236359_at	NM_174934																				
4.17	3.85	0.32	3.31E-01	6.90E-01	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	chrXp11.23-p11.22	207439_s_at	NM_001032289 /// NM_001042498 /// NM_005660																				
6.51	6.18	0.32	3.31E-01	6.90E-01	DERL1	Der1-like domain family, member 1	chr8q24.13	218172_s_at	NM_001134671 /// NM_024295																				
5.33	5.11	0.22	3.31E-01	6.90E-01	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	chr1q32.1	213329_at	NM_001042758 /// NM_015326																				
7.32	7.04	0.28	3.31E-01	6.90E-01	RANBP9	RAN binding protein 9	chr6p23	202582_s_at	NM_005493																				
3.38	3.15	0.23	3.31E-01	6.91E-01	TCF21	transcription factor 21	chr6pter-qter	229529_at	NM_003206 /// NM_198392																				
3.37	3.14	0.23	3.31E-01	6.91E-01	RPL13	ribosomal protein L13	chr16q24.3|17p11.2	214976_at	NM_000977 /// NM_033251																				
5.54	5.23	0.31	3.31E-01	6.91E-01	SESN2	sestrin 2	chr1p35.3	223196_s_at	NM_031459																				
7.77	7.41	0.36	3.31E-01	6.91E-01	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	chr1p31.1	203810_at	NM_007034																				
2.56	2.41	0.15	3.32E-01	6.91E-01	RERE	arginine-glutamic acid dipeptide (RE) repeats	chr1p36.2-p36.1	1557349_at	NM_001042681 /// NM_001042682 /// NM_012102																				
3.13	2.95	0.19	3.32E-01	6.91E-01	LOC285398 /// RFT1	hypothetical locus LOC285398 /// RFT1 homolog (S. cerevisiae)	chr3p21.1	1558289_at	NM_052859																				
10.49	10.35	0.14	3.32E-01	6.91E-01	ARF1	ADP-ribosylation factor 1	chr1q42	200065_s_at	NM_001024226 /// NM_001024227 /// NM_001024228 /// NM_001658																				
4.68	4.16	0.51	3.32E-01	6.91E-01	PION	pigeon homolog (Drosophila)	chr7q11.23	222150_s_at	NM_017439																				
2.00	1.90	0.10	3.32E-01	6.91E-01	LOC158434	hypothetical protein LOC158434	chr9q22.33	1563827_at	---																				
3.10	2.91	0.19	3.32E-01	6.91E-01	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	chrXp11.3-p11.23	207617_at	NM_001356																				
2.32	2.19	0.13	3.32E-01	6.91E-01	DEFB108B /// DEFB108P1 /// LOC100133128	defensin, beta 108B /// defensin, beta 108, pseudogene 1 /// Beta-defensin 108B-like	chr11q13.4 /// chr4p16.1 /// chr8p23-p22	1561165_a_at	NM_001002035 /// XM_001720802																				
2.63	2.41	0.22	3.32E-01	6.91E-01	---	---	---	239726_at	---																				
2.35	2.24	0.11	3.32E-01	6.91E-01	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	chr19q13.4	210146_x_at	NM_001080978 /// NM_005874																				
1.96	1.85	0.11	3.32E-01	6.91E-01	TINAG	tubulointerstitial nephritis antigen	chr6p11.2-p12	240480_at	NM_014464																				
5.55	5.40	0.14	3.32E-01	6.91E-01	---	---	---	227608_at	---																				
7.58	7.34	0.24	3.32E-01	6.92E-01	GSPT1	G1 to S phase transition 1	chr16p13.1	201912_s_at	NM_001130006 /// NM_001130007 /// NM_002094																				
2.19	2.06	0.13	3.32E-01	6.92E-01	---	---	---	242582_at	---																				
8.83	8.64	0.19	3.32E-01	6.92E-01	DAZAP2	DAZ associated protein 2	chr12q12	212595_s_at	NM_014764																				
3.24	3.05	0.20	3.32E-01	6.92E-01	SOX12	SRY (sex determining region Y)-box 12	chr20p13	228358_at	NM_006943																				
5.66	5.44	0.23	3.33E-01	6.92E-01	GRAP	GRB2-related adaptor protein	chr17p11.2	229726_at	NM_006613																				
5.20	4.97	0.23	3.33E-01	6.92E-01	TOLLIP	toll interacting protein	chr11p15.5	233881_s_at	NM_019009																				
3.35	3.16	0.19	3.33E-01	6.92E-01	C18orf25	chromosome 18 open reading frame 25	chr18q21.1	217508_s_at	NM_001008239 /// NM_145055																				
3.72	3.54	0.18	3.33E-01	6.92E-01	GAP43	growth associated protein 43	chr3q13.1-q13.2	216963_s_at	NM_001130064 /// NM_002045																				

2.74	2.58	0.16	3.33E-01	6.92E-01	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	chr4p16.1	228010_at	NM_020416 /// NM_181876																				
7.62	7.14	0.48	3.33E-01	6.92E-01	YAP1	Yes-associated protein 1, 65kDa	chr11q13	224895_at	NM_001130145 /// NM_006106																				
3.69	3.50	0.18	3.33E-01	6.92E-01	ART5	ADP-ribosyltransferase 5	chr11p15.4	1552524_at	NM_001079536 /// NM_053017																				
3.20	3.00	0.20	3.33E-01	6.92E-01	---	---	---	243180_at	---																				
4.19	3.95	0.24	3.33E-01	6.92E-01	---	---	---	239375_at	---																				
2.17	2.06	0.11	3.33E-01	6.92E-01	PAX3	paired box 3	chr2q35-q37|2q35	231666_at	NM_000438 /// NM_001127366 /// NM_013942 /// NM_181457 /// NM_181458 /// NM_181459 /// NM_181460 /// NM_181461																				
7.38	7.22	0.16	3.33E-01	6.92E-01	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	chr17p13.3	200815_s_at	NM_000430																				
3.74	3.52	0.22	3.33E-01	6.92E-01	CCL26	chemokine (C-C motif) ligand 26	chr7q11.23	223710_at	NM_006072																				
2.79	2.64	0.15	3.33E-01	6.92E-01	---	---	---	1565913_at	---																				
9.95	9.37	0.58	3.33E-01	6.92E-01	VCAN	versican	chr5q14.3	221731_x_at	NM_001126336 /// NM_004385																				
5.77	5.51	0.26	3.33E-01	6.92E-01	ZSWIM5	zinc finger, SWIM-type containing 5	chr1p34.1	232336_at	NM_020883																				
2.56	2.44	0.12	3.33E-01	6.92E-01	---	---	---	244880_at	---																				
7.05	6.75	0.30	3.33E-01	6.92E-01	ZNF580	zinc finger protein 580	chr19q13.42	220748_s_at	NM_016202 /// NM_207115																				
9.61	9.42	0.20	3.33E-01	6.92E-01	CTSB	cathepsin B	chr8p22	200838_at	NM_001908 /// NM_147780 /// NM_147781 /// NM_147782 /// NM_147783																				
5.85	5.61	0.24	3.33E-01	6.92E-01	MTO1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	chr6q13	222014_x_at	NM_001123226 /// NM_012123 /// NM_133645																				
5.83	5.56	0.28	3.33E-01	6.92E-01	MAPKBP1	mitogen-activated protein kinase binding protein 1	chr15q15.1	213394_at	NM_001128608 /// NM_014994																				
3.00	2.77	0.22	3.33E-01	6.92E-01	NR4A3	nuclear receptor subfamily 4, group A, member 3	chr9q22	216979_at	NM_006981 /// NM_173198 /// NM_173199 /// NM_173200																				
3.50	3.32	0.18	3.33E-01	6.92E-01	41341	membrane-associated ring finger (C3HC4) 8	chr10q11.21	231933_at	NM_001002265 /// NM_001002266 /// NM_145021																				
3.34	3.20	0.15	3.33E-01	6.92E-01	MKRN2	makorin ring finger protein 2	chr3p25	216995_x_at	NM_014160																				
8.34	8.19	0.15	3.33E-01	6.92E-01	ADSL	adenylosuccinate lyase	chr22q13.1|22q13.2	202144_s_at	NM_000026 /// NM_001123378																				
6.04	5.55	0.49	3.34E-01	6.93E-01	FBXO33	F-box protein 33	chr14q21.1	227521_at	NM_203301																				
2.66	2.51	0.15	3.34E-01	6.93E-01	---	---	---	231241_at	---																				
3.35	3.17	0.17	3.34E-01	6.93E-01	SLC6A18	solute carrier family 6, member 18	chr5p15.33	238215_at	NM_182632																				
6.24	6.08	0.17	3.34E-01	6.93E-01	CCDC124	coiled-coil domain containing 124	chr19p13.11	225454_at	NM_138442																				

9.97	9.69	0.28	3.34E-01	6.93E-01	LAPTM5	lysosomal multispanning membrane protein 5	chr1p34	201721_s_at	NM_006762
2.01	1.87	0.14	3.34E-01	6.93E-01	---	---	---	1567576_at	---
6.67	6.32	0.34	3.34E-01	6.93E-01	---	---	---	243249_at	---
3.48	3.25	0.23	3.34E-01	6.93E-01	SF3B2	splicing factor 3b, subunit 2, 145kDa	chr11q13.1	1558230_at	NM_006842
2.77	2.53	0.24	3.34E-01	6.93E-01	---	---	---	229006_at	---
3.13	2.98	0.15	3.34E-01	6.93E-01	AZGP1P1	alpha-2-glycoprotein 1, zinc-binding pseudogene 1	chr7q22.1	234955_at	XR_017216 /// XR_037935 /// XR_039311 /// XR_039317
2.99	2.81	0.18	3.34E-01	6.93E-01	TRPC2	transient receptor potential cation channel, subfamily C, member 2 (pseudogene)	chr11p15.4-p15.3	215288_at	NR_002720
10.93	10.78	0.15	3.34E-01	6.93E-01	LAPTM4A	lysosomal protein transmembrane 4 alpha	chr2p24.1	200673_at	NM_014713
4.50	4.29	0.21	3.34E-01	6.93E-01	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	chr9q34.13	219198_at	NM_012204
2.55	2.39	0.16	3.34E-01	6.93E-01	LZTS1	leucine zipper, putative tumor suppressor 1	chr8p22	221722_x_at	NM_021020
2.52	2.38	0.14	3.34E-01	6.93E-01	GNG4	guanine nucleotide binding protein (G protein), gamma 4	chr1q42.3	1566513_a_at	NM_001098721 /// NM_001098722 /// NM_004485
3.75	3.56	0.19	3.34E-01	6.93E-01	MCM9	minichromosome maintenance complex component 9	chr6q22.31	219673_at	NM_153255
3.36	3.17	0.18	3.34E-01	6.93E-01	MAMDC4	MAM domain containing 4	chr9q34.3	229473_at	NM_206920
2.54	2.44	0.10	3.34E-01	6.93E-01	PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	chr6q21	1553684_at	NM_001111298 /// NM_173672
4.33	4.06	0.27	3.34E-01	6.93E-01	ZSCAN2	zinc finger and SCAN domain containing 2	chr15q25.2	231188_at	NM_001007072 /// NM_017894 /// NM_181877
2.76	2.64	0.12	3.34E-01	6.93E-01	---	---	---	242830_at	---
2.10	1.95	0.15	3.34E-01	6.93E-01	---	---	---	1559360_at	---
7.72	7.50	0.23	3.34E-01	6.93E-01	NMRAL1	NmrA-like family domain containing 1	chr16p13.3	231271_x_at	NM_020677
3.56	3.40	0.16	3.34E-01	6.93E-01	PHF20	PHD finger protein 20	chr20q11.22-q11.23	235389_at	NM_016436
2.10	1.94	0.17	3.34E-01	6.93E-01	---	---	---	1566846_at	---
7.29	7.05	0.24	3.34E-01	6.93E-01	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	chr14q11.2	217815_at	NM_007192
3.26	3.12	0.15	3.35E-01	6.93E-01	---	---	---	237352_at	---
5.37	4.65	0.71	3.35E-01	6.93E-01	SOCS2	suppressor of cytokine signaling 2	chr12q	203372_s_at	NM_003877
5.29	4.78	0.52	3.35E-01	6.93E-01	PNN	pinin, desmosome associated protein	chr14q21.1	1567214_a_at	NM_002687
5.42	5.13	0.28	3.35E-01	6.93E-01	SBK1	SH3-binding domain kinase 1	chr16p11.2	226549_at	NM_001024401
2.60	2.46	0.14	3.35E-01	6.93E-01	---	---	---	1568923_at	---
3.94	3.76	0.18	3.35E-01	6.93E-01	RASSF1	Ras association (RalGDS/AF-6) domain family member 1	chr3p21.3	240278_at	NM_007182 /// NM_170712 /// NM_170713 /// NM_170714
3.29	3.02	0.28	3.35E-01	6.93E-01	COL9A2	collagen, type IX, alpha 2	chr1p33-p32	213622_at	NM_001852
2.68	2.51	0.17	3.35E-01	6.93E-01	ELL2	elongation factor, RNA polymerase II, 2	chr5q15	214445_at	NM_012081
5.82	5.60	0.23	3.35E-01	6.93E-01	REEP4	receptor accessory protein 4	chr8p21.3	218777_at	NM_025232

7.19	7.05	0.13	3.35E-01	6.93E-01	CTNND1	catenin (cadherin-associated protein), delta 1	chr11q11	208862_s_at	NM_001085458 /// NM_001085459 /// NM_001085460 /// NM_001085461 /// NM_001085462 /// NM_001085463 /// NM_001085464 /// NM_001085465 /// NM_001085466 /// NM_001085467 /// NM_001085468 /// NM_001085469 /// NM_001331																			
2.75	2.62	0.13	3.35E-01	6.94E-01	FCAR	Fc fragment of IgA, receptor for	chr19q13.2-q13.4	211816_x_at	NM_002000 /// NM_133269 /// NM_133271 /// NM_133272 /// NM_133273 /// NM_133274 /// NM_133277 /// NM_133278 /// NM_133279																			
8.01	7.83	0.18	3.35E-01	6.94E-01	APLP2	amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	208703_s_at	NM_001642																			
2.54	2.41	0.13	3.35E-01	6.94E-01	---	---	---	1560449_at	---																			
8.43	8.18	0.26	3.35E-01	6.94E-01	BIN1	bridging integrator 1	chr2q14	214439_x_at	NM_004305 /// NM_139343 /// NM_139344 /// NM_139345 /// NM_139346 /// NM_139347 /// NM_139348 /// NM_139349 /// NM_139350 /// NM_139351																			
2.41	2.26	0.16	3.35E-01	6.94E-01	---	---	---	241776_at	---																			
2.17	2.06	0.11	3.35E-01	6.94E-01	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	chr12p12.2-p11.2	220658_s_at	NM_020183																			
6.14	5.86	0.29	3.36E-01	6.94E-01	HPS6	Hermansky-Pudlak syndrome 6	chr10q24.32	219052_at	NM_024747																			
4.59	4.27	0.32	3.36E-01	6.94E-01	TTC39A	tetratricopeptide repeat domain 39A	chr1p32.3	210652_s_at	NM_001080494																			
8.85	8.37	0.48	3.36E-01	6.94E-01	GSTA4	glutathione S-transferase A4	chr6p12.1	235405_at	NM_001512																			
3.30	3.10	0.20	3.36E-01	6.94E-01	---	---	---	230583_s_at	---																			
1.95	1.84	0.11	3.36E-01	6.94E-01	EPHA7	EPH receptor A7	chr6q16.1	238533_at	NM_004440																			
5.87	5.60	0.27	3.36E-01	6.94E-01	IGF1R	insulin-like growth factor 1 receptor	chr15q26.3	203627_at	NM_000875																			
2.30	2.17	0.13	3.36E-01	6.94E-01	TMED6	transmembrane emp24 protein transport domain containing 6	chr16q22.1	236430_at	NM_144676																			
2.83	2.64	0.18	3.36E-01	6.95E-01	---	---	---	235530_at	---																			

5.91	5.71	0.20	3.36E-01	6.95E-01	RAB4A	RAB4A, member RAS oncogene family	chr1q42-q43	203581_at	NM_004578																				
10.76	10.59	0.17	3.36E-01	6.95E-01	PCBP2	poly(rC) binding protein 2	chr12q13.12-q13.13	204031_s_at	NM_001098620 /// NM_001128911 /// NM_001128912 /// NM_001128913 /// NM_001128914 /// NM_005016 /// NM_031989																				
2.83	2.68	0.15	3.36E-01	6.95E-01	MTMR1	myotubularin related protein 1	chrXq28	216303_s_at	NM_003828																				
4.40	4.04	0.36	3.36E-01	6.95E-01	---	---	---	226034_at	---																				
13.14	13.04	0.10	3.36E-01	6.95E-01	RPL37A	ribosomal protein L37a	chr2q35	201429_s_at	NM_000998																				
2.39	2.25	0.15	3.36E-01	6.95E-01	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	chr8q21.11	1562458_at	NM_001001481 /// NM_018299																				
4.17	3.79	0.38	3.36E-01	6.95E-01	C4orf41	chromosome 4 open reading frame 41	chr4q35.1	218179_s_at	NM_021942 /// NM_199053																				
10.28	10.15	0.13	3.36E-01	6.95E-01	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	chr11q23.3	208746_x_at	NM_006476																				
5.63	4.77	0.85	3.36E-01	6.95E-01	SOCS3	suppressor of cytokine signaling 3	chr17q25.3	227697_at	NM_003955																				
2.88	2.65	0.23	3.36E-01	6.95E-01	CTTN	cortactin	chr11q13	214782_at	NM_005231 /// NM_138565																				
4.61	4.39	0.22	3.36E-01	6.95E-01	---	---	---	229446_at	---																				
4.46	4.15	0.32	3.36E-01	6.95E-01	ZFYVE21	zinc finger, FYVE domain containing 21	chr14q32.33	219929_s_at	NM_024071																				
3.18	3.06	0.13	3.36E-01	6.95E-01	KIAA2018	KIAA2018	chr3q13.2	242508_at	NM_001009899																				
4.67	4.32	0.35	3.36E-01	6.95E-01	---	---	---	231370_at	---																				
4.79	4.39	0.41	3.36E-01	6.95E-01	GLIPR1	GLI pathogenesis-related 1	chr12q21.2	204221_x_at	NM_006851																				
3.45	3.25	0.21	3.37E-01	6.95E-01	ARG2	arginase, type II	chr14q24.1-q24.3	203945_at	NM_001172																				
3.10	2.92	0.18	3.37E-01	6.95E-01	PAX7	paired box 7	chr1p36.2-p36.12	208060_at	NM_002584 /// NM_013945																				
3.56	3.41	0.15	3.37E-01	6.95E-01	ZBTB40	zinc finger and BTB domain containing 40	chr1pter-q31.3	203958_s_at	NM_001083621 /// NM_014870																				
10.60	10.48	0.12	3.37E-01	6.95E-01	EIF1	eukaryotic translation initiation factor 1	chr17q21.2	212227_x_at	NM_005801																				

2.03	1.93	0.10	3.37E-01	6.95E-01	SNRPN	small nuclear ribonucleoprotein polypeptide N	chr15q11.2	1559342_a_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																				
4.22	3.93	0.29	3.37E-01	6.95E-01	---	---	---	227027_at	---																			
3.34	3.14	0.20	3.37E-01	6.95E-01	SPINT1	serine peptidase inhibitor, Kunitz type 1	chr15q15.1	202826_at	NM_001032367 /// NM_003710 /// NM_181642																			
2.81	2.63	0.18	3.37E-01	6.95E-01	---	---	---	229226_at	---																			
3.76	3.54	0.21	3.37E-01	6.95E-01	CENTB5	centaurin, beta 5	---	225542_at	NM_030649																			
2.98	2.81	0.17	3.37E-01	6.95E-01	KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4	chr1p21	235467_s_at	NM_001039574 /// NM_004978 /// NM_153763																			
6.83	6.59	0.24	3.37E-01	6.95E-01	CD99L2	CD99 molecule-like 2	chrXq28	223041_at	NM_031462 /// NM_134445 /// NM_134446																			
7.87	7.62	0.25	3.37E-01	6.95E-01	USP11	ubiquitin specific peptidase 11	chrXp11.23	208723_at	NM_004651																			

11.64	11.54	0.11	3.37E-01	6.95E-01	LOC388474 /// LOC401640 /// LOC441034 /// LOC644029 /// LOC728139 /// LOC728179 /// LOC728992 /// RPL7A	similar to ribosomal protein L7a /// similar to ribosomal protein L7a /// similar to hCG2028724 /// similar to ribosomal protein L7a /// similar to ribosomal protein L7a /// similar to LOC100037086 protein /// hypothetical LOC728992 /// ribosomal protein L7a	chr10p11.22 /// chr15q21.1 /// chr18q12.2 /// chr22q11.21 /// chr3q13.33 /// chr4q25 /// chr6p24.3 /// chr9q34	234873_x_at	NM_000972 /// NR_000016 /// NR_000017 /// NR_002447 /// NR_002448 /// XM_001720549 /// XM_001722043 /// XM_001723546 /// XR_015301 /// XR_015348 /// XR_015445 /// XR_015663 /// XR_015742 /// XR_016809 /// XR_017380 /// XR_017397 /// XR_018917 /// XR_019233 /// XR_019285 /// XR_038254 /// XR_038629 /// XR_039323 /// XR_039369 /// XR_039455 /// XR_039533 /// XR_039725
2.26	2.10	0.15	3.37E-01	6.95E-01	---	---	---	220701_at	---
2.38	2.22	0.15	3.37E-01	6.95E-01	---	---	---	241893_at	---
2.96	2.80	0.16	3.37E-01	6.96E-01	C9orf79	chromosome 9 open reading frame 79	chr9q22.1	1559559_at	NM_178828
2.66	2.47	0.19	3.37E-01	6.96E-01	LOC401022	hypothetical LOC401022	chr2q31.2	228601_at	---
2.25	2.12	0.13	3.37E-01	6.96E-01	CXCR7	Chemokine (C-X-C motif) receptor 7	chr2q37.3	232746_at	NM_020311
2.98	2.84	0.14	3.37E-01	6.96E-01	HELZ	Helicase with zinc finger	chr17q24.2	240486_at	NM_014877
2.18	2.07	0.10	3.38E-01	6.96E-01	---	---	---	236765_at	---
7.02	6.87	0.15	3.38E-01	6.96E-01	FAM161B	Family with sequence similarity 161, member B	chr14q24.3	242608_x_at	NM_152445
2.49	2.37	0.12	3.38E-01	6.96E-01	LOC100130825	Hypothetical protein LOC100130825	chr12q24.33	1557235_at	XM_001720026 /// XM_001722728 /// XM_001726773
2.75	2.51	0.24	3.38E-01	6.96E-01	LOC284402	hypothetical protein LOC284402	chr19q13.11	237748_at	NM_001025591
6.53	6.40	0.13	3.38E-01	6.96E-01	FKSG49	FKSG49	chr5q13.3	224288_x_at	XR_041698
6.22	5.89	0.33	3.38E-01	6.96E-01	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	chr11q24	211817_s_at	NM_000890
2.75	2.48	0.27	3.38E-01	6.96E-01	C2orf49	chromosome 2 open reading frame 49	chr2q12.2	243093_at	NM_024093
2.55	2.42	0.13	3.38E-01	6.96E-01	---	---	---	1566691_at	---
7.58	7.34	0.24	3.38E-01	6.96E-01	---	---	---	221725_at	---
4.26	4.04	0.22	3.38E-01	6.96E-01	BAT4	HLA-B associated transcript 4	chr6p21.3	225476_at	NM_033177
2.81	2.67	0.14	3.38E-01	6.96E-01	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	chr14q11.2-q21	211081_s_at	NM_006575 /// NM_198794
8.56	8.33	0.23	3.38E-01	6.96E-01	HDHD3	haloacid dehalogenase-like hydrolase domain containing 3	chr9q32	221256_s_at	NM_031219

6.83	6.61	0.22	3.38E-01	6.96E-01	PEX19	peroxisomal biogenesis factor 19	chr1q23.2	201706_s_at	NM_001131039 /// NM_002857
3.55	3.39	0.16	3.38E-01	6.96E-01	---	---	---	241847_at	---
2.73	2.60	0.13	3.38E-01	6.96E-01	ANXA6	annexin A6	chr5q32-q34	244250_at	NM_001155 /// NM_004033
3.43	3.28	0.15	3.38E-01	6.96E-01	---	---	---	1556165_at	---
3.65	3.52	0.13	3.38E-01	6.96E-01	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	chr16p12.3	227954_at	NM_001034841
3.19	3.06	0.13	3.38E-01	6.96E-01	OR7A17	olfactory receptor, family 7, subfamily A, member 17	chr19p13.12	208509_s_at	NM_030901
3.04	2.84	0.20	3.38E-01	6.96E-01	LOC440993	hypothetical gene supported by AK128346	chr3q29	229820_at	XR_039810
3.96	3.61	0.35	3.38E-01	6.96E-01	SCAMP1	secretory carrier membrane protein 1	chr5q13.3-q14.1	206667_s_at	NM_004866
2.21	2.08	0.14	3.38E-01	6.96E-01	---	---	---	243150_at	---
6.49	6.19	0.31	3.38E-01	6.96E-01	C6orf120	chromosome 6 open reading frame 120	chr6q27	221786_at	NM_001029863
3.03	2.64	0.38	3.39E-01	6.97E-01	---	---	---	244219_at	---
4.94	4.47	0.47	3.39E-01	6.97E-01	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	chr12p11	208159_x_at	NM_004399 /// NM_030653 /// NM_152438
3.89	3.67	0.22	3.39E-01	6.97E-01	---	---	---	235355_at	---
4.26	4.05	0.20	3.39E-01	6.97E-01	LOC100128325	similar to LOC389556	chr7q32.2	243171_at	XM_001715116 /// XM_001715830 /// XM_001718745
7.53	7.23	0.30	3.39E-01	6.97E-01	SDHD	succinate dehydrogenase complex, subunit D, integral membrane protein	chr11q23	202026_at	NM_003002
6.92	6.56	0.35	3.39E-01	6.97E-01	NOP5/NOP58	nucleolar protein NOP5/NOP58	chr2q33.1	223096_at	NM_015934
3.31	3.19	0.13	3.39E-01	6.97E-01	---	---	---	240526_at	---
3.33	3.14	0.19	3.39E-01	6.97E-01	USP34	ubiquitin specific peptidase 34	chr2p15	242647_at	NM_014709
2.01	1.88	0.13	3.39E-01	6.97E-01	RPP30	ribonuclease P/MRP 30kDa subunit	chr10q23.31	1556062_at	NM_001104546 /// NM_006413
6.46	6.24	0.22	3.39E-01	6.97E-01	SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)	chr17p12-p13	223221_at	NM_004589
4.28	4.10	0.17	3.39E-01	6.97E-01	MTERFD2	MTERF domain containing 2	chr2q37.3	226486_at	NM_182501
3.20	3.08	0.12	3.39E-01	6.97E-01	---	---	---	1561626_at	---
2.46	2.33	0.13	3.39E-01	6.97E-01	CRAMP1L /// HN1L	Crm, cramped-like (Drosophila) /// hematological and neurological expressed 1-like	chr16p13.3	240930_at	NM_020825 /// NM_144570
2.96	2.75	0.20	3.39E-01	6.97E-01	---	---	---	228944_at	---
6.38	6.21	0.17	3.39E-01	6.97E-01	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	chr17p13.2	223460_at	NM_032294 /// NM_172206 /// NM_172207
4.43	4.00	0.44	3.39E-01	6.97E-01	GABPA	GA binding protein transcription factor, alpha subunit 60kDa	chr21q21-q22.1|21q21.3	210188_at	NM_002040
7.07	6.85	0.22	3.39E-01	6.97E-01	DOLK	dolichol kinase	chr9q34.11	204488_at	NM_014908
4.31	3.86	0.44	3.39E-01	6.97E-01	THBD	thrombomodulin	chr20p11.2	203888_at	NM_000361
2.37	2.25	0.12	3.39E-01	6.97E-01	---	---	---	240286_at	---
2.39	2.28	0.11	3.39E-01	6.97E-01	LOC647131	hypothetical LOC647131	chr13q14.2	231367_s_at	XM_001714900 /// XM_934407 /// XM_945302
3.50	3.30	0.21	3.39E-01	6.97E-01	---	---	---	233920_at	---
5.41	5.23	0.18	3.39E-01	6.97E-01	ARMC9	armadillo repeat containing 9	chr2q37.1	219637_at	NM_025139
4.66	4.27	0.38	3.39E-01	6.97E-01	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	chr1q22-q24	211205_x_at	NM_003557
6.82	6.66	0.17	3.39E-01	6.97E-01	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	chr19p13	201396_s_at	NM_003021
5.11	4.77	0.34	3.39E-01	6.97E-01	TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	chr10q25.3	241606_s_at	NM_139169
3.69	3.52	0.17	3.39E-01	6.97E-01	EXDL2	exonuclease 3'-5' domain-like 2	chr14q24.1	1555808_a_at	NM_018199
2.25	2.13	0.12	3.39E-01	6.97E-01	RP3-527F8.2	Hypothetical protein LOC100128420	chrXq26.3	1559648_at	XM_001720337 /// XM_001721317 /// XM_001721335
6.97	6.35	0.63	3.39E-01	6.97E-01	NCAM1	neural cell adhesion molecule 1	chr11q23.1	227394_at	NM_000615 /// NM_001076682 /// NM_181351

2.35	2.20	0.15	3.39E-01	6.97E-01	LOC285941	hypothetical protein LOC285941	chr7p15.2	1559627_at	XM_001722179 /// XM_379477 /// XM_380092 /// XM_938991																				
4.37	4.00	0.37	3.40E-01	6.97E-01	YTHDC2	YTH domain containing 2	chr5q22.2	213077_at	NM_022828																				
3.60	3.47	0.14	3.40E-01	6.97E-01	SIN3B	SIN3 homolog B, transcription regulator (yeast)	chr19p13.11	242129_at	NM_015260																				
6.92	6.69	0.24	3.40E-01	6.97E-01	LIN7C	lin-7 homolog C (C. elegans)	chr11p14	221568_s_at	NM_018362																				
2.70	2.49	0.21	3.40E-01	6.97E-01	---	---	---	236260_at	---																				
2.56	2.41	0.15	3.40E-01	6.97E-01	CENPF	centromere protein F, 350/400ka (mitosin)	chr1q32-q41	209172_s_at	NM_016343																				
2.22	2.11	0.11	3.40E-01	6.97E-01	CAPN6	calpain 6	chrXq23	217387_at	NM_014289																				
2.36	2.20	0.16	3.40E-01	6.97E-01	---	---	---	216815_at	---																				
3.13	2.93	0.20	3.40E-01	6.97E-01	WNT9A	wingless-type MMTV integration site family, member 9A	chr1q42	230643_at	NM_003395																				
2.19	2.03	0.16	3.40E-01	6.97E-01	MGC5590	hypothetical protein MGC5590	chr13q14.11	220930_s_at	XM_930060 /// XM_941452																				
3.20	3.06	0.14	3.40E-01	6.97E-01	LHX4	LIM homeobox 4	chr1q25.2	1553157_at	NM_033343																				
3.55	3.38	0.18	3.40E-01	6.97E-01	NECAP2	NECAP endocytosis associated 2	chr1p36.13	230123_at	NM_018090																				
6.15	5.83	0.32	3.40E-01	6.97E-01	ANKH	ankylosis, progressive homolog (mouse)	chr5p15.1	223092_at	NM_054027																				
2.92	2.78	0.14	3.40E-01	6.97E-01	---	---	---	242674_at	---																				
4.28	4.14	0.14	3.40E-01	6.97E-01	CHAF1B	chromatin assembly factor 1, subunit B (p60)	chr21q22.13	204775_at	NM_005441																				
5.89	5.52	0.37	3.40E-01	6.97E-01	NIPSNAP3A	nipsnap homolog 3A (C. elegans)	chr9q31.1	224436_s_at	NM_015469																				
5.07	4.92	0.15	3.40E-01	6.97E-01	RGS14	regulator of G-protein signaling 14	chr5q35.3	38290_at	NM_006480																				
2.14	2.04	0.11	3.40E-01	6.97E-01	LOC440346	hypothetical LOC440346	chr16p12.1	1569823_at	---																				
2.22	2.06	0.16	3.40E-01	6.97E-01	---	---	---	1564051_at	---																				
2.88	2.66	0.22	3.40E-01	6.97E-01	CCDC52	coiled-coil domain containing 52	chr3q13.2	234995_at	NM_144718																				
3.67	3.36	0.31	3.40E-01	6.97E-01	ZNF70	Zinc finger protein 70	chr22q11.2|22q11.23	243816_at	NM_021916																				
4.46	4.30	0.15	3.40E-01	6.97E-01	WHSC1	Wolf-Hirschhorn syndrome candidate 1	chr4p16.3	222778_s_at	NM_001042424 /// NM_007331 /// NM_133330 /// NM_133331 /// NM_133334 /// NM_133335																				
5.36	5.19	0.17	3.40E-01	6.97E-01	BCL2L13	BCL2-like 13 (apoptosis facilitator)	chr22q11.1	224035_s_at	NM_015367																				
4.22	3.98	0.24	3.40E-01	6.97E-01	EHBP1L1	EH domain binding protein 1-like 1	chr11q13.1	221755_at	NM_001099409																				
2.56	2.46	0.10	3.40E-01	6.97E-01	---	---	---	1556621_a_at	---																				
5.18	4.90	0.29	3.40E-01	6.97E-01	CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9q34.3	212710_at	NM_015447																				
6.78	6.53	0.25	3.40E-01	6.97E-01	PTPN2	protein tyrosine phosphatase, non-receptor type 2	chr18p11.3-p11.2	213136_at	NM_002828 /// NM_080422 /// NM_080423																				
2.11	2.00	0.10	3.40E-01	6.97E-01	NKAIN2	Na+/K+ transporting ATPase interacting 2	chr6q21	1554601_at	NM_001040214																				
5.71	5.52	0.19	3.40E-01	6.97E-01	NARFL	nuclear prelamin A recognition factor-like	chr16p13.3	218742_at	NM_022493																				
3.25	3.10	0.16	3.40E-01	6.97E-01	POLE	polymerase (DNA directed), epsilon	chr12q24.3	1561940_at	NM_006231																				
6.51	6.29	0.22	3.40E-01	6.97E-01	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	chr1p34.2	201404_x_at	NM_002794																				
12.26	12.11	0.15	3.40E-01	6.97E-01	RPL12	ribosomal protein L12	chr9q34	200809_x_at	NM_000976																				
9.33	9.17	0.16	3.40E-01	6.97E-01	NGRN	neugrin, neurite outgrowth associated	chr15q26.1	217722_s_at	NM_001033088 /// NM_016645																				
3.26	3.00	0.26	3.40E-01	6.97E-01	NHSL1	NHS-like 1	chr6q23.3	226490_at	XM_001723403 /// XM_496826 /// XM_941807																				

7.13	6.96	0.17	3.40E-01	6.97E-01	CTNND1	catenin (cadherin-associated protein), delta 1	chr11q11	211240_x_at	NM_001085458 /// NM_001085459 /// NM_001085460 /// NM_001085461 /// NM_001085462 /// NM_001085463 /// NM_001085464 /// NM_001085465 /// NM_001085466 /// NM_001085467 /// NM_001085468 /// NM_001085469 /// NM_001331																			
3.04	2.84	0.20	3.40E-01	6.97E-01	HKR1	GLI-Kruppel family member HKR1	chr19q13.12	1569980_x_at	NM_181786																			
2.56	2.43	0.13	3.40E-01	6.97E-01	NRP2	neuropilin 2	chr2q33.3	210842_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279																			
7.37	7.09	0.29	3.41E-01	6.97E-01	C1orf57	chromosome 1 open reading frame 57	chr1q42.2	223272_s_at	NM_032324																			
2.76	2.64	0.12	3.41E-01	6.97E-01	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	chr14q24	1554094_at	NM_001249																			
7.05	6.76	0.29	3.41E-01	6.97E-01	C1orf71	chromosome 1 open reading frame 71	chr1q44	225550_at	NM_152609																			
2.65	2.52	0.13	3.41E-01	6.97E-01	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	chr1p22.1-p21	1569102_at	NM_000350																			
4.70	4.48	0.22	3.41E-01	6.97E-01	GADD45B	Growth arrest and DNA-damage-inducible, beta	chr19p13.3	213560_at	NM_015675																			
4.71	4.50	0.21	3.41E-01	6.97E-01	IGSF22	immunoglobulin superfamily, member 22	chr11p15.1	1553857_at	NM_173588																			
2.58	2.45	0.12	3.41E-01	6.97E-01	---	---	---	233745_at	---																			
2.80	2.61	0.19	3.41E-01	6.97E-01	HPYR1	Helicobacter pylori responsive 1	chr8q24.22	1566916_at	---																			
6.49	6.14	0.36	3.41E-01	6.97E-01	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	chr22q12.2	209431_s_at	NM_014323 /// NM_032050 /// NM_032051 /// NM_032052																			
3.37	3.23	0.14	3.41E-01	6.97E-01	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	chr1p31.1	1562753_at	NM_030965																			
2.09	1.95	0.14	3.41E-01	6.97E-01	---	---	---	1561161_at	---																			
2.38	2.26	0.11	3.41E-01	6.97E-01	---	---	---	1566778_at	---																			
6.08	5.84	0.24	3.41E-01	6.97E-01	N-PAC	cytokine-like nuclear factor n-pac	chr16p13.3	218506_x_at	NM_032569																			
7.26	7.07	0.19	3.41E-01	6.97E-01	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	chr11p15.5	211779_x_at	NM_012305																			
4.04	3.61	0.42	3.41E-01	6.97E-01	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	chr8q24	204933_s_at	NM_002546																			
8.60	8.18	0.42	3.41E-01	6.97E-01	STARD10	StAR-related lipid transfer (START) domain containing 10	chr11q13	223103_at	NM_006645																			
3.04	2.89	0.15	3.41E-01	6.97E-01	---	---	---	222180_at	---																			
2.64	2.49	0.15	3.41E-01	6.97E-01	C9orf84	chromosome 9 open reading frame 84	chr9q31.3	233504_at	NM_001080551 /// NM_173521																			
6.97	6.73	0.24	3.41E-01	6.98E-01	ZNF219	zinc finger protein 219	chr14q11	219314_s_at	NM_001101672 /// NM_001102454 /// NM_016423																			
7.61	7.46	0.15	3.41E-01	6.98E-01	MEIS3P1	Meis homeobox 3 pseudogene 1	chr17p12	214077_x_at	NR_002211																			
7.15	6.90	0.24	3.41E-01	6.98E-01	H1F0	H1 histone family, member 0	chr22q13.1	208886_at	NM_005318																			
2.88	2.73	0.15	3.41E-01	6.98E-01	---	---	---	240948_at	---																			
2.30	2.16	0.14	3.41E-01	6.98E-01	PSEN1	presenilin 1	chr14q24.3	1559206_at	NM_000021 /// NM_007318																			

2.94	2.76	0.17	3.41E-01	6.98E-01	APAF1	apoptotic peptidase activating factor 1	chr12q23	211554_s_at	NM_001160 /// NM_013229 /// NM_181861 /// NM_181868 /// NM_181869
3.75	3.63	0.12	3.41E-01	6.98E-01	ARL10	ADP-ribosylation factor-like 10	chr5q35.2	242411_at	NM_173664
4.38	3.93	0.45	3.41E-01	6.98E-01	MFAP5	microfibrillar associated protein 5	chr12p13.1-p12.3	209758_s_at	NM_003480
2.59	2.46	0.13	3.42E-01	6.98E-01	---	---	---	242183_at	---
4.62	4.46	0.16	3.42E-01	6.98E-01	TBC1D20	TBC1 domain family, member 20	chr20p13	226664_at	NM_144628
9.62	9.39	0.24	3.42E-01	6.98E-01	CD14	CD14 molecule	chr5q22-q32|5q31.1	201743_at	NM_000591 /// NM_001040021
7.55	7.27	0.28	3.42E-01	6.98E-01	TMEM50B	transmembrane protein 50B	chr21q22.11	219600_s_at	NM_006134
1.96	1.84	0.12	3.42E-01	6.98E-01	C3orf16	chromosome 3 open reading frame 16	chr3q25.1	1561927_at	XM_001131739 /// XM_001132074 /// XM_001717444
2.25	2.14	0.11	3.42E-01	6.98E-01	---	---	---	238588_at	---
2.68	2.51	0.17	3.42E-01	6.98E-01	---	---	---	1568748_at	---
7.05	6.91	0.14	3.42E-01	6.98E-01	RFK	riboflavin kinase	chr9q21.13	203225_s_at	NM_018339
2.28	2.17	0.11	3.42E-01	6.98E-01	CCNB2	Cyclin B2	chr15q22.2	232768_at	NM_004701
2.46	2.28	0.18	3.42E-01	6.98E-01	---	---	---	243498_at	---
1.99	1.89	0.10	3.42E-01	6.98E-01	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	chr5q21	1554460_at	NM_005668 /// NM_175052
3.42	3.26	0.16	3.42E-01	6.98E-01	PLXNA1	plexin A1	chr3q21.3	1558140_at	NM_032242
6.93	6.66	0.27	3.42E-01	6.98E-01	HIATL1	hippocampus abundant transcript-like 1	chr9q22.32	223073_at	NM_032558
8.73	8.56	0.17	3.42E-01	6.98E-01	STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	chr20q13.1	207320_x_at	NM_001037328 /// NM_004602 /// NM_017452 /// NM_017453 /// NM_017454
5.90	5.47	0.43	3.42E-01	6.98E-01	RNF41	ring finger protein 41	chr12q13.2	201962_s_at	NM_005785 /// NM_194358 /// NM_194359
5.26	5.07	0.19	3.42E-01	6.98E-01	ZER1	zer-1 homolog (C. elegans)	chr9q34.11	202456_s_at	NM_006336
5.96	5.65	0.31	3.42E-01	6.98E-01	---	---	---	225176_at	---
4.66	4.40	0.26	3.42E-01	6.98E-01	KLHL22	kelch-like 22 (Drosophila)	chr22q11.21	221838_at	NM_032775
2.28	2.15	0.13	3.42E-01	6.98E-01	HIF3A	hypoxia inducible factor 3, alpha subunit	chr19q13.32	1555318_at	NM_022462 /// NM_152794 /// NM_152795
4.96	4.72	0.24	3.42E-01	6.98E-01	---	---	---	225776_at	---
6.50	6.15	0.36	3.42E-01	6.98E-01	CMTM7	CKLF-like MARVEL transmembrane domain containing 7	chr3p22.3	226017_at	NM_138410 /// NM_181472
6.28	5.94	0.35	3.42E-01	6.98E-01	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	chr14q11.2	216092_s_at	NM_012244 /// NM_182728
4.76	4.51	0.25	3.42E-01	6.98E-01	LIMK2	LIM domain kinase 2	chr22q12.2	202193_at	NM_001031801 /// NM_005569 /// NM_016733
2.98	2.81	0.17	3.43E-01	6.98E-01	SEC14L2	SEC14-like 2 (S. cerevisiae)	chr22q12.2	230316_at	NM_012429
3.03	2.89	0.13	3.43E-01	6.98E-01	KCNA5	potassium voltage-gated channel, shaker-related subfamily, member 5	chr12p13	206762_at	NM_002234
5.31	5.07	0.24	3.43E-01	6.98E-01	TSPAN10	tetraspanin 10	chr17q25.3	223795_at	NM_031945
4.98	4.76	0.22	3.43E-01	6.98E-01	S100PBP	S100P binding protein	chr1p35.1	222610_s_at	NM_001017406 /// NM_022753
2.38	2.16	0.22	3.43E-01	6.98E-01	SLMAP	sarcolemma associated protein	chr3p21.2-p14.3	222924_at	NM_007159

3.80	3.56	0.24	3.43E-01	6.98E-01	SEMA5B	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	chr3q21.1	223610_at	NM_001031702																				
5.98	5.85	0.12	3.43E-01	6.98E-01	TAOK1	TAO kinase 1	chr17q11.2	216310_at	NM_020791																				
2.07	1.96	0.11	3.43E-01	6.98E-01	---	---	---	233505_at	---																				
2.53	2.41	0.12	3.43E-01	6.98E-01	LOC100132911	similar to DPH3 homolog B (CSL-type zinc finger-containing protein 1)	chr20q13.33	233000_x_at	XR_039213 /// XR_039224 /// XR_039287																				
2.83	2.69	0.14	3.43E-01	6.98E-01	ROPN1L	ropporin 1-like	chr5p15.2	223609_at	NM_031916																				
7.59	7.31	0.27	3.43E-01	6.98E-01	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	chr12q11-q13	201389_at	NM_002205																				
2.32	2.21	0.11	3.43E-01	6.98E-01	OSBP	oxysterol binding protein	chr11q12-q13	1563051_at	NM_002556																				
5.13	4.85	0.29	3.43E-01	6.99E-01	RAB12	RAB12, member RAS oncogene family	chr18p11.22	236019_at	NM_001025300																				
6.10	5.72	0.37	3.43E-01	6.99E-01	ABI1	abl-interactor 1	chr10p11.2	209027_s_at	NM_001012750 /// NM_001012751 /// NM_001012752 /// NM_005470																				
4.32	4.06	0.25	3.43E-01	6.99E-01	MBD1	methyl-CpG binding domain protein 1	chr18q21	1555611_s_at	NM_002384 /// NM_015844 /// NM_015845 /// NM_015846 /// NM_015847																				
2.12	1.97	0.15	3.43E-01	6.99E-01	---	---	---	1561679_at	---																				
5.66	5.54	0.12	3.43E-01	6.99E-01	LOC729623 /// PRKAR1B	similar to protein kinase, cAMP-dependent, regulatory, type I, beta /// protein kinase, cAMP-dependent, regulatory, type I, beta	chr7p22	212555_at	NM_002735 /// XM_001716155																				
8.30	8.08	0.23	3.43E-01	6.99E-01	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	chr13q14.1	218435_at	NM_013238																				
2.02	1.89	0.13	3.43E-01	6.99E-01	---	---	---	1561704_at	---																				
11.75	11.63	0.12	3.43E-01	6.99E-01	ACTG1	actin, gamma 1	chr17q25	211995_x_at	NM_001614																				
2.39	2.24	0.14	3.43E-01	6.99E-01	---	---	---	1562351_at	---																				
3.17	3.01	0.16	3.43E-01	6.99E-01	ATP8B3	ATPase, class I, type 8B, member 3	chr19p13.3	1554704_at	NM_138813																				
2.91	2.79	0.12	3.43E-01	6.99E-01	---	---	---	1562222_at	---																				
2.38	2.26	0.12	3.43E-01	6.99E-01	CSMD1	CUB and Sushi multiple domains 1	chr8p23.2	1553405_a_at	NM_033225																				
2.40	2.21	0.19	3.43E-01	6.99E-01	---	---	---	1563391_at	---																				
2.03	1.89	0.13	3.43E-01	6.99E-01	ANKRD13C	ankyrin repeat domain 13C	chr1p32.3-p31.3	1556361_s_at	NM_030816																				
6.76	6.58	0.18	3.43E-01	6.99E-01	---	---	---	223964_x_at	---																				
6.18	5.86	0.31	3.44E-01	6.99E-01	MGC5370	hypothetical protein MGC5370	chr12q14.3	225160_x_at	---																				
3.87	3.76	0.12	3.44E-01	6.99E-01	---	---	---	239333_x_at	---																				
2.06	1.95	0.11	3.44E-01	6.99E-01	---	---	---	240019_at	---																				
2.73	2.56	0.17	3.44E-01	6.99E-01	CCDC135	coiled-coil domain containing 135	chr16q13	223905_at	NM_032269																				
5.60	5.28	0.32	3.44E-01	6.99E-01	ZNHIT2	zinc finger, HIT type 2	chr11q13	219050_s_at	NM_014205																				
5.17	4.98	0.20	3.44E-01	6.99E-01	---	---	---	215182_x_at	---																				
3.27	3.11	0.15	3.44E-01	6.99E-01	---	---	---	1569461_at	---																				
3.94	3.79	0.15	3.44E-01	6.99E-01	SPN	sialophorin	chr16p11.2	216981_x_at	NM_001030288 /// NM_003123																				
2.04	1.93	0.11	3.44E-01	6.99E-01	---	---	---	240649_at	---																				
6.05	5.81	0.24	3.44E-01	6.99E-01	TMEM25	transmembrane protein 25	chr11q23.3	226647_at	NM_032780																				
1.97	1.86	0.11	3.44E-01	6.99E-01	MYO3B	myosin IIIB	chr2q31.1-q31.2	1552578_a_at	NM_001083615 /// NM_138995																				
4.02	3.79	0.23	3.44E-01	6.99E-01	TMEM183A	transmembrane protein 183A	chr1q32.1	212164_at	NM_138391																				
3.31	3.13	0.18	3.44E-01	6.99E-01	---	---	---	229859_at	---																				
3.62	3.35	0.26	3.44E-01	6.99E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	1558078_at	NR_003655 /// XR_042143 /// XR_042182																				
2.42	2.14	0.28	3.44E-01	6.99E-01	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	chr11q14.3-q21	1554506_x_at	NM_005467																				
4.70	4.56	0.13	3.44E-01	6.99E-01	---	---	---	227907_at	---																				
7.82	7.55	0.27	3.44E-01	6.99E-01	LGMN	legumain	chr14q32.1	201212_at	NM_001008530 /// NM_005606																				
2.53	2.36	0.17	3.44E-01	6.99E-01	JAK1	Janus kinase 1 (a protein tyrosine kinase)	chr1p32.3-p31.3	240613_at	NM_002227																				
7.34	7.15	0.19	3.44E-01	6.99E-01	PRPS1	phosphoribosyl pyrophosphate synthetase 1	chrXq21.32-q24	209440_at	NM_002764																				
2.32	2.21	0.11	3.44E-01	6.99E-01	---	---	---	241693_at	---																				
2.01	1.91	0.10	3.44E-01	6.99E-01	ST6GAL2	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	chr2q11.2-q12.1	228821_at	NM_032528																				

7.58	7.37	0.21	3.44E-01	6.99E-01	TNIP1	TNFAIP3 interacting protein 1	chr5q32-q33.1	207196_s_at	NM_006058																				
1.96	1.85	0.11	3.45E-01	6.99E-01	KYNU	kynureninase (L-kynurenine hydrolase)	chr2q22.2	210662_at	NM_001032998 /// NM_003937																				
3.16	2.95	0.21	3.45E-01	6.99E-01	USP53	ubiquitin specific peptidase 53	chr4q26	231817_at	NM_019050																				
2.45	2.34	0.11	3.45E-01	6.99E-01	SYMPK	symplekin	chr19q13.3	1559587_at	NM_004819																				
5.17	4.99	0.18	3.45E-01	6.99E-01	CDX1	caudal type homeobox 1	chr5q31-q33	206430_at	NM_001804																				
2.45	2.30	0.15	3.45E-01	6.99E-01	---	---	---	215738_at	---																				
8.53	8.27	0.26	3.45E-01	6.99E-01	BIN1	bridging integrator 1	chr2q14	210201_x_at	NM_004305 /// NM_139343 /// NM_139344 /// NM_139345 /// NM_139346 /// NM_139347 /// NM_139348 /// NM_139349 /// NM_139350 /// NM_139351																				
2.56	2.44	0.12	3.45E-01	6.99E-01	NGRN /// TTLL13	neugrin, neurite outgrowth associated /// tubulin tyrosine ligase-like family, member 13	chr15q26.1	1568843_at	NM_001029964 /// NM_001033088 /// NM_016645																				
2.05	1.91	0.14	3.45E-01	7.00E-01	TCAM1	testicular cell adhesion molecule 1 homolog (mouse)	chr17q23.3	233320_at	NR_002947																				
2.28	2.16	0.12	3.45E-01	7.00E-01	---	---	---	1556781_at	---																				
5.03	4.83	0.21	3.45E-01	7.00E-01	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	chr16p13.3|16p13.3-p13.11	235215_at	NM_005236																				
4.83	4.46	0.38	3.45E-01	7.00E-01	CYCS	cytochrome c, somatic	chr7p15.2	229415_at	NM_018947																				
4.50	4.35	0.15	3.45E-01	7.00E-01	PDCD6	Aryl-hydrocarbon receptor repressor	chr5p15.33	222152_at	NM_013232 /// XM_001714855 /// XM_001720072 /// XM_001723249																				
2.60	2.46	0.14	3.45E-01	7.00E-01	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18	chr1q23	221371_at	NM_005092																				
1.98	1.88	0.10	3.45E-01	7.00E-01	---	---	---	234623_x_at	---																				
8.43	8.26	0.17	3.45E-01	7.00E-01	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	chr11p11.2	217772_s_at	NM_014342																				
6.76	6.36	0.40	3.45E-01	7.00E-01	KIF1B	kinesin family member 1B	chr1p36.2	226968_at	NM_015074 /// NM_183416																				
2.82	2.68	0.14	3.45E-01	7.00E-01	IGFL1	IGF-like family member 1	chr19q13.32	239430_at	NM_198541																				
2.19	2.07	0.12	3.45E-01	7.00E-01	HSFY1 /// HSFY2	heat shock transcription factor, Y-linked 1 /// heat shock transcription factor, Y linked 2	chrYq11.222	224007_at	NM_001001877 /// NM_033108 /// NM_152584 /// NM_153716 /// NR_003509 /// NR_003510																				
2.64	2.46	0.18	3.46E-01	7.00E-01	MICAL2	Microtubule associated monoxygenase, calponin and LIM domain containing 2	chr11p15.3	236475_at	NM_014632																				
5.94	5.62	0.31	3.46E-01	7.00E-01	MAPK10	mitogen-activated protein kinase 10	chr4q22.1-q23	204813_at	NM_002753 /// NM_138980 /// NM_138981 /// NM_138982																				

6.06	5.90	0.16	3.46E-01	7.00E-01	LOC100129250	similar to hCG1811779	chr9p21.1	78383_at	XM_001722063 /// XM_001723459 /// XM_001725563																			
7.36	6.81	0.55	3.46E-01	7.00E-01	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	chr13q32-q34	223501_at	NM_006573																			
2.73	2.62	0.11	3.46E-01	7.00E-01	MGC4771	hypothetical LOC84754	chr2q37.1	210723_x_at	---																			
4.91	4.58	0.33	3.46E-01	7.00E-01	C12orf30	chromosome 12 open reading frame 30	chr12q24.13	225888_at	NM_024953																			
2.15	2.02	0.14	3.46E-01	7.00E-01	RRM1	Ribonucleotide reductase M1	chr11p15.5	231028_at	NM_001033																			
7.46	6.82	0.63	3.46E-01	7.00E-01	WFDC1	WAP four-disulfide core domain 1	chr16q24.3	219478_at	NM_021197																			
6.49	6.24	0.24	3.46E-01	7.00E-01	ADAM17	ADAM metallopeptidase domain 17	chr2p25	213532_at	NM_003183																			
2.92	2.83	0.10	3.46E-01	7.00E-01	---	---	---	237960_at	---																			
9.72	9.53	0.18	3.46E-01	7.00E-01	UQCRC1	ubiquinol-cytochrome c reductase core protein I	chr3p21.3	201903_at	NM_003365																			
5.73	5.38	0.34	3.46E-01	7.00E-01	MTX3	metaxin 3	chr5q14.1	226528_at	NM_001010891																			
5.86	5.55	0.31	3.46E-01	7.00E-01	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	chr7q36.3	209015_s_at	NM_005494 /// NM_058246																			
4.36	3.98	0.38	3.46E-01	7.00E-01	PPIL4	peptidylprolyl isomerase (cyclophilin)-like 4	chr6q24-q25	226472_at	NM_139126																			
3.72	3.44	0.27	3.46E-01	7.00E-01	TESK2	testis-specific kinase 2	chr1p32	205486_at	NM_007170																			
3.32	3.13	0.19	3.46E-01	7.00E-01	ZNF324B /// ZNF584	zinc finger protein 324B /// zinc finger protein 584	chr19q13.43	222318_at	NM_173548 /// NM_207395																			
3.12	2.97	0.15	3.46E-01	7.00E-01	TRBV10-2	T cell receptor beta variable 10-2	chr7q34	211608_at	---																			
8.17	7.94	0.23	3.46E-01	7.00E-01	TXN2	thioredoxin 2	chr22q13.1	209078_s_at	NM_012473																			
3.11	2.76	0.35	3.46E-01	7.00E-01	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	205408_at	NM_001009569 /// NM_004641																			
1.97	1.87	0.10	3.46E-01	7.00E-01	C10orf126	chromosome 10 open reading frame 126	chr10p12.1	1553915_at	---																			
9.15	8.95	0.20	3.46E-01	7.01E-01	CYC1	cytochrome c-1	chr8q24.3	201066_at	NM_001916																			
2.44	2.31	0.13	3.47E-01	7.01E-01	TROVE2	TROVE domain family, member 2	chr1q31	212839_s_at	NM_001042369 /// NM_001042370 /// NM_004600																			
7.02	6.72	0.29	3.47E-01	7.01E-01	LOC100131612 /// MED27	similar to cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa /// mediator complex subunit 27	chr9q34.1-q34.3	51176_at	NM_004269 /// XM_001715326																			
5.32	4.95	0.37	3.47E-01	7.01E-01	LOC100131989	hypothetical LOC100131989	chr2q33.3	235360_at	XM_001720713 /// XM_001725037 /// XM_001725073																			
3.48	3.27	0.20	3.47E-01	7.01E-01	---	---	---	1563105_at	---																			
2.27	2.14	0.13	3.47E-01	7.01E-01	---	---	---	1564654_at	---																			
2.56	2.40	0.16	3.47E-01	7.01E-01	TRPV3	transient receptor potential cation channel, subfamily V, member 3	chr17p13.3	1555291_at	NM_145068																			
3.32	3.14	0.18	3.47E-01	7.01E-01	LOC389906 /// LOC441528 /// LOC728687 /// LOC729162	similar to Serine/threonine-protein kinase PRKX (Protein kinase PKX1) /// hypothetical protein LOC441528 /// similar to hCG1981372 /// similar to LOC389906 protein	chrXp22.33	1569629_x_at	XM_001128169 /// XM_001713861 /// XM_001715777 /// XM_928240 /// XM_942518 /// XR_041386																			
9.47	9.30	0.17	3.47E-01	7.01E-01	COX5A	cytochrome c oxidase subunit Va	chr15q24.1	203663_s_at	NM_004255																			
8.07	7.88	0.19	3.47E-01	7.01E-01	FLII	flightless I homolog (Drosophila)	chr17p11.2	212024_x_at	NM_002018																			
2.81	2.57	0.24	3.47E-01	7.01E-01	KLHL20	kelch-like 20 (Drosophila)	chr1q24.1-q24.3	204176_at	NM_014458																			
5.26	5.01	0.25	3.47E-01	7.01E-01	GDPD5	glycerophosphodiester phosphodiesterase domain containing 5	chr11q13.4-q13.5	32502_at	NM_030792																			
7.77	7.51	0.26	3.47E-01	7.01E-01	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	chr22q12-q13	222474_s_at	NM_020243																			
3.64	3.33	0.32	3.47E-01	7.01E-01	CXCL10	chemokine (C-X-C motif) ligand 10	chr4q21	204533_at	NM_001565																			
2.38	2.26	0.11	3.47E-01	7.01E-01	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	chr8p11.1	238090_at	NM_152419																			
2.03	1.91	0.12	3.47E-01	7.01E-01	---	---	---	238796_at	---																			
8.73	8.56	0.17	3.47E-01	7.01E-01	LRRC59	leucine rich repeat containing 59	chr17q21.33	222231_s_at	NM_018509																			
2.56	2.38	0.18	3.47E-01	7.01E-01	AP4E1	Adaptor-related protein complex 4, epsilon 1 subunit	chr15q21.2	241174_at	NM_007347																			
2.18	2.04	0.14	3.48E-01	7.01E-01	---	---	---	234178_at	---																			
6.41	6.24	0.18	3.48E-01	7.01E-01	MED8	mediator complex subunit 8	chr1p34.2	213127_s_at	NM_052877 /// NM_201542																			

2.08	1.97	0.11	3.48E-01	7.01E-01	---	---	---	241500_at	---
2.18	2.06	0.12	3.48E-01	7.01E-01	---	---	---	243686_at	---
8.00	7.71	0.29	3.48E-01	7.01E-01	SFRS1	splicing factor, arginine/serine-rich 1	chr17q21.3-q22	208863_s_at	NM_001078166 /// NM_006924
1.96	1.84	0.12	3.48E-01	7.01E-01	TPD52	tumor protein D52	chr8q21	201691_s_at	NM_001025252 /// NM_001025253 /// NM_005079
2.69	2.52	0.17	3.48E-01	7.01E-01	FRMD4A	FERM domain containing 4A	chr10p13	1554033_at	NM_018027
7.95	7.68	0.27	3.48E-01	7.01E-01	COQ9	coenzyme Q9 homolog (S. cerevisiae)	chr16q13	212228_s_at	NM_020312
1.98	1.88	0.10	3.48E-01	7.01E-01	VWDE	von Willebrand factor D and EGF domains	chr7p21.3	1562226_at	XM_001715460 /// XM_371878 /// XM_374405 /// XM_936911
5.14	5.01	0.14	3.48E-01	7.01E-01	---	---	---	1558876_at	---
2.62	2.47	0.15	3.48E-01	7.02E-01	C2orf59	chromosome 2 open reading frame 59	chr2p11.2	1552258_at	XR_042051 /// XR_042052
4.83	4.64	0.19	3.48E-01	7.02E-01	N6AMT1	N-6 adenine-specific DNA methyltransferase 1 (putative)	chr21q21.3	220311_at	NM_013240 /// NM_182749
3.77	3.62	0.15	3.48E-01	7.02E-01	THAP6	THAP domain containing 6	chr4q21.1	230169_at	NM_144721
5.35	5.05	0.30	3.48E-01	7.02E-01	---	---	---	1562265_at	---
6.32	6.10	0.21	3.48E-01	7.02E-01	LTV1	LTV1 homolog (S. cerevisiae)	chr6q24.2	225748_at	NM_032860
8.05	7.71	0.34	3.48E-01	7.02E-01	ARMCX2	armadillo repeat containing, X-linked 2	chrXq21.33-q22.2	203404_at	NM_014782 /// NM_177949
2.85	2.63	0.22	3.48E-01	7.02E-01	---	---	---	243636_s_at	---
6.87	6.65	0.21	3.48E-01	7.02E-01	NLRX1	NLR family member X1	chr11q23.3	219680_at	NM_024618 /// NM_170722
2.19	2.06	0.13	3.48E-01	7.02E-01	LPA	lipoprotein, Lp(a)	chr6q26	207584_at	NM_005577
3.23	3.02	0.21	3.48E-01	7.02E-01	HECTD1	HECT domain containing 1	chr14q12	241955_at	NM_015382
6.21	5.88	0.34	3.48E-01	7.02E-01	TBC1D10B	TBC1 domain family, member 10B	chr16p11.2	220947_s_at	NM_015527
7.78	7.58	0.20	3.49E-01	7.02E-01	TRAPPC3	trafficking protein particle complex 3	chr1p34.3	203512_at	NM_014408
6.30	6.06	0.25	3.49E-01	7.02E-01	CRTAP	cartilage associated protein	chr3p22.3	227138_at	NM_006371
6.96	6.64	0.32	3.49E-01	7.02E-01	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	chr2p22.1	225386_s_at	NM_138394
3.21	3.04	0.16	3.49E-01	7.02E-01	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	chr17q21-q22	210967_x_at	NM_000723 /// NM_199247 /// NM_199248
6.35	6.02	0.33	3.49E-01	7.02E-01	RMI1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	chr9q21.32	218979_at	NM_024945
8.98	8.72	0.26	3.49E-01	7.02E-01	ZMIZ1	zinc finger, MIZ-type containing 1	chr10q22.3	212124_at	NM_020338
2.45	2.31	0.14	3.49E-01	7.02E-01	---	---	---	231350_at	---
2.22	2.12	0.11	3.49E-01	7.02E-01	HELLS	helicase, lymphoid-specific	chr10q24.2	227350_at	NM_018063
11.41	11.24	0.17	3.49E-01	7.02E-01	HLA-A	major histocompatibility complex, class I, A	chr6p21.3	215313_x_at	NM_002116 /// XM_001713645
3.73	3.54	0.19	3.49E-01	7.02E-01	KIAA1632	KIAA1632	chr18q12.3-q21.1	228453_at	NM_020964
6.78	6.57	0.21	3.49E-01	7.02E-01	PTCD1	pentatricopeptide repeat domain 1	chr7q22.1	218956_s_at	NM_015545
4.95	4.71	0.24	3.49E-01	7.02E-01	HPS1	Hermansky-Pudlak syndrome 1	chr10q23.1-q23.3	203309_s_at	NM_000195 /// NM_182639
2.13	2.01	0.12	3.49E-01	7.03E-01	COL9A1	collagen, type IX, alpha 1	chr6q12-q14	1555527_at	NM_001851 /// NM_078485
5.80	5.64	0.17	3.49E-01	7.03E-01	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	chr1q21	202913_at	NM_014784 /// NM_198236
2.45	2.29	0.16	3.49E-01	7.03E-01	---	---	---	1568636_a_at	---
4.43	4.28	0.15	3.49E-01	7.03E-01	ITFG2	integrin alpha FG-GAP repeat containing 2	chr12p13.33	220590_at	NM_018463
3.13	2.78	0.35	3.49E-01	7.03E-01	PTGFR	prostaglandin F receptor (FP)	chr1p31.1	1555097_a_at	NM_000959 /// NM_001039585

5.66	5.26	0.40	3.49E-01	7.03E-01	MTMR3	myotubularin related protein 3	chr22q12.2	226956_at	NM_021090 /// NM_153050 /// NM_153051																			
4.07	3.80	0.27	3.50E-01	7.03E-01	CHTF18	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	chr16p13.3	226569_s_at	NM_022092																			
7.39	7.22	0.18	3.50E-01	7.03E-01	HMOX2	heme oxygenase (decycling) 2	chr16p13.3	218120_s_at	NM_001127204 /// NM_001127205 /// NM_001127206 /// NM_002134																			
2.26	2.15	0.11	3.50E-01	7.03E-01	---	---	---	241777_x_at	---																			
7.90	7.72	0.18	3.50E-01	7.03E-01	NOL7	nucleolar protein 7, 27kDa	chr6p23	210097_s_at	NM_016167																			
3.09	2.98	0.11	3.50E-01	7.03E-01	GLCCI1	glucocorticoid induced transcript 1	chr7p21.3	1560316_s_at	NM_138426																			
3.79	3.58	0.20	3.50E-01	7.03E-01	LOC100131637	hypothetical protein LOC100131637	chr8q21.2	231237_x_at	XM_001716033 /// XM_001716143 /// XM_001716209																			
2.57	2.44	0.13	3.50E-01	7.03E-01	NUMA1	Nuclear mitotic apparatus protein 1	chr11q13	235539_at	NM_006185																			
2.93	2.80	0.14	3.50E-01	7.03E-01	FCHSD2	FCH and double SH3 domains 2	chr11q13.4	1554360_at	NM_014824																			
2.02	1.91	0.11	3.50E-01	7.03E-01	RYR2	ryanodine receptor 2 (cardiac)	chr1q42.1-q43	214044_at	NM_001035																			
7.68	7.50	0.19	3.50E-01	7.03E-01	TSPAN31	tetraspanin 31	chr12q13.3	203226_s_at	NM_005981																			
4.15	3.99	0.16	3.50E-01	7.03E-01	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	chr19q13.4	211100_x_at	NM_001130917 /// NM_006866																			
6.02	5.64	0.38	3.50E-01	7.03E-01	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	chr16q21-q22.1	1555705_a_at	NM_001048251 /// NM_144601 /// NM_181553 /// NM_181554																			
7.71	7.55	0.16	3.50E-01	7.03E-01	C16orf33	chromosome 16 open reading frame 33	chr16p13.3	218493_at	NM_024571																			
3.46	3.27	0.19	3.50E-01	7.04E-01	CENPA	centromere protein A	chr2p24-p21	210821_x_at	NM_001042426 /// NM_001809																			
2.02	1.90	0.11	3.50E-01	7.04E-01	---	---	---	1569958_at	---																			
6.96	6.73	0.23	3.50E-01	7.04E-01	POLR3GL	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	chr1q21.1	223269_at	NM_032305																			
2.59	2.42	0.17	3.50E-01	7.04E-01	---	---	---	203808_at	---																			
2.62	2.47	0.15	3.50E-01	7.04E-01	RGSL1	regulator of G-protein signaling like 1	chr1q25	211446_at	XM_001721759 /// XM_001725941 /// XM_001726587																			
3.09	2.93	0.16	3.51E-01	7.04E-01	C21orf67	chromosome 21 open reading frame 67	chr21q22.3	1555627_s_at	XR_039924 /// XR_039925 /// XR_039926																			
7.42	7.20	0.21	3.51E-01	7.04E-01	HNRNPF	heterogeneous nuclear ribonucleoprotein F	chr10q11.21-q11.22	201376_s_at	NM_001098204 /// NM_001098205 /// NM_001098206 /// NM_001098207 /// NM_001098208 /// NM_004966																			
7.76	7.49	0.27	3.51E-01	7.04E-01	HK1	hexokinase 1	chr10q22	200697_at	NM_000188 /// NM_033496 /// NM_033497 /// NM_033498 /// NM_033500																			

2.44	2.33	0.11	3.51E-01	7.04E-01	---	---	---	1556700_a_at	---
8.55	8.36	0.19	3.51E-01	7.04E-01	MRPL24	mitochondrial ribosomal protein L24	chr1q21-q22	218270_at	NM_024540 /// NM_145729
11.93	11.78	0.14	3.51E-01	7.04E-01	GLTSCR2	glioma tumor suppressor candidate region gene 2	chr19q13.3	217807_s_at	NM_015710
3.03	2.88	0.16	3.51E-01	7.04E-01	AVIL	Advillin	chr12q14.1	1568706_s_at	NM_006576
5.18	4.93	0.25	3.51E-01	7.04E-01	ZC3H10	zinc finger CCCH-type containing 10	chr12q13.2	227430_at	NM_032786
4.01	3.84	0.17	3.51E-01	7.04E-01	C9orf40	chromosome 9 open reading frame 40	chr9q21.13	222781_s_at	NM_017998
3.97	3.63	0.34	3.51E-01	7.04E-01	---	---	---	217482_at	---
4.86	4.70	0.17	3.51E-01	7.04E-01	---	---	---	232949_at	---
3.18	2.99	0.19	3.51E-01	7.04E-01	---	---	---	1557265_at	---
6.64	6.38	0.26	3.51E-01	7.04E-01	PMM1	phosphomannomutase 1	chr22q13.2	203467_at	NM_002676
3.64	3.53	0.10	3.51E-01	7.04E-01	---	---	---	1555856_s_at	---
2.58	2.45	0.14	3.51E-01	7.04E-01	DSCR8	Down syndrome critical region gene 8	chr21q22.2	241224_x_at	XR_040165 /// XR_040166 /// XR_040167
8.47	8.17	0.31	3.51E-01	7.04E-01	SFRS1	splicing factor, arginine/serine-rich 1	chr17q21.3-q22	211784_s_at	NM_001078166 /// NM_006924
3.73	3.51	0.22	3.51E-01	7.04E-01	---	---	---	239452_at	---
2.31	2.14	0.17	3.51E-01	7.04E-01	---	---	---	232576_at	---
2.76	2.61	0.15	3.51E-01	7.04E-01	---	---	---	216931_at	---
2.23	2.11	0.12	3.51E-01	7.04E-01	AP3B2	adaptor-related protein complex 3, beta 2 subunit	chr15q	1570032_at	NM_004644
6.24	6.00	0.24	3.51E-01	7.04E-01	SLC30A6	solute carrier family 30 (zinc transporter), member 6	chr2p22.3	226161_at	NM_017964
4.54	4.37	0.17	3.51E-01	7.04E-01	HAAO	3-hydroxyanthranilate 3,4-dioxygenase	chr2p21	205657_at	NM_012205
2.02	1.92	0.09	3.52E-01	7.04E-01	---	---	---	1556238_at	---
2.69	2.57	0.12	3.52E-01	7.04E-01	LOC730057	Hypothetical LOC730057	chr3p14.1	234078_at	XM_001132251 /// XM_001132871 /// XM_001716450
3.60	3.44	0.17	3.52E-01	7.04E-01	C21orf122	chromosome 21 open reading frame 122	chr21q22.3	223768_at	XR_040045 /// XR_040046 /// XR_040047
6.96	6.79	0.18	3.52E-01	7.04E-01	CSRP2BP	CSRP2 binding protein	chr20p11.23	228544_s_at	NM_020536 /// NM_177926
4.61	4.42	0.19	3.52E-01	7.05E-01	---	---	---	235134_at	---
6.21	6.03	0.18	3.52E-01	7.05E-01	FOXC1	forkhead box C1	chr6p25	213260_at	NM_001453
3.61	3.22	0.39	3.52E-01	7.05E-01	ITCH	Itchy E3 ubiquitin protein ligase homolog (mouse)	chr20q11.22-q11.23	236235_at	NM_031483
7.20	6.65	0.55	3.52E-01	7.05E-01	---	---	---	240385_at	---
3.69	3.24	0.44	3.52E-01	7.05E-01	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2	chr2p22.2-p22.1	1553603_s_at	NM_022374
3.13	2.97	0.16	3.52E-01	7.05E-01	DTNA	dystrobrevin, alpha	chr18q12	205741_s_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981
7.53	7.29	0.24	3.52E-01	7.05E-01	APRT	adenine phosphoribosyltransferase	chr16q24	203219_s_at	NM_000485 /// NM_001030018
2.78	2.68	0.10	3.52E-01	7.05E-01	---	---	---	1566242_at	---
6.98	6.84	0.15	3.52E-01	7.05E-01	NRBP1	nuclear receptor binding protein 1	chr2p23	217765_at	NM_013392
2.26	2.14	0.12	3.52E-01	7.05E-01	---	---	---	237399_at	---
2.11	1.99	0.12	3.52E-01	7.05E-01	ZNF254	zinc finger protein 254	chr19p12	236133_x_at	NM_203282
2.33	2.21	0.12	3.52E-01	7.05E-01	---	---	---	1562163_at	---

4.53	4.32	0.21	3.52E-01	7.05E-01	MRPL4	mitochondrial ribosomal protein L4	chr19p13.2	223742_at	NM_015956 /// NM_146387 /// NM_146388
4.06	3.91	0.16	3.52E-01	7.05E-01	UBA2	ubiquitin-like modifier activating enzyme 2	chr19q12	229587_at	NM_005499
2.90	2.77	0.14	3.52E-01	7.05E-01	LPO	lactoperoxidase	chr17q23.1	210682_at	NM_006151
4.45	4.27	0.18	3.52E-01	7.05E-01	BBS10	Bardet-Biedl syndrome 10	chr12q21.2	219487_at	NM_024685
5.91	5.70	0.20	3.53E-01	7.05E-01	LSM12	LSM12 homolog (S. cerevisiae)	chr17q21.31	212529_at	NM_152344
3.40	3.28	0.13	3.53E-01	7.05E-01	SCAMP5	Secretory carrier membrane protein 5	chr15q24.1-q24.2	234568_at	NM_138967
3.92	3.80	0.12	3.53E-01	7.05E-01	---	---	---	235796_at	---
3.31	3.16	0.15	3.53E-01	7.05E-01	---	---	---	236393_at	---
2.23	2.11	0.12	3.53E-01	7.05E-01	C11orf30	chromosome 11 open reading frame 30	chr11q13.5	1569349_at	NM_020193
4.68	4.48	0.20	3.53E-01	7.05E-01	LOC285708	hypothetical protein LOC285708	chr5q21.2	1564281_at	---
7.56	7.27	0.28	3.53E-01	7.05E-01	PLSCR3	phospholipid scramblase 3	chr17p13.1	218828_at	NM_020360
2.60	2.48	0.13	3.53E-01	7.05E-01	ZNF91	zinc finger protein 91	chr19p13.1-p12	236128_at	NM_003430
7.00	6.71	0.29	3.53E-01	7.05E-01	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	chr7p11.2	201326_at	NM_001009186 /// NM_001762
2.68	2.55	0.14	3.53E-01	7.06E-01	RNF187	Ring finger protein 187	chr1q42.13	229207_x_at	XM_001129309 /// XM_001715919 /// XM_928029
2.63	2.48	0.15	3.53E-01	7.06E-01	---	---	---	237601_at	---
6.77	6.58	0.19	3.53E-01	7.06E-01	DHPS	deoxyhypusine synthase	chr19p13.2-p13.1	211558_s_at	NM_001930 /// NM_013406 /// NM_013407
2.96	2.80	0.16	3.53E-01	7.06E-01	---	---	---	1565974_at	---
5.27	4.88	0.38	3.53E-01	7.06E-01	DMTF1	cyclin D binding myb-like transcription factor 1	chr7q21	203301_s_at	NM_021145
3.04	2.84	0.20	3.53E-01	7.06E-01	---	---	---	1557413_a_at	---
2.77	2.54	0.22	3.54E-01	7.06E-01	---	---	---	1558365_at	---
2.03	1.92	0.11	3.54E-01	7.06E-01	PDE8B	phosphodiesterase 8B	chr5q14.1	235115_at	NM_001029851 /// NM_001029852 /// NM_001029853 /// NM_001029854 /// NM_003719
3.28	3.18	0.10	3.54E-01	7.06E-01	---	---	---	240142_at	---
6.97	6.73	0.23	3.54E-01	7.06E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	218915_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833
4.20	3.24	0.96	3.54E-01	7.06E-01	RAB12	RAB12, member RAS oncogene family	chr18p11.22	235059_at	NM_001025300
3.12	2.29	0.83	3.54E-01	7.06E-01	SOD2	superoxide dismutase 2, mitochondrial	chr6q25.3	215078_at	NM_000636 /// NM_001024465 /// NM_001024466
2.43	2.34	0.10	3.54E-01	7.06E-01	---	---	---	1559867_at	---
3.13	2.95	0.18	3.54E-01	7.06E-01	RFPL1S /// RFPL3S	ret finger protein-like 1 antisense /// ret finger protein-like 3 antisense	chr22q12 /// chr22q12.3	214408_s_at	NR_001450 /// NR_002596 /// NR_002727

6.65	6.51	0.14	3.54E-01	7.06E-01	SAPS3	SAPS domain family, member 3	chr11q13	217928_s_at	NM_018312																			
2.21	2.08	0.12	3.54E-01	7.06E-01	---	---	---	243427_at	---																			
2.23	2.09	0.13	3.54E-01	7.06E-01	C8orf45	chromosome 8 open reading frame 45	chr8q13.1	1569677_a_at	NM_173518																			
2.15	2.02	0.13	3.54E-01	7.06E-01	DSC1	desmocollin 1	chr18q12.2|18q12.1	207324_s_at	NM_004948 /// NM_024421																			
7.12	6.91	0.21	3.54E-01	7.06E-01	MTX2	metaxin 2	chr2q31.1	203517_at	NM_001006635 /// NM_006554																			
8.19	7.75	0.44	3.54E-01	7.06E-01	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	chr6p21.3	206093_x_at	NM_019105 /// NM_032470 /// NR_001284																			
2.79	2.66	0.14	3.54E-01	7.06E-01	---	---	---	1555875_at	---																			
4.03	3.43	0.60	3.54E-01	7.06E-01	ELL2	elongation factor, RNA polymerase II, 2	chr5q15	214446_at	NM_012081																			
7.23	6.90	0.33	3.54E-01	7.06E-01	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	chr10p12.1	230925_at	NM_019043																			
3.40	3.17	0.23	3.54E-01	7.06E-01	FAM168A	family with sequence similarity 168, member A	chr11q13.4	36612_at	NM_015159																			
4.84	4.54	0.30	3.54E-01	7.06E-01	FAM126A	family with sequence similarity 126, member A	chr7p15.3	227239_at	NM_032581																			
2.46	2.33	0.12	3.54E-01	7.06E-01	hCG_1730474	HCG1730474	chr11q12.1	215349_at	XR_041749 /// XR_041750 /// XR_041751																			
11.14	10.74	0.40	3.54E-01	7.06E-01	VIM	vimentin	chr10p13	201426_s_at	NM_003380																			
5.41	5.22	0.19	3.55E-01	7.07E-01	MAGEE1	melanoma antigen family E, 1	chrXq13.3	229286_at	NM_020932																			
3.30	3.19	0.11	3.55E-01	7.07E-01	TM9SF1	Transmembrane 9 superfamily member 1	chr14q11.2	238948_at	NM_001014842 /// NM_006405																			
3.74	3.53	0.22	3.55E-01	7.07E-01	ZNF548	zinc finger protein 548	chr19q13.43	1553719_s_at	NM_152909																			
2.26	2.12	0.14	3.55E-01	7.07E-01	---	---	---	234543_at	---																			
6.10	5.96	0.14	3.55E-01	7.07E-01	---	---	---	64418_at	---																			
2.40	2.28	0.12	3.55E-01	7.07E-01	SCLY	selenocysteine lyase	chr2q37.3	59705_at	NM_016510																			

2.27	2.11	0.16	3.55E-01	7.07E-01	SNRPN	small nuclear ribonucleoprotein polypeptide N	chr15q11.2	1559343_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																				
10.72	10.58	0.14	3.55E-01	7.07E-01	TUBA1B	tubulin, alpha 1b	chr12q13.12	212639_x_at	NM_006082																			
2.42	2.30	0.11	3.55E-01	7.07E-01	---	---	---	1570645_at	---																			
2.65	2.44	0.22	3.55E-01	7.07E-01	---	---	---	1559006_at	---																			
3.52	3.26	0.25	3.55E-01	7.07E-01	DPY19L1	dpy-19-like 1 (C. elegans)	chr7p14.3	1560916_a_at	NM_015283																			
3.18	3.03	0.15	3.55E-01	7.07E-01	ZACN	zinc activated ligand-gated ion channel	chr17q25.3	1555550_at	NM_180990																			
2.80	2.64	0.16	3.55E-01	7.07E-01	TMCO2	transmembrane and coiled-coil domains 2	chr1p34.2	231264_at	NM_001008740																			
4.97	4.84	0.13	3.55E-01	7.07E-01	ARNT	aryl hydrocarbon receptor nuclear translocator	chr1q21	218222_x_at	NM_001668 /// NM_178426 /// NM_178427																			
3.37	3.19	0.18	3.55E-01	7.07E-01	LOC643072	hypothetical LOC643072	chr2q24.2	228412_at	XR_041307 /// XR_041308 /// XR_041309																			

5.41	5.24	0.17	3.55E-01	7.07E-01	OGG1	8-oxoguanine DNA glycosylase	chr3p26.2	205301_s_at	NM_002542 /// NM_016819 /// NM_016820 /// NM_016821 /// NM_016826 /// NM_016827 /// NM_016828 /// NM_016829																				
7.55	7.38	0.16	3.55E-01	7.07E-01	WARS	tryptophanyl-tRNA synthetase	chr14q32.31	200629_at	NM_004184 /// NM_173701 /// NM_213645 /// NM_213646																				
3.04	2.88	0.16	3.55E-01	7.07E-01	IVL	involucrin	chr1q21	214599_at	NM_005547																				
9.27	8.95	0.32	3.55E-01	7.07E-01	C4A /// C4B	complement component 4A (Rodgers blood group) /// complement component 4B (Childo blood group)	chr6p21.3	214428_x_at	NM_000592 /// NM_001002029 /// NM_007293																				
2.07	1.98	0.09	3.55E-01	7.07E-01	---	---	---	233744_at	---																				
2.32	2.21	0.10	3.55E-01	7.07E-01	LOC253724	hypothetical LOC253724	chr12q23.3	1570008_at	XR_015316 /// XR_041116 /// XR_041117																				
3.28	3.09	0.19	3.55E-01	7.07E-01	---	---	---	242523_at	---																				
2.18	2.08	0.10	3.55E-01	7.07E-01	---	---	---	1557498_a_at	---																				
2.34	2.16	0.18	3.56E-01	7.07E-01	---	---	---	232752_at	---																				
3.09	2.89	0.19	3.56E-01	7.07E-01	---	---	---	239540_at	---																				
3.32	2.80	0.52	3.56E-01	7.07E-01	---	---	---	239624_at	---																				
6.91	6.72	0.19	3.56E-01	7.07E-01	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	chr22q13.2-q13.33	1554691_a_at	NM_007229																				
5.40	5.08	0.33	3.56E-01	7.07E-01	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	chr1q32	204484_at	NM_002646																				
3.43	3.23	0.20	3.56E-01	7.07E-01	METTL2A /// METTL2B	methyltransferase like 2A /// methyltransferase like 2B	chr17q23.2 /// chr7q32.1	221079_s_at	NM_001005372 /// NM_018396 /// NM_181725																				
6.67	6.44	0.22	3.56E-01	7.07E-01	RNF26	ring finger protein 26	chr11q23	224947_at	NM_032015																				
2.93	2.80	0.14	3.56E-01	7.07E-01	CLP1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	chr11q12	1566151_at	NM_006831																				
7.33	6.54	0.78	3.56E-01	7.07E-01	NCAM1	neural cell adhesion molecule 1	chr11q23.1	212843_at	NM_000615 /// NM_001076682 /// NM_181351																				
2.10	1.98	0.12	3.56E-01	7.07E-01	MGAT4A	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	chr2q12	1569136_at	NM_012214																				
2.10	1.99	0.11	3.56E-01	7.07E-01	---	---	---	237365_at	---																				
5.92	5.45	0.46	3.56E-01	7.07E-01	ZNF185	zinc finger protein 185 (LIM domain)	chrXq28	203585_at	NM_007150																				
8.49	8.18	0.31	3.56E-01	7.07E-01	RNF145	ring finger protein 145	chr5q33.3	226077_at	NM_144726																				
4.10	3.87	0.22	3.56E-01	7.07E-01	---	---	---	236114_at	---																				
8.19	7.72	0.46	3.56E-01	7.07E-01	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	chr6p21.3	216333_x_at	NM_019105 /// NM_032470 /// NR_001284																				
2.66	2.51	0.15	3.56E-01	7.07E-01	MEFV	Mediterranean fever	chr16p13.3	208262_x_at	NM_000243																				
6.92	6.69	0.23	3.56E-01	7.07E-01	TCF12	transcription factor 12	chr15q21	208986_at	NM_003205 /// NM_207036 /// NM_207037 /// NM_207038 /// NM_207040																				
2.34	2.23	0.12	3.56E-01	7.07E-01	---	---	---	240118_at	---																				
2.13	2.01	0.12	3.56E-01	7.07E-01	CNBD1	cyclic nucleotide binding domain containing 1	chr8q21.3	1552587_at	NM_173538																				

2.19	2.07	0.12	3.56E-01	7.07E-01	---	---	---	234090_at	---
6.85	6.54	0.30	3.56E-01	7.07E-01	DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	chr17q23.1	218277_s_at	NM_024612
2.89	2.61	0.28	3.56E-01	7.07E-01	CEP152	centrosomal protein 152kDa	chr15q21.1	239413_at	NM_014985
2.28	2.16	0.12	3.56E-01	7.08E-01	---	---	---	240663_at	---
5.42	5.23	0.19	3.57E-01	7.08E-01	LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	chr3q29	221536_s_at	NM_018385
6.59	6.13	0.46	3.57E-01	7.08E-01	CDK7	cyclin-dependent kinase 7	chr5q12.1	211297_s_at	NM_001799
4.90	4.67	0.22	3.57E-01	7.08E-01	NRBF2	nuclear receptor binding factor 2	chr10q21.2	221803_s_at	NM_030759
2.68	2.50	0.18	3.57E-01	7.08E-01	---	---	---	235502_at	---
2.49	2.35	0.14	3.57E-01	7.08E-01	---	---	---	217210_at	---
5.48	5.32	0.16	3.57E-01	7.08E-01	ARFRP1 /// IGLJ3	ADP-ribosylation factor related protein 1 /// immunoglobulin lambda joining 3	chr20q13.3 /// chr22q11.1-q11.2	215984_s_at	NM_001134758 /// NM_003224
5.13	4.94	0.19	3.57E-01	7.08E-01	GOLGA1	golgi autoantigen, golgin subfamily a, 1	chr9q33.3	203384_s_at	NM_002077
3.98	3.74	0.23	3.57E-01	7.08E-01	---	---	---	234359_at	---
2.19	2.07	0.12	3.57E-01	7.08E-01	LOC285556	hypothetical protein LOC285556	chr4q23	236523_at	XM_001717423 /// XM_373030 /// XM_939505
2.54	2.39	0.15	3.57E-01	7.08E-01	PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	chr6q25.1	226122_at	NM_001029884
4.83	4.54	0.29	3.57E-01	7.08E-01	GAPVD1	GTPase activating protein and VPS9 domains 1	chr9q33.3	214869_x_at	NM_015635
5.11	4.95	0.16	3.57E-01	7.08E-01	NUMB	numb homolog (Drosophila)	chr14q24.3	209073_s_at	NM_001005743 /// NM_001005744 /// NM_001005745 /// NM_003744
4.58	4.42	0.16	3.57E-01	7.08E-01	---	---	---	216354_at	---
3.45	3.25	0.20	3.57E-01	7.08E-01	RHCE	Rh blood group, CcEe antigens	chr1p36.11	216317_x_at	NM_020485 /// NM_138616 /// NM_138617 /// NM_138618
2.22	2.09	0.13	3.57E-01	7.08E-01	ZNF519	zinc finger protein 519	chr18p11.21	1568873_at	NM_145287
4.18	3.97	0.20	3.57E-01	7.08E-01	WDFY4	WDFY family member 4	chr10q11.22	229597_s_at	NM_020945 /// XM_001124973 /// XM_001124974 /// XM_001714299 /// XM_001719015
2.05	1.92	0.13	3.57E-01	7.08E-01	---	---	---	1559147_at	---
6.31	5.95	0.36	3.57E-01	7.08E-01	CLEC11A	C-type lectin domain family 11, member A	chr19q13.3	211709_s_at	NM_002975
6.27	5.74	0.53	3.57E-01	7.08E-01	GIPC2	GIPC PDZ domain containing family, member 2	chr1p31.1	236548_at	NM_017655
4.15	3.88	0.27	3.57E-01	7.08E-01	---	---	---	225716_at	---
3.91	3.70	0.21	3.57E-01	7.08E-01	OSBPL7	oxysterol binding protein-like 7	chr17q21	227946_at	NM_145798
7.72	7.59	0.12	3.57E-01	7.08E-01	LAMP1	lysosomal-associated membrane protein 1	chr13q34	201551_s_at	NM_005561
6.74	6.20	0.53	3.57E-01	7.08E-01	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	chr1q21	200798_x_at	NM_021960 /// NM_182763
7.03	6.77	0.26	3.57E-01	7.08E-01	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	chr14q11.2	213345_at	NM_004554
3.77	3.62	0.15	3.57E-01	7.08E-01	---	---	---	1569380_a_at	---
6.11	5.65	0.46	3.58E-01	7.08E-01	HBG1 /// HBG2	hemoglobin, gamma A /// hemoglobin, gamma G	chr11p15.5	213515_x_at	NM_000184 /// NM_000559
2.17	2.02	0.15	3.58E-01	7.08E-01	---	---	---	239459_s_at	---
5.09	4.86	0.23	3.58E-01	7.08E-01	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	chr1q21.1	225278_at	NM_005399
1.89	1.80	0.09	3.58E-01	7.08E-01	---	---	---	220884_at	---
3.31	3.12	0.18	3.58E-01	7.08E-01	NFKBIL2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	chr8q24.3	1558329_at	NM_013432
2.40	2.27	0.13	3.58E-01	7.08E-01	MTBP	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa	chr8q24.12	1552518_s_at	NM_022045
6.87	6.69	0.18	3.58E-01	7.08E-01	PITPNA	phosphatidylinositol transfer protein, alpha	chr17p13.3	201191_at	NM_006224
3.13	2.94	0.19	3.58E-01	7.08E-01	RHOB	Ras homolog gene family, member B	chr2p24	226417_at	NM_004040

2.00	1.89	0.11	3.58E-01	7.08E-01	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	chr18q22-q23	1552904_at	NM_138966 /// NM_138999 /// NM_153181																				
10.37	10.17	0.20	3.58E-01	7.08E-01	TPI1	triosephosphate isomerase 1	chr12p13	213011_s_at	NM_000365																				
5.30	4.66	0.65	3.58E-01	7.08E-01	CRYBB2 /// CRYBB2P1	crystallin, beta B2 /// crystallin, beta B2 pseudogene 1	chr22q11.2-q12.1 /// chr22q11.2-q12.1|22q11.23	206777_s_at	NM_000496																				
10.00	9.85	0.15	3.58E-01	7.08E-01	CLTA	clathrin, light chain (Lca)	chr9p13	204050_s_at	NM_001076677 /// NM_001833 /// NM_007096																				
2.35	2.24	0.11	3.58E-01	7.08E-01	---	---	---	1562786_at	---																				
2.59	2.47	0.12	3.58E-01	7.08E-01	---	---	---	242808_at	---																				
2.10	1.99	0.11	3.58E-01	7.09E-01	---	---	---	1556580_a_at	---																				
2.45	2.32	0.13	3.58E-01	7.09E-01	FAM29A	family with sequence similarity 29, member A	chr9p22.1	218602_s_at	NM_017645																				
2.16	2.03	0.12	3.58E-01	7.09E-01	---	---	---	1564819_at	---																				
2.88	2.73	0.15	3.58E-01	7.09E-01	ALOX5	Arachidonate 5-lipoxygenase	chr10q11.2	213952_s_at	NM_000698																				
5.65	5.39	0.26	3.58E-01	7.09E-01	CEMP1	Cementum protein 1	chr16p13.3	227841_at	NM_001048212																				
2.45	2.34	0.11	3.59E-01	7.09E-01	---	---	---	244080_at	---																				
3.22	3.05	0.17	3.59E-01	7.09E-01	WNT9A	wingless-type MMTV integration site family, member 9A	chr1q42	1553045_at	NM_003395																				
2.35	2.21	0.14	3.59E-01	7.09E-01	---	---	---	234398_at	---																				
3.29	3.13	0.16	3.59E-01	7.09E-01	TMEM180	transmembrane protein 180	chr10q24.32	219745_at	NM_024789																				
4.50	4.24	0.26	3.59E-01	7.09E-01	MYST1	MYST histone acetyltransferase 1	chr16p11.2	214885_at	NM_032188 /// NM_182958																				
3.30	3.02	0.28	3.59E-01	7.09E-01	MICB	MHC class I polypeptide-related sequence B	chr6p21.3	206247_at	NM_005931																				
2.45	2.31	0.14	3.59E-01	7.09E-01	ELF5	E74-like factor 5 (ets domain transcription factor)	chr11p13-p12	220625_s_at	NM_001422 /// NM_198381																				
3.85	3.61	0.24	3.59E-01	7.09E-01	---	---	---	1558017_s_at	---																				
4.42	4.27	0.15	3.59E-01	7.09E-01	HLA-DOA	major histocompatibility complex, class II, DO alpha	chr6p21.3	217001_x_at	NM_002119																				
3.11	2.97	0.14	3.59E-01	7.09E-01	ACTBL3	actin, beta-like 3	chr2q21.1	210926_at	XM_001723159 /// XM_001723912 /// XM_001724405																				
4.49	4.19	0.30	3.59E-01	7.09E-01	RWDD3	RWD domain containing 3	chr1p21.3	205087_at	NM_001128142 /// NM_015485																				
6.20	5.97	0.23	3.59E-01	7.09E-01	---	---	---	227501_at	---																				
2.42	2.30	0.12	3.59E-01	7.09E-01	ZNF238	zinc finger protein 238	chr1q44-qter	207164_s_at	NM_006352 /// NM_205768																				
7.98	7.83	0.16	3.59E-01	7.09E-01	ADSL	adenylosuccinate lyase	chr22q13.1|22q13.2	210250_x_at	NM_000026 /// NM_001123378																				
2.03	1.92	0.11	3.59E-01	7.10E-01	---	---	---	1560748_at	---																				
4.13	3.96	0.17	3.59E-01	7.10E-01	DHODH	dihydroorotate dehydrogenase	chr16q22	213632_at	NM_001361																				
2.20	2.09	0.12	3.59E-01	7.10E-01	SOX1	SRY (sex determining region Y)-box 1	chr13q34	237472_at	NM_005986																				
2.68	2.54	0.14	3.59E-01	7.10E-01	CD28	CD28 molecule	chr2q33	211856_x_at	NM_006139																				
6.11	5.78	0.33	3.59E-01	7.10E-01	IWS1	IWS1 homolog (S. cerevisiae)	chr2q14.3	224768_at	NM_017969																				
2.25	2.13	0.12	3.59E-01	7.10E-01	GAFA1	FGF2-associated protein GAFA1	chr14q11.2	1554901_at	XM_001715150 /// XM_001717260 /// XM_001721859																				
2.18	2.09	0.10	3.59E-01	7.10E-01	---	---	---	231426_at	---																				
3.06	2.91	0.15	3.59E-01	7.10E-01	LOC90499	hypothetical protein LOC90499	chr2q11.1	234016_at	XR_042126 /// XR_042127																				
8.14	7.81	0.33	3.60E-01	7.10E-01	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	chr1q23	204232_at	NM_004106																				
3.72	3.46	0.26	3.60E-01	7.10E-01	KLF6	Kruppel-like factor 6	chr10p15	211610_at	NM_001300																				
5.70	5.19	0.50	3.60E-01	7.10E-01	ZNF207	zinc finger protein 207	chr17q11.2	1556035_s_at	NM_001032293 /// NM_001098507 /// NM_003457																				

3.79	3.61	0.18	3.60E-01	7.10E-01	ZNF200	zinc finger protein 200	chr16p13.3	214706_at	NM_003454 /// NM_198087 /// NM_198088																				
2.23	2.08	0.14	3.60E-01	7.10E-01	C6orf190	chromosome 6 open reading frame 190	chr6q22.33	1558972_s_at	NM_001010923																				
2.64	2.47	0.16	3.60E-01	7.10E-01	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	chr3q22.3	217620_s_at	NM_006219																				
2.16	2.04	0.12	3.60E-01	7.10E-01	KAT2B	K(lysine) acetyltransferase 2B	chr3p24	239585_at	NM_003884																				
3.52	3.25	0.27	3.60E-01	7.10E-01	FOXK2	forkhead box K2	chr17q25	242938_s_at	NM_004514																				
2.38	2.18	0.20	3.60E-01	7.10E-01	NSMCE4A	non-SMC element 4 homolog A (S. cerevisiae)	chr10q26.13	228506_at	NM_017615																				
6.91	6.58	0.33	3.60E-01	7.10E-01	C12orf23	chromosome 12 open reading frame 23	chr12q23.3	224759_s_at	NM_152261																				
5.36	5.16	0.20	3.60E-01	7.10E-01	SLC25A33	solute carrier family 25, member 33	chr1p36.22	223296_at	NM_032315																				
2.53	2.34	0.19	3.60E-01	7.10E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	236970_s_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844																				
6.18	5.99	0.20	3.60E-01	7.10E-01	FXC1	fracture callus 1 homolog (rat)	chr11p15.5-p15.3	217981_s_at	NM_012192																				
5.30	5.08	0.22	3.60E-01	7.10E-01	C20orf196	chromosome 20 open reading frame 196	chr20p12.3	235064_s_at	NM_152504																				
2.41	2.30	0.11	3.60E-01	7.10E-01	LOC91149	hypothetical protein LOC91149	chr2q31.1	1563528_at	---																				
3.32	3.17	0.15	3.60E-01	7.10E-01	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	chr17q11.2	208776_at	NM_002815																				
2.59	2.44	0.14	3.60E-01	7.10E-01	TMEM16D	Transmembrane protein 16D	chr12q23.1-q23.2	239883_s_at	NM_178826																				
8.72	8.52	0.20	3.60E-01	7.10E-01	STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	chr20q13.1	208948_s_at	NM_001037328 /// NM_004602 /// NM_017452 /// NM_017453 /// NM_017454																				
2.29	2.15	0.14	3.61E-01	7.10E-01	SSH2	slingshot homolog 2 (Drosophila)	chr17q11.2	1554114_s_at	NM_033389																				
2.33	2.22	0.11	3.61E-01	7.10E-01	---	---	---	1561258_at	---																				
2.29	2.18	0.11	3.61E-01	7.10E-01	ALB	albumin	chr4q11-q13	214837_at	NM_000477																				
8.00	7.70	0.30	3.61E-01	7.10E-01	TOR1AIP1	torsin A interacting protein 1	chr1q24.2	212408_at	NM_015602																				
3.02	2.85	0.16	3.61E-01	7.10E-01	---	---	---	242740_at	---																				
3.02	2.89	0.13	3.61E-01	7.10E-01	---	---	---	1564421_at	---																				
6.35	6.15	0.19	3.61E-01	7.10E-01	LOC100130886 /// TMEM164	hypothetical protein LOC100130886 /// transmembrane protein 164	chrXq22.3	220486_x_at	NM_032227 /// XM_001714477																				
4.64	4.46	0.19	3.61E-01	7.10E-01	HOMER3	homer homolog 3 (Drosophila)	chr19p13.11	222222_s_at	NM_004838																				
3.25	3.08	0.17	3.61E-01	7.10E-01	ITIH4	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	chr3p21-p14	37201_at	NM_002218																				
8.10	7.62	0.47	3.61E-01	7.10E-01	NQO1	NAD(P)H dehydrogenase, quinone 1	chr16q22.1	210519_s_at	NM_000903 /// NM_001025433 /// NM_001025434																				
8.10	7.94	0.16	3.61E-01	7.10E-01	CARS	cysteinyl-tRNA synthetase	chr11p15.5	212971_at	NM_001014437 /// NM_001014438 /// NM_001751 /// NM_139273																				
3.91	3.76	0.15	3.61E-01	7.10E-01	---	---	---	233570_at	---																				
2.36	2.20	0.16	3.61E-01	7.10E-01	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	chr6p22-p21	226933_s_at	NM_001546																				
7.45	7.19	0.26	3.61E-01	7.10E-01	CLTB	clathrin, light chain (Lcb)	chr4q2-q3|5q35	211043_s_at	NM_001834 /// NM_007097																				
3.46	3.29	0.17	3.61E-01	7.10E-01	---	---	---	239276_at	---																				
6.03	5.86	0.17	3.61E-01	7.10E-01	C1orf144	chromosome 1 open reading frame 144	chr1p36.13	212002_at	NM_001114600 /// NM_015609																				
5.59	5.37	0.22	3.61E-01	7.10E-01	ISY1 /// RAB43	ISY1 splicing factor homolog (S. cerevisiae) /// RAB43, member RAS oncogene family	chr3q21.3	225632_s_at	NM_020701 /// NM_198490																				
6.04	5.85	0.19	3.61E-01	7.10E-01	AMOTL1	angiomotin like 1	chr11q14.3	225450_at	NM_130847																				

3.97	3.71	0.26	3.61E-01	7.10E-01	LOC100128501	hypothetical protein LOC100128501	chr9q34.11	229296_at	XM_001721187 /// XM_001721927 /// XM_001726452
2.84	2.71	0.13	3.61E-01	7.10E-01	HOXB6	homeobox B6	chr17q21.3	205365_at	NM_018952
2.85	2.70	0.15	3.61E-01	7.10E-01	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	chr2q31	206670_s_at	NM_000817 /// NM_013445
4.04	3.82	0.21	3.61E-01	7.10E-01	UCKL1	Uridine-cytidine kinase 1-like 1	chr20q13.33	232727_at	NM_017859
5.66	5.45	0.21	3.61E-01	7.10E-01	TREX2 /// UCHL5IP	three prime repair exonuclease 2 /// UCHL5 interacting protein	chrXq28	213334_x_at	NM_017518 /// NM_080701 /// NM_207107
2.82	2.52	0.30	3.61E-01	7.10E-01	---	---	---	244271_at	---
6.14	6.00	0.14	3.61E-01	7.10E-01	FCHSD2	FCH and double SH3 domains 2	chr11q13.4	203620_s_at	NM_014824
2.35	2.16	0.20	3.61E-01	7.10E-01	---	---	---	227985_at	---
5.69	5.42	0.27	3.61E-01	7.10E-01	TRIM13	tripartite motif-containing 13	chr13q14	203659_s_at	NM_001007278 /// NM_005798 /// NM_052811 /// NM_213590
4.78	4.59	0.19	3.61E-01	7.10E-01	AKAP8L	A kinase (PRKA) anchor protein 8-like	chr19p13.12	222160_at	NM_014371
5.29	5.08	0.21	3.61E-01	7.10E-01	HIF1AN	hypoxia-inducible factor 1, alpha subunit inhibitor	chr10q24	226648_at	NM_017902
4.45	3.83	0.63	3.61E-01	7.10E-01	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	chr5q12.1	227180_at	NM_001104558 /// NM_024930
4.08	3.88	0.21	3.61E-01	7.10E-01	UBE2C	ubiquitin-conjugating enzyme E2C	chr20q13.12	202954_at	NM_007019 /// NM_181799 /// NM_181800 /// NM_181801 /// NM_181802 /// NM_181803
2.08	1.96	0.12	3.62E-01	7.10E-01	TMEM135	transmembrane protein 135	chr11q14.2	1554866_at	NM_022918
2.43	2.30	0.12	3.62E-01	7.10E-01	---	---	---	1561608_at	---
4.03	3.84	0.19	3.62E-01	7.10E-01	MYEF2	myelin expression factor 2	chr15q21.1	229464_at	NM_016132
3.55	3.19	0.37	3.62E-01	7.11E-01	LOC348751	hypothetical protein LOC348751	chr2q33.1	1556667_at	XM_001716816 /// XM_929974 /// XM_936759
2.12	2.02	0.10	3.62E-01	7.11E-01	RFX3	regulatory factor X, 3 (influences HLA class II expression)	chr9p24.2	238810_at	NM_002919 /// NM_134428
3.61	3.47	0.14	3.62E-01	7.11E-01	PDZRN3	PDZ domain containing ring finger 3	chr3p13	1555587_at	NM_015009
2.65	2.50	0.15	3.62E-01	7.11E-01	LNPEP	leucyl/cystinyl aminopeptidase	chr5q15	236728_at	NM_005575 /// NM_175920
2.35	2.19	0.16	3.62E-01	7.11E-01	MUC20	mucin 20, cell surface associated	chr3q29	231941_s_at	NM_001098516 /// NM_152673 /// XM_001726694
2.92	2.81	0.12	3.62E-01	7.11E-01	---	---	---	1556690_s_at	---
2.23	2.12	0.11	3.62E-01	7.11E-01	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	chr5q22.2	238779_at	NM_152624
2.20	2.08	0.12	3.62E-01	7.11E-01	---	---	---	1566783_at	---
2.31	2.19	0.12	3.62E-01	7.11E-01	---	---	---	243765_at	---
4.48	4.22	0.26	3.62E-01	7.11E-01	ZNF639	zinc finger protein 639	chr3q26.32	222624_s_at	NM_016331
5.64	5.22	0.42	3.62E-01	7.11E-01	VASN	vasorin	chr16p13.3	225867_at	NM_138440
7.46	7.25	0.21	3.62E-01	7.11E-01	NUDCD3	NudC domain containing 3	chr7p13-p12	201270_x_at	NM_015332
6.86	6.66	0.21	3.62E-01	7.11E-01	WWTR1	WW domain containing transcription regulator 1	chr3q23-q24	202133_at	NM_015472
5.63	5.47	0.17	3.63E-01	7.11E-01	---	---	---	1566177_at	---
8.38	7.96	0.43	3.63E-01	7.11E-01	MT1F	metallothionein 1F	chr16q13	213629_x_at	NM_005949
3.79	3.64	0.15	3.63E-01	7.11E-01	SRGAP2P1	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 1	chr1p11.2	1568957_x_at	---
2.55	2.39	0.16	3.63E-01	7.11E-01	---	---	---	242693_at	---
2.61	2.43	0.18	3.63E-01	7.11E-01	EIF1	eukaryotic translation initiation factor 1	chr17q21.2	212225_at	NM_005801

2.24	2.12	0.12	3.63E-01	7.11E-01	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	chr16p13.11	237354_at	NM_015027																				
5.81	5.62	0.19	3.63E-01	7.11E-01	COX11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	chr17q22	203551_s_at	NM_004375																				
5.51	5.15	0.36	3.63E-01	7.11E-01	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	chr20p13	211572_s_at	NM_005116 /// NM_203327																				
3.86	3.64	0.22	3.63E-01	7.12E-01	---	---	---	1556322_a_at	---																				
11.37	11.21	0.16	3.63E-01	7.12E-01	RPL10A	ribosomal protein L10a	chr6p21.3-p21.2	200036_s_at	NM_007104																				
3.15	2.99	0.15	3.63E-01	7.12E-01	PLEKHG4B	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	chr5p15.33	230441_at	NM_052909																				
3.88	3.71	0.17	3.63E-01	7.12E-01	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	chr9q22.33	235903_at	NM_173551																				
3.41	3.23	0.19	3.63E-01	7.12E-01	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	chr6q27	230622_at	NM_001040000 /// NM_001040001 /// NM_005936																				
2.45	2.24	0.21	3.63E-01	7.12E-01	---	---	---	240994_at	---																				
2.82	2.64	0.19	3.63E-01	7.12E-01	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	chr10q24	228585_at	NM_001098175 /// NM_001776																				
5.52	5.02	0.49	3.63E-01	7.12E-01	NR2C1	nuclear receptor subfamily 2, group C, member 1	chr12q22	204791_at	NM_001032287 /// NM_001127362 /// NM_003297																				
2.83	2.59	0.23	3.63E-01	7.12E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	1566507_a_at	NM_012347 /// NM_033480 /// NM_033481																				
3.36	3.16	0.19	3.63E-01	7.12E-01	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger), member 7	chrXp11.3-p11.23|Xp11.3	1552671_a_at	NM_032591																				
4.85	4.62	0.22	3.63E-01	7.12E-01	GLMN	glomulin, FKBP associated protein	chr1p22.1	207153_s_at	NM_053274																				
2.18	2.05	0.13	3.64E-01	7.12E-01	---	---	---	1554951_at	---																				
6.50	6.05	0.45	3.64E-01	7.12E-01	EPB41L2	erythrocyte membrane protein band 4.1-like 2	chr6q23	201718_s_at	NM_001431																				
2.05	1.93	0.12	3.64E-01	7.12E-01	C4orf10	chromosome 4 open reading frame 10	chr4p16.3	214685_at	NR_015453																				
2.28	2.16	0.12	3.64E-01	7.12E-01	MGC2848	hypothetical protein MGC2848	chr3q22.1	1553935_at	---																				
3.13	2.96	0.17	3.64E-01	7.12E-01	WIPF1	WAS/WASL interacting protein family, member 1	chr2q31.1	231182_at	NM_001077269 /// NM_003387																				
2.45	2.31	0.14	3.64E-01	7.12E-01	---	---	---	1556520_at	---																				
8.89	8.76	0.13	3.64E-01	7.12E-01	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	chr9q12	214864_s_at	NM_012203																				
2.39	2.25	0.14	3.64E-01	7.12E-01	DDX43	DEAD (Asp-Glu-Ala-Asp) box polypeptide 43	chr6q12-q13	220004_at	NM_018665																				
3.81	3.62	0.19	3.64E-01	7.12E-01	MPRIP	Myosin phosphatase Rho interacting protein	chr17p11.2	233278_at	NM_015134 /// NM_201274																				
5.17	4.95	0.23	3.64E-01	7.12E-01	ZNF776	zinc finger protein 776	chr19q13.43	228652_at	NM_173632																				
2.86	2.67	0.19	3.64E-01	7.12E-01	PHC3	polyhomeotic homolog 3 (Drosophila)	chr3q26.2	1552644_a_at	NM_024947																				
4.81	4.51	0.30	3.64E-01	7.12E-01	BCL2L11	BCL2-like 11 (apoptosis facilitator)	chr2q13	1555372_at	NM_006538 /// NM_138621 /// NM_207002																				
9.94	9.81	0.13	3.64E-01	7.12E-01	SNX3	sorting nexin 3	chr6q21	208781_x_at	NM_003795																				
3.63	3.50	0.13	3.64E-01	7.12E-01	ZNF409	zinc finger protein 409	chr14q11.2	207699_at	XM_375065 /// XM_941446																				
3.21	3.00	0.21	3.64E-01	7.12E-01	LOC644656	Hypothetical protein LOC644656	chr11p15.4	229870_at	XM_927762																				
2.11	1.98	0.13	3.64E-01	7.13E-01	DSEL	dermatan sulfate epimerase-like	chr18q22.1	244852_at	NM_032160																				
2.33	2.20	0.13	3.64E-01	7.13E-01	C19orf69	Chromosome 19 open reading frame 69	---	231632_at	NM_001130514																				
10.25	10.09	0.16	3.64E-01	7.13E-01	COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	chr11q12-q13	201119_s_at	NM_004074																				
6.89	6.50	0.38	3.65E-01	7.13E-01	GADD45A	growth arrest and DNA-damage-inducible, alpha	chr1p31.2-p31.1	203725_at	NM_001924																				
7.67	7.47	0.21	3.65E-01	7.13E-01	MRCL3	myosin regulatory light chain MRCL3	chr18p11.31	201319_at	NM_006471																				
2.48	2.34	0.13	3.65E-01	7.13E-01	---	---	---	237244_at	---																				
6.16	5.81	0.36	3.65E-01	7.13E-01	UBA2	ubiquitin-like modifier activating enzyme 2	chr19q12	201177_s_at	NM_005499																				
4.03	3.76	0.27	3.65E-01	7.13E-01	ODF2	outer dense fiber of sperm tails 2	chr9q34.11	225617_at	NM_002540 /// NM_153437																				
7.42	7.22	0.20	3.65E-01	7.13E-01	SKAP2	src kinase associated phosphoprotein 2	chr7p21-p15	225639_at	NM_003930																				
6.32	6.01	0.31	3.65E-01	7.13E-01	RNF41	ring finger protein 41	chr12q13.2	201961_s_at	NM_005785 /// NM_194358 /// NM_194359																				

9.53	9.03	0.50	3.65E-01	7.13E-01	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	chr11p15.5	213348_at	NM_000076 /// NM_001122630 /// NM_001122631																			
6.52	6.34	0.18	3.65E-01	7.13E-01	KIF1C	kinesin family member 1C	chr17p13.2	209244_s_at	NM_006612																			
2.85	2.67	0.18	3.65E-01	7.13E-01	HERC2	hect domain and RLD 2	chr15q13	222461_s_at	NM_004667																			
6.18	5.91	0.27	3.65E-01	7.13E-01	MGC21881	hypothetical locus MGC21881	chr9q21.11	228040_at	NR_015363 /// XR_041522 /// XR_041523																			
2.35	2.22	0.13	3.65E-01	7.13E-01	KRTAP9-4	keratin associated protein 9-4	chr17q12-q21	233640_x_at	NM_033191																			
2.77	2.66	0.11	3.65E-01	7.13E-01	JAK1	Janus kinase 1 (a protein tyrosine kinase)	chr1p32.3-p31.3	1562103_at	NM_002227																			
5.38	5.15	0.23	3.65E-01	7.13E-01	SAFB	scaffold attachment factor B	chr19p13.3-p13.2	201747_s_at	NM_002967																			
7.32	7.12	0.21	3.65E-01	7.13E-01	ZNF212	zinc finger protein 212	chr7q36.1	203985_at	NM_012256																			
8.55	8.35	0.20	3.65E-01	7.13E-01	ARPC4 /// TTLL3	actin related protein 2/3 complex, subunit 4, 20kDa /// tubulin tyrosine ligase-like family, member 3	chr3p25.3	217817_at	NM_001024959 /// NM_001024960 /// NM_001025930 /// NM_005718 /// NM_015644																			
8.56	8.39	0.17	3.65E-01	7.13E-01	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	chr12q24.11	208736_at	NM_005719																			
3.41	2.90	0.50	3.65E-01	7.13E-01	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	chr14q32.2	219528_s_at	NM_022898 /// NM_138576																			
9.06	8.87	0.20	3.65E-01	7.13E-01	CLIC1	chloride intracellular channel 1	chr6p22.1-p21.2	208659_at	NM_001288																			
1.95	1.83	0.12	3.65E-01	7.13E-01	GPR113	G protein-coupled receptor 113	chr2p23.3	236608_at	NM_153835																			
4.16	3.90	0.27	3.65E-01	7.13E-01	LOC100129899	hypothetical protein LOC100129899	chr16p11.2	238771_at	XM_001714827 /// XM_001715004 /// XM_001717825																			
4.17	3.94	0.23	3.65E-01	7.13E-01	SH3RF2	SH3 domain containing ring finger 2	chr5q32	228892_at	NM_152550																			
6.79	6.58	0.20	3.66E-01	7.13E-01	RBM8A	RNA binding motif protein 8A	chr1q12	213852_at	NM_005105																			
4.78	4.55	0.23	3.66E-01	7.13E-01	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	chr7p22	222786_at	NM_018641																			
3.16	2.98	0.18	3.66E-01	7.13E-01	---	---	---	1563131_at	---																			
6.00	5.55	0.44	3.66E-01	7.14E-01	PTGR1	prostaglandin reductase 1	chr9q31.3	228825_at	NM_012212																			
8.16	8.00	0.16	3.66E-01	7.14E-01	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	chr1p36.1-p35	202772_at	NM_000191																			
3.01	2.88	0.13	3.66E-01	7.14E-01	TKT	transketolase	chr3p14.3	228205_at	NM_001064																			
2.23	2.13	0.11	3.66E-01	7.14E-01	---	---	---	242607_at	---																			
3.68	3.43	0.25	3.66E-01	7.14E-01	PAPOLG	poly(A) polymerase gamma	chr2p16.1	222273_at	NM_022894																			
3.29	3.05	0.23	3.66E-01	7.14E-01	ADAM11	ADAM metallopeptidase domain 11	chr17q21.3	207880_at	NM_002390																			
4.58	4.19	0.39	3.66E-01	7.14E-01	CPNE1 /// RBM12	copine I /// RNA binding motif protein 12	chr20q11.21 /// chr20q11.22	212170_at	NM_003915 /// NM_006047 /// NM_152838 /// NM_152925 /// NM_152926 /// NM_152927 /// NM_152928 /// NM_152929 /// NM_152930 /// NM_152931																			
4.17	3.97	0.20	3.66E-01	7.14E-01	---	---	---	238827_at	---																			
2.28	2.16	0.13	3.66E-01	7.14E-01	IL15	interleukin 15	chr4q31	217371_s_at	NM_000585 /// NM_172174																			
2.40	2.28	0.12	3.67E-01	7.14E-01	---	---	---	214160_at	---																			
7.14	6.57	0.57	3.67E-01	7.14E-01	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	chr18p11.2	208568_at	NM_000529																			
1.95	1.84	0.11	3.67E-01	7.14E-01	---	---	---	216709_at	---																			
5.80	5.60	0.20	3.67E-01	7.14E-01	MMP14	matrix metallopeptidase 14 (membrane-inserted)	chr14q11-q12	160020_at	NM_004995																			

9.43	9.26	0.17	3.67E-01	7.14E-01	RNF187	ring finger protein 187	chr1q42.13	212155_at	XM_001129309 /// XM_001715919 /// XM_928029
2.99	2.54	0.45	3.67E-01	7.14E-01	DDX3Y /// LOC100130220	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked /// hypothetical protein LOC100130220	chrYq11	1570360_s_at	NM_001122665 /// NM_004660 /// XM_001713697
2.31	2.19	0.13	3.67E-01	7.14E-01	ADAD1	adenosine deaminase domain containing 1 (testis-specific)	chr4q27	231448_at	NM_139243
5.77	5.56	0.21	3.67E-01	7.14E-01	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	chrXp11.21	204408_at	NM_014481
4.17	4.02	0.15	3.67E-01	7.14E-01	---	---	---	1561871_at	---
2.54	2.39	0.15	3.67E-01	7.14E-01	LOC170425	hypothetical protein LOC170425	chr10q23.1	1563821_at	---
7.57	7.04	0.53	3.67E-01	7.14E-01	HSPB6	heat shock protein, alpha-crystallin-related, B6	chr19q13.12	214767_s_at	NM_144617
3.27	3.10	0.17	3.67E-01	7.14E-01	REM2	RAS (RAD and GEM)-like GTP binding 2	chr14q11.2	235699_at	NM_173527
2.11	1.99	0.12	3.67E-01	7.14E-01	EIF5B	Eukaryotic translation initiation factor 5B	chr2q11.2	214313_s_at	NM_015904
3.40	3.21	0.19	3.67E-01	7.14E-01	FLJ31813	hypothetical protein FLJ31813	chr10q11.22	239051_at	XM_942128
4.94	4.64	0.30	3.67E-01	7.14E-01	---	---	---	232218_at	---
2.35	2.23	0.12	3.67E-01	7.15E-01	---	---	---	231037_at	---
5.47	5.33	0.14	3.67E-01	7.15E-01	SH2D4A	SH2 domain containing 4A	chr8p21.2	219749_at	NM_022071
3.91	3.47	0.43	3.67E-01	7.15E-01	FZD7	frizzled homolog 7 (Drosophila)	chr2q33	203705_s_at	NM_003507
6.63	6.37	0.26	3.67E-01	7.15E-01	DNM2	dynamin 2	chr19p13.2	202253_s_at	NM_001005360 /// NM_001005361 /// NM_001005362 /// NM_004945
3.42	3.28	0.14	3.67E-01	7.15E-01	TCOF1	Treacher Collins-Franceschetti syndrome 1	chr5q32-q33.1	244686_at	NM_000356 /// NM_001008656 /// NM_001008657
2.41	2.28	0.12	3.67E-01	7.15E-01	---	---	---	1560464_at	---
4.92	4.64	0.27	3.67E-01	7.15E-01	STIM2	stromal interaction molecule 2	chr4p15.2	234140_s_at	NM_020860
2.51	2.38	0.13	3.67E-01	7.15E-01	---	---	---	220857_at	---
3.56	3.35	0.21	3.68E-01	7.15E-01	NLRP1	NLR family, pyrin domain containing 1	chr17p13.2	210113_s_at	NM_001033053 /// NM_014922 /// NM_033004 /// NM_033006 /// NM_033007
5.78	5.40	0.38	3.68E-01	7.15E-01	AADACL1	arylacetamide deacetylase-like 1	chr3q26.31	225847_at	NM_020792
3.46	3.28	0.18	3.68E-01	7.15E-01	---	---	---	234797_at	---
5.35	4.99	0.36	3.68E-01	7.15E-01	KTELC1	KTEL (Lys-Tyr-Glu-Leu) containing 1	chr3q13.33	222681_at	NM_020231 /// NM_152305
3.09	2.87	0.22	3.68E-01	7.15E-01	NDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	chr16p13.11	230219_at	NM_017668
3.70	3.49	0.20	3.68E-01	7.15E-01	LOC149134	hypothetical LOC149134	chr1q44	230541_at	XR_040996 /// XR_040997 /// XR_040998
3.37	3.17	0.19	3.68E-01	7.15E-01	C9orf45	chromosome 9 open reading frame 45	chr9q33.2	223522_at	XR_017862 /// XR_017965 /// XR_040211
5.86	5.63	0.22	3.68E-01	7.15E-01	INTS5	integrator complex subunit 5	chr11q12.3	221818_at	NM_030628
2.37	2.21	0.17	3.68E-01	7.15E-01	ALG10B	asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	chr12q12	242900_at	NM_001013620
2.38	2.24	0.14	3.68E-01	7.15E-01	RNF165	ring finger protein 165	chr18q21.1	230143_at	NM_152470
12.26	12.11	0.15	3.68E-01	7.15E-01	RPL12	ribosomal protein L12	chr9q34	200088_x_at	NM_000976
3.84	3.67	0.17	3.68E-01	7.15E-01	CCDC85A	Coiled-coil domain containing 85A	chr2p16.1	243382_at	NM_001080433
3.50	3.12	0.38	3.68E-01	7.15E-01	LUZP2	leucine zipper protein 2	chr11p14.3	215323_at	NM_001009909
7.30	6.99	0.31	3.68E-01	7.15E-01	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	chr1p34.2	57163_at	NM_022821
4.19	4.04	0.15	3.68E-01	7.15E-01	ASPHD1	aspartate beta-hydroxylase domain containing 1	chr16p11.2	214993_at	NM_181718
2.44	2.30	0.14	3.68E-01	7.15E-01	LOC157381	hypothetical protein LOC157381	chr8q24.13	1562703_at	---

3.32	3.15	0.17	3.68E-01	7.15E-01	---	---	---	238228_at	---
3.66	3.53	0.13	3.68E-01	7.15E-01	ACN9	ACN9 homolog (S. cerevisiae)	chr7q21.3	218981_at	NM_020186
2.60	2.49	0.11	3.68E-01	7.15E-01	---	---	---	1561887_at	---
4.19	3.98	0.22	3.68E-01	7.15E-01	STX17	syntaxin 17	chr9q31.1	218666_s_at	NM_017919
4.59	4.36	0.23	3.68E-01	7.15E-01	---	---	---	239329_at	---
3.52	3.09	0.43	3.68E-01	7.15E-01	ANGEL2	angel homolog 2 (Drosophila)	chr1q32.3	221826_at	NM_144567
6.75	6.53	0.23	3.69E-01	7.16E-01	MED15	mediator complex subunit 15	chr22q11.2	222175_s_at	NM_001003891 /// NM_015889
7.19	6.90	0.29	3.69E-01	7.16E-01	POLDIP3	polymerase (DNA-directed), delta interacting protein 3	chr22q13.2	212100_s_at	NM_032311 /// NM_178136
8.66	8.43	0.23	3.69E-01	7.16E-01	ENO1	enolase 1, (alpha)	chr1p36.3-p36.2	217294_s_at	NM_001428
7.62	7.45	0.17	3.69E-01	7.16E-01	MRPS34	mitochondrial ribosomal protein S34	chr16p13.3	218112_at	NM_023936
2.63	2.49	0.14	3.69E-01	7.16E-01	WDR72	WD repeat domain 72	chr15q21.3	236741_at	NM_182758
2.12	1.98	0.14	3.69E-01	7.16E-01	CHD4	Chromodomain helicase DNA binding protein 4	chr12p13	1560419_at	NM_001273
4.31	4.15	0.15	3.69E-01	7.16E-01	---	---	---	234462_at	---
4.33	4.09	0.24	3.69E-01	7.16E-01	C9orf167	chromosome 9 open reading frame 167	chr9q34.3	219620_x_at	NM_017723
2.40	2.27	0.14	3.69E-01	7.16E-01	IQCA1	IQ motif containing with AAA domain 1	chr2q37.2-q37.3	1561485_at	NM_024726
2.06	1.91	0.15	3.69E-01	7.16E-01	KIAA1524	KIAA1524	chr3q13.13	1553810_a_at	NM_020890
3.50	3.16	0.34	3.69E-01	7.16E-01	STT3B	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	chr3p23	238303_at	NM_178862
4.51	4.31	0.20	3.69E-01	7.16E-01	RABEP1	Rabaptin, RAB GTPase binding effector protein 1	chr17p13.2	231002_s_at	NM_001083585 /// NM_004703
2.40	2.16	0.25	3.69E-01	7.16E-01	CAMK2D	Calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	chr4q26	231042_s_at	NM_001221 /// NM_172115 /// NM_172127 /// NM_172128
2.15	2.01	0.14	3.69E-01	7.16E-01	---	---	---	217375_at	---
5.09	4.93	0.15	3.69E-01	7.16E-01	ZNF160	zinc finger protein 160	chr19q13.41	224014_at	NM_001102603 /// NM_033288 /// NM_198893
3.39	3.15	0.25	3.69E-01	7.16E-01	C15orf49	chromosome 15 open reading frame 49	chr15q11.2	221001_at	XR_040061 /// XR_040062
2.19	2.09	0.10	3.69E-01	7.16E-01	---	---	---	235230_at	---
2.85	2.62	0.23	3.69E-01	7.16E-01	UTX	ubiquitously transcribed tetratricopeptide repeat, X chromosome	chrXp11.2	203991_s_at	NM_021140
4.35	4.23	0.13	3.69E-01	7.16E-01	FTCD	formiminotransferase cyclodeaminase	chr21q22.3	224300_x_at	NM_006657 /// NM_206965
2.76	2.59	0.17	3.69E-01	7.16E-01	---	---	---	1562474_at	---
4.14	3.98	0.16	3.69E-01	7.16E-01	CDRT4	CMT1A duplicated region transcript 4	chr17p12	244698_at	NM_173622
6.01	5.83	0.17	3.69E-01	7.16E-01	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	chr17q25.3	204970_s_at	NM_002359 /// NM_032711
2.61	2.51	0.10	3.69E-01	7.16E-01	DNAH1	Dynein, axonemal, heavy chain 1	chr3p21.1	242591_at	NM_015512
7.46	7.33	0.13	3.70E-01	7.16E-01	ACAA1	acetyl-Coenzyme A acyltransferase 1	chr3p23-p22	202025_x_at	NM_001130410 /// NM_001607 /// NR_024024
3.73	3.54	0.19	3.70E-01	7.16E-01	---	---	---	230240_at	---
3.06	2.90	0.17	3.70E-01	7.16E-01	SDK1	sidekick homolog 1, cell adhesion molecule (chicken)	chr7p22.2	229407_at	NM_001079653 /// NM_152744
2.83	2.67	0.16	3.70E-01	7.16E-01	---	---	---	1569760_at	---
3.58	3.44	0.14	3.70E-01	7.16E-01	NKPD1	NTPase, KAP family P-loop domain containing 1	chr19q13.32	1560430_at	NM_001131067 /// NM_198478
2.60	2.46	0.13	3.70E-01	7.16E-01	---	---	---	234384_at	---
12.75	12.65	0.10	3.70E-01	7.16E-01	RPL32	ribosomal protein L32	chr3p25-p24	200674_s_at	NM_000994 /// NM_001007073 /// NM_001007074
3.12	2.92	0.20	3.70E-01	7.16E-01	ZNF552	zinc finger protein 552	chr19q13.43	219741_x_at	NM_024762
6.73	6.47	0.26	3.70E-01	7.16E-01	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	chr18q11.2	202690_s_at	NM_006938

5.26	4.79	0.48	3.70E-01	7.16E-01	HLA-B /// HLA-C /// MICA /// XXbac-BPG181B23.1	major histocompatibility complex, class I, B /// major histocompatibility complex, class I, C /// MHC class I polypeptide-related sequence A /// MHC class I polypeptide-related sequence A	chr6p21.3 /// chr6p21.33	205904_at	NM_000247 /// NM_002117 /// NM_005514 /// XM_001713607 /// XM_001715881 /// XM_001717045 /// XM_001719879																					
7.21	6.93	0.29	3.70E-01	7.16E-01	DUSP23	dual specificity phosphatase 23	chr1q23.2	223402_at	NM_017823																				
6.80	6.56	0.24	3.70E-01	7.16E-01	TSTA3	tissue specific transplantation antigen P35B	chr8q24.3	36936_at	NM_003313																				
7.77	7.56	0.21	3.70E-01	7.16E-01	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	chr6p21.3	213540_at	NM_014234																				
7.71	7.37	0.34	3.70E-01	7.16E-01	TMEM41A	transmembrane protein 41A	chr3q27.2	235037_at	NM_080652																				
6.49	6.29	0.20	3.70E-01	7.16E-01	SEMA3F	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	chr3p21.3	35666_at	NM_004186																				
2.64	2.54	0.10	3.70E-01	7.17E-01	ZNF3	zinc finger protein 3	chr7q22.1	232497_at	NM_017715 /// NM_032924																				
10.18	10.08	0.10	3.70E-01	7.17E-01	CCNI	Cyclin I	chr4q21.1	208655_at	NM_006835																				
3.21	3.05	0.17	3.70E-01	7.17E-01	HRC	histidine rich calcium binding protein	chr19q13.3	207066_at	NM_002152																				
2.42	2.30	0.11	3.71E-01	7.17E-01	PDILT	protein disulfide isomerase-like protein of the testis	chr16p12.3	1554970_at	NM_174924																				
2.63	2.49	0.14	3.71E-01	7.17E-01	---	---	---	1556972_at	---																				
6.25	5.96	0.29	3.71E-01	7.17E-01	KIAA0528	KIAA0528	chr12p12.1	212943_at	NM_014802																				
3.27	2.97	0.30	3.71E-01	7.17E-01	FBXL4	F-box and leucine-rich repeat protein 4	chr6q16.1-q16.3	235450_at	NM_012160																				
6.11	5.89	0.22	3.71E-01	7.17E-01	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)	chr19q13.11	222099_s_at	NM_001114093 /// NM_015578																				
5.62	5.27	0.34	3.71E-01	7.17E-01	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	chr1p21	203566_s_at	NM_000028 /// NM_000642 /// NM_000643 /// NM_000644 /// NM_000645 /// NM_000646																				
2.78	2.67	0.10	3.71E-01	7.17E-01	PLAC8L1	PLAC8-like 1	chr5q32	237783_at	NM_001029869																				
4.76	4.61	0.15	3.71E-01	7.17E-01	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	chr19p13.11	221056_x_at	NM_021235																				
6.11	5.87	0.24	3.71E-01	7.17E-01	BBS1 /// DPP3	Bardet-Biedl syndrome 1 /// dipeptidyl-peptidase 3	chr11q12-q13.1 /// chr11q13.1	218567_x_at	NM_005700 /// NM_024649 /// NM_130443																				
3.86	3.69	0.18	3.71E-01	7.17E-01	CDKL3	cyclin-dependent kinase-like 3	chr5q31	236017_at	NM_001113575 /// NM_016508																				
2.60	2.47	0.12	3.71E-01	7.17E-01	TREML4	triggering receptor expressed on myeloid cells-like 4	chr6p21.1	1564052_at	NM_198153																				
4.92	4.70	0.21	3.71E-01	7.17E-01	TRIM4	tripartite motif-containing 4	chr7q22-q31.1	224159_x_at	NM_033017 /// NM_033091																				
6.75	6.55	0.20	3.71E-01	7.17E-01	ATP6V0E2	ATPase, H+ transporting V0 subunit e2	chr7q36.1	213587_s_at	NM_001100592 /// NM_145230																				
2.71	2.55	0.16	3.71E-01	7.17E-01	C8orf77	chromosome 8 open reading frame 77	chr8q24.3	1558790_s_at	XR_041327 /// XR_041328																				
5.28	5.06	0.23	3.71E-01	7.17E-01	FOXRED2	FAD-dependent oxidoreductase domain containing 2	chr22q12.3	231846_at	NM_001102371 /// NM_024955																				
2.47	2.34	0.13	3.71E-01	7.17E-01	OTUD4	OTU domain containing 4	chr4q31.21	238848_at	NM_001102653 /// NM_017493 /// NM_199324																				
2.55	2.38	0.18	3.71E-01	7.17E-01	---	---	---	215900_at	---																				
4.44	4.29	0.15	3.71E-01	7.17E-01	ARHGAP19	Rho GTPase activating protein 19	chr10q24.1	212738_at	NM_032900																				
4.21	3.96	0.25	3.71E-01	7.17E-01	MXD1	MAX dimerization protein 1	chr2p13-p12	226275_at	NM_002357																				

2.65	2.49	0.16	3.71E-01	7.17E-01	---	---	---	237315_at	---
3.26	3.10	0.15	3.72E-01	7.18E-01	GFI1B	growth factor independent 1B transcription repressor	chr9q34.13	237403_at	NM_004188
5.93	5.70	0.23	3.72E-01	7.18E-01	GIMAP6	GTPase, IMAP family member 6	---	219777_at	NM_001007224 /// NM_024711 /// NR_024115
3.29	3.17	0.11	3.72E-01	7.18E-01	PPP1R3F	Protein phosphatase 1, regulatory (inhibitor) subunit 3F	chrXp11.23	231197_at	NM_033215
2.66	2.45	0.21	3.72E-01	7.18E-01	MFSD8	Major facilitator superfamily domain containing 8	chr4q28.1-q28.2	243407_at	NM_152778
2.11	2.01	0.11	3.72E-01	7.18E-01	---	---	---	230883_at	---
6.32	6.04	0.28	3.72E-01	7.18E-01	NUP54	nucleoporin 54kDa	chr4q21.1	218256_s_at	NM_017426
6.71	6.44	0.26	3.72E-01	7.18E-01	PDXP	pyridoxal (pyridoxine, vitamin B6) phosphatase	chr22cen-q12.3	223290_at	NM_020315
6.99	6.70	0.29	3.72E-01	7.18E-01	COTL1	coactosin-like 1 (Dictyostelium)	chr16q24.1	221059_s_at	NM_021149
4.78	4.46	0.33	3.72E-01	7.18E-01	RBM15	RNA binding motif protein 15	chr1p13	1555762_s_at	NM_022768
6.67	6.46	0.21	3.72E-01	7.18E-01	MCM3	minichromosome maintenance complex component 3	chr6p12	201555_at	NM_002388
2.30	2.15	0.15	3.72E-01	7.18E-01	---	---	---	1564078_at	---
2.24	2.10	0.13	3.72E-01	7.18E-01	---	---	---	1564632_at	---
4.64	4.50	0.13	3.72E-01	7.18E-01	LOC285014	hypothetical protein LOC285014	chr2q11.2	235418_at	---
10.05	9.65	0.39	3.72E-01	7.18E-01	IGFBP7	insulin-like growth factor binding protein 7	chr4q12	201163_s_at	NM_001553
5.46	5.26	0.20	3.72E-01	7.18E-01	GPX7	glutathione peroxidase 7	chr1p32	213170_at	NM_015696
3.12	2.89	0.24	3.72E-01	7.18E-01	NAGS	N-acetylglutamate synthase	chr17q21.31	229432_at	NM_153006
11.52	11.35	0.16	3.72E-01	7.18E-01	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	chr12p13	AFFX-HUMGAPDH/M33197_5_at	NM_002046
5.80	5.43	0.37	3.72E-01	7.18E-01	METAP2	methionyl aminopeptidase 2	chr12q22	227993_at	NM_006838
3.84	3.68	0.16	3.72E-01	7.18E-01	APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	chr19p13.3	205146_x_at	NM_004886
2.49	2.33	0.16	3.72E-01	7.18E-01	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	chr13q14	1554934_at	NM_018191
7.85	7.66	0.19	3.72E-01	7.18E-01	CHD4	chromodomain helicase DNA binding protein 4	chr12p13	201184_s_at	NM_001273
2.38	2.22	0.16	3.72E-01	7.18E-01	---	---	---	243846_x_at	---
2.61	2.48	0.12	3.72E-01	7.18E-01	---	---	---	1557848_at	---
6.69	6.48	0.20	3.73E-01	7.18E-01	C19orf24	chromosome 19 open reading frame 24	chr19p13.3	221587_s_at	NM_017914
2.08	1.96	0.12	3.73E-01	7.18E-01	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	chr15q25.1	1554333_at	NM_001130182 /// NM_001130183 /// NM_018602
7.32	7.08	0.24	3.73E-01	7.18E-01	CBX6 /// NPTXR	chromobox homolog 6 /// neuronal pentraxin receptor	chr22q13.1	202048_s_at	NM_014292 /// NM_014293
2.47	2.32	0.15	3.73E-01	7.18E-01	FLJ30719	hypothetical protein FLJ30719	chr11q24.2	1553456_at	XR_041947 /// XR_041948 /// XR_041949
2.16	2.06	0.11	3.73E-01	7.18E-01	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	chr2q33.3-q34	214053_at	NM_001042599 /// NM_005235
1.85	1.76	0.09	3.73E-01	7.18E-01	---	---	---	233295_at	---
4.86	4.51	0.34	3.73E-01	7.18E-01	EML4	echinoderm microtubule associated protein like 4	chr2p22-p21	223069_s_at	NM_019063
7.43	7.25	0.19	3.73E-01	7.18E-01	CLN3	ceroid-lipofuscinosis, neuronal 3	chr16p12.1	209275_s_at	NM_000086 /// NM_001042432
2.31	2.20	0.12	3.73E-01	7.18E-01	C10orf47	chromosome 10 open reading frame 47	chr10p14	230051_at	NM_153256
3.22	3.00	0.22	3.73E-01	7.18E-01	ZNF341	zinc finger protein 341	chr20q11.22	1553532_a_at	NM_032819
4.47	4.12	0.34	3.73E-01	7.18E-01	TTC33	tetratricopeptide repeat domain 33	chr5p15.2-p12	219421_at	NM_012382
2.75	2.60	0.15	3.73E-01	7.19E-01	---	---	---	1569580_a_at	---
4.23	4.06	0.17	3.73E-01	7.19E-01	---	---	---	239670_at	---
2.71	2.57	0.14	3.73E-01	7.19E-01	MS4A8B	membrane-spanning 4-domains, subfamily A, member 8B	chr11q12.2	224355_s_at	NM_031457
5.77	5.61	0.16	3.73E-01	7.19E-01	RHBDD1	rhomboid domain containing 1	chr2q36.3	226945_at	NM_032276
3.70	3.47	0.24	3.73E-01	7.19E-01	FAM73A	family with sequence similarity 73, member A	chr1p31.1	235125_x_at	NM_198549
2.63	2.52	0.11	3.74E-01	7.19E-01	---	---	---	230768_at	---
4.46	4.27	0.19	3.74E-01	7.19E-01	PARVG	parvin, gamma	chr22q13.2-q13	233510_s_at	NM_022141
4.91	4.50	0.42	3.74E-01	7.19E-01	RANBP2	RAN binding protein 2	chr2q12.3	226922_at	NM_006267
5.09	4.86	0.22	3.74E-01	7.19E-01	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	chrXp11.4	227156_at	NM_001126054 /// NM_001126055 /// NM_003688
3.22	3.06	0.16	3.74E-01	7.19E-01	---	---	---	1556397_at	---
2.28	2.17	0.11	3.74E-01	7.19E-01	---	---	---	235843_at	---
3.05	2.89	0.17	3.74E-01	7.19E-01	MDS2	myelodysplastic syndrome 2 translocation associated	chr1p36	1562731_s_at	---

4.22	3.90	0.32	3.74E-01	7.19E-01	IRF7	interferon regulatory factor 7	chr11p15.5	208436_s_at	NM_001572 /// NM_004029 /// NM_004031
2.72	2.43	0.28	3.74E-01	7.19E-01	---	---	---	1562528_at	---
2.78	2.61	0.17	3.74E-01	7.19E-01	ZNF528	zinc finger protein 528	chr19q13	215019_x_at	NM_032423
1.97	1.86	0.11	3.74E-01	7.19E-01	TRIM55	tripartite motif-containing 55	chr8q13.1	236175_at	NM_033058 /// NM_184085 /// NM_184086 /// NM_184087
4.58	4.34	0.24	3.74E-01	7.19E-01	IL1RL1	Interleukin 1 receptor-like 1	chr2q12	242809_at	NM_003856 /// NM_016232
4.46	4.27	0.19	3.74E-01	7.19E-01	SLC4A11	solute carrier family 4, sodium borate transporter, member 11	chr20p12	233550_s_at	NM_032034
3.89	3.67	0.22	3.74E-01	7.19E-01	---	---	---	235053_at	---
2.31	2.17	0.14	3.74E-01	7.19E-01	---	---	---	239500_at	---
5.16	5.01	0.15	3.74E-01	7.19E-01	LOC284454	hypothetical protein LOC284454	chr19p13.13	235317_at	---
7.24	7.01	0.22	3.74E-01	7.19E-01	CTF8	chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	chr16q22.1	224732_at	NM_001039690 /// NM_001040144 /// NM_001040146
10.33	10.23	0.10	3.74E-01	7.19E-01	NDUFS5 /// RPL10	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) /// ribosomal protein L10	chr1p34.2-p33 /// chrXq28	201757_at	NM_004552 /// NM_006013
1.95	1.84	0.12	3.74E-01	7.19E-01	---	---	---	237433_at	---
2.44	2.34	0.10	3.74E-01	7.19E-01	---	---	---	1556271_at	---
5.09	4.60	0.49	3.74E-01	7.19E-01	41521	Septin 4	chr17q22-q23	233006_at	NM_004574 /// NM_080415 /// NM_080416
3.07	2.92	0.15	3.74E-01	7.19E-01	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	chr19p13.3	207111_at	NM_001974
4.19	3.82	0.36	3.75E-01	7.19E-01	FBXL4	F-box and leucine-rich repeat protein 4	chr6q16.1-q16.3	209943_at	NM_012160
3.93	3.74	0.19	3.75E-01	7.19E-01	CD68 /// EIF4A1	CD68 molecule /// eukaryotic translation initiation factor 4A, isoform 1	chr17p13	203507_at	NM_001040059 /// NM_001251 /// NM_001416
2.91	2.77	0.14	3.75E-01	7.19E-01	---	---	---	236036_at	---
4.38	4.16	0.22	3.75E-01	7.19E-01	SLC38A10	solute carrier family 38, member 10	chr17q25.3	230448_at	NM_001037984 /// NM_138570
3.09	2.94	0.15	3.75E-01	7.19E-01	SIRT2	Sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	chr19q13	1558331_at	NM_012237 /// NM_030593
5.36	5.00	0.36	3.75E-01	7.19E-01	---	---	---	227278_at	---
3.88	3.59	0.30	3.75E-01	7.19E-01	RNFT1	ring finger protein, transmembrane 1	chr17q23.1	227268_at	NM_016125
4.02	3.80	0.22	3.75E-01	7.19E-01	DIXDC1	DIX domain containing 1	chr11q23.1	1558342_x_at	NM_001037954 /// NM_033425
7.65	7.40	0.26	3.75E-01	7.19E-01	PGLS	6-phosphogluconolactonase	chr19p13.2	218387_s_at	NM_012088
3.02	2.84	0.19	3.75E-01	7.19E-01	SCRG1	scrapie responsive protein 1	chr4q31-q32	205475_at	NM_007281
2.24	2.04	0.19	3.75E-01	7.19E-01	LOC653602	hypothetical LOC653602	chr2p24.3	229546_at	XR_041664 /// XR_041665 /// XR_041666
4.99	4.75	0.24	3.75E-01	7.19E-01	RSPH10B2	radial spoke head 10 homolog B2 (Chlamydomonas)	chr7p22.1	1555272_at	NM_001099697
2.35	2.24	0.10	3.75E-01	7.19E-01	RARA	retinoic acid receptor, alpha	chr17q21	1565358_at	NM_000964 /// NM_001024809
4.01	3.85	0.16	3.75E-01	7.19E-01	---	---	---	238589_s_at	---
4.78	4.58	0.20	3.75E-01	7.19E-01	LOC285014	hypothetical protein LOC285014	chr2q11.2	235621_at	---
2.43	2.32	0.11	3.75E-01	7.19E-01	MS4A15	membrane-spanning 4-domains, subfamily A, member 15	chr11q12.2	1564194_a_at	NM_001098835 /// NM_152717
4.84	4.66	0.17	3.75E-01	7.19E-01	SBF1	SET binding factor 1	chr22q13.33	212393_at	NM_002972

2.38	2.27	0.11	3.76E-01	7.20E-01	FLJ35767	FLJ35767 protein	chr17q25.3	241367_at	NM_207459
4.40	4.05	0.35	3.76E-01	7.20E-01	LPCAT2	lysophosphatidylcholine acyltransferase 2	chr16q12.2	227889_at	NM_017839
2.73	2.58	0.15	3.76E-01	7.20E-01	RETNLB	resistin like beta	chr3q13.1	223969_s_at	NM_032579
2.79	2.65	0.14	3.76E-01	7.20E-01	LOC100130815	hypothetical protein LOC100130815	chr14q32.2	1564471_at	XM_001724166 /// XM_001724619 /// XM_001726375
6.31	5.97	0.33	3.76E-01	7.20E-01	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	chr1p	203379_at	NM_001006665 /// NM_002953
4.71	4.50	0.21	3.76E-01	7.20E-01	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	chr6p21.1	203927_at	NM_004556
3.40	3.21	0.19	3.76E-01	7.20E-01	---	---	---	235403_at	---
7.00	6.89	0.11	3.76E-01	7.20E-01	GIGYF2	GRB10 interacting GYF protein 2	chr2q37.1	212261_at	NM_001103146 /// NM_001103147 /// NM_001103148 /// NM_015575
7.47	7.19	0.28	3.76E-01	7.20E-01	PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	chrXq22.3	219485_s_at	NM_002814 /// NM_170750
2.51	2.41	0.10	3.76E-01	7.20E-01	SYTL1	synaptotagmin-like 1	chr1p36.11	227134_at	NM_032872
9.93	9.74	0.19	3.76E-01	7.20E-01	LASS2	LAG1 homolog, ceramide synthase 2	chr1q21.2	222212_s_at	NM_022075 /// NM_181746
6.83	6.68	0.15	3.76E-01	7.20E-01	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	chr21q22.3|21q22.2	201328_at	NM_005239
2.85	2.70	0.15	3.76E-01	7.20E-01	PEX26	peroxisomal biogenesis factor 26	chr22q11.21	235098_at	NM_001127649 /// NM_017929
2.52	2.38	0.14	3.76E-01	7.20E-01	---	---	---	1561896_at	---
3.42	2.94	0.48	3.76E-01	7.20E-01	RANBP2 /// RGPD1 /// RGPD2 /// RGPD3 /// RGPD4 /// RGPD5 /// RGPD6 /// RGPD7 /// RGPD8	RAN binding protein 2 /// RANBP2-like and GRIP domain containing 1 /// RANBP2-like and GRIP domain containing 2 /// RANBP2-like and GRIP domain containing 3 /// RANBP2-like and GRIP domain containing 4 /// RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 6 /// RANBP2-like and GRIP domain containing 7 /// RANBP2-like and GRIP domain containing 8	chr2p11.2 /// chr2q12.3 /// chr2q13	242712_x_at	NM_001024457 /// NM_001037866 /// NM_001078170 /// NM_001123363 /// NM_005054 /// NM_006267 /// NM_032260 /// XM_001133591 /// XM_001721299 /// XM_001722279 /// XM_929931
2.38	2.24	0.14	3.76E-01	7.20E-01	---	---	---	231449_at	---
2.51	2.38	0.13	3.76E-01	7.20E-01	---	---	---	241575_at	---
1.98	1.86	0.11	3.76E-01	7.20E-01	---	---	---	215441_at	---
5.81	5.65	0.15	3.76E-01	7.20E-01	---	---	---	228541_x_at	---
2.80	2.68	0.12	3.76E-01	7.20E-01	---	---	---	211435_at	---
3.24	3.08	0.16	3.77E-01	7.20E-01	RACGAP1	Rac GTPase activating protein 1	chr12q13.13	222077_s_at	NM_001126103 /// NM_001126104 /// NM_013277
2.15	2.05	0.11	3.77E-01	7.20E-01	---	---	---	240985_at	---
3.43	3.25	0.18	3.77E-01	7.20E-01	---	---	---	1563509_at	---
10.18	10.00	0.18	3.77E-01	7.20E-01	TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	chr17p13	209154_at	NM_014604
2.48	2.35	0.13	3.77E-01	7.20E-01	---	---	---	1566937_at	---
4.11	3.97	0.14	3.77E-01	7.20E-01	---	---	---	243022_at	---
3.97	3.80	0.17	3.77E-01	7.20E-01	CSPP1	centrosome and spindle pole associated protein 1	chr8q13.2	221925_s_at	NM_001077204 /// NM_024790
2.30	2.19	0.11	3.77E-01	7.20E-01	UBQLN3	ubiquilin 3	chr11p15	220422_at	NM_017481
2.23	2.12	0.10	3.77E-01	7.20E-01	OTC	ornithine carbamoyltransferase	chrXp21.1	207200_at	NM_000531
6.77	6.53	0.23	3.77E-01	7.20E-01	ZNF294	zinc finger protein 294	chr21q22.11	215596_s_at	NM_015565

1.99	1.89	0.10	3.77E-01	7.20E-01	---	---	---	1556461_at	---
1.96	1.87	0.09	3.77E-01	7.21E-01	---	---	---	241184_x_at	---
2.75	2.47	0.28	3.77E-01	7.21E-01	IGSF1	immunoglobulin superfamily, member 1	chrXq25	223807_at	NM_001555 /// NM_205833
3.66	3.52	0.14	3.77E-01	7.21E-01	EDA	ectodysplasin A	chrXq12-q13.1|Xq12	211130_x_at	NM_001005609 /// NM_001005610 /// NM_001005611 /// NM_001005612 /// NM_001005615 /// NM_001399
8.35	7.97	0.38	3.77E-01	7.21E-01	STARD10	StAR-related lipid transfer (START) domain containing 10	chr11q13	232322_x_at	NM_006645
1.97	1.88	0.09	3.77E-01	7.21E-01	GLYATL1	glycine-N-acyltransferase-like 1	chr11q12.1	1562089_at	NM_080661
3.06	2.74	0.32	3.77E-01	7.21E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	243487_at	NM_014423
4.46	4.28	0.18	3.77E-01	7.21E-01	EFCAB4A	EF-hand calcium binding domain 4A	chr11p15.5	227429_at	NM_173584
5.56	5.32	0.23	3.77E-01	7.21E-01	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	chr4q13.3	227119_at	NM_144571
4.99	4.82	0.18	3.78E-01	7.21E-01	CCDC24	coiled-coil domain containing 24	chr1p34.1	228994_at	NM_152499
2.81	2.67	0.14	3.78E-01	7.21E-01	TRIM46	tripartite motif-containing 46	chr1q22	220909_at	NM_025058
2.28	2.17	0.11	3.78E-01	7.21E-01	---	---	---	238919_at	---
3.12	2.94	0.18	3.78E-01	7.21E-01	IFNA1 /// IFNA13	interferon, alpha 1 /// interferon, alpha 13	chr9p22	208344_x_at	NM_006900 /// NM_024013
3.51	3.38	0.13	3.78E-01	7.21E-01	---	---	---	217580_x_at	---
3.64	3.46	0.18	3.78E-01	7.21E-01	---	---	---	1556645_s_at	---
2.49	2.37	0.12	3.78E-01	7.21E-01	FLJ33996 /// LOC100127971	hypothetical protein FLJ33996 /// hypothetical protein LOC100127971	chr12q13.13	244708_at	XM_001720872 /// XM_001720877 /// XM_001725504 /// XR_000901 /// XR_001317
3.11	2.93	0.18	3.78E-01	7.21E-01	TMEM84	transmembrane protein 84	chr15q23	240912_x_at	NM_173610
7.65	7.24	0.41	3.78E-01	7.21E-01	LY6E	lymphocyte antigen 6 complex, locus E	chr8q24.3	202145_at	NM_001127213 /// NM_002346
2.86	2.49	0.37	3.78E-01	7.22E-01	PGAP1	post-GPI attachment to proteins 1	chr2q33.1	244321_at	NM_024989
6.17	5.88	0.29	3.78E-01	7.22E-01	PYGO2	pygopus homolog 2 (Drosophila)	chr1q21.3	225370_at	NM_138300
5.24	5.06	0.18	3.78E-01	7.22E-01	HMGB3	high-mobility group box 3	chrXq28	225601_at	NM_005342
2.12	2.03	0.09	3.78E-01	7.22E-01	---	---	---	1569544_at	---
5.35	5.08	0.27	3.78E-01	7.22E-01	CEP120	centrosomal protein 120kDa	chr5q23.2	226449_at	NM_153223
7.67	7.25	0.42	3.78E-01	7.22E-01	MIRN21	microRNA 21	chr17q23.1	224917_at	---
1.99	1.85	0.14	3.79E-01	7.22E-01	LOC283922 /// PDPR	hypothetical protein LOC283922 /// pyruvate dehydrogenase phosphatase regulatory subunit	chr16q22.1 /// chr16q22.3	1558999_x_at	NM_017990 /// XR_037801 /// XR_040466 /// XR_040467
2.77	2.59	0.18	3.79E-01	7.22E-01	LOC728190	Hypothetical LOC728190	chr10q23.2	1558794_at	XR_040767
2.41	2.29	0.11	3.79E-01	7.22E-01	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	chr17p13.1	206717_at	NM_002472
2.80	2.65	0.14	3.79E-01	7.22E-01	---	---	---	244479_at	---
7.65	7.24	0.40	3.79E-01	7.22E-01	RREB1	Ras responsive element binding protein 1	chr6p25	228487_s_at	NM_001003698 /// NM_001003699 /// NM_002955
2.59	2.45	0.14	3.79E-01	7.22E-01	---	---	---	241197_at	---
6.37	6.16	0.21	3.79E-01	7.22E-01	UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative)	chr7p13	218837_s_at	NM_015983
9.41	9.20	0.21	3.79E-01	7.22E-01	HLA-E	major histocompatibility complex, class I, E	chr6p21.3	200905_x_at	NM_005516
2.84	2.72	0.12	3.79E-01	7.23E-01	TEX15	testis expressed 15	chr8p12	221448_s_at	NM_031271
6.20	5.92	0.28	3.79E-01	7.23E-01	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	chr3p14.1	214835_s_at	NM_003848
2.65	2.48	0.16	3.79E-01	7.23E-01	KIF4A	kinesin family member 4A	chrXq13.1	218355_at	NM_012310
7.47	7.20	0.26	3.79E-01	7.23E-01	RAB10	RAB10, member RAS oncogene family	chr2p23.3	222981_s_at	NM_016131
6.96	6.71	0.25	3.79E-01	7.23E-01	CUL5	cullin 5	chr11q22-q23	203531_at	NM_003478
2.06	1.97	0.10	3.79E-01	7.23E-01	---	---	---	231581_at	---
7.87	7.69	0.18	3.80E-01	7.23E-01	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	chr16p11.2	212064_x_at	NM_001042539 /// NM_002383

3.44	3.02	0.42	3.80E-01	7.23E-01	SEC31A	SEC31 homolog A (S. cerevisiae)	chr4q21.22	215009_s_at	NM_001077206 /// NM_001077207 /// NM_001077208 /// NM_014933 /// NM_016211
1.94	1.83	0.11	3.80E-01	7.23E-01	MCM3APAS	minichromosome maintenance complex component 3 associated protein antisense	chr21q22.3	1560542_at	NR_002776
2.16	2.06	0.10	3.80E-01	7.23E-01	LOC338809	hypothetical protein LOC338809	chr12q22	1556514_at	NM_001037671
2.16	2.05	0.11	3.80E-01	7.23E-01	PPP1R3A	protein phosphatase 1, regulatory (inhibitor) subunit 3A	chr7q31.1	206895_at	NM_002711
5.66	5.45	0.21	3.80E-01	7.23E-01	CD300LG	CD300 molecule-like family member g	chr17q21.31	1555656_at	NM_145273
6.35	6.11	0.25	3.80E-01	7.23E-01	GMEB2	glucocorticoid modulatory element binding protein 2	chr20q13.33	222251_s_at	NM_012384
2.11	2.01	0.10	3.80E-01	7.23E-01	---	---	---	1566047_at	---
2.34	2.23	0.11	3.80E-01	7.23E-01	LOC283482	hypothetical protein LOC283482	chr13q33.1	1561175_at	XM_001721848
2.82	2.61	0.21	3.80E-01	7.23E-01	FLT3	fms-related tyrosine kinase 3	chr13q12	206674_at	NM_004119
2.35	2.23	0.12	3.80E-01	7.23E-01	---	---	---	228833_s_at	---
3.11	2.96	0.15	3.80E-01	7.23E-01	PLD6	Phospholipase D family, member 6	chr17p11.2	244430_at	NM_178836
6.29	5.98	0.31	3.80E-01	7.23E-01	KIAA1539	KIAA1539	chr9p13.3	207765_s_at	NM_025182
5.28	5.07	0.21	3.80E-01	7.23E-01	MAPKAP1	mitogen-activated protein kinase associated protein 1	chr9q33.3	222426_at	NM_001006617 /// NM_001006618 /// NM_001006619 /// NM_001006620 /// NM_001006621 /// NM_024117
10.26	10.14	0.12	3.80E-01	7.23E-01	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	chr11q23.3	210453_x_at	NM_006476
7.71	7.49	0.22	3.81E-01	7.24E-01	RHOG	ras homolog gene family, member G (rho G)	chr11p15.5-p15.4	203175_at	NM_001665
3.60	2.92	0.67	3.81E-01	7.24E-01	AHRR /// PDCD6	aryl-hydrocarbon receptor repressor /// programmed cell death 6	chr5p15.3 /// chr5p15.33	229354_at	NM_013232 /// NM_020731 /// XM_001714855 /// XM_001720072 /// XM_001723249
4.95	4.76	0.20	3.81E-01	7.24E-01	PIGT	phosphatidylinositol glycan anchor biosynthesis, class T	chr20q12-q13.12	1568986_x_at	NM_015937
7.51	7.09	0.42	3.81E-01	7.24E-01	PTGFRN	prostaglandin F2 receptor negative regulator	chr1p13.1	224937_at	NM_020440
3.92	3.73	0.20	3.81E-01	7.24E-01	TRAF3	TNF receptor-associated factor 3	chr14q32.32	221571_at	NM_003300 /// NM_145725 /// NM_145726
2.15	2.05	0.10	3.81E-01	7.24E-01	---	---	---	1559310_at	---
4.41	4.17	0.24	3.81E-01	7.24E-01	ECE2	endothelin converting enzyme 2	chr3q27.1|.	227103_s_at	NM_001037324 /// NM_001100120 /// NM_001100121 /// NM_014693 /// NM_032331
2.69	2.45	0.24	3.81E-01	7.24E-01	LY75	lymphocyte antigen 75	chr2q24	205668_at	NM_002349
2.56	2.40	0.15	3.81E-01	7.24E-01	TTLL10	tubulin tyrosine ligase-like family, member 10	chr1p36.33	236418_at	NM_001130045 /// NM_153254
2.23	2.13	0.10	3.81E-01	7.24E-01	---	---	---	244184_at	---
5.07	4.79	0.28	3.81E-01	7.24E-01	STK38L	serine/threonine kinase 38 like	chr12p11.23	212572_at	NM_015000
2.57	2.46	0.10	3.81E-01	7.24E-01	---	---	---	231410_at	---
4.22	4.07	0.15	3.81E-01	7.24E-01	TRO	trophinin	chrXp11.22-p11.21	211700_s_at	NM_001039705 /// NM_016157 /// NM_177556

7.47	7.30	0.17	3.81E-01	7.24E-01	PCBP2	poly(rC) binding protein 2	chr12q13.12-q13.13	213263_s_at	NM_001098620 /// NM_001128911 /// NM_001128912 /// NM_001128913 /// NM_001128914 /// NM_005016 /// NM_031989																				
2.84	2.74	0.10	3.81E-01	7.24E-01	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	chr14q11.2	210164_at	NM_004131																				
4.90	4.58	0.33	3.81E-01	7.24E-01	EFCAB2	EF-hand calcium binding domain 2	chr1q44	233375_at	NM_032328																				
2.71	2.58	0.13	3.81E-01	7.24E-01	---	---	---	1556236_at	---																				
3.67	3.57	0.10	3.81E-01	7.24E-01	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	chr12q13	1563253_s_at	NM_001005915 /// NM_001982																				
4.78	4.62	0.16	3.81E-01	7.24E-01	STXBP2	syntaxin binding protein 2	chr19p13.3-p13.2	1570420_at	NM_001127396 /// NM_006949																				
3.52	3.30	0.22	3.81E-01	7.24E-01	CENPJ	centromere protein J	chr13q12.12	223513_at	NM_018451																				
2.59	2.45	0.14	3.81E-01	7.24E-01	---	---	---	1562691_at	---																				
2.48	2.28	0.21	3.82E-01	7.24E-01	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	chr11q14.3-q21	233815_at	NM_005467																				
2.97	2.81	0.16	3.82E-01	7.24E-01	MACROD1	MACRO domain containing 1	chr11q11	1559731_x_at	NM_014067																				
7.20	7.01	0.19	3.82E-01	7.24E-01	SLC35A4	solute carrier family 35, member A4	chr5q31.3	224626_at	NM_080670																				
2.70	2.54	0.16	3.82E-01	7.24E-01	---	---	---	236389_x_at	---																				
3.88	3.57	0.31	3.82E-01	7.24E-01	C15orf52	chromosome 15 open reading frame 52	chr15q15.1	227272_at	NM_207380																				
3.63	3.46	0.16	3.82E-01	7.24E-01	LOC388889	hypothetical LOC388889	chr22q12.1	232340_at	---																				
5.14	4.92	0.22	3.82E-01	7.24E-01	DENND3	DENN/MADD domain containing 3	chr8q24.3	212975_at	NM_014957																				
4.26	4.07	0.19	3.82E-01	7.24E-01	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	chr5q31	213591_at	NM_001182																				
3.04	2.86	0.18	3.82E-01	7.24E-01	SEC24D	SEC24 related gene family, member D (S. cerevisiae)	chr4q26	202375_at	NM_014822																				
6.76	6.50	0.26	3.82E-01	7.24E-01	H1FX	H1 histone family, member X	chr3q21.3	204805_s_at	NM_006026																				
2.09	2.00	0.09	3.82E-01	7.25E-01	FCAR	Fc fragment of IgA, receptor for	chr19q13.2-q13.4	207674_at	NM_002000 /// NM_133269 /// NM_133271 /// NM_133272 /// NM_133273 /// NM_133274 /// NM_133277 /// NM_133278 /// NM_133279																				
3.99	3.63	0.36	3.82E-01	7.25E-01	TLR4	toll-like receptor 4	chr9q32-q33	224341_x_at	NM_138554																				
4.61	4.38	0.23	3.82E-01	7.25E-01	DHDDS	dehydrodolichyl diphosphate synthase	chr1p36.11	224064_s_at	NM_024887 /// NM_205861																				
2.24	2.14	0.10	3.82E-01	7.25E-01	---	---	---	215408_at	---																				
2.38	2.24	0.14	3.82E-01	7.25E-01	SLCO6A1	solute carrier organic anion transporter family, member 6A1	chr5q21.1	1552745_at	NM_173488																				
3.83	3.71	0.12	3.83E-01	7.25E-01	---	---	---	208347_at	---																				
3.84	3.71	0.13	3.83E-01	7.25E-01	EDA2R	ectodysplasin A2 receptor	chrXq12	221399_at	NM_021783 /// XM_001715146																				
3.24	3.11	0.13	3.83E-01	7.25E-01	---	---	---	233715_at	---																				
3.80	3.64	0.16	3.83E-01	7.25E-01	---	---	---	224132_at	---																				
5.59	5.37	0.22	3.83E-01	7.25E-01	FAM175A	family with sequence similarity 175, member A	chr4q21.21-q21.23	226521_s_at	NM_139076																				
5.90	5.66	0.24	3.83E-01	7.25E-01	---	---	---	239238_at	---																				
5.53	5.26	0.27	3.83E-01	7.25E-01	FAM91A1	family with sequence similarity 91, member A1	chr8q24.13	226294_x_at	NM_144963																				
3.19	3.04	0.15	3.83E-01	7.25E-01	SMAD3	SMAD family member 3	chr15q22.33	205396_at	NM_005902																				
2.36	2.24	0.11	3.83E-01	7.25E-01	MCTP2	multiple C2 domains, transmembrane 2	chr15q26.2	1554833_at	NM_018349																				
6.22	5.97	0.25	3.83E-01	7.25E-01	BCL9L	B-cell CLL/lymphoma 9-like	chr11q23.3	227616_at	NM_182557																				

2.62	2.48	0.14	3.83E-01	7.25E-01	DPY19L1P1	dpy-19-like 1 pseudogene 1 (C. elegans)	chr7p14.3	215102_at	XM_001716398 /// XM_001717640 /// XM_001717874																			
6.52	6.30	0.23	3.83E-01	7.25E-01	GCAT	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	chr22q13.1	36475_at	NM_014291																			
7.07	6.88	0.18	3.83E-01	7.25E-01	PTPRS	protein tyrosine phosphatase, receptor type, S	chr19p13.3	226571_s_at	NM_002850 /// NM_130853 /// NM_130854 /// NM_130855																			
3.55	3.39	0.15	3.83E-01	7.25E-01	---	---	---	1559220_at	---																			
2.37	2.24	0.13	3.83E-01	7.25E-01	FCHO2	FCH domain only 2	chr5q13.2	1555153_s_at	NM_138782																			
4.99	4.79	0.20	3.83E-01	7.25E-01	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	chr17q12	1553047_at	NM_003559																			
6.11	5.99	0.11	3.83E-01	7.25E-01	DCTN5	dynactin 5 (p25)	chr16p12.1	209232_s_at	NM_032486																			
2.32	2.05	0.26	3.83E-01	7.25E-01	MMRN1	multimerin 1	chr4q22	205612_at	NM_007351																			
2.45	2.30	0.15	3.83E-01	7.25E-01	PGAP1	post-GPI attachment to proteins 1	chr2q33.1	241801_at	NM_024989																			
2.75	2.64	0.11	3.83E-01	7.25E-01	KCNQ1OT1	KCNQ1 overlapping transcript 1 (non-protein coding)	chr11p15	243435_at	NR_002728																			
4.80	4.58	0.22	3.83E-01	7.25E-01	GATAD2B	GATA zinc finger domain containing 2B	chr1q21.3	238076_at	NM_020699																			
3.73	3.60	0.13	3.83E-01	7.25E-01	---	---	---	235664_at	---																			
4.76	4.39	0.37	3.83E-01	7.25E-01	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	chr4q21.23	226187_at	NM_001263																			
2.40	2.25	0.15	3.83E-01	7.25E-01	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	chr4q21.1	236331_at	NM_003948																			
2.10	1.98	0.12	3.83E-01	7.26E-01	---	---	---	231679_at	---																			
6.86	6.68	0.17	3.84E-01	7.26E-01	VRK3	vaccinia related kinase 3	chr19q13	221998_s_at	NM_001025778 /// NM_016440																			
2.68	2.50	0.17	3.84E-01	7.26E-01	---	---	---	239970_at	---																			
2.96	2.81	0.15	3.84E-01	7.26E-01	RNF39	ring finger protein 39	chr6p21.3	219916_s_at	NM_025236 /// NM_170769																			
6.55	6.16	0.39	3.84E-01	7.26E-01	EMP1	epithelial membrane protein 1	chr12p12.3	201324_at	NM_001423																			
2.11	1.98	0.14	3.84E-01	7.26E-01	---	---	---	244638_at	---																			
4.38	4.20	0.18	3.84E-01	7.26E-01	MAP2K6	mitogen-activated protein kinase kinase 6	chr17q24.3	205698_s_at	NM_002758																			
2.54	2.40	0.14	3.84E-01	7.26E-01	---	---	---	215745_at	---																			
5.78	5.53	0.25	3.84E-01	7.26E-01	TMF1	TATA element modulatory factor 1	chr3p21-p12	214948_s_at	NM_007114																			

9.99	9.61	0.37	3.84E-01	7.26E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	215193_x_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447																			
6.15	5.88	0.27	3.84E-01	7.26E-01	ZDHHC2	zinc finger, DHHC-type containing 2	chr8p21.3-p22	222730_s_at	NM_016353																				
7.27	6.95	0.32	3.84E-01	7.26E-01	MKNK2	MAP kinase interacting serine/threonine kinase 2	chr19p13.3	223199_at	NM_017572 /// NM_199054																				
3.01	2.88	0.14	3.84E-01	7.26E-01	---	---	---	240516_at	---																				
7.65	7.37	0.28	3.84E-01	7.26E-01	TSPAN18	Tetraspanin 18	chr11p11.2	227307_at	NM_001031730 /// NM_130783																				
4.56	4.36	0.20	3.84E-01	7.26E-01	MKS1	Meckel syndrome, type 1	chr17q22	218630_at	NM_017777																				
3.28	3.16	0.13	3.84E-01	7.26E-01	TSPAN16	tetraspanin 16	chr19p13.2	242180_at	NM_012466																				
7.80	7.60	0.20	3.84E-01	7.26E-01	PCBD1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	chr10q22	203557_s_at	NM_000281																				
2.55	2.42	0.13	3.85E-01	7.26E-01	APOA2	apolipoprotein A-II	chr1q21-q23	219465_at	NM_001643																				
6.70	6.46	0.24	3.85E-01	7.26E-01	C16orf5	chromosome 16 open reading frame 5	chr16p13.3	223960_s_at	NM_013399																				
4.52	4.20	0.32	3.85E-01	7.26E-01	ZNF500	zinc finger protein 500	chr16p13.3	213641_at	NM_021646																				
6.37	6.22	0.14	3.85E-01	7.26E-01	FAM168A	family with sequence similarity 168, member A	chr11q13.4	212357_at	NM_015159																				
3.64	3.44	0.20	3.85E-01	7.26E-01	CDCP1	CUB domain containing protein 1	chr3p21.31	218451_at	NM_022842 /// NM_178181																				
4.15	3.94	0.21	3.85E-01	7.26E-01	B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	chr17q25.3	213589_s_at	NM_001009905																				

4.16	4.01	0.15	3.85E-01	7.26E-01	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	chr5p15.33	231021_at	NM_001003841 /// XM_001716583 /// XM_001720416 /// XM_001722996																			
5.65	5.29	0.36	3.85E-01	7.26E-01	ROBO4	roundabout homolog 4, magic roundabout (Drosophila)	chr11q24.2	226028_at	NM_019055																			
2.90	2.73	0.17	3.85E-01	7.26E-01	GYG2	glycogenin 2	chrXp22.3	210963_s_at	NM_001079855 /// NM_003918																			
5.44	5.28	0.16	3.85E-01	7.26E-01	GPR137	G protein-coupled receptor 137	chr11cen-q22.3	43934_at	NM_020155																			
2.02	1.92	0.10	3.85E-01	7.26E-01	---	---	---	241030_at	---																			
7.22	7.03	0.18	3.85E-01	7.26E-01	BIN1	bridging integrator 1	chr2q14	214643_x_at	NM_004305 /// NM_139343 /// NM_139344 /// NM_139345 /// NM_139346 /// NM_139347 /// NM_139348 /// NM_139349 /// NM_139350 /// NM_139351																			
2.72	2.53	0.18	3.85E-01	7.26E-01	---	---	---	240201_at	---																			
2.27	2.15	0.12	3.85E-01	7.26E-01	PSPH	phosphoserine phosphatase	chr7p15.2-p15.1	244819_x_at	NM_004577																			
8.39	8.19	0.20	3.85E-01	7.26E-01	GNB2	guanine nucleotide binding protein (G protein), beta polypeptide 2	chr7q21.3-q22.1|7q22	200852_x_at	NM_005273																			
7.63	7.37	0.25	3.85E-01	7.26E-01	ACLY	ATP citrate lyase	chr17q12-q21	201128_s_at	NM_001096 /// NM_198830																			
2.26	2.14	0.12	3.85E-01	7.27E-01	EFHC2	EF-hand domain (C-terminal) containing 2	chrXp11.3	220591_s_at	NM_025184																			
2.80	2.61	0.19	3.85E-01	7.27E-01	METT10D	methyltransferase 10 domain containing	chr17p13.3	220797_at	NM_024086																			
2.91	2.72	0.19	3.85E-01	7.27E-01	HOXA11	homeobox A11	chr7p15-p14	208493_at	NM_005523																			
2.78	2.67	0.11	3.86E-01	7.27E-01	SCRT1	scratch homolog 1, zinc finger protein (Drosophila)	chr8q24.3	221026_s_at	NM_031309																			
5.72	5.58	0.15	3.86E-01	7.27E-01	APLP2	Amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	228520_s_at	NM_001642																			
3.92	3.77	0.15	3.86E-01	7.27E-01	---	---	---	241003_at	---																			
2.60	2.48	0.12	3.86E-01	7.27E-01	CILP2	cartilage intermediate layer protein 2	chr19p13.11	1552288_at	NM_153221																			
3.22	2.94	0.28	3.86E-01	7.27E-01	CCAR1	Cell division cycle and apoptosis regulator 1	chr10q21.3	239014_at	NM_018237																			
2.71	2.51	0.20	3.86E-01	7.27E-01	psiTPTE22	TPTE pseudogene	chr22q11.2	243952_at	NR_001591 /// XR_042159																			
3.61	3.46	0.14	3.86E-01	7.27E-01	GANC	glucosidase, alpha; neutral C	chr15q15.2	236077_at	NM_198141																			
4.02	3.88	0.14	3.86E-01	7.27E-01	WASL	Wiskott-Aldrich syndrome-like	chr7q31.3	205810_s_at	NM_003941																			
4.12	3.85	0.27	3.86E-01	7.27E-01	SYNE1	spectrin repeat containing, nuclear envelope 1	chr6q25	244070_at	NM_015293 /// NM_033071 /// NM_133650 /// NM_182961																			
2.61	2.46	0.15	3.86E-01	7.27E-01	EZH1	enhancer of zeste homolog 1 (Drosophila)	chr17q21.1-q21.3	239198_at	NM_001991																			
5.87	5.36	0.51	3.86E-01	7.27E-01	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	chr13q12-q14	212295_s_at	NM_003045																			
5.16	4.84	0.31	3.86E-01	7.27E-01	PIGN	phosphatidylinositol glycan anchor biosynthesis, class N	chr18q21.33	219048_at	NM_012327 /// NM_176787																			
4.96	4.35	0.62	3.86E-01	7.27E-01	---	---	---	1558388_a_at	---																			
6.39	6.24	0.15	3.86E-01	7.27E-01	RBL2	retinoblastoma-like 2 (p130)	chr16q12.2	212331_at	NM_005611																			
4.96	4.76	0.19	3.86E-01	7.28E-01	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	chr17q21	1557943_at	NM_033133																			
2.41	2.30	0.11	3.86E-01	7.28E-01	---	---	---	AFFX-TrpnX-5_at	---																			
4.41	4.23	0.18	3.87E-01	7.28E-01	CTSL2	cathepsin L2	chr9q22.2	210074_at	NM_001333																			
2.80	2.64	0.16	3.87E-01	7.28E-01	---	---	---	244389_at	---																			
7.31	7.08	0.23	3.87E-01	7.28E-01	MTDH	Metadherin	chr8q22.1	212248_at	NM_178812																			
3.57	3.45	0.12	3.87E-01	7.28E-01	---	---	---	244421_at	---																			
3.02	2.86	0.15	3.87E-01	7.28E-01	---	---	---	1558960_a_at	---																			

4.10	3.94	0.16	3.87E-01	7.28E-01	---	---	---	238141_s_at	---
5.65	5.46	0.19	3.87E-01	7.28E-01	B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	chr5q35.2-q35.3	222191_s_at	NM_007255
5.55	5.20	0.35	3.87E-01	7.28E-01	STAP2	signal transducing adaptor family member 2	chr19p13.3	221610_s_at	NM_001013841 /// NM_017720
2.15	2.03	0.12	3.87E-01	7.28E-01	---	---	---	240647_at	---
4.13	3.79	0.34	3.87E-01	7.28E-01	CCNJ	cyclin J	chr10pter-q26.12	219470_x_at	NM_001134375 /// NM_001134376 /// NM_019084
4.31	4.08	0.22	3.87E-01	7.28E-01	GPX8	glutathione peroxidase 8	chr5q11.2	228141_at	NM_001008397
2.35	2.21	0.14	3.87E-01	7.28E-01	PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	chr3q25	206157_at	NM_002852
4.66	4.39	0.27	3.87E-01	7.28E-01	---	---	---	226826_at	---
3.68	3.56	0.12	3.87E-01	7.28E-01	WNT5A	wingless-type MMTV integration site family, member 5A	chr3p21-p14	205990_s_at	NM_003392
3.82	3.59	0.23	3.87E-01	7.28E-01	EAF1	ELL associated factor 1	chr3p24.3	226952_at	NM_033083
2.75	2.62	0.13	3.87E-01	7.28E-01	---	---	---	1557776_at	---
6.30	6.07	0.23	3.87E-01	7.28E-01	PBX1	pre-B-cell leukemia homeobox 1	chr1q23	205253_at	NM_002585
2.81	2.62	0.19	3.87E-01	7.28E-01	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	chr18p11.32	212579_at	NM_015295
3.08	2.93	0.15	3.87E-01	7.28E-01	---	---	---	242886_at	---
2.65	2.51	0.14	3.87E-01	7.28E-01	---	---	---	1563244_at	---
8.67	8.52	0.15	3.87E-01	7.28E-01	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	chr1p32	200040_at	NM_006559
2.15	2.04	0.11	3.87E-01	7.28E-01	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	chr18q21.3	204614_at	NM_002575
4.07	3.91	0.17	3.88E-01	7.29E-01	EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	chr15q24.1	219207_at	NM_025083
4.32	4.01	0.30	3.88E-01	7.29E-01	PROM2	prominin 2	chr2q11.1	1562378_s_at	NM_144707
6.16	5.80	0.37	3.88E-01	7.29E-01	---	---	---	238091_at	---
5.48	5.32	0.15	3.88E-01	7.29E-01	HIST1H2AG /// HIST1H2AH /// HIST1H2AI /// HIST1H2AJ /// HIST1H2AK /// HIST1H2AL /// HIST1H2AM /// HIST1H3F	histone cluster 1, H2ag /// histone cluster 1, H2ah /// histone cluster 1, H2ai /// histone cluster 1, H2aj /// histone cluster 1, H2ak /// histone cluster 1, H2al /// histone cluster 1, H2am /// histone cluster 1, H3f	chr6p21.33 /// chr6p22-p21.3 /// chr6p22.1	208583_x_at	NM_003509 /// NM_003510 /// NM_003511 /// NM_003514 /// NM_021018 /// NM_021064 /// NM_021066 /// NM_080596
2.38	2.28	0.10	3.88E-01	7.29E-01	PHLDB2	pleckstrin homology-like domain, family B, member 2	chr3q13.2	1554779_s_at	NM_001134437 /// NM_001134438 /// NM_001134439 /// NM_145753
6.39	6.17	0.22	3.88E-01	7.29E-01	MTO1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	chr6q13	233665_x_at	NM_001123226 /// NM_012123 /// NM_133645
10.83	10.67	0.16	3.88E-01	7.29E-01	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	chr5q31.3-q32	200665_s_at	NM_003118
2.89	2.69	0.20	3.88E-01	7.29E-01	GBP5	guanylate binding protein 5	chr1p22.2	229625_at	NM_001134486 /// NM_052942
2.15	2.05	0.10	3.88E-01	7.29E-01	ARHGAP29	Rho GTPase activating protein 29	chr1p22.1	1554736_at	NM_004815
2.25	2.15	0.10	3.88E-01	7.29E-01	LOC349408	hypothetical protein LOC349408	chrXp22.31	1562805_at	---
4.85	4.68	0.17	3.88E-01	7.29E-01	SLC37A1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	chr21q22.3	218928_s_at	NM_018964
4.83	4.53	0.30	3.88E-01	7.29E-01	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	chr1p36.1	212911_at	NM_015291
2.25	2.14	0.11	3.89E-01	7.29E-01	C12orf59	chromosome 12 open reading frame 59	chr12p13.2	236646_at	NM_153022
4.00	3.87	0.13	3.89E-01	7.29E-01	SEC13	SEC13 homolog (S. cerevisiae)	chr3p25-p24	239617_at	NM_183352
2.15	1.99	0.16	3.89E-01	7.29E-01	CPA6	carboxypeptidase A6	chr8q13.2	224028_at	NM_001127445 /// NM_020361
6.32	6.11	0.21	3.89E-01	7.29E-01	HPCAL1	hippocalcin-like 1	chr2p25.1	205462_s_at	NM_002149 /// NM_134421
6.52	6.24	0.28	3.89E-01	7.29E-01	DSE	dermatan sulfate epimerase	chr6q22	218854_at	NM_001080976 /// NM_013352

2.84	2.69	0.15	3.89E-01	7.30E-01	DNAH6 /// DNHL1 /// LOC200383	dynein, axonemal, heavy chain 6 /// dynein heavy chain-like 1 /// similar to Dynein heavy chain at 16F	chr2p11.2	215341_at	NM_001370 /// NM_173645																				
3.68	3.51	0.16	3.89E-01	7.30E-01	---	---	---	239464_at	---																				
4.30	4.18	0.12	3.89E-01	7.30E-01	ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	chr22q13.1	1560713_a_at	NM_052906																				
5.03	4.85	0.18	3.89E-01	7.30E-01	ARID1B	AT rich interactive domain 1B (SWI1-like)	chr6q25.1	1566989_at	NM_017519 /// NM_020732 /// NM_175863																				
2.80	2.66	0.14	3.89E-01	7.30E-01	NCR1	natural cytotoxicity triggering receptor 1	chr19q13.42	217088_s_at	NM_004829																				
3.32	3.21	0.11	3.89E-01	7.30E-01	CPN1	carboxypeptidase N, polypeptide 1	chr10q24.2	206256_at	NM_001308																				
7.99	7.72	0.26	3.89E-01	7.30E-01	GNPDA1	glucosamine-6-phosphate deaminase 1	chr5q21	202382_s_at	NM_005471																				
7.00	6.71	0.29	3.89E-01	7.30E-01	TSPAN6	tetraspanin 6	chrXq22	209109_s_at	NM_003270																				
4.39	4.18	0.21	3.89E-01	7.30E-01	SRPX2	sushi-repeat-containing protein, X-linked 2	chrXq21.33-q23	205499_at	NM_014467																				
2.31	2.17	0.14	3.89E-01	7.30E-01	---	---	---	236349_at	---																				
3.62	3.40	0.23	3.89E-01	7.30E-01	---	---	---	230161_at	---																				
10.15	9.75	0.40	3.89E-01	7.30E-01	HLA-DRA	major histocompatibility complex, class II, DR alpha	chr6p21.3	210982_s_at	NM_019111																				
2.99	2.85	0.13	3.89E-01	7.30E-01	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	chr1p22.1-p21	210082_at	NM_000350																				
2.39	2.27	0.11	3.89E-01	7.30E-01	SPRR1A	small proline-rich protein 1A	chr1q21-q22	213796_at	NM_005987																				
4.20	4.00	0.20	3.89E-01	7.30E-01	TMEM70	transmembrane protein 70	chr8q21.11	226083_at	NM_001040613 /// NM_017866																				
2.48	2.36	0.13	3.89E-01	7.30E-01	ACRV1	acrosomal vesicle protein 1	chr11q23-q24	208013_s_at	NM_001612 /// NM_020069 /// NM_020107 /// NM_020108 /// NM_020109 /// NM_020110 /// NM_020111 /// NM_020113 /// NM_020115																				
6.19	5.86	0.33	3.89E-01	7.30E-01	DARS	aspartyl-tRNA synthetase	chr2q21.3	201624_at	NM_001349																				
2.29	2.14	0.15	3.90E-01	7.30E-01	---	---	---	1563370_at	---																				
5.98	5.74	0.24	3.90E-01	7.30E-01	PXMP2	peroxisomal membrane protein 2, 22kDa	chr12q24.33	219076_s_at	NM_018663 /// XM_001713955																				
2.33	2.22	0.11	3.90E-01	7.30E-01	---	---	---	239759_at	---																				
5.32	5.11	0.20	3.90E-01	7.30E-01	CASKIN2	CASK interacting protein 2	chr17q25.1	61297_at	NM_020753																				
4.86	4.63	0.22	3.90E-01	7.30E-01	DARS2	aspartyl-tRNA synthetase 2, mitochondrial	chr1q25.1	218365_s_at	NM_018122																				
7.22	6.92	0.29	3.90E-01	7.30E-01	RPA1	replication protein A1, 70kDa	chr17p13.3	201528_at	NM_002945																				
2.13	2.03	0.10	3.90E-01	7.30E-01	---	---	---	1561776_at	---																				
2.72	2.59	0.13	3.90E-01	7.30E-01	---	---	---	1556762_a_at	---																				
2.09	1.96	0.12	3.90E-01	7.30E-01	PRKXP1	protein kinase, X-linked, pseudogene 1	chr15q26.3	235987_at	---																				
6.68	6.48	0.20	3.90E-01	7.30E-01	MARK4	MAP/microtubule affinity-regulating kinase 4	chr19q13.3	55065_at	NM_031417																				
5.02	4.79	0.24	3.90E-01	7.31E-01	C8orf55	chromosome 8 open reading frame 55	chr8q24.3	218500_at	NM_016647																				
2.90	2.71	0.19	3.90E-01	7.31E-01	MIPOL1	mirror-image polydactyly 1	chr14q13.3-q21.1	244246_at	NM_138731																				
4.03	3.84	0.19	3.90E-01	7.31E-01	GEMIN8	gem (nuclear organelle) associated protein 8	chrXp22.2	230758_at	NM_001042479 /// NM_001042480 /// NM_017856																				
5.71	5.45	0.26	3.90E-01	7.31E-01	NKIRAS2	NFKB inhibitor interacting Ras-like 2	chr17q21.2	222105_s_at	NM_001001349 /// NM_017595																				
5.27	5.14	0.12	3.90E-01	7.31E-01	CINP	cyclin-dependent kinase 2-interacting protein	chr14q32.31	218267_at	NM_032630																				
4.02	3.71	0.31	3.91E-01	7.31E-01	NFYA	nuclear transcription factor Y, alpha	chr6p21.3	204107_at	NM_002505 /// NM_021705 /// XM_001716589 /// XM_001717592 /// XM_001718396																				
6.10	5.95	0.15	3.91E-01	7.31E-01	JARID2	jumonji, AT rich interactive domain 2	chr6p24-p23	203297_s_at	NM_004973																				

7.96	7.71	0.25	3.91E-01	7.31E-01	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4	chr17q24-q25	214721_x_at	NM_012121
2.51	2.37	0.14	3.91E-01	7.31E-01	TPM3	tropomyosin 3	chr1q21.2	238079_at	NM_001043351 /// NM_001043352 /// NM_001043353 /// NM_152263 /// NM_153649
2.44	2.31	0.13	3.91E-01	7.31E-01	KIAA0746	KIAA0746 protein	chr4p15.2	230232_at	NM_015187
7.57	7.31	0.27	3.91E-01	7.31E-01	LHFP	lipoma HMGIC fusion partner	chr13q12	218656_s_at	NM_005780
5.55	5.34	0.21	3.91E-01	7.31E-01	ZNF395	zinc finger protein 395	chr8p21.1	221123_x_at	NM_018660
4.57	4.33	0.24	3.91E-01	7.31E-01	---	---	---	1560297_at	---
2.88	2.72	0.16	3.91E-01	7.31E-01	---	---	---	244853_at	---
3.16	2.97	0.19	3.91E-01	7.31E-01	LOC284276	hypothetical LOC284276	chr18q23	1558849_at	XR_041397 /// XR_041398 /// XR_041399
3.86	3.73	0.14	3.91E-01	7.31E-01	SPG20	spastic paraplegia 20 (Troyer syndrome)	chr13q13.3	216965_x_at	NM_015087
3.07	2.81	0.26	3.91E-01	7.31E-01	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	chr6q22.31	223551_at	NM_032471 /// NM_181794 /// NM_181795
6.37	6.23	0.14	3.91E-01	7.31E-01	LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	chr3q29	221535_at	NM_018385
2.30	2.13	0.16	3.91E-01	7.31E-01	---	---	---	236971_at	---
4.19	3.74	0.45	3.91E-01	7.31E-01	---	---	---	238156_at	---
2.40	2.29	0.11	3.91E-01	7.31E-01	---	---	---	237191_x_at	---
2.34	2.18	0.16	3.91E-01	7.31E-01	---	---	---	243665_s_at	---
2.32	2.17	0.15	3.91E-01	7.31E-01	---	---	---	241774_at	---
2.89	2.77	0.12	3.91E-01	7.31E-01	AMN	amnionless homolog (mouse)	chr14q32.3	223587_s_at	NM_030943
8.67	8.51	0.16	3.91E-01	7.31E-01	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	chr9q33.2-q34.11	218160_at	NM_014222
5.58	5.43	0.16	3.91E-01	7.31E-01	TAF12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa	chr1p35.3	209463_s_at	NM_005644
2.12	1.99	0.12	3.91E-01	7.31E-01	---	---	---	1556187_at	---
5.70	5.53	0.17	3.91E-01	7.31E-01	INTS1	integrator complex subunit 1	chr7p22.3	212212_s_at	NM_001080453
2.33	2.21	0.12	3.91E-01	7.31E-01	---	---	---	1556444_a_at	---
8.70	8.41	0.29	3.91E-01	7.31E-01	SLC30A1	Solute carrier family 30 (zinc transporter), member 1	chr1q32-q41	212907_at	NM_021194
2.54	2.43	0.11	3.91E-01	7.31E-01	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	210398_x_at	NM_000150 /// NM_001040701
2.60	2.44	0.16	3.91E-01	7.31E-01	---	---	---	1569680_at	---
2.68	2.57	0.11	3.91E-01	7.31E-01	PRR6	Proline rich 6	chr17p11.2	230436_s_at	NM_181716
4.94	4.50	0.44	3.92E-01	7.31E-01	SFRP1	secreted frizzled-related protein 1	chr8p12-p11.1	202037_s_at	NM_003012
5.30	5.12	0.18	3.92E-01	7.31E-01	ZNF512	zinc finger protein 512	chr2p23	225050_at	NM_032434
6.53	6.24	0.29	3.92E-01	7.32E-01	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	chr4q13-q21	209068_at	NM_031372 /// NR_003249
3.86	3.64	0.22	3.92E-01	7.32E-01	SURF1	surfeit 1	chr9q34.2	217646_at	NM_003172
6.07	5.82	0.24	3.92E-01	7.32E-01	RGNEF	Rho-guanine nucleotide exchange factor	chr5q13.2	1554003_at	NM_001080479
3.97	3.59	0.37	3.92E-01	7.32E-01	FGD6	FYVE, RhoGEF and PH domain containing 6	chr12q22	1555137_a_at	NM_018351
7.61	7.37	0.24	3.92E-01	7.32E-01	NR2F6	nuclear receptor subfamily 2, group F, member 6	chr19p13.1	209262_s_at	NM_005234
2.97	2.79	0.17	3.92E-01	7.32E-01	CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	chr12p13.33	228083_at	NM_172364
4.35	4.13	0.22	3.92E-01	7.32E-01	KIAA1704	KIAA1704	chr13q13-q14	223606_x_at	NM_018559
3.57	3.36	0.21	3.92E-01	7.32E-01	FLYWCH1	FLYWCH-type zinc finger 1	chr16p13.3	225952_at	NM_020912 /// NM_032296
3.41	3.10	0.30	3.93E-01	7.32E-01	---	---	---	231218_at	---
2.71	2.54	0.17	3.93E-01	7.32E-01	---	---	---	236795_at	---
4.05	3.87	0.18	3.93E-01	7.32E-01	ALAS2	aminolevulinate, delta-, synthase 2	chrXp11.21	238813_at	NM_000032 /// NM_001037967 /// NM_001037968 /// NM_001037969
4.45	3.78	0.67	3.93E-01	7.32E-01	PON3	paraoxonase 3	chr7q21.3	213695_at	NM_000940
2.55	2.46	0.09	3.93E-01	7.32E-01	---	---	---	1560208_at	---

8.01	7.74	0.27	3.93E-01	7.32E-01	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	chrXq28	202219_at	NM_005629
3.10	2.91	0.19	3.93E-01	7.32E-01	---	---	---	237307_at	---
2.53	2.40	0.13	3.93E-01	7.32E-01	UEVLD	UEV and lactate/malate dehyrogenase domains	chr11p15.1	1554396_at	NM_001040697 /// NM_018314
3.37	3.19	0.18	3.93E-01	7.32E-01	---	---	---	232690_at	---
3.30	3.14	0.16	3.93E-01	7.32E-01	---	---	---	243410_at	---
5.17	4.99	0.18	3.93E-01	7.32E-01	LTB4R	leukotriene B4 receptor	chr14q11.2-q12	210128_s_at	NM_181657
5.92	5.67	0.25	3.93E-01	7.32E-01	TSPAN33	tetraspanin 33	chr7q32.1	225775_at	NM_178562
9.66	9.46	0.20	3.93E-01	7.32E-01	RAN	RAN, member RAS oncogene family	chr12q24.3	200750_s_at	NM_006325
2.98	2.87	0.12	3.93E-01	7.32E-01	---	---	---	238194_at	---
3.10	2.93	0.17	3.93E-01	7.32E-01	---	---	---	1569763_at	---
3.73	3.54	0.20	3.93E-01	7.32E-01	---	---	---	239231_at	---
2.35	2.25	0.10	3.93E-01	7.32E-01	---	---	---	237356_at	---
7.34	7.11	0.23	3.93E-01	7.33E-01	IQGAP2	IQ motif containing GTPase activating protein 2	chr5q13.3	203474_at	NM_006633
2.12	2.03	0.09	3.94E-01	7.33E-01	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	chr5p13.2	238335_at	NM_001012339 /// NM_194283
2.60	2.50	0.09	3.94E-01	7.33E-01	NXPH2	neurexophilin 2	chr2q22.1	1559355_at	NM_007226
3.42	3.31	0.10	3.94E-01	7.33E-01	CCNYL1	Cyclin Y-like 1	chr2q33.3	227280_s_at	NM_152523
3.73	3.54	0.19	3.94E-01	7.33E-01	NKD1	naked cuticle homolog 1 (Drosophila)	chr16q12	1553115_at	NM_033119
4.68	4.33	0.35	3.94E-01	7.33E-01	ZNF10	zinc finger protein 10	chr12q24.33	229848_at	NM_015394
4.14	3.96	0.18	3.94E-01	7.33E-01	SPON1	spondin 1, extracellular matrix protein	chr11p15.2	209437_s_at	NM_006108
2.70	2.57	0.12	3.94E-01	7.33E-01	---	---	---	231351_at	---
2.21	2.08	0.12	3.94E-01	7.33E-01	GBA3	glucosidase, beta, acid 3 (cytosolic)	chr4p15.31	222943_at	NM_001128432 /// NM_020973
2.39	2.28	0.11	3.94E-01	7.33E-01	ADAM21	ADAM metallopeptidase domain 21	chr14q24.1	1552579_a_at	NM_003813
3.24	3.04	0.20	3.94E-01	7.33E-01	MYEF2	myelin expression factor 2	chr15q21.1	222772_at	NM_016132
7.07	6.79	0.28	3.94E-01	7.33E-01	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	chr21q22.3	211113_s_at	NM_004915 /// NM_016818 /// NM_207174 /// NM_207627 /// NM_207628 /// NM_207629
3.30	3.18	0.12	3.94E-01	7.34E-01	PGLS	6-phosphogluconolactonase	chr19p13.2	1554316_at	NM_012088
4.49	3.89	0.60	3.94E-01	7.34E-01	TNIK	TRAF2 and NCK interacting kinase	chr3q26.2-q26.31	211828_s_at	NM_015028
2.53	2.39	0.14	3.94E-01	7.34E-01	HGD /// LOC100132552 /// LOC727722	homogentisate 1,2-dioxygenase (homogentisate oxidase) /// similar to homogentisate 1,2-dioxygenase /// homogentisate 1,2-dioxygenase like	chr3q13.33	205221_at	NM_000187 /// XM_001713606 /// XM_001719739
4.45	4.27	0.18	3.94E-01	7.34E-01	---	---	---	1560451_at	---
2.14	2.03	0.11	3.95E-01	7.34E-01	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	chr5p13.2	234094_x_at	NM_001012339 /// NM_194283
7.89	7.66	0.23	3.95E-01	7.34E-01	ALG2	asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)	chr9q22.33	225621_at	NM_033087
2.00	1.90	0.10	3.95E-01	7.34E-01	---	---	---	1564767_at	---
2.30	2.15	0.15	3.95E-01	7.34E-01	---	---	---	237954_x_at	---
8.38	8.22	0.16	3.95E-01	7.34E-01	HEBP2	heme binding protein 2	chr6q24	203430_at	NM_014320
2.28	2.14	0.14	3.95E-01	7.34E-01	---	---	---	215837_x_at	---
3.32	3.10	0.22	3.95E-01	7.34E-01	KIAA0907	KIAA0907	chr1q22	230028_at	NM_014949
3.61	3.48	0.13	3.95E-01	7.34E-01	GRIA3	glutamate receptor, ionotrophic, AMPA 3	chrXq25-q26	208032_s_at	NM_000828 /// NM_007325
6.90	6.75	0.15	3.95E-01	7.34E-01	MGC9913	hypothetical protein MGC9913	chr19q13.43	244741_s_at	---
4.94	4.63	0.32	3.95E-01	7.34E-01	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	chr1q43	226969_at	NM_000254
4.70	4.49	0.21	3.95E-01	7.34E-01	VRK3	vaccinia related kinase 3	chr19q13	221999_at	NM_001025778 /// NM_016440
4.60	4.35	0.25	3.95E-01	7.34E-01	TSEN54	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	chr17q25.1	241402_at	NM_207346
5.68	5.53	0.15	3.95E-01	7.34E-01	RNF213	ring finger protein 213	chr17q25.3	225931_s_at	NM_020914
2.47	2.30	0.17	3.95E-01	7.34E-01	TBL2	transducin (beta)-like 2	chr7q11.23	212679_at	NM_012453
6.44	6.18	0.26	3.95E-01	7.34E-01	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	chr22q13.2-q13.31	202937_x_at	NM_015703
2.17	2.07	0.10	3.95E-01	7.34E-01	ABI2	Abl interactor 2	chr2q33	216113_at	NM_005759
4.04	3.89	0.15	3.95E-01	7.34E-01	---	---	---	222358_x_at	---
7.04	6.89	0.15	3.95E-01	7.34E-01	RNF213	ring finger protein 213	chr17q25.3	225929_s_at	NM_020914

3.41	3.25	0.16	3.95E-01	7.34E-01	---	---	---	1557450_s_at	---
2.44	2.27	0.17	3.95E-01	7.34E-01	---	---	---	1564840_at	---
7.00	6.78	0.23	3.96E-01	7.34E-01	USP33	ubiquitin specific peptidase 33	chr1p31.1	212513_s_at	NM_015017 /// NM_201624 /// NM_201626
2.56	2.43	0.13	3.96E-01	7.34E-01	GDEP	Gene differentially expressed in prostate	chr4q21.1	1554591_at	XR_000540 /// XR_000635
3.05	2.81	0.24	3.96E-01	7.34E-01	---	---	---	235505_s_at	---
8.07	7.66	0.41	3.96E-01	7.34E-01	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	chr1q23.3	209340_at	NM_003115
2.47	2.37	0.10	3.96E-01	7.34E-01	FOXQ1	forkhead box Q1	chr6p25	227475_at	NM_033260
4.55	4.31	0.24	3.96E-01	7.34E-01	ZNF680	zinc finger protein 680	chr7q11.21	229533_x_at	NM_001130022 /// NM_178558
8.69	8.54	0.15	3.96E-01	7.34E-01	PPA2	pyrophosphatase (inorganic) 2	chr4q25	220741_s_at	NM_001034191 /// NM_006903 /// NM_176866 /// NM_176867 /// NM_176869
7.03	6.77	0.25	3.96E-01	7.34E-01	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	chr14q11.2	204588_s_at	NM_001126105 /// NM_001126106 /// NM_003982
2.18	2.04	0.13	3.96E-01	7.34E-01	PKP4	plakophilin 4	chr2q23-q31	214874_at	NM_001005476 /// NM_003628
5.77	5.51	0.26	3.96E-01	7.34E-01	BAK1	BCL2-antagonist/killer 1	chr6p21.3	203728_at	NM_001188
3.63	3.48	0.15	3.96E-01	7.34E-01	C8orf76	chromosome 8 open reading frame 76	chr8q24.13	1554063_at	NM_032847
3.44	3.26	0.18	3.96E-01	7.34E-01	LOC284395	hypothetical protein LOC284395	chr19q12	1563872_at	XM_378787 /// XM_943993
8.08	7.78	0.30	3.96E-01	7.34E-01	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	chr11q13.5	207714_s_at	NM_001235
6.13	5.94	0.20	3.96E-01	7.34E-01	TBC1D25	TBC1 domain family, member 25	chrXp11.3-p11.23	227820_at	NM_002536
2.15	2.05	0.11	3.96E-01	7.34E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	234541_s_at	NM_015313
3.17	3.01	0.16	3.96E-01	7.34E-01	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	chr18q12-q21	1569891_at	NM_001001937 /// NM_004046
6.69	6.44	0.25	3.96E-01	7.34E-01	PTPN23	protein tyrosine phosphatase, non-receptor type 23	chr3p21.3	223150_s_at	NM_015466
2.14	2.04	0.10	3.96E-01	7.34E-01	C6orf141	chromosome 6 open reading frame 141	chr6p12.3	1554314_at	XR_040195 /// XR_040196 /// XR_040197 /// XR_040198 /// XR_040199 /// XR_040200
5.75	5.45	0.30	3.96E-01	7.34E-01	GM2A	GM2 ganglioside activator	chr5q31.3-q33.1	209727_at	NM_000405
2.88	2.77	0.11	3.96E-01	7.34E-01	---	---	---	1561532_at	---
6.37	6.05	0.32	3.96E-01	7.34E-01	EPC1	enhancer of polycomb homolog 1 (Drosophila)	chr10p11	225417_at	NM_025209
2.36	2.25	0.11	3.96E-01	7.34E-01	SP2	Sp2 transcription factor	chr17q21.32	237795_s_at	NM_003110
3.15	2.60	0.55	3.96E-01	7.34E-01	TRIB1	tribbles homolog 1 (Drosophila)	chr8q24.13	239818_x_at	NM_025195
3.95	3.58	0.37	3.96E-01	7.34E-01	---	---	---	235008_at	---
3.86	3.71	0.16	3.97E-01	7.34E-01	GIT2	G protein-coupled receptor kinase interactor 2	chr12q24.1	204982_at	NM_014776 /// NM_057169 /// NM_057170 /// NM_139201
4.53	4.29	0.23	3.97E-01	7.34E-01	---	---	---	231317_at	---
2.42	2.31	0.11	3.97E-01	7.34E-01	TMEM59	transmembrane protein 59	chr1p36-p31	241018_at	NM_004872
5.45	5.25	0.20	3.97E-01	7.34E-01	NISCH	nischarin	chr3p21.1	227392_at	NM_007184
9.17	8.87	0.30	3.97E-01	7.35E-01	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	chr19p13.2	200666_s_at	NM_006145
9.10	8.92	0.19	3.97E-01	7.35E-01	PRDX6	peroxiredoxin 6	chr1q25.1	200845_s_at	NM_004905
6.81	5.99	0.82	3.97E-01	7.35E-01	KLF4	Kruppel-like factor 4 (gut)	chr9q31	221841_s_at	NM_004235

3.26	3.10	0.16	3.97E-01	7.35E-01	C8orf51	chromosome 8 open reading frame 51	chr8q24	207458_at	XR_042123 /// XR_042124 /// XR_042125																				
5.75	5.40	0.35	3.97E-01	7.35E-01	---	---	---	235190_at	---																				
3.69	3.54	0.15	3.97E-01	7.35E-01	---	---	---	243593_s_at	---																				
5.38	5.15	0.24	3.97E-01	7.35E-01	BOP1	block of proliferation 1	chr8q24.3	212563_at	NM_015201																				
2.04	1.96	0.08	3.97E-01	7.35E-01	---	---	---	241772_at	---																				
2.14	2.01	0.13	3.97E-01	7.35E-01	NAV3	Neuron navigator 3	chr12q14.3	216632_at	NM_014903																				
4.29	4.14	0.15	3.98E-01	7.35E-01	KIF25	kinesin family member 25	chr6q27	208128_x_at	NM_005355 /// NM_030615																				
4.38	4.19	0.19	3.98E-01	7.35E-01	GPR4	G protein-coupled receptor 4	chr19q13.3	206236_at	NM_005282																				
2.70	2.61	0.09	3.98E-01	7.35E-01	LOC284017	hypothetical protein LOC284017	chr17p13.3	233855_at	---																				
4.13	3.88	0.24	3.98E-01	7.35E-01	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1	chr19p13.3	227420_at	NM_152362																				
3.11	2.97	0.14	3.98E-01	7.35E-01	NUDT17	nudix (nucleoside diphosphate linked moiety X)-type motif 17	chr1q21.1	1561847_at	NM_001012758																				
2.01	1.91	0.10	3.98E-01	7.35E-01	---	---	---	1570103_at	---																				
1.94	1.86	0.08	3.98E-01	7.35E-01	VWDE	von Willebrand factor D and EGF domains	chr7p21.3	239552_at	XM_001715460 /// XM_371878 /// XM_374405 /// XM_936911																				
4.63	4.33	0.30	3.98E-01	7.35E-01	---	---	---	227974_at	---																				
3.00	2.82	0.19	3.98E-01	7.35E-01	CD80	CD80 molecule	chr3q13.3-q21	207176_s_at	NM_005191																				
3.09	2.95	0.15	3.98E-01	7.35E-01	C10orf93	chromosome 10 open reading frame 93	chr10q26.3	1552964_at	NM_173572																				
2.33	2.20	0.12	3.98E-01	7.35E-01	PRL	prolactin	chr6p22.2-p21.3	205445_at	NM_000948																				
3.00	2.73	0.28	3.98E-01	7.35E-01	HCG4	HLA complex group 4	chr6p21.3	206685_at	NR_002139																				
2.29	2.18	0.10	3.98E-01	7.35E-01	RP11-78J21.1	Heterogeneous nuclear ribonucleoprotein A1-like	chr13q14.3	238696_at	NM_001011724 /// NM_001011725																				
2.40	2.24	0.16	3.98E-01	7.35E-01	LOC284751	hypothetical LOC284751	chr20q13.13	1556896_at	NM_001025463																				
3.06	2.92	0.14	3.98E-01	7.35E-01	TSPAN17	tetraspanin 17	chr5q35.3	1558119_at	NM_001006616 /// NM_012171 /// NM_130465																				
4.60	4.35	0.25	3.98E-01	7.35E-01	C16orf35	chromosome 16 open reading frame 35	chr16p13.3	210672_s_at	NM_001039476 /// NM_001077350																				
3.02	2.88	0.14	3.98E-01	7.35E-01	ZNF169	zinc finger protein 169	chr9q22.32	1560922_s_at	NM_194320																				
2.15	2.04	0.11	3.98E-01	7.35E-01	ZDHHC21	zinc finger, DHHC-type containing 21	chr9p22.3	243550_at	NM_178566																				
2.58	2.43	0.15	3.98E-01	7.35E-01	XYLT1	xylosyltransferase I	chr16p12.3	232574_at	NM_022166																				
2.43	2.32	0.12	3.98E-01	7.35E-01	---	---	---	1563360_at	---																				
2.42	2.29	0.13	3.98E-01	7.35E-01	TACR3	tachykinin receptor 3	chr4q25	208183_at	NM_001059																				
3.55	3.31	0.24	3.98E-01	7.35E-01	ZNF177	zinc finger protein 177	chr19p13.2	207417_s_at	NM_003451																				
2.30	2.21	0.10	3.98E-01	7.35E-01	LRRC28	leucine rich repeat containing 28	chr15q26.3	239471_at	NM_144598																				
3.24	3.08	0.15	3.98E-01	7.36E-01	---	---	---	244347_at	---																				
3.33	3.18	0.15	3.98E-01	7.36E-01	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	chr11q13	1560151_x_at	NM_001532																				
7.57	7.39	0.18	3.99E-01	7.36E-01	ANXA7	annexin A7	chr10q21.1-q21.2	201366_at	NM_001156 /// NM_004034																				
3.91	3.65	0.25	3.99E-01	7.36E-01	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	chr6q26-q27	205421_at	NM_021977																				
2.76	2.60	0.16	3.99E-01	7.36E-01	NHLRC3	NHL repeat containing 3	chr13q13.3	236953_s_at	NM_001012754 /// NM_001017370																				
2.11	1.99	0.12	3.99E-01	7.36E-01	USP45	ubiquitin specific peptidase 45	chr6q16.3	238057_at	NM_001080481																				
2.30	2.18	0.12	3.99E-01	7.36E-01	---	---	---	242975_s_at	---																				
1.99	1.91	0.08	3.99E-01	7.36E-01	C20orf106 /// C20orf107	chromosome 20 open reading frame 106 /// chromosome 20 open reading frame 107	chr20q13.31	233086_at	NM_001012971 /// NM_001013646																				
3.10	2.96	0.14	3.99E-01	7.36E-01	CCNY	cyclin Y	chr10p11.21	224649_x_at	NM_145012 /// NM_181698																				
4.20	4.07	0.13	3.99E-01	7.36E-01	HSPC111	hypothetical protein HSPC111	chr5q35.2	213833_x_at	NM_016391																				

2.27	2.15	0.12	3.99E-01	7.36E-01	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	chr18q22-q23	1562713_a_at	NM_138966 /// NM_138999 /// NM_153181																				
5.97	5.56	0.40	3.99E-01	7.36E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	203639_s_at	NM_000141 /// NM_022970																				
3.13	2.94	0.19	3.99E-01	7.36E-01	WDR91	WD repeat domain 91	chr7q33	230888_at	NM_014149																				
2.15	2.03	0.12	3.99E-01	7.36E-01	C8orf38	Chromosome 8 open reading frame 38	chr8q22.1	1556571_at	NM_152416																				
7.34	7.07	0.27	3.99E-01	7.36E-01	FAM21A /// FAM21B /// FAM21C /// FAM21D	family with sequence similarity 21, member A /// family with sequence similarity 21, member B /// family with sequence similarity 21, member C /// family with sequence similarity 21, member D	chr10q11.1 /// chr10q11.22 /// chr10q11.23	214946_x_at	NM_001005751 /// NM_015262 /// NM_018232 /// XM_370557																				
3.14	3.06	0.09	3.99E-01	7.36E-01	LOC149086	hypothetical protein LOC149086	chr1p35.2	1566647_s_at	XR_017808 /// XR_041107 /// XR_041108																				
4.68	4.47	0.21	4.00E-01	7.37E-01	---	---	---	81811_at	---																				
2.89	2.76	0.14	4.00E-01	7.37E-01	PKLR	pyruvate kinase, liver and RBC	chr1q21	207858_s_at	NM_000298 /// NM_181871																				
2.65	2.52	0.13	4.00E-01	7.37E-01	OLA1	Obg-like ATPase 1	chr2q31.1	224525_s_at	NM_001011708 /// NM_013341																				
8.00	7.89	0.11	4.00E-01	7.37E-01	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	chr12q12-q14	201805_at	NM_002733 /// NM_212461																				
2.17	2.04	0.12	4.00E-01	7.37E-01	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	chr2q31-q33|2q31.1	1554742_at	NM_000534 /// NM_001128143 /// NM_001128144																				
6.46	6.25	0.22	4.00E-01	7.37E-01	TMEM189-UBE2V1 /// UBE2V1	TMEM189-UBE2V1 /// ubiquitin-conjugating enzyme E2 variant 1	chr20q13.2	201001_s_at	NM_001032288 /// NM_003349 /// NM_021988 /// NM_022442 /// NM_199144 /// NM_199203																				
5.44	5.06	0.38	4.00E-01	7.37E-01	L3MBTL3	l(3)mbt-like 3 (Drosophila)	chr6q23	229393_at	NM_001007102 /// NM_032438																				
3.12	3.01	0.11	4.00E-01	7.37E-01	LOC100135777	hypothetical LOC100135777	---	1554332_a_at	---																				
2.85	2.72	0.13	4.00E-01	7.37E-01	KDSR	3-ketodihydrosphingosine reductase	chr18q21.3	1558279_a_at	NM_002035																				
5.27	4.76	0.51	4.00E-01	7.37E-01	ABHD5	abhydrolase domain containing 5	chr3p21	218739_at	NM_016006																				
4.65	4.20	0.45	4.00E-01	7.37E-01	---	---	---	215126_at	---																				
6.75	6.54	0.21	4.00E-01	7.37E-01	PELP1	proline, glutamate and leucine rich protein 1	chr17p13.2	215354_s_at	NM_014389																				
2.36	2.24	0.12	4.00E-01	7.37E-01	TTBK2	tau tubulin kinase 2	chr15q15.2	1554295_x_at	NM_173500																				
5.46	5.28	0.18	4.00E-01	7.37E-01	RNASEH2B	ribonuclease H2, subunit B	chr13q14.3	229210_at	NM_024570																				
3.08	2.99	0.10	4.00E-01	7.37E-01	LOC644165 /// LOC728216	similar to breakpoint cluster region /// hypothetical LOC728216	chr22q11.21 /// chr22q11.23	1553591_at	XM_001128283 /// XM_001721519 /// XM_933701																				
4.14	3.93	0.20	4.00E-01	7.37E-01	GALK1	galactokinase 1	chr17q24	204374_s_at	NM_000154																				
2.25	2.11	0.14	4.01E-01	7.37E-01	LOC283856	hypothetical protein LOC283856	chr16q13	1560707_at	---																				
4.60	4.40	0.20	4.01E-01	7.37E-01	JAG2	jagged 2	chr14q32	32137_at	NM_002226 /// NM_145159																				
4.56	4.24	0.32	4.01E-01	7.37E-01	WRN	Werner syndrome	chr8p12-p11.2	205667_at	NM_000553																				
3.82	3.52	0.31	4.01E-01	7.37E-01	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	chr1q43-q44	222880_at	NM_005465 /// NM_181690																				
2.40	2.29	0.11	4.01E-01	7.37E-01	---	---	---	1557659_a_at	---																				
8.45	8.26	0.19	4.01E-01	7.37E-01	HLA-E	major histocompatibility complex, class I, E	chr6p21.3	217456_x_at	NM_005516																				
2.23	2.11	0.13	4.01E-01	7.37E-01	KIF15	kinesin family member 15	chr3p21.31	219306_at	NM_020242																				

2.30	2.21	0.10	4.01E-01	7.37E-01	CPA1	carboxypeptidase A1 (pancreatic)	chr7q32	205615_at	NM_001868
5.45	5.10	0.35	4.01E-01	7.37E-01	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	chr16q23	203350_at	NM_001030007 /// NM_001128
2.99	2.87	0.12	4.01E-01	7.37E-01	---	---	---	1561439_at	---
4.13	3.87	0.26	4.01E-01	7.38E-01	---	---	---	238999_at	---
2.66	2.45	0.21	4.01E-01	7.38E-01	---	---	---	242637_at	---
2.00	1.90	0.10	4.01E-01	7.38E-01	ZNF215	zinc finger protein 215	chr11p15.4	1555510_at	NM_013250
3.80	3.52	0.27	4.01E-01	7.38E-01	---	---	---	1559232_a_at	---
2.74	2.60	0.14	4.01E-01	7.38E-01	---	---	---	1566182_at	---
2.13	2.04	0.09	4.01E-01	7.38E-01	---	---	---	231503_at	---
7.83	7.64	0.18	4.01E-01	7.38E-01	TRAPPC1	trafficking protein particle complex 1	chr17p13.1	225294_s_at	NM_021210
2.38	2.22	0.16	4.01E-01	7.38E-01	---	---	---	233237_at	---
5.38	5.25	0.13	4.01E-01	7.38E-01	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	chr11p11.2	229535_at	NM_175732
5.53	5.25	0.27	4.01E-01	7.38E-01	FBXO38	F-box protein 38	chr5q33.1	221257_x_at	NM_030793 /// NM_205836
6.59	6.45	0.15	4.01E-01	7.38E-01	C14orf172	chromosome 14 open reading frame 172	chr14q32.33	221907_at	NM_152307
2.80	2.58	0.23	4.02E-01	7.38E-01	TMPO	thymopoietin	chr12q22	209754_s_at	NM_001032283 /// NM_001032284 /// NM_003276
7.33	7.18	0.14	4.02E-01	7.38E-01	SNRPB2	small nuclear ribonucleoprotein polypeptide B"	chr20p12.2-p11.22	202505_at	NM_003092 /// NM_198220
2.22	2.12	0.10	4.02E-01	7.38E-01	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	chr16p13.3	1558088_a_at	NM_003345 /// NM_194259 /// NM_194260 /// NM_194261
2.54	2.44	0.10	4.02E-01	7.38E-01	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	205183_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370
3.06	2.66	0.40	4.02E-01	7.38E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	235412_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735
2.98	2.77	0.20	4.02E-01	7.38E-01	KRT76	keratin 76	chr12q13.13	207878_at	NM_015848
2.07	1.96	0.11	4.02E-01	7.38E-01	---	---	---	237821_at	---
2.05	1.95	0.11	4.02E-01	7.38E-01	---	---	---	AFFX-r2-Bs-dap-5_at	---
8.42	8.29	0.13	4.02E-01	7.38E-01	C8orf59	chromosome 8 open reading frame 59	chr8q21.2	226165_at	NM_001099670 /// NM_001099671 /// NM_001099672 /// NM_001099673
3.22	3.07	0.15	4.02E-01	7.38E-01	BTBD14A	BTB (POZ) domain containing 14A	chr9q34.3	230050_at	NM_144653
6.64	6.43	0.21	4.02E-01	7.38E-01	AAAS	achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A)	chr12q13	218075_at	NM_015665
2.24	2.12	0.12	4.02E-01	7.38E-01	TMC1	transmembrane channel-like 1	chr9q21.12	1564591_a_at	NM_138691
2.16	2.07	0.09	4.02E-01	7.38E-01	---	---	---	238946_at	---
8.79	8.66	0.13	4.03E-01	7.39E-01	WSB2	WD repeat and SOCS box-containing 2	chr12q24.23	201760_s_at	NM_018639
10.42	10.28	0.14	4.03E-01	7.39E-01	HSPC152	hypothetical protein HSPC152	chr11q13.1	217774_s_at	NM_016404
7.32	7.14	0.19	4.03E-01	7.39E-01	OPRS1	opioid receptor, sigma 1	chr9p13.3	201692_at	NM_005866 /// NM_147157
6.33	6.10	0.23	4.03E-01	7.39E-01	ZCCHC7	zinc finger, CCHC domain containing 7	chr9p13.2	226496_at	NM_032226
4.68	4.57	0.11	4.03E-01	7.39E-01	TUBA4B	tubulin, alpha 4b (pseudogene)	chr2q35	207490_at	NR_003063
3.77	3.65	0.13	4.03E-01	7.39E-01	PER1	period homolog 1 (Drosophila)	chr17p13.1-p12	242832_at	NM_002616
6.56	6.23	0.33	4.03E-01	7.39E-01	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	chr14q32.12	223160_s_at	NM_032560
6.48	6.25	0.22	4.03E-01	7.39E-01	WASL	Wiskott-Aldrich syndrome-like	chr7q31.3	224813_at	NM_003941

3.17	2.90	0.26	4.03E-01	7.39E-01	ING3	inhibitor of growth family, member 3	chr7q31	231863_at	NM_019071 /// NM_198267
2.64	2.47	0.18	4.03E-01	7.39E-01	TRIM8	tripartite motif-containing 8	chr10q24.3	223131_s_at	NM_030912
4.68	4.50	0.18	4.03E-01	7.39E-01	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal	chr11p15.4-p15.1	216230_x_at	NM_000543 /// NM_001007593
5.25	5.09	0.17	4.03E-01	7.39E-01	NDRG3	NDRG family member 3	chr20q11.21-q11.23	221082_s_at	NM_022477 /// NM_032013
3.40	3.21	0.19	4.03E-01	7.39E-01	---	---	---	239535_at	---
8.30	8.15	0.16	4.03E-01	7.39E-01	RNF10	ring finger protein 10	chr12q24.31	207801_s_at	NM_014868
5.65	5.15	0.50	4.03E-01	7.39E-01	MOSPD1	motile sperm domain containing 1	chrXq26.3	1557455_s_at	NM_019556
5.98	5.67	0.32	4.03E-01	7.39E-01	RAMP3	receptor (G protein-coupled) activity modifying protein 3	chr7p13-p12	205326_at	NM_005856
5.30	4.89	0.42	4.04E-01	7.39E-01	POMZP3 /// ZP3	POM (POM121 homolog, rat) and ZP3 fusion /// zona pellucida glycoprotein 3 (sperm receptor)	chr7q11.23	204148_s_at	NM_001110354 /// NM_007155 /// NM_012230 /// NM_152992
4.86	4.67	0.19	4.04E-01	7.39E-01	AMDHD2	amidohydrolase domain containing 2	chr16p13.3	219082_at	NM_015944
4.67	4.36	0.31	4.04E-01	7.39E-01	---	---	---	241786_at	---
5.76	5.50	0.26	4.04E-01	7.39E-01	NAGA	N-acetylgalactosaminidase, alpha-	chr22q13-qter|22q11	202944_at	NM_000262
3.99	3.66	0.34	4.04E-01	7.39E-01	---	---	---	230820_at	---
4.07	3.75	0.33	4.04E-01	7.39E-01	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	chr10q11.21	222235_s_at	NM_018590
6.57	6.24	0.33	4.04E-01	7.39E-01	RPL37	Ribosomal protein L37	chr5p13	224763_at	NM_000997
2.62	2.49	0.13	4.04E-01	7.39E-01	CSTF2	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	chrXq22.1	238821_at	NM_001325
4.59	4.22	0.37	4.04E-01	7.39E-01	RRAD	Ras-related associated with diabetes	chr16q22	204803_s_at	NM_001128850 /// NM_004165
2.65	2.46	0.19	4.04E-01	7.39E-01	LBP	lipopolysaccharide binding protein	chr20q11.23-q12	214461_at	NM_004139
2.94	2.73	0.22	4.04E-01	7.39E-01	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	chr5q33.1	242422_at	NM_005754 /// NM_198395
2.54	2.39	0.15	4.04E-01	7.39E-01	MYO10	myosin X	chr5p15.1-p14.3	1554026_a_at	NM_012334
2.80	2.63	0.18	4.04E-01	7.39E-01	---	---	---	1567611_at	---
3.22	2.94	0.27	4.04E-01	7.40E-01	LOC645323	hypothetical LOC645323	chr5q14.3	238850_at	XR_041118 /// XR_041119 /// XR_041120
2.30	2.20	0.09	4.04E-01	7.40E-01	---	---	---	222298_at	---
2.22	2.12	0.10	4.04E-01	7.40E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1565111_x_at	NM_153003
6.95	6.79	0.16	4.04E-01	7.40E-01	FUZ	fuzzy homolog (Drosophila)	chr19q13.33	221187_s_at	NM_025129
6.61	6.08	0.53	4.04E-01	7.40E-01	UGCG	UDP-glucose ceramide glucosyltransferase	chr9q31	221765_at	NM_003358
3.39	3.24	0.15	4.04E-01	7.40E-01	GORASP1	Golgi reassembly stacking protein 1, 65kDa	chr3p22-p21.33	243677_at	NM_031899
1.92	1.82	0.10	4.04E-01	7.40E-01	---	---	---	222322_at	---
2.24	2.12	0.12	4.04E-01	7.40E-01	LOC100130354	hypothetical protein LOC100130354	chr3p24.2	208413_at	XM_001722489 /// XM_001723395 /// XM_001725893
4.06	3.96	0.11	4.04E-01	7.40E-01	---	---	---	240274_at	---
2.45	2.35	0.10	4.04E-01	7.40E-01	LOC154872	hypothetical LOC154872	chr7q31.33	237271_at	XR_041807 /// XR_041808 /// XR_041809 /// XR_041810
6.64	6.46	0.18	4.04E-01	7.40E-01	MEF2D	myocyte enhancer factor 2D	chr1q12-q23	225641_at	NM_005920
4.41	4.31	0.10	4.04E-01	7.40E-01	---	---	---	239408_at	---
3.78	3.60	0.17	4.05E-01	7.40E-01	LOC338963	hypothetical protein LOC338963	chr15q25.2	1563878_a_at	XR_040082 /// XR_040083 /// XR_040084
2.20	2.10	0.10	4.05E-01	7.40E-01	---	---	---	1562595_at	---
3.59	3.48	0.11	4.05E-01	7.40E-01	WDR73	WD repeat domain 73	chr15q25.2	233242_at	NM_032856
7.04	6.85	0.19	4.05E-01	7.40E-01	CCNK	cyclin K	chr14q32	225824_at	NM_001099402 /// NM_003858
3.54	3.37	0.17	4.05E-01	7.40E-01	CCDC61	coiled-coil domain containing 61	chr19q13.32	228472_at	NM_001080402

8.08	7.82	0.27	4.05E-01	7.40E-01	LOC401115	hypothetical LOC401115	chr4p16.3	229860_x_at	XM_001716080 /// XM_379250 /// XM_937968																				
9.95	9.59	0.36	4.05E-01	7.40E-01	OAT	ornithine aminotransferase (gyrate atrophy)	chr10q26	201599_at	NM_000274																				
2.01	1.90	0.11	4.05E-01	7.40E-01	---	---	---	207744_at	---																				
5.45	5.16	0.29	4.05E-01	7.40E-01	RDH13	retinol dehydrogenase 13 (all-trans/9-cis)	chr19q13.42	225467_s_at	NM_138412																				
7.43	7.23	0.19	4.05E-01	7.40E-01	EPHB4	EPH receptor B4	chr7q22	202894_at	NM_004444																				
4.58	4.08	0.49	4.05E-01	7.40E-01	ENTPD4 /// LOXL2	ectonucleoside triphosphate diphosphohydrolase 4 /// lysyl oxidase-like 2	chr8p21.3 /// chr8p21.3-p21.2	202998_s_at	NM_001128930 /// NM_002318 /// NM_004901																				
2.38	2.24	0.14	4.05E-01	7.40E-01	---	---	---	1563316_at	---																				
2.98	2.87	0.11	4.05E-01	7.40E-01	KLHL23	kelch-like 23 (Drosophila)	chr2q31.1	241682_at	NM_144711																				
2.20	2.05	0.14	4.05E-01	7.40E-01	---	---	---	1566645_at	---																				
7.40	7.07	0.33	4.05E-01	7.40E-01	DHRS3	dehydrogenase/reductase (SDR family) member 3	chr1p36.1	202481_at	NM_004753																				
4.21	3.95	0.26	4.05E-01	7.40E-01	RARB	retinoic acid receptor, beta	chr3p24	205080_at	NM_000965 /// NM_016152																				
5.22	5.00	0.22	4.05E-01	7.40E-01	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	chr19p12	210811_s_at	NM_019070																				
10.01	9.66	0.35	4.05E-01	7.40E-01	HLA-DRA	major histocompatibility complex, class II, DR alpha	chr6p21.3	208894_at	NM_019111																				
2.39	2.27	0.12	4.06E-01	7.40E-01	---	---	---	233194_at	---																				
1.90	1.80	0.09	4.06E-01	7.40E-01	hCG_2015956 /// LOC100127893 /// LOC100131085 /// LOC388401 /// LOC441896 /// LOC641900 /// LOC728380 /// LOC728843 /// RPL7	hCG2015956 /// similar to ribosomal protein L7 /// hypothetical LOC100131085 /// similar to ribosomal protein L7 /// similar to ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// hypothetical LOC728380 /// hypothetical LOC728843 /// ribosomal protein L7	chr17q21.33 /// chr1p13.3 /// chr2p22.2 /// chr5q14.1 /// chr5q34 /// chr6p22.3 /// chr8q21.11	216588_at	NM_000971 /// XM_001719048 /// XM_001722435 /// XM_943842 /// XR_015391 /// XR_015500 /// XR_015600 /// XR_015705 /// XR_016234 /// XR_016879 /// XR_018042 /// XR_018794 /// XR_038286 /// XR_038691 /// XR_038779 /// XR_038885 /// XR_038901 /// XR_038947 /// XR_039043 /// XR_039090 /// XR_039345 /// XR_039473 /// XR_039795																				
8.79	8.60	0.19	4.06E-01	7.40E-01	NPTN	neuroplastin	chr15q22	202228_s_at	NM_012428 /// NM_017455																				
2.18	2.06	0.11	4.06E-01	7.40E-01	RHEBL1	Ras homolog enriched in brain like 1	chr12q13.12	1570253_a_at	NM_144593																				
4.39	4.23	0.16	4.06E-01	7.40E-01	UCN3	urocortin 3 (stresscopin)	chr10p15.1	1552676_at	NM_053049																				
5.67	5.51	0.16	4.06E-01	7.40E-01	THAP3	THAP domain containing, apoptosis associated protein 3	chr1p36.31	213192_at	NM_138350																				

3.93	3.82	0.11	4.06E-01	7.41E-01	LOC91316	Similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific)	chr22q11.23	239924_at	XR_038140 /// XR_040205 /// XR_040206
3.89	3.78	0.11	4.06E-01	7.41E-01	KANK1	KN motif and ankyrin repeat domains 1	chr9p24.3	238789_at	NM_015158 /// NM_153186
4.67	4.46	0.21	4.06E-01	7.41E-01	DIDO1	death inducer-obliterator 1	chr20q13.33	227335_at	NM_022105 /// NM_033081 /// NM_080796 /// NM_080797
4.32	4.10	0.21	4.06E-01	7.41E-01	CD8A	CD8a molecule	chr2p12	205758_at	NM_001768 /// NM_171827
2.19	2.08	0.11	4.06E-01	7.41E-01	TFE3	Transcription factor binding to IGHM enhancer 3	chrXp11.22	1567704_at	NM_006521
3.56	3.36	0.19	4.06E-01	7.41E-01	DLEC1	deleted in lung and esophageal cancer 1	chr3p22-p21.3	206798_x_at	NM_007335 /// NM_007337
4.97	4.83	0.15	4.06E-01	7.41E-01	MRPS12	mitochondrial ribosomal protein S12	chr19q13.1-q13.2	210008_s_at	NM_021107 /// NM_033362 /// NM_033363
2.12	2.03	0.09	4.06E-01	7.41E-01	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	chr17p13.1	34471_at	NM_002472
3.33	3.19	0.14	4.06E-01	7.41E-01	TSPAN5	tetraspanin 5	chr4q23	209890_at	NM_005723
2.17	2.08	0.09	4.07E-01	7.41E-01	LOC646903	hypothetical LOC646903	chr3q25.1	237116_at	XR_017284 /// XR_019133
2.46	2.30	0.16	4.07E-01	7.41E-01	CIDEC	cell death-inducing DFFA-like effector c	chr3p25.3	1554839_at	NM_022094
6.37	6.26	0.11	4.07E-01	7.41E-01	FAM63A	family with sequence similarity 63, member A	chr1q21.2	226062_x_at	NM_001040217 /// NM_018379
3.17	3.06	0.11	4.07E-01	7.41E-01	LOC147299	hypothetical protein LOC147299	chr18q23	1557590_at	---
6.14	5.83	0.31	4.07E-01	7.41E-01	C12orf52	chromosome 12 open reading frame 52	chr12q24.13	44065_at	NM_032848
5.84	5.64	0.20	4.07E-01	7.41E-01	CYTH4	cytohesin 4	chr22q12.3-q13.1	219183_s_at	NM_013385
6.48	6.16	0.32	4.07E-01	7.41E-01	SLC44A2	solute carrier family 44, member 2	chr19p13.1	225175_s_at	NM_020428
5.46	5.24	0.21	4.07E-01	7.41E-01	SSBP2	single-stranded DNA binding protein 2	chr5q14.1	210829_s_at	NM_012446
5.03	4.86	0.16	4.07E-01	7.41E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	217610_at	NR_003655 /// XR_042143 /// XR_042182
6.55	6.34	0.21	4.07E-01	7.41E-01	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	chr6p21.3	204279_at	NM_002800 /// NM_148954
2.57	2.44	0.13	4.07E-01	7.41E-01	PRDM2	PR domain containing 2, with ZNF domain	chr1p36.21	216433_s_at	NM_001007257 /// NM_012231 /// NM_015866
2.36	2.26	0.10	4.07E-01	7.41E-01	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	chr16q12.2	216610_at	NM_001043
2.15	2.04	0.11	4.07E-01	7.41E-01	---	---	---	1566094_at	---
4.13	3.90	0.22	4.07E-01	7.41E-01	SORCS2	sortilin-related VPS10 domain containing receptor 2	chr4p16.1	228720_at	NM_020777
3.65	3.54	0.11	4.07E-01	7.41E-01	MAGOH2	mago-nashi homolog 2, proliferation-associated (Drosophila)	chr17p13.1	217693_x_at	---
2.88	2.73	0.15	4.07E-01	7.41E-01	LOC727978 /// LOC728210	Similar to hCG2042473 /// Similar to hCG2042473	chr3q29	238777_x_at	XM_001126286 /// XM_001126873 /// XM_001714108 /// XM_001732873
2.01	1.93	0.09	4.07E-01	7.41E-01	---	---	---	1561229_at	---
3.20	3.05	0.15	4.07E-01	7.41E-01	LGALS12	lectin, galactoside-binding, soluble, 12	chr11q13	223828_s_at	NM_033101
2.68	2.54	0.14	4.07E-01	7.41E-01	---	---	---	1563484_at	---
2.12	2.01	0.11	4.07E-01	7.41E-01	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	chr14q11.2	220474_at	NM_030631
4.57	4.39	0.18	4.07E-01	7.41E-01	---	---	---	1569478_s_at	---
2.06	1.96	0.10	4.07E-01	7.41E-01	---	---	---	232411_at	---
2.16	2.04	0.12	4.08E-01	7.42E-01	---	---	---	1569646_a_at	---

5.12	4.97	0.15	4.08E-01	7.42E-01	---	---	---	239463_at	---
2.19	2.08	0.11	4.08E-01	7.42E-01	---	---	---	1562727_at	---
7.27	7.14	0.13	4.08E-01	7.42E-01	ABHD12	abhydrolase domain containing 12	chr20p11.21	224742_at	NM_001042472 /// NM_015600
2.20	2.08	0.12	4.08E-01	7.42E-01	LOC158830	similar to Ab2-183	chrXq13.1	231377_at	NM_001025265
2.67	2.50	0.17	4.08E-01	7.42E-01	BRAP	BRCA1 associated protein	chr12q24	209922_at	NM_006768
6.85	6.58	0.26	4.08E-01	7.42E-01	AGK	acylglycerol kinase	chr7q34	222132_s_at	NM_018238
2.13	2.04	0.09	4.08E-01	7.42E-01	PLGLB2	plasminogen-like B2	chr2p11-q11	230120_s_at	NM_002665
2.46	2.36	0.10	4.08E-01	7.42E-01	LOC728460	similar to FLJ32921 protein	chr5q23.2	231434_at	XM_001128581 /// XM_001129498 /// XM_001723364
5.68	5.45	0.23	4.08E-01	7.42E-01	COIL	coilin	chr17q22-q23	203654_s_at	NM_004645
4.47	4.29	0.18	4.08E-01	7.42E-01	HCG18	HLA complex group 18	chr6p21.3	225584_at	NR_024052 /// NR_024053 /// XM_933653 /// XM_936164 /// XM_944855
3.91	3.73	0.18	4.08E-01	7.42E-01	MTA2	metastasis associated 1 family, member 2	chr11q12-q13.1	203444_s_at	NM_004739
5.26	5.02	0.24	4.08E-01	7.42E-01	---	---	---	228991_at	---
5.06	4.71	0.35	4.08E-01	7.42E-01	EPB41L5	erythrocyte membrane protein band 4.1 like 5	chr2q14.2	225855_at	NM_020909
9.29	8.92	0.37	4.08E-01	7.42E-01	LOC283666	hypothetical LOC283666	chr15q21.3	226682_at	---
5.85	5.61	0.24	4.09E-01	7.42E-01	VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	chr13q14.3	222478_at	NM_016075
2.07	1.96	0.11	4.09E-01	7.42E-01	LOC645485	hypothetical LOC645485	chr12p11.21	1560251_at	XM_932931 /// XM_944437
3.01	2.84	0.17	4.09E-01	7.42E-01	PLXNA3	plexin A3	chrXq28	1553139_s_at	NM_017514
7.64	7.33	0.32	4.09E-01	7.42E-01	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2	chr2p22.2-p22.1	222700_at	NM_022374
5.98	5.75	0.23	4.09E-01	7.43E-01	UHRF1BP1	UHRF1 binding protein 1	chr6p21	226135_at	NM_017754
7.35	7.16	0.19	4.09E-01	7.43E-01	YTHDF2	YTH domain family, member 2	chr1p35	217812_at	NM_016258
3.46	3.10	0.36	4.09E-01	7.43E-01	LOC283666	Hypothetical LOC283666	chr15q21.3	240951_at	---
3.62	3.50	0.12	4.09E-01	7.43E-01	MYO9B	myosin IXB	chr19p13.1	208452_x_at	NM_001130065 /// NM_004145
2.51	2.33	0.18	4.09E-01	7.43E-01	LOC100133236	Hypothetical protein LOC100133236	chr1q32.1	238250_at	XM_001714136 /// XM_001714243 /// XM_001714262
3.19	2.96	0.23	4.09E-01	7.43E-01	C12orf66	chromosome 12 open reading frame 66	chr12q14.2	1554067_at	NM_152440
7.29	7.11	0.18	4.09E-01	7.43E-01	FBXO18	F-box protein, helicase, 18	chr10p15.1	224683_at	NM_032807 /// NM_178150
2.67	2.51	0.16	4.09E-01	7.43E-01	GAS5	growth arrest-specific 5 (non-protein coding)	chr1q25.1	1560402_at	NR_002578
2.40	2.29	0.11	4.10E-01	7.43E-01	ZBTB20	Zinc finger and BTB domain containing 20	chr3q13.2	244581_at	NM_015642
2.95	2.41	0.55	4.10E-01	7.43E-01	ZNF460	zinc finger protein 460	chr19q13.4	216279_at	NM_006635
3.55	3.39	0.16	4.10E-01	7.43E-01	MRPL44	mitochondrial ribosomal protein L44	chr2q36.1	218202_x_at	NM_022915
4.62	4.48	0.14	4.10E-01	7.43E-01	NR6A1	nuclear receptor subfamily 6, group A, member 1	chr9q33-q34.1	211402_x_at	NM_001489 /// NM_033334
8.12	7.65	0.47	4.10E-01	7.43E-01	SRGN	serglycin	chr10q22.1	201858_s_at	NM_002727
6.17	5.90	0.27	4.10E-01	7.43E-01	C9orf103	chromosome 9 open reading frame 103	chr9q21-q22	227865_at	NM_001001551
4.90	4.65	0.24	4.10E-01	7.43E-01	KIAA1462	KIAA1462	chr10p11.23	213316_at	NM_020848
2.97	2.79	0.18	4.10E-01	7.43E-01	LOC441086	hypothetical gene supported by BC039003	chr5q13.3	1562920_at	XM_001714443 /// XM_001715645
1.96	1.86	0.09	4.10E-01	7.43E-01	---	---	---	1556888_at	---
6.67	6.44	0.22	4.10E-01	7.43E-01	---	---	---	227319_at	---
5.91	5.73	0.17	4.10E-01	7.43E-01	ALG12	asparagine-linked glycosylation 12 homolog (S. cerevisiae, alpha-1,6-mannosyltransferase)	chr22q13.33	218444_at	NM_024105
3.17	2.98	0.18	4.10E-01	7.43E-01	KALRN	kalirin, RhoGEF kinase	chr3q21.1-q21.2	206078_at	NM_001024660 /// NM_003947 /// NM_007064

7.79	7.58	0.21	4.10E-01	7.43E-01	CLSTN1	calsyntenin 1	chr1p36.22	201561_s_at	NM_001009566 /// NM_014944
2.30	2.15	0.15	4.10E-01	7.43E-01	---	---	---	215477_at	---
2.36	2.26	0.10	4.10E-01	7.43E-01	SKP2	S-phase kinase-associated protein 2 (p45)	chr5p13	210567_s_at	NM_005983 /// NM_032637
3.91	3.70	0.22	4.10E-01	7.43E-01	---	---	---	244561_at	---
2.74	2.62	0.12	4.10E-01	7.43E-01	41342	membrane-associated ring finger (C3HC4) 9	chr12q14.1	230001_at	NM_138396
6.11	5.89	0.23	4.10E-01	7.43E-01	TUBGCP3	tubulin, gamma complex associated protein 3	chr13q34	203690_at	NM_006322
1.95	1.86	0.09	4.10E-01	7.44E-01	TSPAN2	tetraspanin 2	chr1p13.2	214606_at	NM_005725
3.48	3.33	0.15	4.10E-01	7.44E-01	FRS3	fibroblast growth factor receptor substrate 3	chr6p21.1	219907_at	NM_006653
8.20	8.06	0.15	4.10E-01	7.44E-01	FAM108A1	family with sequence similarity 108, member A1	chr19p13.3	221267_s_at	NM_001130111 /// NM_031213
4.74	4.34	0.40	4.10E-01	7.44E-01	PDK1	pyruvate dehydrogenase kinase, isozyme 1	chr2q31.1	206686_at	NM_002610
2.14	1.98	0.16	4.11E-01	7.44E-01	LOC286434 /// LOC389906 /// LOC441528 /// LOC728687 /// LOC729162	hypothetical protein LOC286434 /// similar to Serine/threonine-protein kinase PRKX (Protein kinase PKX1) /// hypothetical protein LOC441528 /// similar to hCG1981372 /// similar to LOC389906 protein	chrXp22.33	222031_at	XM_001128169 /// XM_001713861 /// XM_001715777 /// XM_001717193 /// XM_928240 /// XM_942518 /// XR_041386
5.94	5.75	0.20	4.11E-01	7.44E-01	ERLIN2	ER lipid raft associated 2	chr8p11.2	221543_s_at	NM_001003790 /// NM_001003791 /// NM_007175
3.82	3.50	0.31	4.11E-01	7.44E-01	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	chr2p23.3	223504_at	NM_016544
3.25	3.04	0.20	4.11E-01	7.44E-01	CA14	carbonic anhydrase XIV	chr1q21	219464_at	NM_012113
5.99	5.79	0.19	4.11E-01	7.44E-01	ACAD11 /// NPHP3	acyl-Coenzyme A dehydrogenase family, member 11 /// nephronophthisis 3 (adolescent)	chr3q22.1	225573_at	NM_032169 /// NM_153240
2.16	2.04	0.12	4.11E-01	7.44E-01	HOXD12	homeobox D12	chr2q31-q32|2q31.1	221411_at	NM_021193
5.36	5.13	0.22	4.11E-01	7.44E-01	SEC63	SEC63 homolog (S. cerevisiae)	chr6q21	229969_at	NM_007214
5.23	5.06	0.17	4.11E-01	7.44E-01	DAGLB	diacylglycerol lipase, beta	chr7p22.1	225833_at	NM_139179
3.74	3.50	0.24	4.11E-01	7.44E-01	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	chr2q35	1554080_at	NM_005444
3.12	3.02	0.09	4.11E-01	7.44E-01	C13orf3	chromosome 13 open reading frame 3	chr13q12.11	227165_at	NM_145061
3.05	2.95	0.10	4.11E-01	7.44E-01	---	---	---	1566643_a_at	---
3.23	2.96	0.27	4.11E-01	7.44E-01	FAM13A1	family with sequence similarity 13, member A1	chr4q22.1	1569025_s_at	NM_001015045 /// NM_014883
2.10	2.01	0.09	4.11E-01	7.44E-01	---	---	---	1560346_at	---
4.20	4.03	0.17	4.11E-01	7.44E-01	FAM174B	family with sequence similarity 174, member B	chr15q26.1	221880_s_at	NM_207446
3.24	2.96	0.29	4.11E-01	7.44E-01	SCARA3	scavenger receptor class A, member 3	chr8p21	223843_at	NM_016240 /// NM_182826
3.58	3.44	0.13	4.11E-01	7.44E-01	OR13C4	olfactory receptor, family 13, subfamily C, member 4	chr9q31.1	1567298_at	NM_001001919
3.96	3.76	0.20	4.11E-01	7.44E-01	---	---	---	225328_at	---
2.47	2.36	0.11	4.12E-01	7.44E-01	---	---	---	206962_x_at	---
6.29	6.06	0.23	4.12E-01	7.44E-01	SYS1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	chr20q13.12	224669_at	NM_033542
9.27	9.11	0.16	4.12E-01	7.44E-01	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	chr14q32	200694_s_at	NM_020414
6.14	6.01	0.13	4.12E-01	7.44E-01	NAP1L4	nucleosome assembly protein 1-like 4	chr11p15.5	201414_s_at	NM_005969
2.33	2.23	0.10	4.12E-01	7.44E-01	TRAF1	TNF receptor-associated factor 1	chr9q33-q34	235116_at	NM_005658
4.83	4.66	0.17	4.12E-01	7.44E-01	C10orf57	chromosome 10 open reading frame 57	chr10q22.3	218174_s_at	NM_025125
2.22	2.11	0.11	4.12E-01	7.44E-01	RP11-756A22.3	hypothetical LOC646405	chr13q12.12-q12.13	1562583_s_at	NM_001126062 /// XM_001722635 /// XM_929331 /// XM_940374
6.19	5.97	0.22	4.12E-01	7.44E-01	TWSG1	twisted gastrulation homolog 1 (Drosophila)	chr18p11.3	225406_at	NM_020648
2.10	2.01	0.10	4.12E-01	7.44E-01	---	---	---	1570136_at	---
3.11	2.95	0.16	4.12E-01	7.44E-01	---	---	---	213657_s_at	---
2.33	2.17	0.15	4.12E-01	7.45E-01	---	---	---	1561303_at	---
2.70	2.54	0.16	4.12E-01	7.45E-01	RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)	chr19q13.42	1559190_s_at	NM_138412

5.37	5.18	0.19	4.12E-01	7.45E-01	LOC100134401	hypothetical protein LOC100134401	---	213605_s_at	XM_001717368
3.08	2.90	0.18	4.12E-01	7.45E-01	ARL17	ADP-ribosylation factor-like 17	chr17q21.31	229028_s_at	NM_001039083 /// NM_001103154
4.42	4.20	0.22	4.12E-01	7.45E-01	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	chr19q13.2	206576_s_at	NM_001024912 /// NM_001712
6.65	6.46	0.20	4.12E-01	7.45E-01	MTMR12	myotubularin related protein 12	chr5p13.3	225232_at	NM_001040446
3.49	3.34	0.15	4.12E-01	7.45E-01	LOC284422	similar to HSPC323	chr19p13.3	231982_at	XM_001726225 /// XM_209196 /// XM_939969
6.78	6.61	0.17	4.12E-01	7.45E-01	ARD1A	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	chrXq28	203025_at	NM_003491
4.58	4.41	0.17	4.12E-01	7.45E-01	PGM2L1	Phosphoglucomutase 2-like 1	chr11q13.4	1569448_at	NM_173582
6.10	5.96	0.14	4.12E-01	7.45E-01	SNX27	sorting nexin family member 27	chr1q21.3	221498_at	NM_030918
2.83	2.65	0.18	4.13E-01	7.45E-01	C9orf31	chromosome 9 open reading frame 31	chr9q33.2	221072_at	XR_040686 /// XR_040687 /// XR_040688
2.88	2.71	0.17	4.13E-01	7.45E-01	CLECL1	C-type lectin-like 1	chr12p13.31	244413_at	NM_172004
5.82	5.72	0.10	4.13E-01	7.45E-01	DHRS12	dehydrogenase/reductase (SDR family) member 12	chr13q14.3	204800_s_at	NM_001031719 /// NM_024705
5.73	5.43	0.29	4.13E-01	7.45E-01	TAOK2	TAO kinase 2	chr16p11.2	204986_s_at	NM_004783 /// NM_016151
5.71	5.54	0.17	4.13E-01	7.45E-01	DOCK1	dedicator of cytokinesis 1	chr10q26.13-q26.3	203187_at	NM_001380
4.92	4.59	0.32	4.13E-01	7.45E-01	PLEKHA3	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	chr2q31.2	227658_s_at	NM_019091
2.86	2.73	0.13	4.13E-01	7.45E-01	PPY	pancreatic polypeptide	chr17q21	210670_at	NM_002722
2.97	2.73	0.25	4.13E-01	7.45E-01	---	---	---	230397_at	---
6.04	5.82	0.22	4.13E-01	7.45E-01	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	chr10q24.1	226459_at	NM_152309
2.73	2.61	0.12	4.13E-01	7.45E-01	---	---	---	243155_at	---
7.22	6.98	0.24	4.13E-01	7.45E-01	SLC2A8	solute carrier family 2 (facilitated glucose transporter), member 8	chr9q33.3	218985_at	NM_014580
6.29	6.00	0.29	4.13E-01	7.45E-01	BASP1	brain abundant, membrane attached signal protein 1	chr5p15.1-p14	202391_at	NM_006317
2.95	2.80	0.14	4.13E-01	7.45E-01	LOC100132005	hypothetical LOC100132005	chr6p21.2	1557669_at	XM_001722344 /// XM_001722399 /// XM_001725157
3.58	3.40	0.18	4.13E-01	7.46E-01	CCHCR1	coiled-coil alpha-helical rod protein 1	chr6p21.3	37425_g_at	NM_001105563 /// NM_001105564 /// NM_019052
4.23	4.09	0.14	4.13E-01	7.46E-01	---	---	---	243860_at	---
2.75	2.59	0.16	4.13E-01	7.46E-01	---	---	---	1561060_at	---
3.06	2.93	0.13	4.13E-01	7.46E-01	---	---	---	1563071_at	---
6.44	6.23	0.21	4.13E-01	7.46E-01	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	chr2p13.1	201298_s_at	NM_018221
3.23	2.89	0.34	4.13E-01	7.46E-01	ZBTB10	zinc finger and BTB domain containing 10	chr8q13-q21.1	219312_s_at	NM_001105539 /// NM_023929
3.89	3.77	0.11	4.13E-01	7.46E-01	NOL6	nucleolar protein family 6 (RNA-associated)	chr9p13.3	232566_at	NM_022917 /// NM_139235
2.16	2.04	0.12	4.14E-01	7.46E-01	---	---	---	1560169_at	---
4.83	4.63	0.20	4.14E-01	7.46E-01	EXOSC3	exosome component 3	chr9p11	223490_s_at	NM_001002269 /// NM_016042
2.24	2.12	0.12	4.14E-01	7.46E-01	---	---	---	1566204_at	---
4.79	4.41	0.38	4.14E-01	7.46E-01	ANGPTL1	angiopoietin-like 1	chr1q25.2	239183_at	NM_004673
3.86	3.75	0.11	4.14E-01	7.46E-01	SFTPC	surfactant protein C	chr8p21	38691_s_at	NM_003018
2.48	2.38	0.10	4.14E-01	7.46E-01	---	---	---	236757_at	---
3.32	3.18	0.14	4.14E-01	7.46E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	213763_at	NM_001113239 /// NM_022740
2.51	2.40	0.10	4.14E-01	7.46E-01	ALG10	asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase)	chr12p11.1	1552306_at	NM_032834
2.32	2.22	0.10	4.14E-01	7.46E-01	TTBK2	tau tubulin kinase 2	chr15q15.2	1554294_s_at	NM_173500

2.85	2.73	0.12	4.14E-01	7.46E-01	---	---	---	244082_at	---
4.76	4.51	0.25	4.14E-01	7.46E-01	TM4SF1	transmembrane 4 L six family member 1	chr3q21-q25	209387_s_at	NM_014220
2.38	2.28	0.10	4.14E-01	7.46E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1562591_a_at	NM_153003
3.14	3.00	0.14	4.14E-01	7.46E-01	ALS2CL	ALS2 C-terminal like	chr3p21.31	243276_at	NM_147129 /// NM_182775
2.41	2.29	0.12	4.14E-01	7.46E-01	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	chr15q22-q24	1558356_at	NM_001008224 /// NM_018003
4.22	4.08	0.14	4.14E-01	7.46E-01	ANK1	ankyrin 1, erythrocytic	chr8p11.1	205391_x_at	NM_000037 /// NM_020475 /// NM_020476 /// NM_020477 /// NM_020478 /// NM_020480
3.30	2.95	0.35	4.14E-01	7.46E-01	tcag7.1238	homeo box A11, antisense	chr7p15.2	230666_at	NR_002795
2.81	2.61	0.21	4.14E-01	7.46E-01	MDFIC	MyoD family inhibitor domain containing	chr7q31.1-q31.2	1559942_at	NM_199072
5.24	4.79	0.46	4.14E-01	7.46E-01	---	---	---	1559391_s_at	---
5.17	4.86	0.32	4.14E-01	7.46E-01	STIM2	stromal interaction molecule 2	chr4p15.2	225246_at	NM_020860
7.30	7.11	0.18	4.15E-01	7.46E-01	SH3GL1	SH3-domain GRB2-like 1	chr19p13.3	201851_at	NM_003025
3.01	2.68	0.33	4.15E-01	7.46E-01	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	chr6p21.32	205518_s_at	NR_002174
6.86	6.75	0.11	4.15E-01	7.46E-01	APLP2	amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	211404_s_at	NM_001642
3.40	3.26	0.14	4.15E-01	7.47E-01	PRRG3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	chrXq28	220433_at	NM_024082
2.24	2.13	0.11	4.15E-01	7.47E-01	---	---	---	244603_at	---
2.58	2.45	0.13	4.15E-01	7.47E-01	TACC2	transforming, acidic coiled-coil containing protein 2	chr10q26	1570025_at	NM_006997 /// NM_206860 /// NM_206861 /// NM_206862
2.35	2.23	0.12	4.15E-01	7.47E-01	ZFX	zinc finger protein, X-linked	chrXp21.3	217176_s_at	NM_003410
6.18	6.04	0.14	4.15E-01	7.47E-01	DET1	de-etiolated homolog 1 (Arabidopsis)	chr15q25.3	219641_at	NM_017996
3.68	3.54	0.14	4.15E-01	7.47E-01	B3GALTL	beta 1,3-galactosyltransferase-like	chr13q12.3	227100_at	NM_194318
6.15	5.85	0.30	4.15E-01	7.47E-01	RFX7	regulatory factor X, 7	chr15q21.3	222630_at	NM_022841
5.40	5.13	0.27	4.15E-01	7.47E-01	---	---	---	227290_at	---
8.96	8.69	0.27	4.15E-01	7.47E-01	TIMP2	TIMP metallopeptidase inhibitor 2	chr17q25	224560_at	NM_003255
2.11	1.99	0.12	4.15E-01	7.47E-01	---	---	---	1561086_at	---
1.98	1.89	0.09	4.16E-01	7.47E-01	---	---	---	1554871_at	---
2.48	2.35	0.13	4.16E-01	7.47E-01	---	---	---	236856_x_at	---
2.06	1.93	0.13	4.16E-01	7.47E-01	---	---	---	1559986_at	---
2.04	1.95	0.10	4.16E-01	7.47E-01	RP11-35N6.1	plasticity related gene 3	chr9q31.1	1570250_at	NM_017753 /// NM_207299
6.47	6.26	0.21	4.16E-01	7.47E-01	MRPL11	mitochondrial ribosomal protein L11	chr11q13.3	219162_s_at	NM_016050 /// NM_170738 /// NM_170739
5.16	4.95	0.20	4.16E-01	7.47E-01	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	chr12q24.31	219245_s_at	NM_024623
4.02	3.88	0.14	4.16E-01	7.47E-01	SH3TC1	SH3 domain and tetratricopeptide repeats 1	chr4p16.1	229832_x_at	NM_018986
2.19	2.08	0.12	4.16E-01	7.47E-01	---	---	---	1562201_x_at	---
7.55	7.36	0.18	4.16E-01	7.47E-01	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	chr16p13.11	212053_at	NM_015027
8.35	8.16	0.19	4.16E-01	7.47E-01	PAFAH1B2	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kDa	chr11q23	224777_s_at	NM_002572
2.80	2.63	0.17	4.16E-01	7.47E-01	TRAPPC4	trafficking protein particle complex 4	chr11q23.3	234456_at	NM_016146
8.32	8.20	0.12	4.16E-01	7.47E-01	FKBP2	FK506 binding protein 2, 13kDa	chr11q13.1-q13.3	203391_at	NM_004470 /// NM_057092
4.03	3.93	0.10	4.16E-01	7.47E-01	HIST1H2AB	histone cluster 1, H2ab	chr6p21.3	208569_at	NM_003513
4.30	4.03	0.27	4.16E-01	7.47E-01	---	---	---	235531_at	---
3.87	3.61	0.26	4.16E-01	7.47E-01	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	chr18q21	241396_at	NM_015277

7.40	7.23	0.17	4.16E-01	7.47E-01	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	chr17q21.31	225289_at	NM_003150 /// NM_139276 /// NM_213662																				
3.79	3.61	0.18	4.16E-01	7.47E-01	UCN	urocortin	chr2p23-p21	206072_at	NM_003353																				
2.49	2.37	0.12	4.16E-01	7.47E-01	CSPP1	centrosome and spindle pole associated protein 1	chr8q13.2	227105_at	NM_001077204 /// NM_024790																				
2.92	2.77	0.15	4.16E-01	7.47E-01	---	---	---	237293_at	---																				
7.06	6.79	0.26	4.16E-01	7.47E-01	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	chr6p21.3	215535_s_at	NM_006411 /// NM_032741																				
3.71	3.42	0.30	4.17E-01	7.48E-01	CEP68	centrosomal protein 68kDa	chr2p14	239442_at	NM_015147																				
2.46	2.34	0.11	4.17E-01	7.48E-01	---	---	---	1565602_at	---																				
7.13	6.85	0.29	4.17E-01	7.48E-01	SMAP2	stromal membrane-associated GTPase-activating protein 2	chr1p35.3-p34.1	225282_at	NM_022733																				
5.85	5.73	0.12	4.17E-01	7.48E-01	GOSR2	golgi SNAP receptor complex member 2	chr17q21	210009_s_at	NM_001012511 /// NM_004287 /// NM_054022																				
2.55	2.45	0.10	4.17E-01	7.48E-01	MYPN	myopalladin	chr10q21.3	235367_at	NM_032578																				
2.58	2.46	0.12	4.17E-01	7.48E-01	---	---	---	240460_at	---																				
4.58	4.40	0.17	4.17E-01	7.48E-01	ABHD11	abhydrolase domain containing 11	chr7q11.23	1552800_at	NM_148912																				
2.42	2.31	0.11	4.17E-01	7.48E-01	---	---	---	237501_at	---																				
2.18	2.07	0.12	4.17E-01	7.48E-01	---	---	---	213964_x_at	---																				
7.94	7.73	0.21	4.17E-01	7.48E-01	GM2A	GM2 ganglioside activator	chr5q31.3-q33.1	35820_at	NM_000405																				
3.56	3.44	0.12	4.17E-01	7.48E-01	SYK	spleen tyrosine kinase	chr9q22	209269_s_at	NM_003177																				
2.27	2.17	0.10	4.17E-01	7.48E-01	RGMB	RGM domain family, member B	chr5q21.1	242450_at	NM_001012761 /// NM_173670																				
2.51	2.37	0.15	4.17E-01	7.48E-01	---	---	---	243922_at	---																				
2.29	2.16	0.13	4.17E-01	7.48E-01	VAV3	vav 3 guanine nucleotide exchange factor	chr1p13.3	224221_s_at	NM_001079874 /// NM_006113																				
5.08	4.83	0.25	4.17E-01	7.48E-01	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	chr14q32.2	226684_at	NM_018036																				
2.24	2.14	0.10	4.18E-01	7.48E-01	MDN1	MDN1, midasin homolog (yeast)	chr6q15	234854_at	NM_014611																				
8.05	7.86	0.20	4.18E-01	7.48E-01	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	chr19p13.12-p13.11	202839_s_at	NM_004146																				
5.80	5.66	0.14	4.18E-01	7.48E-01	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	chr2q21.1	213521_at	NM_014369																				
6.69	6.50	0.19	4.18E-01	7.48E-01	TIMM23 /// TIMM23B	translocase of inner mitochondrial membrane 23 homolog (yeast) /// translocase of inner mitochondrial membrane 23 homolog B (yeast)	chr10q11.21-q11.23 /// chr10q11.23	218119_at	NM_006327 /// XM_001715214 /// XM_928114																				
3.62	3.48	0.15	4.18E-01	7.49E-01	---	---	---	217490_at	---																				
3.82	3.55	0.27	4.18E-01	7.49E-01	LPCAT2	lysophosphatidylcholine acyltransferase 2	chr16q12.2	239598_s_at	NM_017839																				
4.72	4.54	0.18	4.18E-01	7.49E-01	MTMR2	myotubularin related protein 2	chr11q22	203212_s_at	NM_016156 /// NM_201278 /// NM_201281 /// NR_023354 /// NR_023355 /// NR_023356																				
2.80	2.57	0.23	4.18E-01	7.49E-01	MBNL2	Muscleblind-like 2 (Drosophila)	chr13q32.1	1553536_at	NM_144778 /// NM_207304																				
2.53	2.35	0.19	4.18E-01	7.49E-01	WNK4	WNK lysine deficient protein kinase 4	chr17q21-q22	244344_at	NM_032387																				
4.79	4.55	0.23	4.18E-01	7.49E-01	LRRC51	leucine rich repeat containing 51	chr11q13.4	226717_at	NM_145309																				
7.85	7.58	0.27	4.18E-01	7.49E-01	CABC1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	chr1q42.13	218168_s_at	NM_020247																				
6.96	6.73	0.23	4.18E-01	7.49E-01	RAP2A	RAP2A, member of RAS oncogene family	chr13q34	225585_at	NM_021033																				
7.58	7.40	0.19	4.18E-01	7.49E-01	SDF4	stromal cell derived factor 4	chr1p36.33	217855_x_at	NM_016176 /// NM_016547																				
5.44	5.22	0.22	4.18E-01	7.49E-01	SIN3A	SIN3 homolog A, transcription regulator (yeast)	chr15q24.2	225135_at	NM_015477																				
3.19	3.04	0.15	4.18E-01	7.49E-01	C12orf47	chromosome 12 open reading frame 47	chr12q24.12	219817_at	NR_015404 /// XR_017874 /// XR_017973																				
2.23	2.12	0.11	4.18E-01	7.49E-01	---	---	---	1556362_at	---																				

6.70	6.58	0.12	4.18E-01	7.49E-01	FKBP15	FK506 binding protein 15, 133kDa	chr9q32	31826_at	NM_015258																				
3.19	3.07	0.12	4.18E-01	7.49E-01	---	---	---	1556837_a_at	---																				
8.64	8.44	0.19	4.18E-01	7.49E-01	C12orf62	chromosome 12 open reading frame 62	chr12q13.13	225772_s_at	NM_032901																				
1.91	1.82	0.09	4.18E-01	7.49E-01	---	---	---	233789_at	---																				
3.29	3.14	0.15	4.19E-01	7.49E-01	---	---	---	1567010_at	---																				
3.20	3.02	0.18	4.19E-01	7.49E-01	GPATCH2	G patch domain containing 2	chr1q41	236026_at	NM_018040																				
2.01	1.92	0.10	4.19E-01	7.49E-01	---	---	---	223873_s_at	---																				
2.49	2.29	0.20	4.19E-01	7.49E-01	CCNT2	cyclin T2	chr2q21.3	214638_s_at	NM_001241 /// NM_058241																				
4.44	4.11	0.33	4.19E-01	7.49E-01	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	chr3q26.2-q27	210180_s_at	NM_004593																				
4.91	4.71	0.20	4.19E-01	7.49E-01	AP1GBP1	AP1 gamma subunit binding protein 1	chr17q12	222715_s_at	NM_007247 /// NM_080550																				
2.74	2.64	0.10	4.19E-01	7.49E-01	---	---	---	233967_at	---																				
3.04	2.85	0.18	4.19E-01	7.49E-01	TP53I11	tumor protein p53 inducible protein 11	chr11p11.2	216919_at	NM_001076787 /// NM_006034																				
4.14	3.90	0.24	4.19E-01	7.49E-01	LOC642031	hypothetical protein LOC642031	---	228522_at	XM_936101																				
5.90	5.60	0.30	4.19E-01	7.50E-01	RASIP1	Ras interacting protein 1	chr19q13.33	220027_s_at	NM_017805																				
6.63	6.40	0.24	4.19E-01	7.50E-01	MAP7D1	MAP7 domain containing 1	chr1p34.3	217943_s_at	NM_018067																				
3.80	3.61	0.20	4.19E-01	7.50E-01	MMEL1	membrane metallo-endopeptidase-like 1	chr1p36	1552930_at	NM_033467																				
5.93	5.68	0.24	4.19E-01	7.50E-01	C1orf216	chromosome 1 open reading frame 216	chr1p34.3	212791_at	NM_152374																				
2.20	2.09	0.11	4.19E-01	7.50E-01	JMJD6	jumonji domain containing 6	chr17q25	1552629_a_at	NM_001081461 /// NM_015167																				
2.35	2.24	0.11	4.19E-01	7.50E-01	ZIC3	Zic family member 3 (odd-paired homolog, Drosophila)	chrXq26.2	207197_at	NM_003413																				
5.55	5.38	0.17	4.19E-01	7.50E-01	JMJD2A	jumonji domain containing 2A	chr1p34.1	203204_s_at	NM_014663																				
2.36	2.23	0.13	4.19E-01	7.50E-01	PSORS1C3	psoriasis susceptibility 1 candidate 3	chr6p21.33	238997_at	NM_001134284 /// XM_001719830 /// XM_001720043 /// XM_001721570 /// XM_001722901 /// XM_001723557																				

5.26	4.98	0.28	4.19E-01	7.50E-01	FAM86A /// FAM86B1 /// FAM86C /// FAM86D /// LOC100125556 /// LOC348926 /// LOC387745 /// LOC645332 /// LOC729375	family with sequence similarity 86, member A /// family with sequence similarity 86, member B1 /// family with sequence similarity 86, member C /// family with sequence similarity 86, member D /// hypothetical LOC100125556 /// hypothetical protein LOC348926 /// similar to CG7889-PA /// hypothetical protein LOC645332 /// similar to family with sequence similarity 86, member C	chr11p15.4 /// chr11q13.2 /// chr11q13.4 /// chr16p13.3 /// chr3p12.3 /// chr3q21.2 /// chr3q21.3 /// chr4p16.3 /// chr8p23.1	222013_x_at	NM_001083537 /// NM_001099653 /// NM_018172 /// NM_152563 /// NM_201400 /// NM_201598 /// NR_003494 /// XR_015558 /// XR_016307 /// XR_017741 /// XR_017820 /// XR_017896 /// XR_017899 /// XR_037819 /// XR_037875 /// XR_037903 /// XR_039934 /// XR_040598 /// XR_040853 /// XR_040854 /// XR_041138 /// XR_041139 /// XR_041140 /// XR_041463 /// XR_041464 /// XR_041465																				
5.30	5.04	0.26	4.20E-01	7.50E-01	TFCP2	transcription factor CP2	chr12q13	207627_s_at	NM_005653																				
3.28	3.17	0.11	4.20E-01	7.50E-01	C18orf22	Chromosome 18 open reading frame 22	chr18q23	215683_at	NM_024805																				
3.70	3.48	0.22	4.20E-01	7.50E-01	ZNF44	Zinc finger protein 44	chr19p13.2	229654_at	NM_016264 /// XM_001718561 /// XM_001719479 /// XM_001719639																				
3.41	3.25	0.16	4.20E-01	7.50E-01	NKX3-1	NK3 homeobox 1	chr8p21	211497_x_at	NM_006167																				
4.07	3.75	0.33	4.20E-01	7.50E-01	IGFBP5	insulin-like growth factor binding protein 5	chr2q33-q36	1555997_s_at	NM_000599																				
4.32	4.06	0.26	4.20E-01	7.50E-01	ECSM2	Endothelial cell-specific molecule 2	chr5q31.2	227779_at	NM_001077693																				
2.54	2.40	0.14	4.20E-01	7.50E-01	CLRN1OS	clarin 1 opposite strand	chr3q21-q25	1560432_at	NR_024066																				
6.27	6.04	0.24	4.20E-01	7.50E-01	PAX8	paired box 8	chr2q12-q14	121_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992																				
2.08	1.98	0.10	4.20E-01	7.50E-01	PROK2	prokineticin 2	chr3p13	232629_at	NM_001126128 /// NM_021935																				

9.50	9.16	0.34	4.20E-01	7.50E-01	FOSL2	FOS-like antigen 2	chr2p23.3	228188_at	NM_005253
3.49	3.38	0.12	4.20E-01	7.50E-01	UNK	unkempt homolog (Drosophila)	chr17q25.1	1562434_at	NM_001080419
5.25	4.99	0.25	4.20E-01	7.50E-01	UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	chr13q34	206959_s_at	NM_023011 /// NM_080687
3.97	3.77	0.19	4.20E-01	7.50E-01	MORC3	MORC family CW-type zinc finger 3	chr21q22.13	213000_at	NM_015358
1.90	1.81	0.09	4.20E-01	7.50E-01	---	---	---	1559492_at	---
3.11	2.97	0.13	4.20E-01	7.50E-01	GLS2	glutaminase 2 (liver, mitochondrial)	chr12q13	205531_s_at	NM_013267
2.20	2.10	0.11	4.20E-01	7.50E-01	LOC201651	similar to Arylacetamide deacetylase (AADAC)	chr3q25.1	1569582_at	XR_017321 /// XR_019163 /// XR_041981
4.87	4.75	0.12	4.20E-01	7.50E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	215536_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447
6.14	5.98	0.16	4.20E-01	7.50E-01	---	---	---	241373_at	---
6.37	6.08	0.29	4.20E-01	7.50E-01	SEH1L	SEH1-like (S. cerevisiae)	chr18p11.21	221931_s_at	NM_001013437 /// NM_031216
6.89	6.61	0.28	4.21E-01	7.50E-01	LOC91461	hypothetical protein BC007901	chr2p21	225380_at	NM_138370
3.89	3.72	0.16	4.21E-01	7.50E-01	KIAA1147	KIAA1147	chr7q34	227502_at	NM_001080392
3.00	2.90	0.10	4.21E-01	7.50E-01	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	chr11q24.2	239796_x_at	NM_001039661 /// NM_148910

2.64	2.53	0.11	4.21E-01	7.50E-01	LOC100131303	Similar to hCG1775037	chr16q22.1	236593_at	XM_001723725 /// XM_001723845 /// XM_001726636																				
2.71	2.59	0.13	4.21E-01	7.50E-01	TTC16	tetratricopeptide repeat domain 16	chr9q34.11	236833_at	NM_144965																				
3.10	2.95	0.15	4.21E-01	7.50E-01	ZNF627	Zinc finger protein 627	chr19p13.2	1563204_at	NM_145295																				
11.24	11.12	0.12	4.21E-01	7.50E-01	CD63	CD63 molecule	chr12q12-q13	200663_at	NM_001040034 /// NM_001780																				
3.17	3.04	0.12	4.21E-01	7.51E-01	RAB26	RAB26, member RAS oncogene family	chr16p13.3	50965_at	NM_014353																				
2.37	2.23	0.14	4.21E-01	7.51E-01	LOC374443	CLR pseudogene	chr12p13.31	240572_s_at	NR_002814																				
2.47	2.33	0.14	4.21E-01	7.51E-01	---	---	---	1561509_at	---																				
5.58	5.49	0.09	4.21E-01	7.51E-01	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	chr21q22.3	209041_s_at	NM_003343 /// NM_182688																				
2.26	2.17	0.09	4.21E-01	7.51E-01	---	---	---	1570106_at	---																				
2.52	2.39	0.13	4.21E-01	7.51E-01	DRAM	Damage-regulated autophagy modulator	chr12q23.2	241992_at	NM_018370																				
2.72	2.58	0.14	4.21E-01	7.51E-01	REPIN1	replication initiator 1	chr7q36.1	222501_s_at	NM_001099695 /// NM_001099696 /// NM_013400 /// NM_014374																				
3.39	3.13	0.26	4.21E-01	7.51E-01	UTY	ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	chrYq11	210322_x_at	NM_007125 /// NM_182659 /// NM_182660																				
2.54	2.46	0.08	4.21E-01	7.51E-01	KLK13	kallikrein-related peptidase 13	chr19q13.3-q13.4	205783_at	NM_015596																				
4.03	3.85	0.17	4.21E-01	7.51E-01	---	---	---	1563302_at	---																				
3.74	3.57	0.17	4.21E-01	7.51E-01	---	---	---	235934_at	---																				
3.09	2.94	0.15	4.21E-01	7.51E-01	KIAA1529	KIAA1529	chr9q22.33	229628_s_at	NM_020893																				
2.95	2.80	0.15	4.21E-01	7.51E-01	KBTBD5	kelch repeat and BTB (POZ) domain containing 5	chr3p22.1	1555044_a_at	NM_152393																				
3.56	3.30	0.25	4.21E-01	7.51E-01	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	chr10q22.1	223722_at	NM_021800 /// NM_201262																				
7.91	7.65	0.26	4.22E-01	7.51E-01	FOXN3	forkhead box N3	chr14q31.3	222494_at	NM_001085471 /// NM_005197																				
1.98	1.86	0.12	4.22E-01	7.51E-01	---	---	---	1558900_at	---																				
2.97	2.83	0.14	4.22E-01	7.51E-01	S100A13	S100 calcium binding protein A13	chr1q21	213481_at	NM_001024210 /// NM_001024211 /// NM_001024212 /// NM_001024213 /// NM_005979 /// XM_001724603																				
4.28	4.10	0.18	4.22E-01	7.51E-01	---	---	---	229108_at	---																				
2.28	2.19	0.09	4.22E-01	7.51E-01	---	---	---	233594_at	---																				
2.49	2.37	0.12	4.22E-01	7.51E-01	LOC340544	Hypothetical protein LOC340544	chrXq22.2	231088_at	---																				
3.80	3.56	0.24	4.22E-01	7.52E-01	---	---	---	243329_at	---																				
6.94	6.74	0.20	4.22E-01	7.52E-01	TPCN1	two pore segment channel 1	chr12q24.13	217914_at	NM_017901																				
4.43	4.33	0.10	4.22E-01	7.52E-01	---	---	---	230581_at	---																				
4.26	4.10	0.16	4.22E-01	7.52E-01	FLJ45482	hypothetical LOC645566	---	1565786_x_at	XM_928583 /// XR_040445 /// XR_040446 /// XR_040447																				

6.96	6.84	0.11	4.22E-01	7.52E-01	TCF7	transcription factor 7 (T-cell specific, HMG-box)	chr5q31.1	205255_x_at	NM_003202 /// NM_201632 /// NM_201633 /// NM_201634 /// NM_213648																			
11.94	11.85	0.10	4.22E-01	7.52E-01	PPIA	peptidylprolyl isomerase A (cyclophilin A)	chr7p13	211765_x_at	NM_021130																			
2.45	2.32	0.12	4.22E-01	7.52E-01	RNF144A	ring finger protein 144A	chr2p25.2-p25.1	1570051_at	NM_014746																			
2.26	2.13	0.13	4.22E-01	7.52E-01	---	---	---	236440_at	---																			
3.71	3.56	0.14	4.22E-01	7.52E-01	FLJ36848	hypothetical LOC647115	chr2p15	231698_at	XM_001726089 /// XM_930136 /// XM_941733																			
7.15	6.87	0.28	4.22E-01	7.52E-01	SAPS3	SAPS domain family, member 3	chr11q13	222467_s_at	NM_018312																			
8.05	7.83	0.22	4.22E-01	7.52E-01	BIN1	bridging integrator 1	chr2q14	202931_x_at	NM_004305 /// NM_139343 /// NM_139344 /// NM_139345 /// NM_139346 /// NM_139347 /// NM_139348 /// NM_139349 /// NM_139350 /// NM_139351																			
4.24	4.13	0.12	4.22E-01	7.52E-01	ZNF843	zinc finger protein 843	chr16p11.2	1555078_at	XM_001720820 /// XM_290712 /// XM_937979																			
5.82	5.49	0.34	4.22E-01	7.52E-01	WSB1	WD repeat and SOCS box-containing 1	chr17q11.1	201294_s_at	NM_015626 /// NM_134265																			
2.88	2.71	0.17	4.22E-01	7.52E-01	---	---	---	241846_at	---																			
3.30	3.13	0.17	4.23E-01	7.52E-01	CDK8	cyclin-dependent kinase 8	chr13q12	1553113_s_at	NM_001260																			
5.12	4.89	0.23	4.23E-01	7.52E-01	SLC25A16	Solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	chr10q21.3	235747_at	NM_152707																			
2.14	2.03	0.11	4.23E-01	7.52E-01	ARSB	arylsulfatase B	chr5q11-q13	1554032_at	NM_000046 /// NM_198709																			
2.11	2.01	0.10	4.23E-01	7.52E-01	GPR39	G protein-coupled receptor 39	chr2q21-q22	229105_at	NM_001508																			
5.32	5.05	0.27	4.23E-01	7.52E-01	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	chr18q23	211105_s_at	NM_006162 /// NM_172387 /// NM_172388 /// NM_172389 /// NM_172390																			
5.43	5.26	0.17	4.23E-01	7.52E-01	PLCG1	phospholipase C, gamma 1	chr20q12-q13.1	216551_x_at	NM_002660 /// NM_182811																			
2.34	2.22	0.12	4.23E-01	7.52E-01	KRT13	keratin 13	chr17q12-q21.2	207935_s_at	NM_002274 /// NM_153490																			
2.15	2.03	0.12	4.23E-01	7.52E-01	---	---	---	243549_at	---																			
2.64	2.50	0.14	4.23E-01	7.52E-01	---	---	---	242960_at	---																			

11.58	11.45	0.13	4.23E-01	7.52E-01	H3F3A /// H3F3B /// LOC440926	H3 histone, family 3A /// H3 histone, family 3B (H3.3B) /// H3 histone, family 3A pseudogene	chr17q25 /// chr1q41 /// chr2q31.1	211940_x_at	NM_002107 /// NM_005324 /// NR_002315 /// XR_042136 /// XR_042137 /// XR_042155																				
2.26	2.15	0.11	4.23E-01	7.52E-01	LUC7L	LUC7-like (S. cerevisiae)	chr16p13.3	1557066_at	NM_018032 /// NM_201412																				
3.30	3.18	0.12	4.23E-01	7.52E-01	---	---	---	241300_at	---																				
1.99	1.87	0.11	4.23E-01	7.52E-01	---	---	---	1564292_at	---																				
6.17	5.84	0.33	4.23E-01	7.52E-01	---	---	---	228827_at	---																				
2.02	1.92	0.10	4.23E-01	7.52E-01	HAL	Histidine ammonia-lyase	chr12q22-q24.1	237967_at	NM_002108																				
6.12	5.97	0.16	4.23E-01	7.52E-01	CHAF1A	chromatin assembly factor 1, subunit A (p150)	chr19p13.3	214426_x_at	NM_005483																				
3.54	3.42	0.12	4.23E-01	7.52E-01	ADCY7	adenylate cyclase 7	chr16q12-q13	1554827_a_at	NM_001114																				
4.17	4.02	0.15	4.23E-01	7.52E-01	EGFL8 /// PPT2	EGF-like-domain, multiple 8 /// palmitoyl-protein thioesterase 2	chr6p21.3 /// chr6p21.32	208469_s_at	NM_005155 /// NM_030652 /// NM_138717																				
2.39	2.28	0.12	4.24E-01	7.52E-01	SP140	SP140 nuclear body protein	chr2q37.1	1565588_at	NM_001005176 /// NM_007237																				
3.18	3.00	0.18	4.24E-01	7.52E-01	EMP1	epithelial membrane protein 1	chr12p12.3	213895_at	NM_001423																				
6.82	6.61	0.21	4.24E-01	7.52E-01	TRA2A	transformer-2 alpha	chr7p15.3	213593_s_at	NM_013293																				
1.98	1.87	0.11	4.24E-01	7.52E-01	---	---	---	238234_at	---																				
3.12	2.98	0.14	4.24E-01	7.52E-01	POLD3	Polymerase (DNA-directed), delta 3, accessory subunit	chr11q14	1554609_at	NM_006591																				
8.73	8.56	0.16	4.24E-01	7.53E-01	LSMD1	LSM domain containing 1	chr17p13.1	225441_x_at	NM_032356																				
2.10	2.00	0.10	4.24E-01	7.53E-01	---	---	---	1561204_at	---																				
6.13	5.90	0.24	4.24E-01	7.53E-01	HCK	hemopoietic cell kinase	chr20q11-q12	208018_s_at	NM_002110																				
8.62	8.38	0.23	4.24E-01	7.53E-01	HNRNPK	heterogeneous nuclear ribonucleoprotein K	chr9q21.32-q21.33	200097_s_at	NM_002140 /// NM_031262 /// NM_031263																				
6.52	6.34	0.18	4.24E-01	7.53E-01	TMEM188	transmembrane protein 188	chr16q12.1	235812_at	NM_153261																				
5.92	5.67	0.26	4.24E-01	7.53E-01	EED	embryonic ectoderm development	chr11q14.2-q22.3	209572_s_at	NM_003797 /// NM_152991																				
2.09	2.00	0.09	4.24E-01	7.53E-01	C3orf50	chromosome 3 open reading frame 50	chr3q26.2	1558411_at	NR_021485 /// XM_001723648 /// XM_001725917 /// XM_001726230																				
3.27	3.16	0.12	4.24E-01	7.53E-01	ART1	ADP-ribosyltransferase 1	chr11p15	1570479_at	NM_004314																				
3.56	3.43	0.13	4.24E-01	7.53E-01	---	---	---	236810_at	---																				
3.13	2.96	0.17	4.24E-01	7.53E-01	ASMT	acetylserotonin O-methyltransferase	chrXp22.3 or Yp11.3	206779_s_at	NM_004043																				
2.28	2.20	0.08	4.25E-01	7.53E-01	ZNF124	zinc finger protein 124	chr1q44	234394_at	NM_003431																				
3.12	2.99	0.14	4.25E-01	7.53E-01	---	---	---	241501_at	---																				
6.63	6.42	0.21	4.25E-01	7.53E-01	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	chr12p12.1	204009_s_at	NM_004985 /// NM_033360																				
2.17	2.08	0.10	4.25E-01	7.53E-01	LOC148709	actin pseudogene	chr1q32.1	1558577_at	NR_002929																				
5.83	4.81	1.02	4.25E-01	7.53E-01	POSTN	periostin, osteoblast specific factor	chr13q13.3	210809_s_at	NM_006475																				
7.04	6.87	0.17	4.25E-01	7.53E-01	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	chrXq28	213843_x_at	NM_005629																				
11.07	10.35	0.73	4.25E-01	7.53E-01	APOC1	apolipoprotein C-I	chr19q13.2	204416_x_at	NM_001645																				
2.46	2.32	0.14	4.25E-01	7.53E-01	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	chr1p34.3	226898_s_at	NM_005066																				
4.58	4.25	0.33	4.25E-01	7.53E-01	---	---	---	226458_at	---																				
4.24	3.99	0.25	4.25E-01	7.53E-01	CRLS1	cardiolipin synthase 1	chr20p13-p12.3	241741_at	NM_001127458 /// NM_019095																				
5.64	5.45	0.19	4.25E-01	7.53E-01	TMEM50B	transmembrane protein 50B	chr21q22.11	222907_x_at	NM_006134																				
2.99	2.88	0.11	4.25E-01	7.53E-01	SFT2D1	SFT2 domain containing 1	chr6q27	1560694_at	NM_145169																				
6.98	6.82	0.16	4.25E-01	7.53E-01	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	chrXq28	210854_x_at	NM_005629																				
2.34	2.22	0.12	4.25E-01	7.53E-01	LOC554201	hypothetical LOC554201	chr2q24.1	1555224_at	---																				

2.54	2.41	0.14	4.25E-01	7.53E-01	LOC440895	LIM and senescent cell antigen-like domains 3-like	chr2q13	229096_at	XM_001726941 /// XM_496582																			
3.40	3.29	0.11	4.25E-01	7.53E-01	MGC24975	hypothetical protein MGC24975	chr19p13.3	1552272_a_at	NM_001134316 /// NM_153359																			
4.79	4.44	0.35	4.25E-01	7.53E-01	---	---	---	214949_at	---																			
7.49	7.32	0.17	4.25E-01	7.53E-01	APLP2	amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	214875_x_at	NM_001642																			
7.70	7.56	0.14	4.25E-01	7.53E-01	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	chr17q21.31	208992_s_at	NM_003150 /// NM_139276 /// NM_213662																			
1.92	1.82	0.10	4.25E-01	7.53E-01	LOC414300	hypothetical LOC414300	chr12q23	1563221_at	---																			
3.57	3.46	0.11	4.26E-01	7.54E-01	---	---	---	236807_at	---																			
2.67	2.53	0.13	4.26E-01	7.54E-01	GUSBL2	glucuronidase, beta-like 2	chr6p11.2	232207_at	NR_003660 /// XR_042150 /// XR_042151																			
6.97	6.84	0.14	4.26E-01	7.54E-01	TULP3	tubby like protein 3	chr12p13.3	205854_at	NM_003324																			
2.85	2.72	0.13	4.26E-01	7.54E-01	ADD2	adducin 2 (beta)	chr2p14-p13	205268_s_at	NM_001617 /// NM_017482 /// NM_017483 /// NM_017484 /// NM_017488																			
8.03	7.73	0.30	4.26E-01	7.54E-01	C10orf32	chromosome 10 open reading frame 32	chr10q24.32	225334_at	NM_144591																			
4.46	4.24	0.22	4.26E-01	7.54E-01	---	---	---	241996_at	---																			
6.01	5.79	0.23	4.26E-01	7.54E-01	LOC27320 /// TNRC18	hypothetical protein LOC27320 /// trinucleotide repeat containing 18	chr7p22.1 /// chr7q11.21	226691_at	NM_001080495 /// XM_376618 /// XM_499300																			
11.89	11.76	0.12	4.26E-01	7.54E-01	H3F3A /// H3F3B /// LOC440926	H3 histone, family 3A /// H3 histone, family 3B (H3.3B) /// H3 histone, family 3A pseudogene	chr17q25 /// chr1q41 /// chr2q31.1	213828_x_at	NM_002107 /// NM_005324 /// NR_002315 /// XR_042136 /// XR_042137 /// XR_042155																			
2.01	1.91	0.10	4.26E-01	7.54E-01	MCART6	mitochondrial carrier triple repeat 6	chrXq22.2	1561660_at	NM_001012755																			
1.91	1.82	0.09	4.26E-01	7.54E-01	DRP2	dystrophin related protein 2	chrXq22	1569881_at	NM_001939																			
3.75	3.64	0.11	4.26E-01	7.54E-01	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	chr11p15.3	235135_at	NM_006284																			
2.27	2.16	0.11	4.26E-01	7.54E-01	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	chr9q22.33	234740_at	NM_001077181 /// NM_003671 /// NM_033331																			
6.39	6.05	0.33	4.26E-01	7.54E-01	TAPT1	transmembrane anterior posterior transformation 1	chr4p15.32	226735_at	NM_153365																			
6.70	6.55	0.16	4.26E-01	7.54E-01	C16orf42	chromosome 16 open reading frame 42	chr16p13.3	213105_s_at	NM_001001410																			
2.41	2.30	0.11	4.26E-01	7.54E-01	LOC729870	Hypothetical LOC729870	chr4q31.3	1560068_a_at	XM_001721662 /// XM_001721664 /// XM_001721706 /// XM_001721707 /// XM_001725930 /// XM_001725931																			

3.72	3.56	0.16	4.26E-01	7.54E-01	HR	hairless homolog (mouse)	chr8p21.2	241355_at	NM_005144 /// NM_018411																				
2.80	2.61	0.19	4.26E-01	7.54E-01	C2orf56	chromosome 2 open reading frame 56	chr2p22.2	220943_s_at	NM_001083946 /// NM_144736																				
3.81	3.68	0.13	4.26E-01	7.54E-01	TOP3A	topoisomerase (DNA) III alpha	chr17p12-p11.2	214299_at	NM_004618																				
2.71	2.61	0.10	4.26E-01	7.54E-01	---	---	---	1569312_at	---																				
10.58	10.43	0.15	4.27E-01	7.54E-01	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	chr17q25	200654_at	NM_000918																				
2.29	2.18	0.11	4.27E-01	7.54E-01	---	---	---	231332_at	---																				
3.18	3.05	0.13	4.27E-01	7.54E-01	SIGLEC6	sialic acid binding Ig-like lectin 6	chr19q13.3	206520_x_at	NM_001245 /// NM_198845 /// NM_198846																				
4.94	4.65	0.29	4.27E-01	7.54E-01	C21orf57	Chromosome 21 open reading frame 57	chr21q22.3	242565_x_at	NM_001006114 /// NM_058181																				
3.72	3.56	0.16	4.27E-01	7.54E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	224066_s_at	NM_001113239 /// NM_022740																				
6.94	6.64	0.30	4.27E-01	7.54E-01	C1RL	complement component 1, r subcomponent-like	chr12p13.31	218983_at	NM_016546																				
3.76	3.64	0.12	4.27E-01	7.54E-01	---	---	---	236956_at	---																				
4.40	4.24	0.16	4.27E-01	7.54E-01	CHRNG	cholinergic receptor, nicotinic, gamma	chr2q33-q34	221355_at	NM_005199																				
1.96	1.86	0.10	4.27E-01	7.54E-01	SLC4A10	solute carrier family 4, sodium bicarbonate transporter-like, member 10	chr2q23-q24	206830_at	NM_022058																				
2.33	2.20	0.12	4.27E-01	7.54E-01	EPHA6	EPH receptor A6	chr3q11.2	233184_at	NM_001080448 /// NM_173655																				
3.24	3.09	0.14	4.27E-01	7.54E-01	TTC27	Tetratricopeptide repeat domain 27	chr2p22.3	244248_at	NM_017735																				
1.99	1.88	0.11	4.27E-01	7.54E-01	---	---	---	1570506_at	---																				
4.90	4.70	0.20	4.27E-01	7.54E-01	GATAD2B	GATA zinc finger domain containing 2B	chr1q21.3	225393_at	NM_020699																				
7.84	7.69	0.15	4.28E-01	7.55E-01	SCAMP3	secretory carrier membrane protein 3	chr1q21	201771_at	NM_005698 /// NM_052837																				
2.60	2.45	0.15	4.28E-01	7.55E-01	CALCOCO2	calcium binding and coiled-coil domain 2	chr17q21.32	1560631_at	NM_005831																				
4.31	4.16	0.15	4.28E-01	7.55E-01	THAP6	THAP domain containing 6	chr4q21.1	227813_at	NM_144721																				
2.50	2.37	0.14	4.28E-01	7.55E-01	ZC3H13	zinc finger CCCH-type containing 13	chr13q14.12	209851_at	NM_015070																				
5.47	5.14	0.33	4.28E-01	7.55E-01	FANCL	Fanconi anemia, complementation group L	chr2p16.1	218397_at	NM_001114636 /// NM_018062																				
3.39	3.28	0.11	4.28E-01	7.55E-01	---	---	---	236803_at	---																				
3.59	3.32	0.28	4.28E-01	7.55E-01	LARP4	La ribonucleoprotein domain family, member 4	chr12q13.13	214155_s_at	NM_052879 /// NM_199188 /// NM_199190																				
2.31	2.23	0.08	4.28E-01	7.55E-01	MGC22265	hypothetical protein MGC22265	chr5p14.3	1555568_at	---																				
4.99	4.64	0.36	4.29E-01	7.55E-01	SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	chr1q21.3	222217_s_at	NM_024330																				
2.39	2.26	0.13	4.29E-01	7.55E-01	---	---	---	216553_x_at	---																				
2.92	2.77	0.15	4.29E-01	7.56E-01	IL1RL1	interleukin 1 receptor-like 1	chr2q12	210442_at	NM_003856 /// NM_016232																				
4.76	4.58	0.19	4.29E-01	7.56E-01	TMEM37	Transmembrane protein 37	chr2q14.2	243849_at	NM_183240																				
3.94	3.82	0.12	4.29E-01	7.56E-01	---	---	---	235724_at	---																				
3.18	2.98	0.20	4.29E-01	7.56E-01	FLJ44896	FLJ44896 protein	chr5p15.33	236046_at	XR_041619 /// XR_041620 /// XR_041621																				
3.13	3.03	0.10	4.29E-01	7.56E-01	XRRA1	X-ray radiation resistance associated 1	chr11q13.4	237666_at	NM_182969																				
2.93	2.77	0.16	4.29E-01	7.56E-01	SNX22	sorting nexin 22	chr15q22.31	1569481_s_at	NM_024798																				
4.83	4.49	0.34	4.29E-01	7.56E-01	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	chr1p34-p33	204468_s_at	NM_005424																				
4.53	4.38	0.15	4.29E-01	7.56E-01	---	---	---	236410_x_at	---																				
3.29	3.15	0.14	4.29E-01	7.56E-01	OIP5	Opa interacting protein 5	chr15q15.1	213599_at	NM_007280																				
2.85	2.72	0.13	4.29E-01	7.56E-01	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	chr6q26	228667_at	NM_020133																				
4.94	4.72	0.22	4.29E-01	7.56E-01	C19orf25	chromosome 19 open reading frame 25	chr19p13.3	226378_s_at	NM_152482																				
6.11	5.84	0.27	4.29E-01	7.56E-01	SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	chr15q25	234725_s_at	NM_020210 /// NM_198925																				

6.17	5.96	0.21	4.29E-01	7.56E-01	EPB49	erythrocyte membrane protein band 4.9 (dematin)	chr8p21.1	204505_s_at	NM_001114135 /// NM_001114136 /// NM_001114137 /// NM_001114138 /// NM_001114139 /// NM_001978																				
7.13	6.64	0.49	4.29E-01	7.56E-01	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	chr11p15.5	219534_x_at	NM_000076 /// NM_001122630 /// NM_001122631																				
2.74	2.59	0.15	4.29E-01	7.56E-01	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	chr9q33.3	210552_s_at	NM_014636																				
2.62	2.48	0.14	4.29E-01	7.56E-01	---	---	---	237344_at	---																				
6.93	6.71	0.22	4.29E-01	7.56E-01	PLEKHO2	pleckstrin homology domain containing, family O member 2	chr15q22.1	204436_at	NM_025201																				
3.41	3.25	0.16	4.29E-01	7.56E-01	GLCCI1	glucocorticoid induced transcript 1	chr7p21.3	227525_at	NM_138426																				
2.76	2.64	0.11	4.29E-01	7.56E-01	TNRC6A	trinucleotide repeat containing 6A	chr16p11.2	1553346_a_at	NM_014494																				
2.67	2.57	0.10	4.30E-01	7.56E-01	LRRC3	leucine rich repeat containing 3	chr21q22.3	221017_s_at	NM_030891																				
3.14	2.98	0.16	4.30E-01	7.56E-01	MTAP	methylthioadenosine phosphorylase	chr9p21	204956_at	NM_002451																				
4.89	4.71	0.18	4.30E-01	7.56E-01	---	---	---	217211_at	---																				
7.45	7.25	0.20	4.30E-01	7.56E-01	THOC7	THO complex 7 homolog (Drosophila)	chr3p14.1	218334_at	NM_025075																				
2.36	2.25	0.11	4.30E-01	7.56E-01	ZNF664	Zinc finger protein 664	chr12q24.31	1569936_a_at	NM_152437																				
2.25	2.14	0.12	4.30E-01	7.56E-01	OSBP2	Oxysterol binding protein 2	chr22q12.2	1569617_at	NM_030758																				
3.05	2.85	0.20	4.30E-01	7.56E-01	ZNRF1	zinc and ring finger 1	chr16q23.1	225962_at	NM_032268																				
2.15	2.08	0.08	4.30E-01	7.56E-01	PHTF2	putative homeodomain transcription factor 2	chr7q11.23-q21	1554822_at	NM_001127357 /// NM_001127358 /// NM_001127359 /// NM_001127360 /// NM_020432																				
6.98	6.72	0.26	4.30E-01	7.56E-01	ANKRD52	ankyrin repeat domain 52	chr12q13.2	228257_at	NM_173595 /// XM_001722431																				
2.25	2.14	0.10	4.30E-01	7.56E-01	---	---	---	1569721_at	---																				
2.72	2.59	0.13	4.30E-01	7.56E-01	LOC100133236	hypothetical protein LOC100133236	chr1q32.1	238308_at	XM_001714136 /// XM_001714243 /// XM_001714262																				
2.90	2.60	0.29	4.30E-01	7.56E-01	SPRED1	sprouty-related, EVH1 domain containing 1	chr15q14	244439_at	NM_152594																				
3.91	3.73	0.18	4.30E-01	7.56E-01	CEP290	centrosomal protein 290kDa	chr12q21.32	205250_s_at	NM_025114																				
2.81	2.65	0.16	4.30E-01	7.56E-01	KCNRG	potassium channel regulator	chr13q14.3	239098_at	NM_173605 /// NM_199464																				
2.00	1.91	0.09	4.30E-01	7.56E-01	ADH1B	Alcohol dehydrogenase 1B (class I), beta polypeptide	chr4q21-q23	243544_at	NM_000668																				
4.18	3.99	0.19	4.30E-01	7.56E-01	POP4	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	chr19q12	227583_at	NM_006627																				
8.62	8.50	0.12	4.30E-01	7.56E-01	TCEAL4	transcription elongation factor A (SII)-like 4	chrXq22.2	202371_at	NM_001006935 /// NM_001006936 /// NM_001006937 /// NM_024863																				
2.73	2.53	0.20	4.30E-01	7.56E-01	CORO2B	coronin, actin binding protein, 2B	chr15q23	209789_at	NM_006091																				
5.65	5.43	0.22	4.30E-01	7.56E-01	ZC3H18	zinc finger CCCH-type containing 18	chr16q24.2-q24.3	226108_at	NM_144604																				
4.67	4.57	0.10	4.30E-01	7.56E-01	LRP10	low density lipoprotein receptor-related protein 10	chr14q11.2	231861_at	NM_014045																				
3.07	2.91	0.16	4.31E-01	7.57E-01	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	chr14q23-q24.2	214923_at	NM_015994																				
6.58	6.42	0.15	4.31E-01	7.57E-01	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	chr19p13.3|19p13.3-p13.2	203092_at	NM_006351																				
2.90	2.79	0.10	4.31E-01	7.57E-01	S100A2	S100 calcium binding protein A2	chr1q21	204268_at	NM_005978																				
5.22	4.98	0.23	4.31E-01	7.57E-01	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	chr1p35-p31.3	201250_s_at	NM_006516																				
6.17	5.95	0.22	4.31E-01	7.57E-01	SOS2	son of sevenless homolog 2 (Drosophila)	chr14q21	212870_at	NM_006939																				
4.81	4.22	0.59	4.31E-01	7.57E-01	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	chr6p21.3	213537_at	NM_033554																				
2.49	2.37	0.12	4.31E-01	7.57E-01	---	---	---	243646_at	---																				

4.55	4.41	0.14	4.31E-01	7.57E-01	FGD2	FYVE, RhoGEF and PH domain containing 2	chr6p21.2	1565754_x_at	NM_173558
5.80	5.67	0.14	4.31E-01	7.57E-01	PTH2	parathyroid hormone 2	chr19q13.33	1555238_at	NM_178449
4.30	4.16	0.14	4.31E-01	7.57E-01	YEATS2	YEATS domain containing 2	chr3q27.1	221203_s_at	NM_018023
5.69	5.35	0.34	4.31E-01	7.57E-01	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	chr2q33.3	213111_at	NM_015040 /// NM_152671
3.03	2.83	0.20	4.31E-01	7.57E-01	FUSIP1 /// LOC642558	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1	chr1p36.11	204299_at	NM_006625 /// NM_054016 /// XM_001713958 /// XM_001713979
3.69	3.52	0.17	4.31E-01	7.57E-01	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	chr2q37.1	203331_s_at	NM_001017915 /// NM_005541
7.39	7.20	0.19	4.31E-01	7.57E-01	C1orf21	chromosome 1 open reading frame 21	chr1q25	223125_s_at	NM_030806
5.12	4.84	0.28	4.31E-01	7.57E-01	---	---	---	236004_at	---
2.53	2.44	0.09	4.31E-01	7.57E-01	ZNF137	zinc finger protein 137	chr19q13.4	207394_at	NM_003438 /// NR_023311
6.99	6.79	0.20	4.31E-01	7.57E-01	COPS7A	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	chr12p13.31	209029_at	NM_016319
2.70	2.53	0.17	4.31E-01	7.57E-01	---	---	---	242353_at	---
2.89	2.76	0.13	4.31E-01	7.57E-01	TIAF1	TGFB1-induced anti-apoptotic factor 1	chr17q11.2	1560553_at	NM_004740
5.37	5.25	0.12	4.31E-01	7.57E-01	NSD1	nuclear receptor binding SET domain protein 1	chr5q35.2-q35.3	219084_at	NM_022455 /// NM_172349
2.64	2.52	0.12	4.31E-01	7.57E-01	PCDHAC1	protocadherin alpha subfamily C, 1	chr5q31	1553237_x_at	NM_018898 /// NM_031882
8.11	7.95	0.15	4.32E-01	7.57E-01	CLNS1A	chloride channel, nucleotide-sensitive, 1A	chr11q13.5-q14	209143_s_at	NM_001293
2.12	2.02	0.10	4.32E-01	7.57E-01	FGF1	fibroblast growth factor 1 (acidic)	chr5q31	1552721_a_at	NM_000800 /// NM_033136 /// NM_033137
3.38	3.24	0.13	4.32E-01	7.57E-01	MATN1	matrilin 1, cartilage matrix protein	chr1p35	206905_s_at	NM_002379
6.63	6.03	0.61	4.32E-01	7.57E-01	HOXB7	homeobox B7	chr17q21.3	204779_s_at	NM_004502
5.74	5.41	0.33	4.32E-01	7.57E-01	TBC1D16	TBC1 domain family, member 16	chr17q25.3	222116_s_at	NM_019020
2.14	2.05	0.09	4.32E-01	7.57E-01	---	---	---	1557519_at	---
2.61	2.48	0.14	4.32E-01	7.57E-01	ACVR1B	activin A receptor, type IB	chr12q13	208223_s_at	NM_004302 /// NM_020327 /// NM_020328
2.52	2.40	0.12	4.32E-01	7.57E-01	SLC4A5	Solute carrier family 4, sodium bicarbonate cotransporter, member 5	chr2p13	234976_x_at	NM_021196 /// NM_133478
2.32	2.21	0.11	4.32E-01	7.57E-01	---	---	---	1561998_at	---
6.33	6.07	0.25	4.32E-01	7.57E-01	WDR26	WD repeat domain 26	chr1q42.11	224897_at	NM_001115113 /// NM_025160
5.04	4.87	0.17	4.32E-01	7.57E-01	ZNF688	zinc finger protein 688	chr16p11.2	213529_at	NM_001024683 /// NM_145271
3.26	3.09	0.17	4.32E-01	7.57E-01	---	---	---	AFFX-M27830_3_at	---
4.59	4.47	0.12	4.32E-01	7.57E-01	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	chr12q12-q13.11	235579_at	NM_004719
2.59	2.47	0.11	4.32E-01	7.57E-01	---	---	---	243073_at	---
3.64	3.48	0.16	4.32E-01	7.57E-01	ZCCHC2	zinc finger, CCHC domain containing 2	chr18q21.33	224503_s_at	NM_017742
3.54	3.33	0.21	4.32E-01	7.57E-01	ZNF193	zinc finger protein 193	chr6p21.3	239406_at	NM_006299
4.54	4.38	0.16	4.32E-01	7.57E-01	HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	chr1p34	220042_x_at	NM_001127714 /// NM_024503
5.78	5.65	0.14	4.32E-01	7.57E-01	RSPRY1	ring finger and SPRY domain containing 1	chr16q13	225773_at	NM_133368
2.29	2.17	0.13	4.32E-01	7.57E-01	---	---	---	1560563_at	---
2.00	1.91	0.09	4.32E-01	7.57E-01	---	---	---	1560989_at	---
3.33	3.19	0.14	4.32E-01	7.57E-01	ICA1L	islet cell autoantigen 1,69kDa-like	chr2q33.1	1554205_s_at	NM_138468 /// NM_178231
6.47	6.05	0.41	4.32E-01	7.57E-01	BTG2	BTG family, member 2	chr1q32	201235_s_at	NM_006763
3.61	2.90	0.71	4.32E-01	7.57E-01	SPINK6	serine peptidase inhibitor, Kazal type 6	chr5q32	1553973_a_at	NM_205841

3.46	3.32	0.14	4.32E-01	7.57E-01	ESR1	estrogen receptor 1	chr6q25.1	217190_x_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742																				
5.77	5.56	0.21	4.32E-01	7.57E-01	STK35	serine/threonine kinase 35	chr20p13	225648_at	NM_080836																				
6.01	5.81	0.21	4.32E-01	7.57E-01	TSPAN4	tetraspanin 4	chr11p15.5	209264_s_at	NM_001025234 /// NM_001025235 /// NM_001025236 /// NM_001025237 /// NM_001025238 /// NM_001025239 /// NM_003271																				
7.56	7.33	0.24	4.32E-01	7.57E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	225229_at	NM_014423																				
2.56	2.46	0.10	4.32E-01	7.57E-01	LOC554206	hypothetical LOC554206	chr16p12.1	1554187_at	XR_040102 /// XR_040103																				
3.31	3.03	0.28	4.32E-01	7.57E-01	TM6SF1	transmembrane 6 superfamily member 1	chr15q24-q26	219892_at	NM_023003																				
2.64	2.53	0.11	4.32E-01	7.57E-01	TACC3	Transforming, acidic coiled-coil containing protein 3	chr4p16.3	1569487_at	NM_006342																				
3.43	3.27	0.16	4.32E-01	7.57E-01	HBB	Hemoglobin, beta	chr11p15.5	1562981_at	NM_000518																				
2.66	2.54	0.12	4.33E-01	7.58E-01	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	chr16p11.2	1563003_at	NM_000887																				
2.57	2.42	0.15	4.33E-01	7.58E-01	LOC728705	hypothetical protein LOC728705	chr12q23.3	239343_at	XM_001128243																				
2.96	2.88	0.09	4.33E-01	7.58E-01	RNF175	ring finger protein 175	chr4q31.3	236465_at	NM_173662																				
2.47	2.32	0.14	4.33E-01	7.58E-01	---	---	---	240881_at	---																				
3.51	3.36	0.15	4.33E-01	7.58E-01	FLJ39534	hypothetical protein FLJ39534	chr3p21.31	1557613_at	---																				
4.51	4.33	0.18	4.33E-01	7.58E-01	RNF170	ring finger protein 170	chr8p11.21	220985_s_at	NM_030954																				
3.53	3.21	0.31	4.33E-01	7.58E-01	WISP1	WNT1 inducible signaling pathway protein 1	chr8q24.1-q24.3	211312_s_at	NM_003882 /// NM_080838																				
2.26	2.15	0.11	4.33E-01	7.58E-01	FBXO11	F-box protein 11	chr2p16.3	219208_at	NM_012167 /// NM_018693 /// NM_025133																				
2.42	2.31	0.11	4.33E-01	7.58E-01	THEM5	thioesterase superfamily member 5	chr1q21.3	1562490_at	NM_182578																				
2.17	2.07	0.10	4.33E-01	7.58E-01	CXCL11	chemokine (C-X-C motif) ligand 11	chr4q21.2	211122_s_at	NM_005409																				
2.64	2.54	0.11	4.34E-01	7.58E-01	---	---	---	241711_at	---																				
2.80	2.72	0.08	4.34E-01	7.58E-01	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	chr21q22.2	211806_s_at	NM_002243 /// NM_170736 /// NM_170737																				
2.57	2.43	0.15	4.34E-01	7.58E-01	LOC286178	hypothetical protein LOC286178	chr8q12.1	1556573_s_at	---																				
3.90	3.55	0.35	4.34E-01	7.58E-01	UBR1	ubiquitin protein ligase E3 component n-recognin 1	chr15q13	238528_at	NM_174916																				
3.73	3.62	0.12	4.34E-01	7.58E-01	BRUNOL4	bruno-like 4, RNA binding protein (Drosophila)	chr18q12	232719_at	NM_001025087 /// NM_001025088 /// NM_001025089 /// NM_020180																				
4.44	4.14	0.30	4.34E-01	7.58E-01	KRI1	KRI1 homolog (S. cerevisiae)	chr19p13.2	227587_at	NM_023008																				
2.54	2.42	0.12	4.34E-01	7.58E-01	LOC221122	hypothetical protein LOC221122	chr11p11.2	1560279_a_at	---																				
2.60	2.44	0.16	4.34E-01	7.58E-01	SPAST	spastin	chr2p24-p21	207724_s_at	NM_014946 /// NM_199436																				
2.48	2.37	0.11	4.34E-01	7.58E-01	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	chr5q12	1554717_a_at	NM_001104631 /// NM_006203																				
5.60	5.43	0.18	4.34E-01	7.58E-01	TICAM1	toll-like receptor adaptor molecule 1	chr19p13.3	213191_at	NM_182919																				
9.60	9.44	0.16	4.34E-01	7.58E-01	MRPL49	mitochondrial ribosomal protein L49	chr11q13	201717_at	NM_004927																				
2.56	2.47	0.10	4.34E-01	7.58E-01	POFUT1	protein O-fucosyltransferase 1	chr20q11	210433_at	NM_015352 /// NM_172236																				

2.51	2.40	0.12	4.34E-01	7.58E-01	KIAA1310	KIAA1310	chr2p12-p11.2	223756_at	NM_001115016 /// NM_017991
5.04	4.88	0.16	4.34E-01	7.58E-01	---	---	---	1555222_a_at	---
2.79	2.65	0.13	4.34E-01	7.59E-01	hCG_1651160	Ssu72 RNA polymerase II CTD phosphatase-like	chr7q31.33	234470_at	NM_001085395
3.73	3.57	0.15	4.34E-01	7.59E-01	---	---	---	1560496_at	---
4.55	4.37	0.18	4.34E-01	7.59E-01	C10orf28	chromosome 10 open reading frame 28	chr10q24.2	228374_at	NM_014472
2.27	2.17	0.10	4.34E-01	7.59E-01	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	chr4p14	213984_at	NM_001100399 /// NM_001100400 /// NM_015200
5.80	5.61	0.19	4.34E-01	7.59E-01	ZNF618	zinc finger protein 618	chr9q32	226590_at	NM_133374
3.51	3.34	0.17	4.34E-01	7.59E-01	ARMCX5	armadillo repeat containing, X-linked 5	chrXq22.1-q22.3	1555902_at	NM_022838
4.58	4.44	0.14	4.34E-01	7.59E-01	---	---	---	231387_at	---
8.00	7.74	0.27	4.34E-01	7.59E-01	C2orf69	chromosome 2 open reading frame 69	chr2q33.1	238974_at	NM_153689
5.81	5.67	0.14	4.35E-01	7.59E-01	SH3GLB2	SH3-domain GRB2-like endophilin B2	chr9q34	224432_at	NM_020145
3.33	3.21	0.12	4.35E-01	7.59E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	228112_at	NM_015512
4.51	4.16	0.36	4.35E-01	7.59E-01	CHD2	chromodomain helicase DNA binding protein 2	chr15q26	1554015_a_at	NM_001042572 /// NM_001271
5.96	5.59	0.37	4.35E-01	7.59E-01	---	---	---	241459_at	---
3.21	3.09	0.12	4.35E-01	7.59E-01	ICA1L	islet cell autoantigen 1,69kDa-like	chr2q33.1	223881_at	NM_138468 /// NM_178231
3.42	3.05	0.37	4.35E-01	7.59E-01	IL1RL1	interleukin 1 receptor-like 1	chr2q12	207526_s_at	NM_003856 /// NM_016232
4.90	4.72	0.17	4.35E-01	7.59E-01	FLJ22374	hypothetical protein FLJ22374	chr7p15.1	235559_at	NM_032222
7.95	7.76	0.20	4.35E-01	7.59E-01	TEX261	testis expressed 261	chr2p13.3	212083_at	NM_144582
3.56	3.35	0.21	4.35E-01	7.59E-01	CDYL2	chromodomain protein, Y-like 2	chr16q23.2	1553647_at	NM_152342
6.09	5.83	0.27	4.35E-01	7.59E-01	SP4	Sp4 transcription factor	chr7p15.3	236265_at	NM_003112
2.31	2.20	0.11	4.35E-01	7.59E-01	MYH2	myosin, heavy chain 2, skeletal muscle, adult	chr17p13.1	204631_at	NM_001100112 /// NM_017534
5.67	5.48	0.19	4.35E-01	7.59E-01	UBFD1	ubiquitin family domain containing 1	chr16p12	205687_at	NM_019116
7.38	7.08	0.29	4.35E-01	7.59E-01	---	---	---	210524_x_at	---
4.52	4.38	0.14	4.35E-01	7.59E-01	LTBP4	latent transforming growth factor beta binding protein 4	chr19q13.1-q13.2	210628_x_at	NM_001042544 /// NM_001042545 /// NM_003573
2.67	2.54	0.13	4.35E-01	7.59E-01	---	---	---	233246_at	---
3.88	3.71	0.16	4.35E-01	7.59E-01	CCNI	Cyclin I	chr4q21.1	227299_at	NM_006835
2.51	2.40	0.11	4.35E-01	7.59E-01	JRK	jerky homolog (mouse)	chr8q24.3	1554916_a_at	NM_001077527 /// NM_003724
6.34	6.10	0.24	4.35E-01	7.59E-01	---	---	---	212528_at	---
2.44	2.35	0.09	4.35E-01	7.59E-01	---	---	---	1557219_at	---
7.10	6.93	0.18	4.35E-01	7.60E-01	CCDC50	coiled-coil domain containing 50	chr3q28	225331_at	NM_174908 /// NM_178335
4.62	4.38	0.24	4.35E-01	7.60E-01	---	---	---	233931_at	---
2.87	2.74	0.13	4.35E-01	7.60E-01	LOC643201	hypothetical protein LOC643201	chr5q35.2	235416_at	XM_001716444 /// XM_001717933 /// XM_932161
5.89	5.58	0.31	4.36E-01	7.60E-01	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	chr9p21-p12	214066_x_at	NM_003995
3.41	3.24	0.17	4.36E-01	7.60E-01	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	chr20q11	1554637_a_at	NM_001032999 /// NM_001039709 /// NM_005093
9.62	9.21	0.41	4.36E-01	7.60E-01	UGCG	UDP-glucose ceramide glucosyltransferase	chr9q31	204881_s_at	NM_003358
3.02	2.89	0.13	4.36E-01	7.60E-01	CLIP1	CAP-GLY domain containing linker protein 1	chr12q24.3	242287_at	NM_002956 /// NM_198240
3.03	2.91	0.11	4.36E-01	7.60E-01	TEKT2	tektin 2 (testicular)	chr1p35.3-p34.1	210323_at	NM_014466
2.44	2.31	0.13	4.36E-01	7.60E-01	---	---	---	240907_at	---
8.05	7.86	0.19	4.36E-01	7.60E-01	HPCAL1	hippocalcin-like 1	chr2p25.1	212552_at	NM_002149 /// NM_134421
4.37	4.19	0.19	4.36E-01	7.60E-01	---	---	---	232790_at	---

5.72	5.46	0.26	4.36E-01	7.60E-01	AGGF1	angiogenic factor with G patch and FHA domains 1	chr5q13.3	222661_at	NM_018046
1.97	1.88	0.09	4.36E-01	7.60E-01	---	---	---	1566637_at	---
3.91	3.78	0.13	4.36E-01	7.60E-01	TNRP	TMF regulated nuclear protein	chr1p36.11	236052_at	NM_001013642
5.57	5.40	0.17	4.36E-01	7.60E-01	TBL3	transducin (beta)-like 3	chr16p13.3	209820_s_at	NM_006453
4.15	3.98	0.17	4.36E-01	7.60E-01	ZNF2	zinc finger protein 2	chr2q11.2	223792_at	NM_001017396 /// NM_021088
6.17	5.83	0.34	4.36E-01	7.60E-01	ESRRG	estrogen-related receptor gamma	chr1q41	207981_s_at	NM_001134285 /// NM_001438 /// NM_206594 /// NM_206595 /// NR_024099
2.44	2.31	0.12	4.36E-01	7.60E-01	---	---	---	224234_at	---
6.96	6.83	0.13	4.36E-01	7.60E-01	PPME1	protein phosphatase methylesterase 1	chr11q13.4	217841_s_at	NM_016147
2.31	2.19	0.12	4.36E-01	7.60E-01	FLJ40606	hypothetical protein LOC643549	chr20q13.12	1560162_at	XR_041973 /// XR_041974 /// XR_041975
5.76	5.57	0.19	4.36E-01	7.60E-01	SYNE1	spectrin repeat containing, nuclear envelope 1	chr6q25	209447_at	NM_015293 /// NM_033071 /// NM_133650 /// NM_182961
5.70	5.44	0.26	4.36E-01	7.60E-01	FRAT1	frequently rearranged in advanced T-cell lymphomas	chr10q24.1	219889_at	NM_005479 /// XM_001714291
2.10	2.00	0.10	4.36E-01	7.60E-01	---	---	---	244277_at	---
2.58	2.44	0.15	4.37E-01	7.60E-01	---	---	---	235752_at	---
5.15	4.94	0.21	4.37E-01	7.60E-01	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	chr6q21	208070_s_at	NM_002912
2.14	2.03	0.12	4.37E-01	7.60E-01	C4orf43	chromosome 4 open reading frame 43	chr4q32.3	218513_at	NM_018352
2.40	2.29	0.10	4.37E-01	7.61E-01	CIB3	calcium and integrin binding family member 3	chr19p13.12	1552750_at	NM_054113
4.48	4.30	0.18	4.37E-01	7.61E-01	DIS3L2	DIS3 mitotic control homolog (S. cerevisiae)-like 2	chr2q37.1	227597_at	NM_152383
2.80	2.71	0.09	4.37E-01	7.61E-01	LPCAT2	Lysophosphatidylcholine acyltransferase 2	chr16q12.2	229791_at	NM_017839
7.74	7.26	0.48	4.37E-01	7.61E-01	---	---	---	238751_at	---
3.01	2.90	0.11	4.37E-01	7.61E-01	HBZ	hemoglobin, zeta	chr16p13.3	206647_at	NM_005332
2.57	2.46	0.11	4.37E-01	7.61E-01	KLK8	kallikrein-related peptidase 8	chr19q13.3-q13.4	1552319_a_at	NM_007196 /// NM_144505 /// NM_144506 /// NM_144507
4.38	4.08	0.29	4.37E-01	7.61E-01	EPSTI1	Epithelial stromal interaction 1 (breast)	chr13q13.3	235276_at	NM_001002264 /// NM_033255
2.23	2.15	0.08	4.37E-01	7.61E-01	---	---	---	1566763_at	---
5.02	4.76	0.26	4.37E-01	7.61E-01	MMRN2	multimerin 2	chr10q23.2	219091_s_at	NM_024756
2.82	2.67	0.15	4.37E-01	7.61E-01	---	---	---	241243_at	---
3.25	3.09	0.16	4.37E-01	7.61E-01	---	---	---	211910_at	---
2.03	1.92	0.11	4.37E-01	7.61E-01	C1orf118	chromosome 1 open reading frame 118	chr1p31.1	1560746_at	XR_041257 /// XR_041258 /// XR_041259
2.47	2.30	0.17	4.37E-01	7.61E-01	---	---	---	240549_at	---
2.34	2.25	0.09	4.37E-01	7.61E-01	---	---	---	237529_at	---
2.83	2.72	0.11	4.38E-01	7.61E-01	GPR15	G protein-coupled receptor 15	chr3q11.2-q13.1	208524_at	NM_005290
4.38	4.18	0.20	4.38E-01	7.61E-01	---	---	---	241460_at	---
3.57	3.43	0.13	4.38E-01	7.61E-01	SLPI	secretory leukocyte peptidase inhibitor	chr20q12	203021_at	NM_003064
5.75	5.56	0.19	4.38E-01	7.61E-01	RNUXA	RNA U, small nuclear RNA export adaptor (phosphorylation regulated)	chr5q23.2	231812_x_at	NM_032177
3.61	3.38	0.23	4.38E-01	7.61E-01	SELI	selenoprotein I	chr2p23.3	1555274_a_at	NM_033505
4.66	4.47	0.19	4.38E-01	7.61E-01	MIPEP	mitochondrial intermediate peptidase	chr13q12	36830_at	NM_005932
2.82	2.74	0.09	4.38E-01	7.61E-01	KLHL10	kelch-like 10 (Drosophila)	chr17q21.2	1552425_a_at	NM_152467
2.05	1.94	0.11	4.38E-01	7.61E-01	C11orf1	chromosome 11 open reading frame 1	chr11q13-q22	218925_s_at	NM_022761
4.68	4.42	0.27	4.38E-01	7.62E-01	LOC100133660	hypothetical LOC100133660	---	230082_at	XR_036844

6.99	6.50	0.50	4.38E-01	7.62E-01	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	chr11p15.5	213182_x_at	NM_000076 /// NM_001122630 /// NM_001122631																				
4.09	3.93	0.15	4.38E-01	7.62E-01	LOC550631	hypothetical LOC550631	chr22q12.2	1568796_at	NM_001017437																				
2.68	2.57	0.11	4.38E-01	7.62E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	208225_at	NM_000141 /// NM_022970																				
11.84	11.73	0.11	4.38E-01	7.62E-01	H3F3A /// H3F3B /// LOC440926	H3 histone, family 3A /// H3 histone, family 3B (H3.3B) /// H3 histone, family 3A pseudogene	chr17q25 /// chr1q41 /// chr2q31.1	208755_x_at	NM_002107 /// NM_005324 /// NR_002315 /// XR_042136 /// XR_042137 /// XR_042155																				
5.38	5.16	0.22	4.38E-01	7.62E-01	ADCY4	adenylate cyclase 4	chr14q12	230800_at	NM_139247																				
6.98	6.68	0.31	4.39E-01	7.62E-01	KIAA1949	KIAA1949	chr6p21.3	224927_at	NM_133471																				
7.09	6.85	0.25	4.39E-01	7.62E-01	WBP2	WW domain binding protein 2	chr17q25	209117_at	NM_012478																				
4.23	4.08	0.15	4.39E-01	7.62E-01	ATP11A	ATPase, class VI, type 11A	chr13q34	216488_s_at	NM_015205 /// NM_032189																				
3.36	3.17	0.19	4.39E-01	7.62E-01	FLJ11235	hypothetical protein FLJ11235	chr5q22.2	220364_at	XR_017726 /// XR_017738 /// XR_039819																				
3.23	3.01	0.22	4.39E-01	7.62E-01	---	---	---	1570338_at	---																				
3.09	2.95	0.14	4.39E-01	7.62E-01	hCG_2024094	hCG2024094	chr10q23.31	232239_at	XR_041961 /// XR_041962 /// XR_041963																				
2.82	2.70	0.12	4.39E-01	7.62E-01	FSTL4	follistatin-like 4	chr5q31.1	1564511_a_at	NM_015082																				
5.27	5.01	0.25	4.39E-01	7.62E-01	ZBTB3	zinc finger and BTB domain containing 3	chr11q12.3	1553858_at	NM_024784																				
3.95	3.72	0.23	4.39E-01	7.62E-01	PRDM10	PR domain containing 10	chr11q25	219515_at	NM_020228 /// NM_199437 /// NM_199438 /// NM_199439																				
2.99	2.83	0.16	4.39E-01	7.62E-01	---	---	---	1559228_at	---																				
6.24	6.03	0.21	4.39E-01	7.62E-01	EXOC7	exocyst complex component 7	chr17q25.1	212026_s_at	NM_001013839 /// NM_015219																				
2.68	2.49	0.19	4.39E-01	7.62E-01	---	---	---	238910_at	---																				
3.29	3.09	0.19	4.39E-01	7.62E-01	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr7p14.3	202904_s_at	NM_001130710 /// NM_012322																				
8.47	8.33	0.14	4.39E-01	7.62E-01	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	chr19p13.3	218188_s_at	NM_012458																				
2.93	2.82	0.11	4.39E-01	7.62E-01	TEC	tec protein tyrosine kinase	chr4p12	206301_at	NM_003215																				
5.79	5.63	0.16	4.39E-01	7.62E-01	TRAFD1	TRAF-type zinc finger domain containing 1	chr12q	35254_at	NM_006700																				
3.64	3.41	0.23	4.40E-01	7.63E-01	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	chr19p13.11	222113_s_at	NM_021235																				
3.57	3.26	0.31	4.40E-01	7.63E-01	---	---	---	244420_at	---																				

2.86	2.71	0.15	4.40E-01	7.63E-01	FCGR2A /// FCGR2B /// FCGR2C	Fc fragment of IgG, low affinity IIa, receptor (CD32) /// Fc fragment of IgG, low affinity IIb, receptor (CD32) /// Fc fragment of IgG, low affinity IIc, receptor for (CD32)	chr1q23 /// chr1q23.3	1565674_at	NM_001002273 /// NM_001002274 /// NM_001002275 /// NM_001005410 /// NM_001005411 /// NM_004001 /// NM_021642 /// NM_201563
2.82	2.64	0.17	4.40E-01	7.63E-01	C21orf2	Chromosome 21 open reading frame 2	chr21q22.3	238965_at	NM_004928
5.08	4.78	0.30	4.40E-01	7.63E-01	WDR19	WD repeat domain 19	chr4p14	220917_s_at	NM_025132
3.08	2.98	0.09	4.40E-01	7.63E-01	LMNB1	lamin B1	chr5q23.3-q31.1	203276_at	NM_005573
2.92	2.81	0.11	4.40E-01	7.63E-01	TRIM29	tripartite motif-containing 29	chr11q22-q23	211001_at	NM_012101
2.65	2.55	0.10	4.40E-01	7.63E-01	MLXIP	MLX interacting protein	chr12q24.31	1554886_a_at	NM_014938
3.38	3.20	0.18	4.40E-01	7.63E-01	LOC147645	hypothetical protein LOC147645	chr19q13.33	238654_at	XM_001718903 /// XM_085831 /// XM_937000
5.90	5.68	0.22	4.40E-01	7.63E-01	CAMTA2	calmodulin binding transcription activator 2	chr17p13.2	212948_at	NM_015099
5.78	5.67	0.12	4.40E-01	7.63E-01	KPNA6	karyopherin alpha 6 (importin alpha 7)	chr1p35.1-p34.3	212101_at	NM_012316
3.15	3.04	0.12	4.40E-01	7.63E-01	---	---	---	244765_at	---
3.24	3.02	0.21	4.40E-01	7.63E-01	ACOT11	acyl-CoA thioesterase 11	chr1p32.3	1554938_a_at	NM_015547 /// NM_147161
4.32	4.04	0.28	4.40E-01	7.63E-01	PRR5	proline rich 5 (renal)	chr22q13	47069_at	NM_001017528 /// NM_001017529 /// NM_001017530 /// NM_015366 /// NM_181333
9.33	9.13	0.20	4.41E-01	7.63E-01	C20orf24	chromosome 20 open reading frame 24	chr20q11.23	223880_x_at	NM_018840 /// NM_199483
5.85	5.48	0.37	4.41E-01	7.63E-01	GRAMD3	GRAM domain containing 3	chr5q23.2	218706_s_at	NM_023927
5.83	5.39	0.44	4.41E-01	7.63E-01	LRRC16A	leucine rich repeat containing 16A	chr6p22.2	230793_at	NM_017640
12.06	11.94	0.11	4.41E-01	7.63E-01	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	chr12p13	213453_x_at	NM_002046
3.95	3.76	0.19	4.41E-01	7.63E-01	---	---	---	230640_at	---
5.79	5.59	0.21	4.41E-01	7.64E-01	VEGFB	vascular endothelial growth factor B	chr11q13	203683_s_at	NM_003377
2.88	2.75	0.13	4.41E-01	7.64E-01	USP28	ubiquitin specific peptidase 28	chr11q23	231837_at	NM_020886
7.52	7.29	0.22	4.41E-01	7.64E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	1566509_s_at	NM_012347 /// NM_033480 /// NM_033481
2.85	2.71	0.14	4.41E-01	7.64E-01	CPEB3	cytoplasmic polyadenylation element binding protein 3	chr10q23.32	205773_at	NM_014912
6.98	6.81	0.17	4.41E-01	7.64E-01	FBXW11	F-box and WD repeat domain containing 11	chr5q35.1	209455_at	NM_012300 /// NM_033644 /// NM_033645
6.56	6.42	0.14	4.41E-01	7.64E-01	EYA3	eyes absent homolog 3 (Drosophila)	chr1p36	226170_at	NM_001990
3.11	2.96	0.15	4.41E-01	7.64E-01	---	---	---	231284_at	---
5.68	5.49	0.19	4.41E-01	7.64E-01	CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	chr18q23	205035_at	NM_004715 /// NM_048368
6.46	6.31	0.15	4.41E-01	7.64E-01	SHQ1	SHQ1 homolog (S. cerevisiae)	chr3p13	219083_at	NM_018130
2.53	2.39	0.14	4.41E-01	7.64E-01	---	---	---	1560590_s_at	---
3.77	3.62	0.15	4.42E-01	7.64E-01	---	---	---	241936_x_at	---
3.34	3.19	0.15	4.42E-01	7.64E-01	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	chr17q21	1555155_at	NM_005937
3.47	3.20	0.26	4.42E-01	7.64E-01	VEZT	vezatin, adherens junctions transmembrane protein	chr12q22	223089_at	NM_017599
2.79	2.66	0.13	4.42E-01	7.64E-01	NPC1L1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	chr7p13	220106_at	NM_001101648 /// NM_013389
2.38	2.28	0.10	4.42E-01	7.64E-01	GNG13	guanine nucleotide binding protein (G protein), gamma 13	chr16p13.3	220806_x_at	NM_016541
1.93	1.84	0.09	4.42E-01	7.64E-01	---	---	---	241653_x_at	---
6.88	6.73	0.15	4.42E-01	7.64E-01	HEXIM1	hexamethylene bis-acetamide inducible 1	chr17q21.31	202815_s_at	NM_006460

2.44	2.32	0.12	4.42E-01	7.64E-01	41344	membrane-associated ring finger (C3HC4) 11	chr5p15.1	239359_at	NM_001102562																				
2.41	2.30	0.11	4.42E-01	7.64E-01	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	chr18q21.3-q22	217272_s_at	NM_012397																				
6.18	5.97	0.21	4.42E-01	7.64E-01	VWA5B2	von Willebrand factor A domain containing 5B2	chr3q27.1	232642_at	XM_001716350 /// XM_291077 /// XM_941833																				
6.43	6.19	0.24	4.42E-01	7.64E-01	C3orf58	chromosome 3 open reading frame 58	chr3q24	226464_at	NM_001134470 /// NM_173552																				
6.21	6.07	0.14	4.42E-01	7.64E-01	C20orf7	chromosome 20 open reading frame 7	chr20p12.1	227160_s_at	NM_001039375 /// NM_024120																				
5.64	5.49	0.15	4.42E-01	7.64E-01	---	---	---	234807_x_at	---																				
4.67	4.55	0.12	4.42E-01	7.64E-01	UNQ6975	NGNL6975	chr2p21	1562601_at	XM_376051 /// XM_941319																				
2.38	2.28	0.10	4.42E-01	7.64E-01	CASS4	Cas scaffolding protein family member 4	chr20q13.31	220888_s_at	NM_020356																				
8.78	8.43	0.35	4.42E-01	7.64E-01	PBX3	pre-B-cell leukemia homeobox 3	chr9q33-q34	204082_at	NM_006195																				
5.51	5.38	0.13	4.42E-01	7.64E-01	DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	chr7p13	238525_at	NM_019082																				
5.21	4.95	0.26	4.42E-01	7.64E-01	RABIF	RAB interacting factor	chr1q32-q41	204478_s_at	NM_002871																				
3.61	3.49	0.12	4.42E-01	7.64E-01	STX2	syntaxin 2	chr12q24.33	207346_at	NM_001980 /// NM_194356																				
4.25	4.04	0.21	4.42E-01	7.64E-01	TMEM55A	transmembrane protein 55A	chr8q21.3	226338_at	NM_018710																				
4.29	4.10	0.19	4.42E-01	7.64E-01	H2AFX	H2A histone family, member X	chr11q23.2-q23.3	213344_s_at	NM_002105																				
6.10	5.92	0.18	4.42E-01	7.64E-01	LOC100130930	hypothetical LOC100130930	chr19p13.3	228251_at	XM_001723136 /// XM_001726287 /// XM_001726431																				
4.11	3.99	0.13	4.42E-01	7.64E-01	SLC25A40	solute carrier family 25, member 40	chr7q21.12	205716_at	NM_018843																				
2.28	2.19	0.09	4.42E-01	7.64E-01	---	---	---	1561855_x_at	---																				
2.29	2.17	0.12	4.43E-01	7.64E-01	LAMB4	laminin, beta 4	chr7q22-q31.2	216622_at	NM_007356																				
3.11	3.01	0.10	4.43E-01	7.64E-01	C10orf27	chromosome 10 open reading frame 27	chr10q22.1	1552887_at	NM_152710																				
3.46	3.32	0.14	4.43E-01	7.64E-01	ARMC7	armadillo repeat containing 7	chr17q25.1	229906_at	NM_024585																				
4.01	3.85	0.16	4.43E-01	7.65E-01	GRID1	glutamate receptor, ionotropic, delta 1	chr10q22	1555267_at	NM_017551																				
2.98	2.87	0.10	4.43E-01	7.65E-01	ZNRD1	zinc ribbon domain containing 1	chr6p21.3	234114_at	NM_014596 /// NM_170783																				
3.74	3.60	0.13	4.43E-01	7.65E-01	---	---	---	1556188_a_at	---																				
2.11	2.02	0.08	4.43E-01	7.65E-01	---	---	---	1561149_at	---																				
4.90	4.70	0.20	4.43E-01	7.65E-01	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	chr7p22	204857_at	NM_001013836 /// NM_001013837 /// NM_003550																				
3.44	3.13	0.31	4.43E-01	7.65E-01	MTF2	metal response element binding transcription factor 2	chr1p22.1	209704_at	NM_007358																				
5.73	5.53	0.19	4.43E-01	7.65E-01	41342	membrane-associated ring finger (C3HC4) 9	chr12q14.1	226454_at	NM_138396																				
5.98	5.77	0.21	4.43E-01	7.65E-01	H2AFV	H2A histone family, member V	chr7p13	227085_at	NM_012412 /// NM_138635 /// NM_201436 /// NM_201516 /// NM_201517																				
7.91	7.74	0.17	4.43E-01	7.65E-01	ELOF1	elongation factor 1 homolog (S. cerevisiae)	chr19p13.2	225156_at	NM_032377																				
2.56	2.41	0.15	4.43E-01	7.65E-01	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	chr19p13.2	1555602_a_at	NM_001420 /// NM_032281																				
4.16	4.01	0.15	4.43E-01	7.65E-01	ASPRV1	aspartic peptidase, retroviral-like 1	chr2p14	235514_at	NM_152792																				
3.06	2.83	0.23	4.43E-01	7.65E-01	---	---	---	244359_s_at	---																				
2.75	2.62	0.13	4.44E-01	7.65E-01	---	---	---	234585_at	---																				
3.01	2.79	0.22	4.44E-01	7.65E-01	ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	chr5q12.1	1554883_a_at	NM_000082 /// NM_001007233 /// NM_001007234																				
2.82	2.65	0.17	4.44E-01	7.65E-01	TRIM42	tripartite motif-containing 42	chr3q23	1566851_at	NM_152616																				
2.52	2.40	0.12	4.44E-01	7.65E-01	C10orf46	Chromosome 10 open reading frame 46	chr10q26.11	227136_s_at	NM_153810																				
1.93	1.83	0.10	4.44E-01	7.65E-01	TF	transferrin	chr3q22.1	220109_at	NM_001063																				

8.20	8.09	0.12	4.44E-01	7.65E-01	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	chr8q11.2	221504_s_at	NM_015941 /// NM_213619 /// NM_213620																			
4.49	4.33	0.16	4.44E-01	7.65E-01	FLJ40288	hypothetical protein FLJ40288	chr7q32.3	1553464_at	XR_040153 /// XR_040154 /// XR_040155 /// XR_040156																			
3.98	3.55	0.44	4.44E-01	7.65E-01	TncRNA	Trophoblast-derived noncoding RNA	chr11q13.1	214657_s_at	NR_002802																			
7.58	7.46	0.13	4.44E-01	7.65E-01	CALU	calumenin	chr7q32.1	200757_s_at	NM_001130674 /// NM_001219																			
4.50	4.18	0.33	4.44E-01	7.65E-01	RGS4	regulator of G-protein signaling 4	chr1q23.3	204339_s_at	NM_001102445 /// NM_001113380 /// NM_001113381 /// NM_005613																			
2.08	1.98	0.10	4.44E-01	7.65E-01	---	---	---	1567702_at	---																			
2.79	2.67	0.11	4.44E-01	7.65E-01	---	---	---	240252_at	---																			
8.75	8.60	0.16	4.44E-01	7.65E-01	HINT2	histidine triad nucleotide binding protein 2	chr9p13.3	224415_s_at	NM_032593																			
2.44	2.29	0.15	4.44E-01	7.65E-01	MCM3AP	minichromosome maintenance complex component 3 associated protein	chr21q22.3	215581_s_at	NM_003906																			
2.73	2.62	0.11	4.44E-01	7.65E-01	---	---	---	1556281_at	---																			
2.46	2.35	0.10	4.44E-01	7.65E-01	---	---	---	228147_at	---																			
2.42	2.32	0.10	4.44E-01	7.66E-01	CLCN5	chloride channel 5	chrXp11.23-p11.22|Xp11.23	232128_s_at	NM_000084 /// NM_001127898 /// NM_001127899																			
2.49	2.38	0.11	4.44E-01	7.66E-01	YSK4	yeast Sps1/Ste20-related kinase 4 (S. cerevisiae)	chr2q21.3	1555804_a_at	NM_001018046 /// NM_025052																			
4.56	4.31	0.25	4.45E-01	7.66E-01	KRBA1	KRAB-A domain containing 1	chr7q36	236275_at	NM_032534																			
2.52	2.42	0.10	4.45E-01	7.66E-01	C11orf80	chromosome 11 open reading frame 80	chr11q13.1	238593_at	NM_024650																			
3.08	2.98	0.10	4.45E-01	7.66E-01	C13orf1	chromosome 13 open reading frame 1	chr13q14	214668_at	NM_001127482 /// NM_020456 /// NR_023351																			
3.24	2.94	0.30	4.45E-01	7.66E-01	FBXL4	F-box and leucine-rich repeat protein 4	chr6q16.1-q16.3	236994_at	NM_012160																			
8.01	7.76	0.25	4.45E-01	7.66E-01	HNRNPA3 /// HNRNPA3P1	heterogeneous nuclear ribonucleoprotein A3 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	chr10q11.21 /// chr2q31.2	211933_s_at	NM_194247 /// NR_002726																			
3.12	2.90	0.22	4.45E-01	7.66E-01	C2orf60	chromosome 2 open reading frame 60	chr2q33.1	235686_at	NM_001039693 /// NR_004862																			
2.34	2.23	0.12	4.45E-01	7.66E-01	---	---	---	1561673_at	---																			
2.01	1.94	0.08	4.45E-01	7.66E-01	LOC643085	hypothetical LOC643085	chr2q11.1	229224_x_at	XR_041320 /// XR_041321 /// XR_041322																			
2.51	2.42	0.09	4.45E-01	7.66E-01	---	---	---	1562950_at	---																			
2.24	2.13	0.10	4.45E-01	7.66E-01	---	---	---	1553882_at	---																			
2.36	2.27	0.09	4.45E-01	7.66E-01	---	---	---	1556297_a_at	---																			
3.42	3.30	0.13	4.45E-01	7.66E-01	INTS1	integrator complex subunit 1	chr7p22.3	212210_at	NM_001080453																			
2.35	2.22	0.13	4.45E-01	7.66E-01	---	---	---	1555187_at	---																			
2.03	1.94	0.09	4.45E-01	7.66E-01	---	---	---	215469_at	---																			
4.46	4.21	0.25	4.45E-01	7.66E-01	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	chr12p11	202660_at	NM_002223																			
4.52	4.33	0.19	4.45E-01	7.66E-01	RECQL4	RecQ protein-like 4	chr8q24.3	1553015_a_at	NM_004260																			
4.28	4.12	0.16	4.45E-01	7.66E-01	MATR3 /// SNHG4	matrin 3 /// small nucleolar RNA host gene 4 (non-protein coding)	chr5q31.2	1564907_s_at	NM_018834 /// NM_199189 /// NR_003141																			
2.82	2.72	0.10	4.45E-01	7.66E-01	---	---	---	244577_at	---																			

8.17	7.97	0.21	4.46E-01	7.66E-01	C20orf30	chromosome 20 open reading frame 30	chr20p12.3	220477_s_at	NM_001009923 /// NM_001009924 /// NM_001009925 /// NM_014145
6.33	6.10	0.23	4.46E-01	7.66E-01	---	---	---	1555743_s_at	---
6.19	6.07	0.12	4.46E-01	7.67E-01	SMARCAL1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	chr2q34-q35	218452_at	NM_001127207 /// NM_014140
3.10	2.90	0.20	4.46E-01	7.67E-01	C16orf55	chromosome 16 open reading frame 55	chr16q24.3	230811_at	NM_153025
3.93	3.83	0.10	4.46E-01	7.67E-01	C2orf70	chromosome 2 open reading frame 70	chr2p23.3	231126_at	NM_001105519
2.36	2.25	0.11	4.46E-01	7.67E-01	LALBA	lactalbumin, alpha-	chr12q13	207816_at	NM_002289
8.31	8.16	0.15	4.46E-01	7.67E-01	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	chr19p13.2	202785_at	NM_005001
3.11	2.97	0.14	4.46E-01	7.67E-01	FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	chr8p12	223976_at	NM_032664
2.74	2.61	0.13	4.46E-01	7.67E-01	---	---	---	1561409_at	---
2.37	2.26	0.11	4.46E-01	7.67E-01	---	---	---	234219_at	---
2.26	2.12	0.13	4.46E-01	7.67E-01	SP100	SP100 nuclear antigen	chr2q37.1	210219_at	NM_001080391 /// NM_003113
3.86	3.70	0.16	4.46E-01	7.67E-01	LOC286297	hypothetical protein LOC286297	chr9q12	1564277_a_at	XM_372109 /// XM_933054 /// XM_933058
6.46	6.33	0.13	4.46E-01	7.67E-01	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	chr21q22.1-q22.2|21q22.11	216954_x_at	NM_001697
2.67	2.53	0.13	4.46E-01	7.67E-01	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif, 17	chr15q24	1552725_s_at	NM_139057
3.06	2.92	0.13	4.46E-01	7.67E-01	SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	chr5p15.3	207212_at	NM_004174
2.11	2.01	0.09	4.46E-01	7.67E-01	NRG4	neuregulin 4	chr15q24.2	242426_at	NM_138573
2.12	2.03	0.09	4.46E-01	7.67E-01	C6orf182	chromosome 6 open reading frame 182	chr6q21	243118_at	NM_001083535 /// NM_173830
3.63	3.39	0.25	4.46E-01	7.67E-01	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	chr6q21	218948_at	NM_018292
3.12	2.96	0.16	4.46E-01	7.67E-01	PIAS2	protein inhibitor of activated STAT, 2	chr18q21.1	37433_at	NM_004671 /// NM_173206
2.27	2.18	0.09	4.47E-01	7.67E-01	ZNF430	zinc finger protein 430	chr19p12	238614_x_at	NM_025189
2.38	2.26	0.12	4.47E-01	7.67E-01	HIST1H2AD /// HIST1H2BN /// HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	histone cluster 1, H2ad /// histone cluster 1, H2bn /// histone cluster 1, H3a /// histone cluster 1, H3b /// histone cluster 1, H3c /// histone cluster 1, H3d /// histone cluster 1, H3e /// histone cluster 1, H3f /// histone cluster 1, H3g /// histone cluster 1, H3h /// histone cluster 1, H3i /// histone cluster 1, H3j	chr6p21.3 /// chr6p22-p21.3 /// chr6p22.1	208506_at	NM_003520 /// NM_003529 /// NM_003530 /// NM_003531 /// NM_003532 /// NM_003533 /// NM_003534 /// NM_003535 /// NM_003536 /// NM_003537 /// NM_021018 /// NM_021065
2.78	2.64	0.14	4.47E-01	7.67E-01	LOC284120	hypothetical LOC284120	chr17q25.3	241394_at	XM_001721080 /// XM_211339
2.65	2.52	0.13	4.47E-01	7.67E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	208876_s_at	NM_002577
2.43	2.34	0.09	4.47E-01	7.67E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	1559427_at	NM_001112732 /// NM_024979
2.19	2.08	0.11	4.47E-01	7.67E-01	FGD4	FYVE, RhoGEF and PH domain containing 4	chr12p11.21	230559_x_at	NM_139241
2.08	1.98	0.10	4.47E-01	7.67E-01	CENTB2	centaurin, beta 2	chr3q29	212477_at	NM_012287
2.83	2.72	0.11	4.47E-01	7.67E-01	---	---	---	234125_at	---
6.09	5.97	0.13	4.47E-01	7.67E-01	C14orf133	chromosome 14 open reading frame 133	chr14q24.3-q31	218431_at	NM_022067

8.51	8.25	0.26	4.47E-01	7.67E-01	TCEA3	transcription elongation factor A (SII), 3	chr1p36.12	226388_at	NM_003196
4.12	3.71	0.41	4.47E-01	7.67E-01	PLD1	phospholipase D1, phosphatidylcholine-specific	chr3q26	232530_at	NM_001130081 /// NM_002662
2.09	2.02	0.08	4.47E-01	7.67E-01	---	---	---	216864_at	---
5.87	5.63	0.25	4.47E-01	7.67E-01	COL16A1	collagen, type XVI, alpha 1	chr1p35-p34	204345_at	NM_001856
3.14	2.94	0.19	4.47E-01	7.67E-01	BIRC5	baculoviral IAP repeat-containing 5	chr17q25	210334_x_at	NM_001012270 /// NM_001012271 /// NM_001168
4.75	4.55	0.21	4.47E-01	7.67E-01	DOCK4	dedicator of cytokinesis 4	chr7q31.1	205003_at	NM_014705
2.22	2.12	0.10	4.47E-01	7.67E-01	---	---	---	232131_at	---
3.63	3.49	0.14	4.47E-01	7.67E-01	TASP1	taspase, threonine aspartase, 1	chr20p12.1	219443_at	NM_017714
2.23	2.14	0.09	4.47E-01	7.67E-01	SR140	U2-associated SR140 protein	chr3q23	236431_at	NM_001080415
6.94	6.84	0.10	4.47E-01	7.67E-01	CCNY	cyclin Y	chr10p11.21	224652_at	NM_145012 /// NM_181698
8.51	8.36	0.15	4.47E-01	7.67E-01	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	chr7p22	217736_s_at	NM_001134335 /// NM_014413
2.95	2.74	0.22	4.47E-01	7.67E-01	GULP1	GULP, engulfment adaptor PTB domain containing 1	chr2q32.3-q33	223837_at	NM_016315
2.34	2.23	0.11	4.48E-01	7.67E-01	---	---	---	217426_at	---
2.96	2.84	0.12	4.48E-01	7.67E-01	TERF2	telomeric repeat binding factor 2	chr16q22.1	1555185_x_at	NM_005652
2.72	2.60	0.12	4.48E-01	7.67E-01	CLIP3	CAP-GLY domain containing linker protein 3	chr19q13.12	235243_at	NM_015526
7.01	6.87	0.14	4.48E-01	7.68E-01	C18orf10	chromosome 18 open reading frame 10	chr18q12.2	213617_s_at	NM_015476
2.32	2.20	0.13	4.48E-01	7.68E-01	---	---	---	1556105_at	---
7.44	7.28	0.17	4.48E-01	7.68E-01	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	chr3p21.31	203658_at	NM_000387
7.92	7.76	0.17	4.48E-01	7.68E-01	TEX264	testis expressed 264	chr3p21.31	218548_x_at	NM_001129884 /// NM_015926 /// NR_024012
4.00	3.84	0.16	4.48E-01	7.68E-01	---	---	---	239324_at	---
3.29	3.03	0.26	4.48E-01	7.68E-01	SPON1	spondin 1, extracellular matrix protein	chr11p15.2	213993_at	NM_006108
6.84	6.64	0.20	4.48E-01	7.68E-01	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	chr11q23.3	209509_s_at	NM_001382 /// NM_203316
7.91	7.73	0.18	4.48E-01	7.68E-01	BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	chr19q13.1-q13.2	202331_at	NM_000709
3.86	3.73	0.13	4.48E-01	7.68E-01	---	---	---	217615_at	---
4.58	4.47	0.10	4.48E-01	7.68E-01	SYTL4	Synaptotagmin-like 4	chrXq21.33	229991_s_at	NM_001129896 /// NM_080737
3.26	3.04	0.21	4.48E-01	7.68E-01	GALT	galactose-1-phosphate uridylyltransferase	chr9p13	232708_at	NM_000155
2.06	1.98	0.08	4.48E-01	7.68E-01	---	---	---	244094_at	---
2.58	2.47	0.11	4.48E-01	7.68E-01	DGAT2L3	diacylglycerol O-acyltransferase 2-like 3	chrXq13.1	1560507_at	NM_001013579
6.36	6.21	0.15	4.48E-01	7.68E-01	UBE2R2	ubiquitin-conjugating enzyme E2R 2	chr9p13.3	226954_at	NM_017811
3.21	3.09	0.12	4.49E-01	7.68E-01	---	---	---	223410_s_at	---
2.63	2.54	0.08	4.49E-01	7.68E-01	PTGIS	prostaglandin I2 (prostacyclin) synthase	chr20q13.13	211892_s_at	NM_000961
3.23	3.02	0.22	4.49E-01	7.68E-01	---	---	---	244216_at	---
2.90	2.79	0.11	4.49E-01	7.68E-01	FBXL12	F-box and leucine-rich repeat protein 12	chr19p13.2	237256_at	NM_017703
2.46	2.35	0.11	4.49E-01	7.68E-01	BCORL1	BCL6 co-repressor-like 1	chrXq25-q26.1	233574_at	NM_021946
5.63	5.47	0.16	4.49E-01	7.68E-01	RAB11FIP1	RAB11 family interacting protein 1 (class I)	chr8p11.22	225177_at	NM_001002233 /// NM_001002814 /// NM_025151
5.93	5.68	0.26	4.49E-01	7.68E-01	C1orf131	chromosome 1 open reading frame 131	chr1q42.2	226242_at	NM_152379
2.15	2.04	0.12	4.49E-01	7.68E-01	hCG_2009921	hypothetical locus LOC441204	chr7p15.2	215297_at	NR_015364 /// XM_001722132 /// XM_001723644 /// XM_001723694 /// XM_499061 /// XM_943507
2.42	2.34	0.09	4.49E-01	7.68E-01	CPO	carboxypeptidase O	chr2q33.3	1553506_at	NM_173077
2.23	2.13	0.10	4.49E-01	7.68E-01	FSIP1	fibrous sheath interacting protein 1	chr15q14	1553622_a_at	NM_152597

2.31	2.22	0.09	4.49E-01	7.68E-01	C11orf57	chromosome 11 open reading frame 57	chr11q23.1	1560029_a_at	NM_001082969 /// NM_001082970 /// NM_018195																			
2.30	2.18	0.12	4.49E-01	7.69E-01	IDS	iduronate 2-sulfatase	chrXq28	202438_x_at	NM_000202 /// NM_006123																			
2.31	2.22	0.09	4.49E-01	7.69E-01	LOC100130548	hypothetical protein LOC100130548	chr9q34.2	1557734_s_at	XM_001719412 /// XM_001722285 /// XM_001722973																			
5.57	5.42	0.15	4.49E-01	7.69E-01	TOR3A	torsin family 3, member A	chr1q25.2	233851_s_at	NM_022371																			
5.92	5.76	0.16	4.49E-01	7.69E-01	C19orf29	chromosome 19 open reading frame 29	chr19p13.3	214892_x_at	NM_001080543 /// NM_021231																			
2.61	2.52	0.10	4.49E-01	7.69E-01	CXCR7	Chemokine (C-X-C motif) receptor 7	chr2q37.3	1559114_a_at	NM_020311																			
2.19	2.07	0.13	4.49E-01	7.69E-01	---	---	---	243785_at	---																			
2.69	2.45	0.23	4.50E-01	7.69E-01	SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	chr4q13.1	222940_at	NM_005420																			
4.75	4.47	0.28	4.50E-01	7.69E-01	CDK2	cyclin-dependent kinase 2	chr12q13	204252_at	NM_001798 /// NM_052827																			
2.40	2.29	0.11	4.50E-01	7.69E-01	---	---	---	1562871_at	---																			
2.13	2.02	0.11	4.50E-01	7.69E-01	C2orf80	chromosome 2 open reading frame 80	chr2q33.3	241998_at	NM_001099334																			
2.47	2.33	0.15	4.50E-01	7.69E-01	C10orf96	chromosome 10 open reading frame 96	chr10q25.3	1555443_at	NM_198515																			
2.48	2.35	0.14	4.50E-01	7.69E-01	LOC339400	hypothetical protein LOC339400	chr1q21.3	241014_at	---																			
4.58	4.34	0.24	4.50E-01	7.69E-01	ORAI2	ORAI calcium release-activated calcium modulator 2	chr7q22.1	231406_at	NM_001126340 /// NM_032831																			
6.67	6.56	0.11	4.50E-01	7.69E-01	C12orf45	chromosome 12 open reading frame 45	chr12q23.3	226349_at	NM_152318																			
2.06	1.97	0.09	4.50E-01	7.69E-01	---	---	---	1561731_at	---																			
3.40	3.30	0.11	4.50E-01	7.69E-01	---	---	---	1566477_at	---																			
2.30	2.19	0.11	4.50E-01	7.69E-01	---	---	---	243415_at	---																			
2.72	2.60	0.12	4.50E-01	7.69E-01	C12orf72	chromosome 12 open reading frame 72	chr12p11.21	1554583_a_at	NM_173802																			
6.05	5.80	0.26	4.50E-01	7.69E-01	---	---	---	238040_at	---																			
3.78	3.53	0.25	4.50E-01	7.69E-01	KCTD9	potassium channel tetramerisation domain containing 9	chr8p21.1	218823_s_at	NM_017634																			
6.78	6.62	0.16	4.50E-01	7.69E-01	MRPL55	mitochondrial ribosomal protein L55	chr1q42.13	225719_s_at	NM_181441 /// NM_181454 /// NM_181455 /// NM_181456 /// NM_181462 /// NM_181463 /// NM_181464 /// NM_181465																			
3.85	3.69	0.16	4.50E-01	7.69E-01	IGH@ /// IGHG1 /// IGHM	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu	chr14q32.33	228518_at	---																			
4.48	4.20	0.27	4.51E-01	7.69E-01	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	chr1q25	221210_s_at	NM_030769																			
5.39	5.14	0.25	4.51E-01	7.69E-01	PDCD2L	programmed cell death 2-like	chr19q13.11	224467_s_at	NM_032346																			
9.97	9.83	0.13	4.51E-01	7.70E-01	FAM127A	family with sequence similarity 127, member A	chrXq26	201828_x_at	NM_001078171																			
8.77	8.48	0.29	4.51E-01	7.70E-01	CYCS	cytochrome c, somatic	chr7p15.2	208905_at	NM_018947																			
1.95	1.85	0.10	4.51E-01	7.70E-01	TRPC3	transient receptor potential cation channel, subfamily C, member 3	chr4q27	210814_at	NM_001130698 /// NM_003305																			
4.21	3.86	0.35	4.51E-01	7.70E-01	SLC39A8	solute carrier family 39 (zinc transporter), member 8	chr4q22-q24	209267_s_at	NM_022154																			
2.70	2.62	0.09	4.51E-01	7.70E-01	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	chr16q12.2	210353_s_at	NM_001043																			
5.00	4.80	0.20	4.51E-01	7.70E-01	UNQ338	hypothetical protein LOC646962	chr9p13.3	235496_at	NM_001039792																			
2.49	2.31	0.18	4.51E-01	7.70E-01	CEP97	centrosomal protein 97kDa	chr3q12.3	219886_at	NM_024548																			
6.41	6.07	0.34	4.51E-01	7.70E-01	ATXN7	ataxin 7	chr3p21.1-p12	204516_at	NM_000333 /// NM_001128149																			

6.49	6.12	0.37	4.51E-01	7.70E-01	PRELP	proline/arginine-rich end leucine-rich repeat protein	chr1q32	228224_at	NM_002725 /// NM_201348																				
3.26	3.15	0.12	4.51E-01	7.70E-01	---	---	---	1564729_at	---																				
3.56	3.39	0.17	4.51E-01	7.70E-01	LOC148413	hypothetical LOC148413	chr1p36.33	225934_at	XR_040142 /// XR_040143 /// XR_040144																				
2.63	2.54	0.09	4.51E-01	7.70E-01	---	---	---	240973_s_at	---																				
6.43	6.25	0.18	4.51E-01	7.70E-01	RYK	RYK receptor-like tyrosine kinase	chr3q22	214172_x_at	NM_001005861 /// NM_002958																				
6.40	6.25	0.15	4.51E-01	7.70E-01	PIGF	phosphatidylinositol glycan anchor biosynthesis, class F	chr2p21-p16	205077_s_at	NM_002643 /// NM_173074																				
2.21	2.12	0.09	4.51E-01	7.70E-01	---	---	---	1562973_at	---																				
6.39	6.27	0.12	4.51E-01	7.70E-01	ACACB	acetyl-Coenzyme A carboxylase beta	chr12q24.11	1552615_at	NM_001093																				
8.80	8.66	0.14	4.51E-01	7.70E-01	LOC100133665 /// TALDO1	similar to transaldolase /// transaldolase 1	chr11p15.5-p15.4	201463_s_at	NM_006755 /// XM_001718819																				
7.48	7.02	0.46	4.51E-01	7.70E-01	JUN	jun oncogene	chr1p32-p31	201464_x_at	NM_002228																				
2.01	1.90	0.10	4.51E-01	7.70E-01	LOC400654	hypothetical gene supported by BC042493	chr18q22.1	1561090_at	---																				
2.11	2.03	0.08	4.52E-01	7.70E-01	---	---	---	241042_at	---																				
2.18	2.07	0.11	4.52E-01	7.70E-01	---	---	---	1557896_at	---																				
6.02	5.80	0.22	4.52E-01	7.70E-01	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	chr17q22-q23	205596_s_at	NM_022739																				
3.49	3.37	0.12	4.52E-01	7.70E-01	LOC100129286	Hypothetical protein LOC100129286	chr2p21	237772_at	XM_001724487 /// XM_001725454 /// XM_001726918																				
5.23	4.99	0.25	4.52E-01	7.70E-01	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	chr1q32.1	228385_at	NM_001031725 /// NM_031306																				
5.33	5.16	0.17	4.52E-01	7.70E-01	VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)	chr2p13-p14	222627_at	NM_001005739 /// NM_016516																				
2.50	2.36	0.14	4.52E-01	7.70E-01	UBE3C	ubiquitin protein ligase E3C	chr7q36.3	1554794_a_at	NM_014671																				
3.34	3.18	0.16	4.52E-01	7.70E-01	ITIH3	inter-alpha (globulin) inhibitor H3	chr3p21.2-p21.1	205755_at	NM_002217																				
6.69	6.52	0.16	4.52E-01	7.70E-01	TMEM127	transmembrane protein 127	chr2q11.2	222887_s_at	NM_017849																				
2.40	2.30	0.10	4.52E-01	7.70E-01	---	---	---	242575_at	---																				
3.05	2.97	0.09	4.52E-01	7.70E-01	C1orf223	chromosome 1 open reading frame 223	chr1p33	230969_at	XM_001717622 /// XM_371248 /// XM_941516																				
2.32	2.17	0.16	4.52E-01	7.70E-01	---	---	---	232202_at	---																				
2.19	2.11	0.08	4.52E-01	7.70E-01	---	---	---	244583_at	---																				
2.59	2.50	0.09	4.52E-01	7.70E-01	---	---	---	215060_at	---																				
4.43	4.13	0.30	4.52E-01	7.70E-01	ZMYM2	zinc finger, MYM-type 2	chr13q11-q12	210281_s_at	NM_003453 /// NM_197968																				
3.83	3.67	0.17	4.52E-01	7.70E-01	---	---	---	235302_at	---																				
4.73	4.49	0.24	4.52E-01	7.70E-01	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	chr1q41	219037_at	NM_016052																				
2.53	2.43	0.11	4.52E-01	7.70E-01	PADI2	peptidyl arginine deiminase, type II	chr1p36.13	1554385_a_at	NM_007365																				
2.43	2.33	0.11	4.52E-01	7.70E-01	---	---	---	233769_at	---																				
4.43	4.28	0.15	4.52E-01	7.70E-01	LOC115110	hypothetical protein LOC115110	chr1p36.32	233960_s_at	---																				
4.99	4.50	0.50	4.52E-01	7.70E-01	SDPR	serum deprivation response (phosphatidylserine binding protein)	chr2q32-q33	218711_s_at	NM_004657																				
2.17	2.09	0.08	4.52E-01	7.70E-01	SPATA9	spermatogenesis associated 9	chr5q15	223840_s_at	NM_031952																				

									NM_001014 /// XM_373949 /// XM_938568 /// XR_015547 /// XR_015651 /// XR_016556 /// XR_017072 /// XR_017607 /// XR_017819 /// XR_017832 /// XR_018990 /// XR_019502 /// XR_019617 /// XR_038061 /// XR_038624 /// XR_038633 /// XR_038707 /// XR_038708 /// XR_038743 /// XR_038761 /// XR_040066 /// XR_042354 /// XR_042409 ///																				
					LOC376693 /// LOC388885 /// LOC391833 /// LOC401817 /// LOC646785 /// LOC728791 /// LOC730187 ///	hypothetical LOC376693 /// similar to ribosomal protein S10 /// similar to hCG2000485 /// similar to ribosomal protein S10 /// similar to ribosomal protein S10 /// similar to ribosomal protein S10 /// similar to ribosomal protein S10 /// ribosomal protein S10	chr15q22.2 /// chr1q32.1 /// chr22q11.23 /// chr2p14 /// chr3q13.31 /// chr5q31.1 /// chr6p21.31 ///																						
4.45	4.23	0.22	4.52E-01	7.70E-01	RPS10 /// RPS10P3	/// ribosomal protein S10 pseudogene 3	chr9q22.1	217336_at	XR_042419																					
7.24	7.03	0.22	4.53E-01	7.70E-01	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	chrXp11.4-p11.2	201895_at	NM_001654																					
3.76	3.65	0.11	4.53E-01	7.70E-01	---	---	---	1559421_at	---																					
2.25	2.12	0.13	4.53E-01	7.70E-01	---	---	---	1562926_at	---																					
5.22	5.02	0.20	4.53E-01	7.70E-01	TMEM110	transmembrane protein 110	chr3p21.1	213851_at	NM_198563																					
7.34	7.23	0.11	4.53E-01	7.70E-01	---	---	---	231658_x_at	---																					

7.62	7.27	0.34	4.53E-01	7.70E-01	CREM	cAMP responsive element modulator	chr10p11.21	209967_s_at	NM_001881 /// NM_181571 /// NM_182717 /// NM_182718 /// NM_182719 /// NM_182720 /// NM_182721 /// NM_182722 /// NM_182723 /// NM_182724 /// NM_182725 /// NM_182769 /// NM_182770 /// NM_182771 /// NM_182772 /// NM_182850 /// NM_182853 /// NM_183011 /// NM_183012 /// NM_183013 /// NM_183060																			
5.13	4.95	0.18	4.53E-01	7.70E-01	---	---	---	237618_at	---																				
2.74	2.64	0.10	4.53E-01	7.70E-01	---	---	---	1557518_a_at	---																				
3.48	3.34	0.14	4.53E-01	7.70E-01	FLJ38717	FLJ38717 protein	chr6p21.1	229914_at	XR_040734 /// XR_040735 /// XR_040736																				
2.42	2.31	0.11	4.53E-01	7.71E-01	NOX3	NADPH oxidase 3	chr6q25.1-q26	221089_at	NM_015718																				
5.80	5.63	0.17	4.53E-01	7.71E-01	LOC375190	hypothetical LOC375190	chr2p23.3	230435_at	XR_040244 /// XR_040245 /// XR_040246																				
2.72	2.62	0.10	4.53E-01	7.71E-01	KLF17	Kruppel-like factor 17	chr1p34.1	1553891_at	NM_173484																				
7.27	7.07	0.20	4.53E-01	7.71E-01	TIMP2	TIMP metallopeptidase inhibitor 2	chr17q25	203167_at	NM_003255																				
5.33	5.09	0.24	4.53E-01	7.71E-01	---	---	---	1568649_at	---																				
4.21	4.01	0.20	4.53E-01	7.71E-01	ZNF280D	zinc finger protein 280D	chr15q21.3	239107_at	NM_001002843 /// NM_001002844 /// NM_017661																				
2.06	1.95	0.11	4.53E-01	7.71E-01	---	---	---	240564_x_at	---																				
4.17	4.04	0.13	4.54E-01	7.71E-01	PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	chr7p21-p11.2	233943_x_at	NM_032639																				
2.49	2.38	0.12	4.54E-01	7.71E-01	---	---	---	233279_at	---																				
8.15	7.99	0.16	4.54E-01	7.71E-01	NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2	chr15q11.2	212129_at	NM_001008860 /// NM_001008892 /// NM_001008894 /// NM_030922																				
7.27	6.93	0.34	4.54E-01	7.71E-01	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	chr10q22	208990_s_at	NM_012207 /// NM_021644																				

2.28	2.17	0.11	4.54E-01	7.71E-01	BDH1	3-hydroxybutyrate dehydrogenase, type 1	chr3q29	1570336_at	NM_004051 /// NM_203314 /// NM_203315																				
5.42	5.30	0.12	4.54E-01	7.71E-01	CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11p11	1555467_a_at	NM_001025596 /// NM_006560 /// NM_198700																				
1.90	1.81	0.08	4.54E-01	7.71E-01	EPS15L2	epidermal growth factor receptor pathway substrate 15-like 2	chr7p12.3	207750_at	---																				
3.71	3.41	0.30	4.54E-01	7.71E-01	YTHDC2	YTH domain containing 2	chr5q22.2	205836_s_at	NM_022828																				
3.86	3.69	0.18	4.54E-01	7.71E-01	---	---	---	233233_at	---																				
3.33	3.22	0.11	4.54E-01	7.71E-01	KCNE3	potassium voltage-gated channel, Isk-related family, member 3	chr11q13-q14	222923_s_at	NM_005472																				
6.06	5.66	0.40	4.54E-01	7.71E-01	---	---	---	1560259_at	---																				
3.01	2.87	0.14	4.54E-01	7.71E-01	SAG	S-antigen; retina and pineal gland (arrestin)	chr2q37.1	206671_at	NM_000541																				
7.31	6.92	0.39	4.54E-01	7.71E-01	CREM	cAMP responsive element modulator	chr10p11.21	214508_x_at	NM_001881 /// NM_181571 /// NM_182717 /// NM_182718 /// NM_182719 /// NM_182720 /// NM_182721 /// NM_182722 /// NM_182723 /// NM_182724 /// NM_182725 /// NM_182769 /// NM_182770 /// NM_182771 /// NM_182772 /// NM_182850 /// NM_182853 /// NM_183011 /// NM_183012 /// NM_183013 /// NM_183060																		
4.61	4.20	0.41	4.54E-01	7.71E-01	TMEM173	transmembrane protein 173	chr5q31.2	224916_at	NM_198282																				
3.91	3.74	0.17	4.54E-01	7.71E-01	---	---	---	242437_at	---																				
2.37	2.25	0.11	4.54E-01	7.71E-01	CSRP3	cysteine and glycine-rich protein 3 (cardiac LIM protein)	chr11p15.1	205553_s_at	NM_001127656 /// NM_003476																				

2.52	2.22	0.30	4.54E-01	7.71E-01	ZNF655	zinc finger protein 655	chr7q22.1	1554726_at	NM_001009958 /// NM_001009960 /// NM_001083956 /// NM_001085366 /// NM_001085367 /// NM_001085368 /// NM_024061 /// NM_138494																				
2.26	2.17	0.09	4.54E-01	7.71E-01	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	chr8q22	213906_at	NM_001080416																				
2.94	2.81	0.13	4.54E-01	7.72E-01	---	---	---	237539_at	---																				
4.81	4.55	0.26	4.54E-01	7.72E-01	C1orf107	chromosome 1 open reading frame 107	chr1q32.2	204699_s_at	NM_014388																				
6.06	5.88	0.18	4.54E-01	7.72E-01	ZBTB47	zinc finger and BTB domain containing 47	chr3p22.1	226500_at	NM_145166																				
2.26	2.16	0.10	4.55E-01	7.72E-01	---	---	---	1556496_a_at	---																				
10.49	10.36	0.14	4.55E-01	7.72E-01	COX5B	cytochrome c oxidase subunit Vb	chr2cen-q13	213735_s_at	NM_001862																				
3.22	3.07	0.15	4.55E-01	7.72E-01	KIAA1648	KIAA1648 protein	chr22q12.1	1555871_at	XM_001720903 /// XM_001723353 /// XM_001726321																				
5.09	4.93	0.17	4.55E-01	7.72E-01	TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	chr1q42.13	213654_at	NM_001025247 /// NM_014409																				
4.77	4.56	0.21	4.55E-01	7.72E-01	NTN4	netrin 4	chr12q22|12q22-q23	223315_at	NM_021229																				
5.92	5.39	0.53	4.55E-01	7.72E-01	GLIPR1	GLI pathogenesis-related 1	chr12q21.2	226142_at	NM_006851																				
9.52	9.16	0.36	4.55E-01	7.72E-01	CXCR4	chemokine (C-X-C motif) receptor 4	chr2q21	211919_s_at	NM_001008540 /// NM_003467																				
2.80	2.63	0.16	4.55E-01	7.72E-01	ATXN1	ataxin 1	chr6p23	242230_at	NM_000332 /// NM_001128164																				
2.37	2.24	0.13	4.55E-01	7.72E-01	PRX	periaxin	chr19q13.13-q13.2	222255_at	NM_020956 /// NM_181882																				
2.83	2.71	0.12	4.55E-01	7.72E-01	VRK3	vaccinia related kinase 3	chr19q13	1566701_at	NM_001025778 /// NM_016440																				
4.12	3.70	0.42	4.55E-01	7.72E-01	RFC3	replication factor C (activator 1) 3, 38kDa	chr13q12.3-q13	204128_s_at	NM_002915 /// NM_181558																				
3.53	3.38	0.14	4.55E-01	7.72E-01	LRRC27	leucine rich repeat containing 27	chr10q26.3	1558484_s_at	NM_030626																				
2.23	2.13	0.10	4.55E-01	7.72E-01	KLHL23	Kelch-like 23 (Drosophila)	chr2q31.1	237756_at	NM_144711																				
6.04	5.91	0.13	4.55E-01	7.72E-01	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	chr20p13	212864_at	NM_003818																				
5.11	4.95	0.15	4.55E-01	7.72E-01	FEN1	flap structure-specific endonuclease 1	chr11q12	204768_s_at	NM_004111																				
3.32	3.19	0.13	4.56E-01	7.72E-01	ARL13B	ADP-ribosylation factor-like 13B	chr3q11.2	228201_at	NM_144996 /// NM_182896																				
2.57	2.43	0.13	4.56E-01	7.73E-01	C12orf72	chromosome 12 open reading frame 72	chr12p11.21	1563475_s_at	NM_173802																				

3.23	3.12	0.11	4.56E-01	7.73E-01	GGT1 /// GGT2 /// GGT3P /// GGT4P /// GGT8P	gamma-glutamyltransferase 1 /// gamma-glutamyltransferase 2 /// gamma-glutamyltransferase 3 pseudogene /// gamma-glutamyltransferase 4 pseudogene /// gamma-glutamyltransferase 8 pseudogene	chr22q11.21 /// chr22q11.23 /// chr2p11.1	244179_x_at	NM_001032364 /// NM_001032365 /// NM_005265 /// NM_013430 /// NR_003267 /// NR_003503 /// XM_001129377 /// XM_001129425 /// XR_038677 /// XR_042175																				
2.26	2.17	0.09	4.56E-01	7.73E-01	---	---	---	233577_at	---																				
2.07	2.00	0.07	4.56E-01	7.73E-01	---	---	---	1561877_at	---																				
6.70	6.48	0.21	4.56E-01	7.73E-01	ZNF146	zinc finger protein 146	chr19q13.1	200050_at	NM_001099638 /// NM_001099639 /// NM_007145																				
1.91	1.82	0.09	4.56E-01	7.73E-01	---	---	---	239080_at	---																				
2.51	2.39	0.12	4.56E-01	7.73E-01	---	---	---	233661_at	---																				
2.78	2.68	0.11	4.56E-01	7.73E-01	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	chr3p14.1	1559257_a_at	NM_001033057 /// NM_004742 /// NM_015520																				
8.08	7.96	0.12	4.56E-01	7.73E-01	TMED9	transmembrane emp24 protein transport domain containing 9	chr5q35.3	208757_at	NM_017510																				
1.86	1.77	0.09	4.56E-01	7.73E-01	---	---	---	1567696_at	---																				
4.69	4.56	0.13	4.56E-01	7.73E-01	---	---	---	213114_at	---																				
7.67	7.48	0.19	4.56E-01	7.73E-01	TXNDC1	thioredoxin domain containing 1	chr14q22.1	209476_at	NM_030755																				
6.01	5.90	0.11	4.56E-01	7.73E-01	CDC2L1 /// CDC2L2	cell division cycle 2-like 1 (PITSLRE proteins) /// cell division cycle 2-like 2 (PITSLRE proteins)	chr1p36.33	215329_s_at	NM_024011 /// NM_033486 /// NM_033487 /// NM_033488 /// NM_033489 /// NM_033492 /// NM_033493 /// NM_033529 /// XM_001713735 /// XM_001713748 /// XM_001715985 /// XM_001716018 /// XM_001716037 /// XM_001716055																				
3.47	3.33	0.13	4.56E-01	7.73E-01	C9orf86	chromosome 9 open reading frame 86	chr9q34.3	219828_at	NM_017995 /// NM_024718																				
6.22	6.11	0.10	4.57E-01	7.73E-01	ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)	chr3p25.3-p25.2	224025_s_at	NM_006395																				
6.89	6.68	0.21	4.57E-01	7.73E-01	NAGA	N-acetylgalactosaminidase, alpha-	chr22q13-qter|22q11	1555041_a_at	NM_000262																				
2.82	2.69	0.13	4.57E-01	7.73E-01	C14orf118	Chromosome 14 open reading frame 118	chr14q22.1-q24.3	231970_at	NM_017926 /// NM_017972																				

6.11	5.94	0.17	4.57E-01	7.73E-01	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	chr15q22.2-q22.3	223507_at	NM_006660																				
2.74	2.55	0.18	4.57E-01	7.74E-01	KCTD15	potassium channel tetramerisation domain containing 15	chr19q13.11	222668_at	NM_001129994 /// NM_001129995 /// NM_024076																				
3.03	2.86	0.17	4.57E-01	7.74E-01	CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9q34.3	220410_s_at	NM_015447																				
7.89	7.70	0.19	4.57E-01	7.74E-01	LOC203547	hypothetical protein LOC203547	chrXq28	225556_at	NM_001017980																				
4.89	4.64	0.25	4.57E-01	7.74E-01	AP4M1	adaptor-related protein complex 4, mu 1 subunit	chr7q22.1	209837_at	NM_004722																				
6.68	6.35	0.33	4.57E-01	7.74E-01	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	chr1p34.1	202743_at	NM_001114172 /// NM_003629																				
8.62	8.47	0.15	4.57E-01	7.74E-01	PINK1	PTEN induced putative kinase 1	chr1p36	209018_s_at	NM_032409																				
5.77	5.54	0.23	4.57E-01	7.74E-01	C15orf39	chromosome 15 open reading frame 39	chr15q24.2	204494_s_at	NM_015492																				
3.14	3.04	0.11	4.57E-01	7.74E-01	KIAA1772	KIAA1772	chr18q11.1-q11.2	233977_at	XR_040952 /// XR_040953 /// XR_040954																				
3.55	3.29	0.26	4.57E-01	7.74E-01	PRR16	proline rich 16	chr5q23.1	1554867_a_at	NM_016644																				
1.94	1.87	0.08	4.57E-01	7.74E-01	---	---	---	237593_at	---																				
4.71	4.48	0.23	4.57E-01	7.74E-01	GYLTL1B	glycosyltransferase-like 1B	chr11p11.2	227829_at	NM_152312																				
2.07	1.96	0.11	4.57E-01	7.74E-01	---	---	---	1562420_at	---																				
5.97	5.78	0.19	4.57E-01	7.74E-01	BRMS1	breast cancer metastasis suppressor 1	chr11q13-q13.2	215631_s_at	NM_001024957 /// NM_015399																				
3.85	3.72	0.13	4.57E-01	7.74E-01	CASP2	caspase 2, apoptosis-related cysteine peptidase	chr7q34-q35	209812_x_at	NM_032982 /// NM_032983																				
2.73	2.63	0.10	4.58E-01	7.74E-01	OSBPL1A	oxysterol binding protein-like 1A	chr18q11.1	1554646_at	NM_018030 /// NM_080597																				
8.02	7.84	0.18	4.58E-01	7.74E-01	C2orf30	chromosome 2 open reading frame 30	chr2p16.2	224628_at	NM_001127397 /// NM_001127398 /// NM_015701																				
2.28	2.16	0.12	4.58E-01	7.74E-01	AFM	afamin	chr4q11-q13	206840_at	NM_001133																				
6.75	6.61	0.14	4.58E-01	7.74E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	207358_x_at	NM_012090 /// NM_033044																				
2.32	2.23	0.09	4.58E-01	7.74E-01	FAM160B1	family with sequence similarity 160, member B1	chr10q25.3	1554288_at	NM_020940																				
5.48	5.33	0.15	4.58E-01	7.74E-01	C9orf30 /// TMEFF1	chromosome 9 open reading frame 30 /// transmembrane protein with EGF-like and two follistatin-like domains 1	chr9q31 /// chr9q31.1	1555841_at	NM_003692 /// NM_080655																				
2.13	2.03	0.10	4.58E-01	7.74E-01	MTRF1	mitochondrial translational release factor 1	chr13q14.1-q14.3	242996_at	NM_004294																				
4.35	4.13	0.21	4.58E-01	7.74E-01	PCNXL3	pecanex-like 3 (Drosophila)	chr11q13.1	227858_at	NM_032223																				
4.89	4.71	0.18	4.58E-01	7.74E-01	---	---	---	238104_at	---																				
4.55	4.10	0.45	4.58E-01	7.74E-01	PLD1	phospholipase D1, phosphatidylcholine-specific	chr3q26	215723_s_at	NM_001130081 /// NM_002662																				
6.24	6.09	0.15	4.58E-01	7.74E-01	PTMS	parathymosin	chr12p13	218045_x_at	NM_002824																				
2.85	2.76	0.09	4.58E-01	7.74E-01	TCP11L2	t-complex 11 (mouse)-like 2	chr12q23.3	1569206_at	NM_152772																				
3.45	3.31	0.15	4.58E-01	7.74E-01	LOC220980	hypothetical protein LOC220980	chr10q11.21	1563632_at	---																				
4.91	4.71	0.20	4.58E-01	7.74E-01	HEL308	DNA helicase HEL308	chr4q21.23	1554341_a_at	NM_133636																				
2.13	2.02	0.10	4.58E-01	7.74E-01	DENND1B	DENN/MADD domain containing 1B	chr1q31.3	1557309_at	NM_019049 /// NM_144977																				
6.11	5.68	0.43	4.58E-01	7.74E-01	AMD1	adenosylmethionine decarboxylase 1	chr6q21-q22	201196_s_at	NM_001033059 /// NM_001634																				
4.76	4.59	0.16	4.58E-01	7.74E-01	SFI1	Sfi1 homolog, spindle assembly associated (yeast)	chr22q12.2	215699_x_at	NM_001007467 /// NM_014775																				
2.85	2.65	0.19	4.58E-01	7.74E-01	C17orf65	chromosome 17 open reading frame 65	chr17q21.31	1555981_at	NM_178542																				
3.79	3.46	0.33	4.58E-01	7.74E-01	KY	kyphoscoliosis peptidase	chr3q22.2	244572_at	NM_178554																				
4.76	4.67	0.09	4.59E-01	7.74E-01	KIF9	kinesin family member 9	chr3p21.31	230701_x_at	NM_022342 /// NM_182902 /// NM_182903																				
2.28	2.18	0.10	4.59E-01	7.74E-01	ZNF486	zinc finger protein 486	chr19p12	1553901_x_at	NM_052852																				
2.76	2.61	0.16	4.59E-01	7.74E-01	JAK2	Janus kinase 2 (a protein tyrosine kinase)	chr9p24	205841_at	NM_004972																				

2.59	2.48	0.11	4.59E-01	7.74E-01	LOC100130349	hypothetical protein LOC100130349	chr2p21	235963_at	XM_001724359 /// XM_001725371 /// XM_001726915																			
4.52	4.38	0.14	4.59E-01	7.74E-01	SIRT6	sirtuin (silent mating type information regulation 2 homolog) 6 (S. cerevisiae)	chr19p13.3	219613_s_at	NM_016539																			
2.35	2.25	0.10	4.59E-01	7.74E-01	ANXA10	annexin A10	chr4q33	210143_at	NM_007193																			
2.40	2.27	0.12	4.59E-01	7.74E-01	---	---	---	1562759_at	---																			
4.68	4.46	0.22	4.59E-01	7.75E-01	WDR24	WD repeat domain 24	chr16p13.3	223293_at	NM_032259																			
2.13	2.02	0.11	4.59E-01	7.75E-01	MSTP9	macrophage stimulating, pseudogene 9	chr1p36.13	215563_s_at	NR_002729																			
2.33	2.24	0.10	4.59E-01	7.75E-01	---	---	---	1559656_a_at	---																			
2.30	2.15	0.15	4.59E-01	7.75E-01	---	---	---	240089_at	---																			
4.75	4.66	0.10	4.59E-01	7.75E-01	LIN52	lin-52 homolog (C. elegans)	chr14q24.3	231959_at	NM_001024674																			
2.55	2.43	0.12	4.59E-01	7.75E-01	ENAH	enabled homolog (Drosophila)	chr1q42.12	1553672_at	NM_001008493 /// NM_018212																			
3.26	3.13	0.13	4.59E-01	7.75E-01	---	---	---	232995_at	---																			
2.64	2.55	0.09	4.59E-01	7.75E-01	C1orf46	chromosome 1 open reading frame 46	chr1q21.3	216935_at	---																			
4.34	4.23	0.11	4.59E-01	7.75E-01	EEF1A1	Eukaryotic translation elongation factor 1 alpha 1	chr6q14.1	1557120_at	NM_001402																			
2.77	2.65	0.12	4.59E-01	7.75E-01	---	---	---	215658_at	---																			
6.88	6.57	0.31	4.59E-01	7.75E-01	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)	chr6p21.3	217362_x_at	NR_001298																			
3.09	2.98	0.11	4.59E-01	7.75E-01	LOC100128909	similar to hCG1817494	chr9q22.2	236008_at	XM_001721350 /// XM_001722147 /// XM_001723661																			
2.41	2.29	0.12	4.59E-01	7.75E-01	STBD1	starch binding domain 1	chr4q24-q25	1557575_at	NM_003943																			
4.27	4.15	0.12	4.59E-01	7.75E-01	ZNF20 /// ZNF625	zinc finger protein 20 /// zinc finger protein 625	chr19p13.2 /// chr19p13.3-p13.2	244406_at	NM_021143 /// NM_145233																			
2.69	2.56	0.13	4.60E-01	7.75E-01	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	chr13q14	222705_s_at	NM_014252																			
3.06	2.96	0.10	4.60E-01	7.75E-01	MAP6D1	MAP6 domain containing 1	chr3q27.1	242838_at	NM_024871																			
4.63	4.48	0.15	4.60E-01	7.75E-01	SERPINA9	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	chr14q32.13	1553499_s_at	NM_001042518 /// NM_175739																			
2.98	2.82	0.16	4.60E-01	7.75E-01	JAKMIP3	janus kinase and microtubule interacting protein 3	chr10q26.3	233076_at	NM_001105521																			
4.69	4.49	0.20	4.60E-01	7.75E-01	UBE2O	ubiquitin-conjugating enzyme E2O	chr17q25.1	218141_at	NM_022066																			
3.44	3.33	0.11	4.60E-01	7.75E-01	MED28	Mediator complex subunit 28	chr4p16	243668_at	NM_025205																			
5.52	5.38	0.14	4.60E-01	7.75E-01	IFNAR2	interferon (alpha, beta and omega) receptor 2	chr21q22.1|21q22.11	204785_x_at	NM_000874 /// NM_207584 /// NM_207585																			
8.22	8.04	0.17	4.60E-01	7.75E-01	ARCN1	archain 1	chr11q23.3	201176_s_at	NM_001655																			
6.81	6.60	0.21	4.60E-01	7.75E-01	LMO2	LIM domain only 2 (rhombotin-like 1)	chr11p13	204249_s_at	NM_005574																			
2.11	2.02	0.09	4.60E-01	7.75E-01	LMOD3	leiomodin 3 (fetal)	chr3p14.1	1564469_at	NM_198271																			
3.26	3.13	0.14	4.60E-01	7.75E-01	---	---	---	242106_at	---																			
3.23	3.14	0.09	4.60E-01	7.75E-01	---	---	---	1564429_at	---																			
2.74	2.63	0.11	4.60E-01	7.75E-01	LOC440900	hypothetical LOC440900	chr2q14.1	243795_s_at	XR_041709 /// XR_041710 /// XR_041711																			
2.43	2.29	0.14	4.60E-01	7.75E-01	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	chr17q24.2	238649_at	NM_012417 /// NM_181671																			
3.89	3.71	0.18	4.61E-01	7.76E-01	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	chr7p14-p13	1554151_at	NM_001003941 /// NM_002541																			
5.67	5.39	0.29	4.61E-01	7.76E-01	MAK16	MAK16 homolog (S. cerevisiae)	chr8p12	211686_s_at	NM_032509																			
2.87	2.77	0.10	4.61E-01	7.76E-01	HEATR3	HEAT repeat containing 3	chr16q12.1	1554478_a_at	NM_182922																			
3.95	3.84	0.11	4.61E-01	7.76E-01	LOC641808 /// MGC35361	similar to Expressed sequence AI847670 /// hypothetical MGC35361	chr7q11.23 /// chr7q22.1	236182_at	XM_001715921 /// XM_001717516 /// XR_041062 /// XR_041063 /// XR_041064																			
5.13	4.90	0.23	4.61E-01	7.76E-01	TMCO4	transmembrane and coiled-coil domains 4	chr1p36.13	227007_at	NM_181719																			

2.67	2.53	0.14	4.61E-01	7.76E-01	GINS4	GINS complex subunit 4 (Sld5 homolog)	chr8p11.21	235029_at	NM_032336
3.59	3.45	0.14	4.61E-01	7.76E-01	---	---	---	1565617_at	---
6.98	6.62	0.36	4.61E-01	7.76E-01	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	chr10q11.1	203666_at	NM_000609 /// NM_001033886 /// NM_199168
2.41	2.31	0.10	4.61E-01	7.76E-01	---	---	---	234856_at	---
6.00	5.77	0.23	4.61E-01	7.76E-01	LOC441108	hypothetical gene supported by AK128882	chr5q31.1	230405_at	NM_001013717
2.71	2.56	0.14	4.61E-01	7.76E-01	GPR133	G protein-coupled receptor 133	chr12q24.33	232267_at	NM_198827
2.49	2.38	0.11	4.61E-01	7.76E-01	---	---	---	235891_at	---
3.61	3.40	0.21	4.61E-01	7.76E-01	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	chr17q21.31	243213_at	NM_003150 /// NM_139276 /// NM_213662
4.24	4.03	0.21	4.61E-01	7.76E-01	HECTD1	HECT domain containing 1	chr14q12	242349_at	NM_015382
7.79	7.55	0.24	4.61E-01	7.76E-01	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	chr4p16	212434_at	NM_025196
3.03	2.90	0.12	4.61E-01	7.76E-01	---	---	---	243687_at	---
4.59	4.43	0.16	4.61E-01	7.76E-01	CYTH1	cytohesin 1	chr17q25	202879_s_at	NM_004762 /// NM_017456
3.25	3.17	0.08	4.62E-01	7.76E-01	---	---	---	244754_at	---
9.30	9.16	0.14	4.62E-01	7.77E-01	PINK1	PTEN induced putative kinase 1	chr1p36	209019_s_at	NM_032409
5.46	5.23	0.24	4.62E-01	7.77E-01	C6orf70	chromosome 6 open reading frame 70	chr6q27	227656_at	NM_018341
2.46	2.35	0.11	4.62E-01	7.77E-01	MBD2	methyl-CpG binding domain protein 2	chr18q21	202485_s_at	NM_003927 /// NM_015832
2.83	2.33	0.49	4.62E-01	7.77E-01	CCNL1	cyclin L1	chr3q25.32	241495_at	NM_020307
6.36	6.17	0.18	4.62E-01	7.77E-01	SKP1	S-phase kinase-associated protein 1	chr5q31	200719_at	NM_006930 /// NM_170679
2.31	2.21	0.11	4.62E-01	7.77E-01	PTGDR	prostaglandin D2 receptor (DP)	chr14q22.1	215937_at	NM_000953
8.61	8.50	0.11	4.62E-01	7.77E-01	SPG21	spastic paraplegia 21 (autosomal recessive, Mast syndrome)	chr15q21-q22	217827_s_at	NM_001127889 /// NM_001127890 /// NM_016630
5.51	5.36	0.15	4.62E-01	7.77E-01	ZFAND3	zinc finger, AN1-type domain 3	chr6pter-p22.3	222493_s_at	NM_021943
4.35	4.15	0.20	4.62E-01	7.77E-01	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	chr2p13.1	201297_s_at	NM_018221
2.79	2.70	0.09	4.62E-01	7.77E-01	---	---	---	1556735_at	---
2.19	2.11	0.08	4.62E-01	7.77E-01	FANCM	Fanconi anemia, complementation group M	chr14q21.3	1554277_s_at	NM_020937
4.87	4.68	0.19	4.63E-01	7.77E-01	ICAM2	intercellular adhesion molecule 2	chr17q23-q25	204683_at	NM_000873 /// NM_001099786 /// NM_001099787 /// NM_001099788 /// NM_001099789
2.95	2.84	0.11	4.63E-01	7.77E-01	---	---	---	1566885_at	---
5.87	5.77	0.10	4.63E-01	7.77E-01	ADRBK1	adrenergic, beta, receptor kinase 1	chr11q13.1	201402_at	NM_001619
2.38	2.28	0.11	4.63E-01	7.77E-01	MRPS18C	mitochondrial ribosomal protein S18C	chr4q21.23	222948_s_at	NM_016067
2.18	2.05	0.13	4.63E-01	7.77E-01	ALOXE3	arachidonate lipoxygenase 3	chr17p13.1	222383_s_at	NM_021628
2.68	2.60	0.08	4.63E-01	7.77E-01	BPTF	bromodomain PHD finger transcription factor	chr17q24.3	231953_at	NM_004459 /// NM_182641
3.37	3.25	0.12	4.63E-01	7.77E-01	---	---	---	240552_at	---
3.09	3.00	0.09	4.63E-01	7.77E-01	TGFB3	transforming growth factor, beta 3	chr14q24	1555540_at	NM_003239
3.03	2.83	0.21	4.63E-01	7.77E-01	---	---	---	1556216_s_at	---
1.98	1.89	0.09	4.63E-01	7.78E-01	C1orf220	chromosome 1 open reading frame 220	chr1q25.2	1563876_at	NM_207467
3.19	3.03	0.16	4.63E-01	7.78E-01	ESM1	endothelial cell-specific molecule 1	chr5q11.2	208394_x_at	NM_007036
2.02	1.94	0.08	4.63E-01	7.78E-01	---	---	---	210464_at	---
2.54	2.41	0.13	4.63E-01	7.78E-01	CXorf25	chromosome X open reading frame 25	chrXp11.3	1564367_at	XM_001714024 /// XM_001714796
2.27	2.14	0.14	4.63E-01	7.78E-01	TRPC1	transient receptor potential cation channel, subfamily C, member 1	chr3q22-q24	211602_s_at	NM_003304
5.64	5.40	0.24	4.63E-01	7.78E-01	SNX1	sorting nexin 1	chr15q22.31	213364_s_at	NM_003099 /// NM_148955 /// NM_152826

4.83	4.74	0.10	4.64E-01	7.78E-01	EXOC3L	exocyst complex component 3-like	chr16q22.1	1554937_x_at	NM_178516
5.29	4.91	0.38	4.64E-01	7.78E-01	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	chr6p21.3	216339_s_at	NM_019105 /// NM_032470 /// NR_001284
5.06	4.88	0.18	4.64E-01	7.78E-01	CHUK	conserved helix-loop-helix ubiquitous kinase	chr10q24-q25	209666_s_at	NM_001278
3.36	3.22	0.15	4.64E-01	7.78E-01	LOC100132740 /// STAG3L1 /// STAG3L2 /// STAG3L3	hypothetical protein LOC100132740 /// stromal antigen 3-like 1 /// stromal antigen 3-like 2 /// stromal antigen 3-like 3	chr7q11.23 /// chr7q11.23-q21.1	235263_at	NM_001002840 /// NM_001013739 /// NM_001025202 /// NM_018991 /// XM_001720660 /// XM_001722108
5.62	5.39	0.23	4.64E-01	7.78E-01	LDB2	LIM domain binding 2	chr4p16	206481_s_at	NM_001130834 /// NM_001290
5.55	5.42	0.13	4.64E-01	7.78E-01	TP53I13	tumor protein p53 inducible protein 13	chr17q11.2	225605_at	NM_138349
3.65	3.54	0.12	4.64E-01	7.78E-01	ALPP /// ALPPL2	alkaline phosphatase, placental (Regan isozyme) /// alkaline phosphatase, placental-like 2	chr2q37	211619_s_at	NM_001632 /// NM_031313
8.01	7.90	0.11	4.64E-01	7.78E-01	FAM49B	family with sequence similarity 49, member B	chr8q24.21	217916_s_at	NM_016623
3.02	2.90	0.12	4.64E-01	7.78E-01	DMN	desmuslin	chr15q26.3	214304_x_at	NM_015286 /// NM_145728
2.98	2.83	0.15	4.64E-01	7.78E-01	---	---	---	241001_at	---
2.93	2.83	0.10	4.64E-01	7.78E-01	---	---	---	1566834_at	---
3.06	2.98	0.08	4.64E-01	7.78E-01	---	---	---	1563983_at	---
4.14	3.95	0.19	4.64E-01	7.78E-01	LOC100130544	hypothetical protein LOC100130544	chr6q25.3	1564248_at	XM_001716277 /// XM_001716352 /// XM_001726880
2.34	2.23	0.11	4.64E-01	7.78E-01	RNF165	ring finger protein 165	chr18q21.1	1569080_at	NM_152470
2.27	2.19	0.08	4.64E-01	7.78E-01	---	---	---	221625_at	---
3.08	2.92	0.16	4.64E-01	7.78E-01	ANKS4B	ankyrin repeat and sterile alpha motif domain containing 4B	chr16p12.2	239087_at	NM_145865
5.21	4.88	0.32	4.64E-01	7.78E-01	TLR4	toll-like receptor 4	chr9q32-q33	221060_s_at	NM_138554
2.32	2.16	0.16	4.64E-01	7.78E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	210365_at	NM_001001890 /// NM_001122607 /// NM_001754
3.58	3.46	0.11	4.64E-01	7.78E-01	DLK2	delta-like 2 homolog (Drosophila)	chr6p21.1	220262_s_at	NM_023932 /// NM_206539
4.44	4.28	0.16	4.64E-01	7.78E-01	KHSRP	KH-type splicing regulatory protein	chr19p13.3	227555_s_at	NM_003685
3.25	3.05	0.20	4.64E-01	7.78E-01	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	chr18q21	210018_x_at	NM_006785 /// NM_173844
3.79	3.59	0.20	4.64E-01	7.78E-01	FBXL6	F-box and leucine-rich repeat protein 6	chr8q24.3	219189_at	NM_012162 /// NM_024555
3.04	2.92	0.12	4.64E-01	7.78E-01	---	---	---	233710_at	---
3.79	3.60	0.19	4.64E-01	7.78E-01	---	---	---	222214_at	---
8.55	8.40	0.15	4.64E-01	7.78E-01	SPAG7	sperm associated antigen 7	chr17p13.2	200053_at	NM_004890
4.16	4.02	0.14	4.64E-01	7.78E-01	POU2F1	POU class 2 homeobox 1	chr1q22-q23	229753_at	NM_002697
5.03	4.90	0.13	4.64E-01	7.78E-01	GRK6	G protein-coupled receptor kinase 6	chr5q35	211543_s_at	NM_001004105 /// NM_001004106 /// NM_002082
3.09	2.96	0.13	4.65E-01	7.78E-01	SCN8A	sodium channel, voltage gated, type VIII, alpha subunit	chr12q13	207049_at	NM_014191
4.59	4.45	0.14	4.65E-01	7.78E-01	SLC35E1	solute carrier family 35, member E1	chr19p13.11	222263_at	NM_024881
3.25	2.97	0.28	4.65E-01	7.78E-01	DIO2	deiodinase, iodothyronine, type II	chr14q24.2-q24.3	231240_at	NM_000793 /// NM_001007023 /// NM_013989
2.67	2.55	0.12	4.65E-01	7.78E-01	AMBN	ameloblastin (enamel matrix protein)	chr4q21	221114_at	NM_016519

5.84	5.69	0.16	4.65E-01	7.78E-01	KRI1	KRI1 homolog (S. cerevisiae)	chr19p13.2	218798_at	NM_023008
5.94	5.82	0.12	4.65E-01	7.78E-01	GCC1	GRIP and coiled-coil domain containing 1	chr7q32.1	218912_at	NM_024523
7.08	6.92	0.17	4.65E-01	7.78E-01	RSU1	Ras suppressor protein 1	chr10p13	201980_s_at	NM_012425 /// NM_152724
2.44	2.31	0.12	4.65E-01	7.78E-01	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	chr12q13-q14	1561973_at	NM_001130420 /// NM_003075 /// NM_139067
2.65	2.55	0.10	4.65E-01	7.79E-01	ZNF397OS	zinc finger protein 397 opposite strand	chr18q12.2	1562988_at	NM_001112734 /// XM_001720071 /// XM_001722380 /// XM_001723235
6.12	5.90	0.21	4.65E-01	7.79E-01	AKT3	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	chr1q43-q44	212609_s_at	NM_005465 /// NM_181690
3.06	2.95	0.11	4.65E-01	7.79E-01	---	---	---	1566980_at	---
3.10	2.97	0.13	4.65E-01	7.79E-01	BMP2	bone morphogenetic protein 2	chr20p12	205290_s_at	NM_001200
2.57	2.47	0.10	4.65E-01	7.79E-01	FBXO41	F-box protein 41	chr2p13.2	236405_at	NM_001080410
4.91	4.67	0.24	4.65E-01	7.79E-01	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	chr5q31	206197_at	NM_003551
3.93	3.71	0.21	4.65E-01	7.79E-01	SNX30	sorting nexin family member 30	chr9q32	226249_at	NM_001012994
6.03	5.88	0.15	4.65E-01	7.79E-01	FPGS	folylpolyglutamate synthase	chr9q34.1	202945_at	NM_001018078 /// NM_004957
3.30	3.18	0.12	4.65E-01	7.79E-01	TBX19	T-box 19	chr1q24.2	206838_at	NM_005149
6.04	5.79	0.26	4.65E-01	7.79E-01	HSPA13	heat shock protein 70kDa family, member 13	chr21q11.1|21q11	202557_at	NM_006948
7.58	7.39	0.19	4.65E-01	7.79E-01	CCDC85B	coiled-coil domain containing 85B	chr11q12.1	204610_s_at	NM_006848
5.35	5.19	0.16	4.65E-01	7.79E-01	SETD5	SET domain containing 5	chr3p25.3	222575_at	NM_001080517
2.60	2.51	0.10	4.65E-01	7.79E-01	---	---	---	234182_at	---
2.82	2.69	0.13	4.65E-01	7.79E-01	---	---	---	238290_at	---
7.32	7.07	0.25	4.66E-01	7.79E-01	C7	complement component 7	chr5p13	235979_at	NM_000587
7.27	7.06	0.22	4.66E-01	7.79E-01	RBM25	RNA binding motif protein 25	chr14q24.3	212033_at	NM_021239
2.42	2.32	0.11	4.66E-01	7.79E-01	---	---	---	216767_at	---
2.11	1.99	0.12	4.66E-01	7.79E-01	CLEC12B	C-type lectin domain family 12, member B	chr12p13.2	231600_at	NM_001129998 /// NM_205852
2.05	1.96	0.09	4.66E-01	7.79E-01	FREM3	FRAS1 related extracellular matrix 3	chr4q31.21	243337_at	XM_001127662 /// XM_001720656 /// XM_094074
4.52	4.37	0.15	4.66E-01	7.79E-01	SPOPL	speckle-type POZ protein-like	chr2q22.1	225659_at	NM_001001664
2.84	2.67	0.17	4.66E-01	7.79E-01	CEP72	centrosomal protein 72kDa	chr5p15.33	219531_at	NM_018140
4.92	4.71	0.21	4.66E-01	7.79E-01	ARSA	arylsulfatase A	chr22q13.31-qter|22q13.33	204443_at	NM_000487 /// NM_001085425 /// NM_001085426 /// NM_001085427 /// NM_001085428
2.36	2.26	0.11	4.66E-01	7.79E-01	---	---	---	1560135_at	---
2.13	2.01	0.12	4.66E-01	7.79E-01	ZNF506	zinc finger protein 506	chr19p13.11	1568720_at	NM_001099269
4.93	4.83	0.10	4.66E-01	7.79E-01	DUS2L	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	chr16q22.1	47105_at	NM_017803
2.62	2.51	0.10	4.66E-01	7.79E-01	ADARB1	Adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	chr21q22.3	234799_at	NM_001033049 /// NM_001112 /// NM_015833 /// NM_015834
2.29	2.16	0.12	4.66E-01	7.79E-01	---	---	---	241699_at	---
2.45	2.32	0.14	4.66E-01	7.79E-01	---	---	---	241468_at	---

4.95	4.74	0.20	4.66E-01	7.79E-01	CCBL1	cysteine conjugate-beta lyase, cytoplasmic	chr9q34.11	206037_at	NM_001122671 /// NM_001122672 /// NM_004059																				
2.68	2.52	0.16	4.66E-01	7.79E-01	HERC6	Hect domain and RLD 6	chr4q22.1	1562785_at	NM_017912																				
2.72	2.61	0.11	4.66E-01	7.79E-01	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	chr2q35	213903_s_at	NM_005444																				
4.08	3.88	0.20	4.66E-01	7.79E-01	COL8A2	collagen, type VIII, alpha 2	chr1p34.2	221900_at	NM_005202																				
5.14	4.99	0.15	4.66E-01	7.79E-01	JOSD2	Josephin domain containing 2	chr19q13.33	227096_at	NM_138334																				
6.72	6.61	0.10	4.66E-01	7.79E-01	PSEN2	presenilin 2 (Alzheimer disease 4)	chr1q31-q42	211373_s_at	NM_000447 /// NM_012486																				
4.11	3.95	0.16	4.67E-01	7.79E-01	BMP8A	bone morphogenetic protein 8a	chr1p34.2	220203_at	NM_181809																				
2.16	2.05	0.11	4.67E-01	7.79E-01	---	---	---	234266_at	---																				
7.66	7.40	0.26	4.67E-01	7.79E-01	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	chr5q23-q31	211763_s_at	NM_003337																				
5.41	5.16	0.25	4.67E-01	7.79E-01	---	---	---	227679_at	---																				
3.53	3.43	0.10	4.67E-01	7.79E-01	LPAR3	lysophosphatidic acid receptor 3	chr1p22.3	220816_at	NM_012152																				
4.47	4.16	0.31	4.67E-01	7.79E-01	SYNJ2	synaptojanin 2	chr6q25.3	212828_at	NM_003898																				
2.24	2.13	0.11	4.67E-01	7.79E-01	IL12A	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	chr3q25.33-q26	207160_at	NM_000882																				
4.74	4.56	0.18	4.67E-01	7.79E-01	RNF216	ring finger protein 216	chr7p22.1	218425_at	NM_207111 /// NM_207116																				
7.78	7.60	0.18	4.67E-01	7.79E-01	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	chr5q33.1	201503_at	NM_005754 /// NM_198395																				
2.14	2.05	0.09	4.67E-01	7.80E-01	---	---	---	233602_at	---																				
2.46	2.27	0.19	4.67E-01	7.80E-01	TM4SF1	transmembrane 4 L six family member 1	chr3q21-q25	215033_at	NM_014220																				
2.53	2.43	0.10	4.67E-01	7.80E-01	RXFP3	relaxin/insulin-like family peptide receptor 3	chr5p15.1-p14	221066_at	NM_016568																				
2.97	2.84	0.12	4.67E-01	7.80E-01	LOC286434 /// LOC389906 /// LOC729162	hypothetical protein LOC286434 /// similar to Serine/threonine-protein kinase PRKX (Protein kinase PKX1) /// similar to LOC389906 protein	chrXp22.33	59433_at	XM_001713861 /// XM_001715777 /// XM_001717193 /// XM_928240 /// XM_942518																				
1.99	1.91	0.08	4.67E-01	7.80E-01	---	---	---	239938_x_at	---																				
2.47	2.38	0.09	4.67E-01	7.80E-01	KRT37	keratin 37	chr17q12-q21	207649_at	NM_003770																				
2.17	2.08	0.09	4.67E-01	7.80E-01	HOXD3	homeobox D3	chr2q31.1	217076_s_at	NM_006898																				
2.73	2.62	0.11	4.68E-01	7.80E-01	---	---	---	233010_at	---																				
3.24	3.13	0.10	4.68E-01	7.80E-01	GNB5	guanine nucleotide binding protein (G protein), beta 5	chr15q21.2	1554346_at	NM_006578 /// NM_016194																				
2.60	2.47	0.12	4.68E-01	7.80E-01	MUC16	mucin 16, cell surface associated	chr19p13.2	220196_at	NM_024690																				
2.63	2.53	0.10	4.68E-01	7.80E-01	OR2S2	olfactory receptor, family 2, subfamily S, member 2	chr9p13.3-p13.1	221409_at	NM_019897																				
6.21	5.99	0.22	4.68E-01	7.80E-01	TBC1D13	TBC1 domain family, member 13	chr9q34.11	44696_at	NM_018201																				
2.14	2.04	0.10	4.68E-01	7.80E-01	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	chr12p12.1	1559203_s_at	NM_004985 /// NM_033360																				
4.95	4.85	0.11	4.68E-01	7.80E-01	FLJ41603	FLJ41603 protein	chr5q33.1	241380_at	NM_001001669																				
2.23	2.14	0.09	4.68E-01	7.80E-01	---	---	---	1562398_at	---																				
5.98	5.85	0.13	4.68E-01	7.80E-01	ZNF592	zinc finger protein 592	chr15q25.3	213389_at	NM_014630																				
3.16	3.04	0.12	4.68E-01	7.80E-01	---	---	---	241158_at	---																				
6.21	6.05	0.16	4.68E-01	7.80E-01	WIZ	widely interspaced zinc finger motifs	chr19p13.1	221783_at	NM_021241																				
3.09	2.98	0.11	4.68E-01	7.80E-01	TRIM29	tripartite motif-containing 29	chr11q22-q23	202504_at	NM_012101																				
5.32	5.12	0.20	4.68E-01	7.80E-01	TNRC6A	trinucleotide repeat containing 6A	chr16p11.2	234734_s_at	NM_014494																				
3.10	2.94	0.17	4.68E-01	7.80E-01	UBE2I	Ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	chr16p13.3	213536_s_at	NM_003345 /// NM_194259 /// NM_194260 /// NM_194261																				
7.78	7.62	0.17	4.69E-01	7.80E-01	ARF6	ADP-ribosylation factor 6	chr14q21.3	224788_at	NM_001663																				
3.88	3.80	0.09	4.69E-01	7.80E-01	TMEM40	transmembrane protein 40	chr3p25.1	219503_s_at	NM_018306																				
3.07	2.88	0.19	4.69E-01	7.80E-01	GOSR2	golgi SNAP receptor complex member 2	chr17q21	213206_at	NM_001012511 /// NM_004287 /// NM_054022																				
5.15	4.85	0.30	4.69E-01	7.80E-01	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	chr11q23.2	202883_s_at	NM_002716 /// NM_181699																				

5.96	5.71	0.25	4.69E-01	7.80E-01	FAM50B	family with sequence similarity 50, member B	chr6p25-pter	205775_at	NM_012135
3.84	3.69	0.15	4.69E-01	7.80E-01	PNPLA7	patatin-like phospholipase domain containing 7	chr9q34.3	228383_at	NM_001098537 /// NM_152286
7.64	7.40	0.24	4.69E-01	7.80E-01	DDEF1	development and differentiation enhancing factor 1	chr8q24.1-q24.2	224796_at	NM_018482
5.26	5.13	0.13	4.69E-01	7.81E-01	RPL14	ribosomal protein L14	chr3p22-p21.2	219138_at	NM_001034996 /// NM_003973
9.07	8.89	0.18	4.69E-01	7.81E-01	NQO2	NAD(P)H dehydrogenase, quinone 2	chr6pter-q12	203814_s_at	NM_000904
3.25	3.12	0.12	4.69E-01	7.81E-01	YPEL1	yippee-like 1 (Drosophila)	chr22q11.2	213996_at	NM_013313
5.36	5.17	0.19	4.69E-01	7.81E-01	YLPM1	YLP motif containing 1	chr14q24.3	214659_x_at	NM_019589
2.37	2.26	0.11	4.69E-01	7.81E-01	RAB33A	RAB33A, member RAS oncogene family	chrXq25	206039_at	NM_004794
2.53	2.42	0.11	4.69E-01	7.81E-01	---	---	---	1561565_at	---
2.34	2.25	0.10	4.69E-01	7.81E-01	C10orf92	chromosome 10 open reading frame 92	chr10q26.3	220539_at	NM_017609
2.31	2.21	0.10	4.70E-01	7.81E-01	---	---	---	1569104_a_at	---
2.12	2.02	0.10	4.70E-01	7.81E-01	MICALL2	MICAL-like 2	chr7p22.3	1555862_s_at	NM_182924
2.34	2.27	0.07	4.70E-01	7.81E-01	BRUNOL5	bruno-like 5, RNA binding protein (Drosophila)	chr19p13	231744_at	NM_021938
7.71	7.53	0.17	4.70E-01	7.81E-01	EAPP	E2F-associated phosphoprotein	chr14q13.1	202623_at	NM_018453
3.13	3.02	0.11	4.70E-01	7.81E-01	DHFR	dihydrofolate reductase	chr5q11.2-q13.2	202533_s_at	NM_000791
9.62	9.47	0.15	4.70E-01	7.81E-01	UQCRH	ubiquinol-cytochrome c reductase hinge protein	chr1p33	202233_s_at	NM_006004
3.38	3.24	0.14	4.70E-01	7.81E-01	CSF1	colony stimulating factor 1 (macrophage)	chr1p21-p13	210557_x_at	NM_000757 /// NM_172210 /// NM_172211 /// NM_172212
6.15	5.98	0.16	4.70E-01	7.81E-01	LOC146346	hypothetical protein LOC146346	chr16q22.3	225918_at	---
1.98	1.89	0.08	4.70E-01	7.81E-01	FAM66C	family with sequence similarity 66, member C	chr12p13.31	1570396_at	XR_040642 /// XR_040643
2.14	2.03	0.12	4.70E-01	7.81E-01	---	---	---	1563085_at	---
2.35	2.25	0.09	4.70E-01	7.81E-01	ATOH7	atonal homolog 7 (Drosophila)	chr10q21.3|10q21.3-q22.1	1552879_a_at	NM_145178
3.07	2.90	0.17	4.70E-01	7.81E-01	---	---	---	244037_at	---
3.12	2.97	0.15	4.70E-01	7.81E-01	LOC100131941	Hypothetical protein LOC100131941	chr13q14.3	1557818_x_at	XM_001714946 /// XM_001716781 /// XM_001718409
2.51	2.41	0.10	4.70E-01	7.81E-01	C21orf29	chromosome 21 open reading frame 29	chr21q22.3	1552570_at	NM_144991
2.38	2.29	0.09	4.70E-01	7.82E-01	GOSR2	golgi SNAP receptor complex member 2	chr17q21	243880_at	NM_001012511 /// NM_004287 /// NM_054022
4.23	4.14	0.09	4.71E-01	7.82E-01	BTF3L2	basic transcription factor 3, like 2	chr8q13.3	217461_x_at	---
3.35	3.24	0.11	4.71E-01	7.82E-01	CXXC4	CXXC finger 4	chr4q22-q24	220277_at	NM_025212
2.58	2.48	0.10	4.71E-01	7.82E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	1565484_x_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284
4.45	4.17	0.28	4.71E-01	7.82E-01	PANX1	pannexin 1	chr11q21	204715_at	NM_015368
5.31	5.16	0.15	4.71E-01	7.82E-01	EVI5	ecotropic viral integration site 5	chr1p22.1	209717_at	NM_005665
3.98	3.86	0.12	4.71E-01	7.82E-01	SLC30A6	solute carrier family 30 (zinc transporter), member 6	chr2p22.3	243643_x_at	NM_017964
3.20	3.10	0.10	4.71E-01	7.82E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	1552677_a_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891
2.09	1.98	0.10	4.71E-01	7.82E-01	---	---	---	227051_at	---
2.46	2.37	0.09	4.71E-01	7.82E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	1554967_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891
3.42	3.28	0.15	4.71E-01	7.82E-01	CLDN4	claudin 4	chr7q11.23	1569421_at	NM_001305
4.60	4.26	0.33	4.71E-01	7.82E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	211401_s_at	NM_000141 /// NM_022970

5.36	4.91	0.45	4.71E-01	7.82E-01	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	chrXq13	207564_x_at	NM_181672 /// NM_181673
7.13	7.00	0.14	4.71E-01	7.82E-01	ASH2L	ash2 (absent, small, or homeotic)-like (Drosophila)	chr8p11.2	209517_s_at	NM_001105214 /// NM_004674
2.30	2.17	0.13	4.72E-01	7.82E-01	TDRD6	tudor domain containing 6	chr6p12.3	232692_at	NM_001010870
2.16	2.04	0.12	4.72E-01	7.83E-01	DPY19L2	dpy-19-like 2 (C. elegans)	chr12q14.2	238784_at	NM_173812
2.17	2.07	0.10	4.72E-01	7.83E-01	KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	chr5q34	1554710_at	NM_004137
3.10	2.99	0.10	4.72E-01	7.83E-01	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	chr2q35	223904_at	NM_017431
2.37	2.28	0.09	4.72E-01	7.83E-01	LOC729799	similar to SEC14-like 1 (S. cerevisiae)	chr11p11.2	217667_at	XR_015983 /// XR_016003 /// XR_038768
4.27	4.12	0.15	4.72E-01	7.83E-01	CCAR1	cell division cycle and apoptosis regulator 1	chr10q21.3	224737_x_at	NM_018237
2.67	2.54	0.13	4.72E-01	7.83E-01	NLRP9	NLR family, pyrin domain containing 9	chr19q13.42	1553527_at	NM_176820
2.76	2.64	0.12	4.72E-01	7.83E-01	---	---	---	236581_at	---
7.28	7.10	0.18	4.72E-01	7.83E-01	CCNB1IP1	cyclin B1 interacting protein 1	chr14q11.2	217988_at	NM_021178 /// NM_182849 /// NM_182851 /// NM_182852
8.42	8.20	0.22	4.72E-01	7.83E-01	CREB3L2	cAMP responsive element binding protein 3-like 2	chr7q34	212345_s_at	NM_194071
9.29	9.00	0.29	4.72E-01	7.83E-01	SRPX	sushi-repeat-containing protein, X-linked	chrXp21.1	204955_at	NM_006307
3.73	3.62	0.11	4.72E-01	7.83E-01	C21orf58	chromosome 21 open reading frame 58	chr21q22.3	1559438_at	NM_058180
5.17	4.89	0.28	4.72E-01	7.83E-01	CCND1	cyclin D1	chr11q13	208711_s_at	NM_053056
6.39	6.10	0.29	4.72E-01	7.83E-01	PLD1	phospholipase D1, phosphatidylcholine-specific	chr3q26	205203_at	NM_001130081 /// NM_002662
4.49	4.40	0.09	4.72E-01	7.83E-01	SFRS14	splicing factor, arginine/serine-rich 14	chr19p12	64371_at	NM_001017392 /// NM_014884
4.10	3.91	0.20	4.72E-01	7.83E-01	ZFP41	zinc finger protein 41 homolog (mouse)	chr8q24.3	227898_s_at	NM_173832
4.58	4.46	0.12	4.72E-01	7.83E-01	NMNAT3	nicotinamide nucleotide adenylyltransferase 3	chr3q23	228090_at	NM_178177
3.24	3.15	0.10	4.72E-01	7.83E-01	CCDC56	Coiled-coil domain containing 56	chr17q21	236998_at	NM_001040431
2.34	2.23	0.10	4.73E-01	7.83E-01	TWISTNB	TWIST neighbor	chr7p15.3	214729_at	NM_001002926
4.02	3.83	0.19	4.73E-01	7.83E-01	GALR3	galanin receptor 3	chr22q13.1	33579_i_at	NM_003614
2.81	2.72	0.10	4.73E-01	7.83E-01	---	---	---	1556682_s_at	---
2.85	2.75	0.10	4.73E-01	7.83E-01	---	---	---	228567_at	---
8.36	8.18	0.17	4.73E-01	7.83E-01	RNASEH2C	ribonuclease H2, subunit C	chr11q13.1	226453_at	NM_032193
4.78	4.54	0.24	4.73E-01	7.83E-01	PIGN	phosphatidylinositol glycan anchor biosynthesis, class N	chr18q21.33	232101_s_at	NM_012327 /// NM_176787
6.73	6.42	0.31	4.73E-01	7.83E-01	---	---	---	235570_at	---
2.67	2.56	0.11	4.73E-01	7.83E-01	---	---	---	232330_at	---
2.79	2.52	0.27	4.73E-01	7.83E-01	LOC100132181	Hypothetical protein LOC100132181	---	227835_at	XM_001722051
2.12	2.04	0.09	4.73E-01	7.83E-01	ODF2L	outer dense fiber of sperm tails 2-like	chr1p22.3	231909_x_at	NM_001007022 /// NM_020729
2.33	2.24	0.09	4.73E-01	7.83E-01	---	---	---	1563531_at	---
4.92	4.73	0.19	4.73E-01	7.83E-01	PHF3	PHD finger protein 3	chr6q12	215718_s_at	NM_015153
5.17	5.03	0.14	4.73E-01	7.83E-01	AVPR1B	arginine vasopressin receptor 1B	chr1q32	208260_at	NM_000707
7.69	7.03	0.66	4.73E-01	7.83E-01	VCAN	versican	chr5q14.3	215646_s_at	NM_001126336 /// NM_004385
3.11	3.01	0.10	4.73E-01	7.83E-01	C1orf167	chromosome 1 open reading frame 167	chr1p36.22	1561976_at	XM_001713965 /// XM_001714773 /// XM_001715322 /// XM_001715329 /// XM_209234 /// XM_938203
2.22	2.11	0.11	4.73E-01	7.83E-01	DPPA4	developmental pluripotency associated 4	chr3q13.13	219651_at	NM_018189

9.13	8.88	0.25	4.73E-01	7.83E-01	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	chr7p15	205292_s_at	NM_002137 /// NM_031243																				
1.95	1.87	0.08	4.73E-01	7.83E-01	---	---	---	217577_at	---																				
2.24	2.16	0.09	4.73E-01	7.83E-01	---	---	---	1565839_a_at	---																				
3.26	3.05	0.20	4.73E-01	7.84E-01	BIVM	basic, immunoglobulin-like variable motif containing	chr13q32-q33.1	233255_s_at	NM_017693																				
3.90	3.68	0.23	4.74E-01	7.84E-01	LOC653390 /// RRN3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene /// RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	chr16p11.2 /// chr16p12	216902_s_at	NM_018427 /// NR_003369																				
3.94	3.85	0.09	4.74E-01	7.84E-01	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	chr19q13.2	211889_x_at	NM_001024912 /// NM_001712																				
6.24	6.07	0.17	4.74E-01	7.84E-01	PRNPIP	prion protein interacting protein	chr1p32	208973_at	NM_024066																				
4.26	4.10	0.16	4.74E-01	7.84E-01	---	---	---	239096_at	---																				
6.45	6.26	0.19	4.74E-01	7.84E-01	RAB8B	RAB8B, member RAS oncogene family	chr15q22.2	226633_at	NM_016530																				
3.10	2.97	0.14	4.74E-01	7.84E-01	TTLL10	tubulin tyrosine ligase-like family, member 10	chr1p36.33	1552418_at	NM_001130045 /// NM_153254																				
3.04	2.92	0.12	4.74E-01	7.84E-01	C20orf173	chromosome 20 open reading frame 173	chr20q11.22	233143_at	XR_042063 /// XR_042064 /// XR_042065																				
3.02	2.93	0.08	4.74E-01	7.84E-01	EVI5L	ecotropic viral integration site 5-like	chr19p13.2	244501_at	NM_145245																				
2.91	2.80	0.11	4.74E-01	7.84E-01	---	---	---	242092_at	---																				
2.24	2.15	0.09	4.74E-01	7.84E-01	LOC731223	hypothetical LOC731223	chr14q24.3	1563373_at	XM_001128868 /// XM_001715691 /// XM_001718540																				
2.24	2.14	0.10	4.74E-01	7.84E-01	LOC338579	hypothetical protein LOC338579	chr10q11.21	1561225_at	XM_936973																				
4.76	4.64	0.12	4.74E-01	7.84E-01	ALPK1	alpha-kinase 1	chr4q25	227438_at	NM_001102406 /// NM_025144																				
5.62	5.40	0.22	4.74E-01	7.84E-01	C16orf68	chromosome 16 open reading frame 68	chr16p13.2	218945_at	NM_024109																				
2.18	2.11	0.08	4.74E-01	7.84E-01	GP5	glycoprotein V (platelet)	chr3q29	211525_s_at	NM_004488																				
2.22	2.13	0.09	4.74E-01	7.84E-01	LRRC38	leucine rich repeat containing 38	chr1p36.21	1558375_at	XM_001713942 /// XM_059074 /// XM_943661																				
4.09	3.80	0.29	4.74E-01	7.84E-01	ERLIN1	ER lipid raft associated 1	chr10q21-q22	202444_s_at	NM_001100626 /// NM_006459																				
10.98	10.45	0.53	4.74E-01	7.84E-01	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	chr16p13.3	214414_x_at	NM_000517 /// NM_000558																				
2.43	2.34	0.09	4.74E-01	7.84E-01	LOC283143	Hypothetical protein LOC283143	chr11q23.2	239685_at	XR_039943 /// XR_039944 /// XR_039945																				
4.71	4.43	0.28	4.74E-01	7.84E-01	TRIM47	tripartite motif-containing 47	chr17q24-q25	225868_at	NM_033452																				
2.39	2.29	0.10	4.75E-01	7.84E-01	CCR8	chemokine (C-C motif) receptor 8	chr3p22	208059_at	NM_005201																				
7.65	7.52	0.14	4.75E-01	7.84E-01	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	chr19p13.3	213887_s_at	NM_002695																				
2.55	2.46	0.09	4.75E-01	7.84E-01	---	---	---	241518_at	---																				
2.54	2.44	0.10	4.75E-01	7.84E-01	CCL27	chemokine (C-C motif) ligand 27	chr9p13	207955_at	NM_006664																				
2.40	2.28	0.12	4.75E-01	7.84E-01	---	---	---	240406_at	---																				
2.68	2.57	0.11	4.75E-01	7.84E-01	FAM71C	family with sequence similarity 71, member C	chr12q23.1	1552526_at	NM_153364																				
6.65	6.46	0.19	4.75E-01	7.84E-01	HADH	hydroxyacyl-Coenzyme A dehydrogenase	chr4q22-q26	211569_s_at	NM_005327																				
2.28	2.18	0.09	4.75E-01	7.84E-01	C13orf37	Chromosome 13 open reading frame 37	chr13q22.1	228530_at	NM_001071775																				
6.35	6.11	0.24	4.75E-01	7.84E-01	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	chr11p15.3	212473_s_at	NM_014632																				
3.77	3.65	0.12	4.75E-01	7.84E-01	RUNX2	runt-related transcription factor 2	chr6p21	221283_at	NM_001015051 /// NM_001024630 /// NM_004348																				
7.16	6.98	0.18	4.75E-01	7.84E-01	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19p13.3	40562_at	NM_002067																				

3.04	2.89	0.15	4.75E-01	7.85E-01	OCIAD1	OCIA domain containing 1	chr4p11	235537_at	NM_001079839 /// NM_001079840 /// NM_001079841 /// NM_001079842 /// NM_017830																				
3.53	3.40	0.13	4.75E-01	7.85E-01	COL11A2	collagen, type XI, alpha 2	chr6p21.3	213870_at	NM_080679 /// NM_080680 /// NM_080681																				
3.02	2.90	0.12	4.75E-01	7.85E-01	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	chr8p22-p21.3	230658_at	NM_001008539 /// NM_003046																				
4.28	4.10	0.18	4.75E-01	7.85E-01	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	chr12p11.21	226258_at	NM_001113402 /// NM_207337 /// NR_004854																				
1.83	1.76	0.07	4.75E-01	7.85E-01	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	chr15q15-q21.1	1555102_at	NM_002009																				
2.78	2.66	0.12	4.75E-01	7.85E-01	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	chr1q24-q25	206411_s_at	NM_001100108 /// NM_005158 /// NM_007314																				
2.37	2.28	0.09	4.75E-01	7.85E-01	---	---	---	1569418_at	---																				
5.58	5.42	0.16	4.75E-01	7.85E-01	GTF2H2 /// GTF2H2B /// LOC728340 /// LOC730394	general transcription factor IIH, polypeptide 2, 44kDa /// general transcription factor IIH, polypeptide 2B /// general transcription factor IIH, polypeptide 2, 44kDa-like /// general transcription factor IIH, polypeptide 2, 44kDa-like	chr5q12.2-q13.3 /// chr5q13.2	221540_x_at	NM_001042490 /// NM_001098728 /// NM_001098729 /// NM_001515 /// XM_001713843																				
7.72	7.44	0.28	4.76E-01	7.85E-01	SPIN1	spindlin 1	chr9q22.1-q22.3	222431_at	NM_006717																				
6.67	6.05	0.62	4.76E-01	7.85E-01	LY6D	lymphocyte antigen 6 complex, locus D	chr8q24-qter	206276_at	NM_003695																				
2.33	2.22	0.11	4.76E-01	7.85E-01	CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	chr18q11.2	223737_x_at	NM_031422																				
5.39	5.28	0.10	4.76E-01	7.85E-01	---	---	---	232700_at	---																				
2.83	2.69	0.14	4.76E-01	7.85E-01	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	chr22q13.1|22q12.3	206628_at	NM_000343																				
5.75	5.19	0.56	4.76E-01	7.85E-01	HOXB7	homeobox B7	chr17q21.3	216973_s_at	NM_004502																				
2.30	2.22	0.08	4.76E-01	7.85E-01	---	---	---	1566702_at	---																				
6.20	5.90	0.30	4.76E-01	7.85E-01	TUBB2A	tubulin, beta 2A	chr6p25	204141_at	NM_001069																				
1.97	1.90	0.07	4.76E-01	7.85E-01	---	---	---	1565820_x_at	---																				
3.10	2.83	0.27	4.76E-01	7.85E-01	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	chr2p16.1	222891_s_at	NM_018014 /// NM_022893 /// NM_138559																				
2.62	2.44	0.18	4.76E-01	7.85E-01	---	---	---	217598_at	---																				
5.12	4.74	0.37	4.76E-01	7.85E-01	SLC2A8	Solute carrier family 2, (facilitated glucose transporter) member 8	chr9q33.3	239426_at	NM_014580																				
2.89	2.78	0.11	4.76E-01	7.85E-01	---	---	---	240971_x_at	---																				
4.61	4.37	0.24	4.76E-01	7.85E-01	DBN1	drebrin 1	chr5q35.3	202806_at	NM_004395 /// NM_080881																				
6.33	6.14	0.19	4.76E-01	7.85E-01	DUSP6	dual specificity phosphatase 6	chr12q22-q23	208892_s_at	NM_001946 /// NM_022652																				
3.11	2.98	0.14	4.77E-01	7.85E-01	---	---	---	236384_at	---																				
3.12	3.00	0.12	4.77E-01	7.85E-01	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	chr14q32.3	216299_s_at	NM_001100118 /// NM_001100119 /// NM_005432																				
7.25	7.02	0.23	4.77E-01	7.85E-01	C14orf1	chromosome 14 open reading frame 1	chr14q24.3	217188_s_at	NM_007176																				
3.54	3.43	0.11	4.77E-01	7.85E-01	TAAR5	trace amine associated receptor 5	chr6q23	221459_at	NM_003967																				
4.96	4.78	0.18	4.77E-01	7.85E-01	SAPS2	SAPS domain family, member 2	chr22q13.33	202792_s_at	NM_014678																				

6.50	6.36	0.14	4.77E-01	7.85E-01	WARS	tryptophanyl-tRNA synthetase	chr14q32.31	200628_s_at	NM_004184 /// NM_173701 /// NM_213645 /// NM_213646
2.20	2.10	0.10	4.77E-01	7.85E-01	FAM80A	family with sequence similarity 80, member A	chr1p34.2	236376_at	NM_173642
2.52	2.42	0.10	4.77E-01	7.85E-01	---	---	---	242580_at	---
6.02	5.79	0.23	4.77E-01	7.86E-01	FUNDC1	FUN14 domain containing 1	chrXp11.3	235346_at	NM_173794
2.94	2.84	0.10	4.77E-01	7.86E-01	TK2	Thymidine kinase 2, mitochondrial	chr16q22-q23.1	240300_at	NM_004614
3.92	3.49	0.43	4.77E-01	7.86E-01	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	chr14q11.2-q21	203553_s_at	NM_006575 /// NM_198794
3.31	3.15	0.16	4.77E-01	7.86E-01	ATAD2	ATPase family, AAA domain containing 2	chr8q24.13	218782_s_at	NM_014109
12.25	12.13	0.11	4.77E-01	7.86E-01	RPS4X	ribosomal protein S4, X-linked	chrXq13.1	213347_x_at	NM_001007
1.91	1.84	0.07	4.77E-01	7.86E-01	---	---	---	1562999_x_at	---
6.87	6.74	0.13	4.77E-01	7.86E-01	LOC728944 /// THAP4	similar to THAP domain-containing protein 4 /// THAP domain containing 4	chr2q37.3	220417_s_at	NM_015963 /// XM_001128859
6.68	6.45	0.23	4.77E-01	7.86E-01	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	chr10q11.2-q21	211764_s_at	NM_003338
5.09	4.89	0.20	4.77E-01	7.86E-01	CASKIN2	CASK interacting protein 2	chr17q25.1	221846_s_at	NM_020753
2.27	2.18	0.09	4.77E-01	7.86E-01	PI15	peptidase inhibitor 15	chr8q21.11	229947_at	NM_015886
6.16	5.87	0.29	4.77E-01	7.86E-01	PGM2	phosphoglucomutase 2	chr4p14	223738_s_at	NM_018290
3.08	2.96	0.12	4.77E-01	7.86E-01	MBD3L2	methyl-CpG binding domain protein 3-like 2	chr19p13.2	1552456_a_at	NM_144614
3.06	2.92	0.14	4.77E-01	7.86E-01	---	---	---	1559702_at	---
3.48	3.35	0.13	4.77E-01	7.86E-01	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	chr9p12	233946_at	NM_018225
5.42	5.19	0.23	4.78E-01	7.86E-01	VWA5A	von Willebrand factor A domain containing 5A	chr11q23	210102_at	NM_001130142 /// NM_014622 /// NM_198315
5.26	5.12	0.14	4.78E-01	7.86E-01	LAMP1	lysosomal-associated membrane protein 1	chr13q34	213728_at	NM_005561
2.75	2.63	0.13	4.78E-01	7.86E-01	SLC6A16	Solute carrier family 6, member 16	chr19q13.1-q13.4	1569940_at	NM_014037
5.72	5.50	0.22	4.78E-01	7.86E-01	LOC728198 /// TAF9B	similar to transcription associated factor TAFII31L /// TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	chrXq13.1-q21.1	226037_s_at	NM_015975 /// XM_001126120
4.36	4.25	0.11	4.78E-01	7.86E-01	NOM1	nucleolar protein with MIF4G domain 1	chr7q36.3	229220_x_at	NM_138400
2.12	2.03	0.08	4.78E-01	7.86E-01	---	---	---	1557580_at	---
10.86	10.34	0.51	4.78E-01	7.86E-01	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	chr16p13.3	211745_x_at	NM_000517 /// NM_000558
2.33	2.22	0.11	4.78E-01	7.86E-01	LOC650794	Similar to FRAS1 related extracellular matrix protein 2	chr13q12.11	236837_x_at	XM_001716126 /// XM_370711 /// XM_939879
7.19	6.93	0.26	4.78E-01	7.86E-01	LY86	lymphocyte antigen 86	chr6p25.1	205859_at	NM_004271
3.22	3.09	0.12	4.78E-01	7.86E-01	MGC23270	hypothetical LOC196872	chr14q32.33	1553780_at	XR_041100
4.70	4.58	0.12	4.78E-01	7.87E-01	LETM1	leucine zipper-EF-hand containing transmembrane protein 1	chr4p16.3	233439_at	NM_012318
2.81	2.67	0.14	4.78E-01	7.87E-01	CD247	CD247 molecule	chr1q22-q23	210031_at	NM_000734 /// NM_198053
3.83	3.66	0.17	4.78E-01	7.87E-01	LYNX1	Ly6/neurotoxin 1	chr8q24.3	1554179_s_at	NM_023946 /// NM_177457 /// NM_177458 /// NM_177476 /// NM_177477

4.33	4.09	0.23	4.78E-01	7.87E-01	FLJ21767 /// LOC100132214 /// LOC100133005 /// LOC100134722 /// RASA4	RAS p21 protein activator 4 pseudogene /// similar to HSPC047 protein /// similar to RAS p21 protein activator 4 /// similar to HSPC047 protein /// RAS p21 protein activator 4	chr7p13 /// chr7q22 /// chr7q22.1	212706_at	NM_001079877 /// NM_006989 /// NR_024116 /// XM_001713977 /// XM_001718200 /// XM_001724280 /// XM_001725218 /// XM_001725602																				
5.21	5.06	0.16	4.78E-01	7.87E-01	PLEK	pleckstrin	chr2p14	203471_s_at	NM_002664																				
2.91	2.77	0.15	4.79E-01	7.87E-01	CD6	CD6 molecule	chr11q13	211900_x_at	NM_006725																				
3.50	3.23	0.27	4.79E-01	7.87E-01	CCDC50	coiled-coil domain containing 50	chr3q28	236831_at	NM_174908 /// NM_178335																				
6.25	5.69	0.56	4.79E-01	7.87E-01	ZNF295	zinc finger protein 295	chr21q22.3	225539_at	NM_001098402 /// NM_001098403 /// NM_020727																				
5.06	4.71	0.35	4.79E-01	7.87E-01	---	---	---	235930_at	---																				
2.15	2.07	0.08	4.79E-01	7.87E-01	LOC729059	hypothetical protein LOC729059	chr1p36.12	231551_at	XR_042045 /// XR_042046 /// XR_042047 /// XR_042048 /// XR_042049 /// XR_042050																				
3.29	3.10	0.19	4.79E-01	7.87E-01	C17orf75	chromosome 17 open reading frame 75	chr17q11.2	203830_at	NM_022344																				
2.46	2.36	0.10	4.79E-01	7.87E-01	---	---	---	241269_at	---																				
1.98	1.90	0.09	4.79E-01	7.87E-01	SEMG2	semenogelin II	chr20q12-q13.1	216030_s_at	NM_003008																				
2.83	2.69	0.14	4.79E-01	7.87E-01	---	---	---	228021_at	---																				
1.96	1.87	0.09	4.79E-01	7.87E-01	DNAH11	Dynein, axonemal, heavy chain 11	chr7p21	237804_at	NM_003777																				
2.47	2.34	0.13	4.79E-01	7.87E-01	CD6	CD6 molecule	chr11q13	1566447_at	NM_006725																				
2.46	2.31	0.15	4.79E-01	7.87E-01	ZNF326	zinc finger protein 326	chr1p22.2	241720_at	NM_182975 /// NM_182976																				
3.99	3.76	0.23	4.79E-01	7.87E-01	SCYL3	SCY1-like 3 (S. cerevisiae)	chr1q24.2	41329_at	NM_020423 /// NM_181093																				
6.16	6.01	0.15	4.79E-01	7.87E-01	DCP1B	DCP1 decapping enzyme homolog B (S. cerevisiae)	chr12p13.33	226093_at	NM_152640																				
5.67	5.46	0.21	4.80E-01	7.87E-01	DKFZP434B0335	DKFZP434B0335 protein	chr7q21.3	227581_at	NM_015395																				
3.68	3.55	0.13	4.80E-01	7.87E-01	NDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	chr16p13.11	222625_s_at	NM_017668																				
5.16	4.97	0.19	4.80E-01	7.87E-01	GLT25D1	glycosyltransferase 25 domain containing 1	chr19p13.11	222644_s_at	NM_024656																				
10.96	10.45	0.50	4.80E-01	7.87E-01	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	chr16p13.3	217414_x_at	NM_000517 /// NM_000558																				
6.60	6.44	0.16	4.80E-01	7.87E-01	NCBP2	nuclear cap binding protein subunit 2, 20kDa	chr3q29	201517_at	NM_001042540 /// NM_007362																				
3.27	3.14	0.13	4.80E-01	7.87E-01	---	---	---	243112_at	---																				
2.48	2.38	0.10	4.80E-01	7.87E-01	B4GALT3	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3	chr1q21-q23	238312_s_at	NM_003779																				
6.97	6.80	0.17	4.80E-01	7.87E-01	POLE3	polymerase (DNA directed), epsilon 3 (p17 subunit)	chr9q33	208828_at	NM_017443																				
2.19	2.09	0.10	4.80E-01	7.87E-01	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	chr1p36.12	1554309_at	NM_003760																				
2.54	2.46	0.08	4.80E-01	7.88E-01	OMG	oligodendrocyte myelin glycoprotein	chr17q11.2	207093_s_at	NM_002544																				
4.74	4.56	0.18	4.80E-01	7.88E-01	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	chr5q31.1	223712_at	NM_032151																				
2.31	2.22	0.09	4.80E-01	7.88E-01	CCDC66	coiled-coil domain containing 66	chr3p14.3	1560177_at	NM_001012506 /// NM_001130911																				
4.94	4.82	0.12	4.80E-01	7.88E-01	C2CD3	C2 calcium-dependent domain containing 3	chr11q13.4	36552_at	NM_015531																				
4.13	4.01	0.12	4.80E-01	7.88E-01	YLPM1	YLP motif containing 1	chr14q24.3	214713_at	NM_019589																				
2.73	2.61	0.12	4.80E-01	7.88E-01	---	---	---	237818_at	---																				
2.22	2.10	0.13	4.80E-01	7.88E-01	---	---	---	241753_at	---																				

8.94	8.80	0.14	4.81E-01	7.88E-01	AURKAIP1	aurora kinase A interacting protein 1	chr1p36.33	218580_x_at	NM_001127229 /// NM_001127230 /// NM_017900																			
7.51	7.36	0.15	4.81E-01	7.88E-01	RBM8A	RNA binding motif protein 8A	chr1q12	222443_s_at	NM_005105																			
4.53	4.29	0.24	4.81E-01	7.88E-01	SF3A2	splicing factor 3a, subunit 2, 66kDa	chr19p13.3|19p13.3-p13.2	37462_i_at	NM_007165																			
4.24	4.08	0.16	4.81E-01	7.88E-01	---	---	---	239469_at	---																			
5.18	4.90	0.27	4.81E-01	7.88E-01	STRN3	striatin, calmodulin binding protein 3	chr14q13-q21	204496_at	NM_001083893 /// NM_014574																			
2.64	2.51	0.13	4.81E-01	7.88E-01	LOC203107	hypothetical protein LOC203107	chr8q22.1	1556613_s_at	---																			
5.70	5.38	0.32	4.81E-01	7.88E-01	FZD5	frizzled homolog 5 (Drosophila)	chr2q33-q34	221245_s_at	NM_003468																			
5.46	5.33	0.14	4.81E-01	7.88E-01	SEPHS1	selenophosphate synthetase 1	chr10p14	208940_at	NM_012247																			
4.48	4.26	0.22	4.81E-01	7.88E-01	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	chr16p11.2	207824_s_at	NM_001042539 /// NM_002383																			
4.17	4.00	0.17	4.81E-01	7.88E-01	CAV3	caveolin 3	chr3p25	208204_s_at	NM_001234 /// NM_033337																			
2.52	2.34	0.18	4.81E-01	7.88E-01	CBX3	Chromobox homolog 3 (HP1 gamma homolog, Drosophila)	chr7p15.2	1555920_at	NM_007276 /// NM_016587																			
2.39	2.29	0.10	4.81E-01	7.88E-01	ADCY10	adenylate cyclase 10 (soluble)	chr1q24	217305_s_at	NM_018417																			
1.99	1.92	0.07	4.81E-01	7.88E-01	---	---	---	1563032_at	---																			
2.23	2.14	0.09	4.81E-01	7.88E-01	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	chr10q24.3-qter	1431_at	NM_000773																			
3.59	3.45	0.14	4.81E-01	7.88E-01	---	---	---	235211_at	---																			
2.33	2.25	0.08	4.81E-01	7.88E-01	C17orf92	chromosome 17 open reading frame 92	chr17q21	230784_at	NM_032391																			
6.10	5.88	0.22	4.81E-01	7.88E-01	NRP2	neuropilin 2	chr2q33.3	225566_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279																			
4.16	4.04	0.12	4.82E-01	7.89E-01	PPP5C	protein phosphatase 5, catalytic subunit	chr19q13.3	215705_at	NM_006247																			
3.81	3.61	0.20	4.82E-01	7.89E-01	PITPNM3	PITPNM family member 3	chr17p13	230076_at	NM_031220																			
2.02	1.95	0.07	4.82E-01	7.89E-01	LOC285733	hypothetical LOC285733	chr6q23.1	244151_at	XM_001724204 /// XM_379432 /// XM_944838																			
4.02	3.92	0.10	4.82E-01	7.89E-01	ADAM12	ADAM metallopeptidase domain 12	chr10q26.3	204943_at	NM_003474 /// NM_021641																			
3.65	3.45	0.20	4.82E-01	7.89E-01	---	---	---	1563573_at	---																			
2.40	2.30	0.10	4.82E-01	7.89E-01	KIAA0125	KIAA0125	chr14q32.33	206478_at	XR_039974 /// XR_039975																			
5.53	5.34	0.19	4.82E-01	7.89E-01	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	chr22q13.1	204691_x_at	NM_001004426 /// NM_003560																			
2.00	1.92	0.07	4.82E-01	7.89E-01	---	---	---	1560543_at	---																			
2.48	2.38	0.09	4.82E-01	7.89E-01	LOC441178	hypothetical LOC441178	chr6q27	1563894_at	XR_040768 /// XR_040769 /// XR_040770																			
2.39	2.25	0.14	4.82E-01	7.89E-01	SDCCAG8	serologically defined colon cancer antigen 8	chr1q43-q44	1554237_at	NM_006642																			
2.52	2.31	0.21	4.82E-01	7.89E-01	ZNF785	zinc finger protein 785	chr16p11.2	1554770_x_at	NM_152458																			
2.13	2.01	0.11	4.82E-01	7.89E-01	DKK2	dickkopf homolog 2 (Xenopus laevis)	chr4q25	224199_at	NM_014421																			
4.25	4.12	0.13	4.83E-01	7.89E-01	LOC440995	hypothetical gene supported by BC034933; BC068085	chr3q29	235911_at	XM_498955 /// XM_942874																			
3.80	3.66	0.15	4.83E-01	7.89E-01	PYGM	phosphorylase, glycogen, muscle	chr11q12-q13.2	205577_at	NM_005609																			
2.83	2.69	0.14	4.83E-01	7.89E-01	MGC2848	hypothetical protein MGC2848	chr3q22.1	1553936_a_at	---																			
2.04	1.95	0.09	4.83E-01	7.89E-01	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	chr6p22-p21.3	1565925_at	NM_005495																			

2.63	2.51	0.13	4.83E-01	7.89E-01	MUC5AC /// MUC5B	mucin 5AC, oligomeric mucus/gel-forming /// mucin 5B, oligomeric mucus/gel-forming	chr11p15.5	222268_x_at	NM_002458 /// NM_017511 /// XM_001134429 /// XM_001714104 /// XM_001714774 /// XM_001719349
2.21	2.13	0.09	4.83E-01	7.89E-01	SART3	squamous cell carcinoma antigen recognized by T cells 3	chr12q24.1	1554276_at	NM_014706
3.19	3.06	0.12	4.83E-01	7.89E-01	---	---	---	214238_at	---
6.67	6.44	0.22	4.83E-01	7.89E-01	GIMAP5	GTPase, IMAP family member 5	chr7q36.1	64064_at	NM_018384
7.53	7.38	0.15	4.83E-01	7.90E-01	LOC440983	hypothetical gene supported by BC066916	chr3q25.1	227338_at	XM_498946 /// XM_944951
2.88	2.76	0.12	4.83E-01	7.90E-01	LRRC7	Leucine rich repeat containing 7	chr1p31.1	242050_at	NM_020794
1.98	1.88	0.09	4.83E-01	7.90E-01	---	---	---	1561213_at	---
2.64	2.53	0.11	4.83E-01	7.90E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	1555032_at	NM_002926 /// NM_198227 /// NM_198229
2.58	2.49	0.09	4.83E-01	7.90E-01	---	---	---	242315_at	---
6.42	6.28	0.15	4.83E-01	7.90E-01	G6PC3	glucose 6 phosphatase, catalytic, 3	chr17q21.31	221759_at	NM_138387
2.18	2.07	0.11	4.83E-01	7.90E-01	HIATL1	hippocampus abundant transcript-like 1	chr9q22.32	233954_at	NM_032558
2.82	2.71	0.11	4.83E-01	7.90E-01	---	---	---	228265_at	---
5.38	5.24	0.14	4.83E-01	7.90E-01	DNHD1L	dynein heavy chain domain 1-like	chr11p15.4	232240_at	XM_929181 /// XM_940957
2.19	2.12	0.08	4.83E-01	7.90E-01	---	---	---	234492_at	---
6.04	5.81	0.24	4.83E-01	7.90E-01	EI24	etoposide induced 2.4 mRNA	chr11q24	216396_s_at	NM_001007277 /// NM_004879
3.08	2.99	0.09	4.83E-01	7.90E-01	GNL1	guanine nucleotide binding protein-like 1	chr6p21.3	238487_at	NM_005275
2.18	2.09	0.10	4.83E-01	7.90E-01	---	---	---	234670_at	---
2.93	2.83	0.10	4.83E-01	7.90E-01	---	---	---	240334_at	---
5.80	5.29	0.51	4.83E-01	7.90E-01	LOC90826	hypothetical protein BC004337	chr4q31.23	228536_at	NM_138364
10.58	10.50	0.09	4.83E-01	7.90E-01	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	chr12q13.13	201322_at	NM_001686
3.34	3.22	0.12	4.84E-01	7.90E-01	TMEM179	Transmembrane protein 179	chr14q32.33	231216_at	NM_207379 /// XM_001717234
2.60	2.47	0.13	4.84E-01	7.90E-01	RPL32P3	ribosomal protein L32 pseudogene 3	chr3q21.3	1558969_a_at	NR_003111
2.20	2.10	0.10	4.84E-01	7.90E-01	---	---	---	231499_s_at	---
2.93	2.81	0.12	4.84E-01	7.90E-01	WHSC1	Wolf-Hirschhorn syndrome candidate 1	chr4p16.3	222777_s_at	NM_001042424 /// NM_007331 /// NM_133330 /// NM_133331 /// NM_133334 /// NM_133335
2.18	2.09	0.09	4.84E-01	7.90E-01	---	---	---	1570125_at	---
4.90	4.69	0.22	4.84E-01	7.90E-01	SERBP1	SERPINE1 mRNA binding protein 1	chr1p31	227369_at	NM_001018067 /// NM_001018068 /// NM_001018069 /// NM_015640
4.66	4.54	0.12	4.84E-01	7.90E-01	ZNF320	zinc finger protein 320	chr19q13.41	241704_x_at	NM_207333
2.31	2.21	0.10	4.84E-01	7.90E-01	---	---	---	1562275_at	---
2.71	2.58	0.13	4.84E-01	7.90E-01	CSPG4	chondroitin sulfate proteoglycan 4	chr15q24.2	214297_at	NM_001897
5.61	5.44	0.18	4.84E-01	7.90E-01	TAPBPL	TAP binding protein-like	chr12p13.31	218746_at	NM_018009
7.41	7.27	0.14	4.84E-01	7.90E-01	C22orf13	chromosome 22 open reading frame 13	chr22q11.2	223039_at	NM_031444
2.88	2.78	0.10	4.84E-01	7.90E-01	SLC35B3	solute carrier family 35, member B3	chr6p24.3	231003_at	NM_015948
5.29	5.13	0.16	4.84E-01	7.90E-01	COL27A1	collagen, type XXVII, alpha 1	chr9q32	225292_at	NM_032888
2.58	2.47	0.11	4.84E-01	7.90E-01	---	---	---	239786_at	---
3.59	3.41	0.18	4.84E-01	7.90E-01	---	---	---	1562505_at	---
2.29	2.18	0.11	4.84E-01	7.90E-01	RPAIN	RPA interacting protein	chr17p13.2	228288_at	NM_001033002

3.61	3.51	0.10	4.84E-01	7.90E-01	WWP2	WW domain containing E3 ubiquitin protein ligase 2	chr16q22.1	1554580_a_at	NM_007014 /// NM_199423 /// NM_199424																				
1.91	1.84	0.07	4.84E-01	7.90E-01	BNC1	basonuclin 1	chr15q25.2	1552487_a_at	NM_001717																				
2.75	2.61	0.14	4.85E-01	7.91E-01	RP11-49G10.8	breast cancer and salivary gland expression gene	chr20q11.21	1555554_at	XR_042114 /// XR_042115 /// XR_042116																				
6.27	6.13	0.15	4.85E-01	7.91E-01	C3orf18	chromosome 3 open reading frame 18	chr3p21.3	219114_at	NM_016210																				
6.73	6.51	0.22	4.85E-01	7.91E-01	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	chr5q31	229083_at	NM_006805																				
2.47	2.36	0.11	4.85E-01	7.91E-01	LOC283033	hypothetical protein LOC283033	chr10q11.21	1564178_at	---																				
5.91	5.57	0.34	4.85E-01	7.91E-01	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	chr10q24.1-q24.3	200898_s_at	NM_012215																				
2.47	2.39	0.09	4.85E-01	7.91E-01	---	---	---	233708_at	---																				
5.29	5.12	0.17	4.85E-01	7.91E-01	DUSP10	dual specificity phosphatase 10	chr1q41	215501_s_at	NM_007207 /// NM_144728 /// NM_144729																				
7.32	7.13	0.19	4.85E-01	7.91E-01	TCEAL8	transcription elongation factor A (SII)-like 8	chrXq22.1	224819_at	NM_001006684 /// NM_153333																				
3.30	3.16	0.14	4.85E-01	7.91E-01	NPY5R	neuropeptide Y receptor Y5	chr4q31-q32	207400_at	NM_006174																				
3.89	3.71	0.17	4.85E-01	7.91E-01	---	---	---	216101_at	---																				
4.76	4.64	0.12	4.85E-01	7.91E-01	C6orf108	Chromosome 6 open reading frame 108	chr6p21.1	213871_s_at	NM_006443 /// NM_199184																				
3.91	3.71	0.20	4.85E-01	7.91E-01	C8orf42	Chromosome 8 open reading frame 42	chr8p23.3	230903_s_at	NM_175075																				
2.50	2.40	0.10	4.85E-01	7.91E-01	---	---	---	241530_at	---																				
3.29	3.13	0.16	4.85E-01	7.91E-01	TTC12	Tetratricopeptide repeat domain 12	chr11q23.1	244571_s_at	NM_017868																				
9.37	9.12	0.24	4.85E-01	7.91E-01	MRPL41	mitochondrial ribosomal protein L41	chr9q34.3	227186_s_at	NM_032477																				
6.28	6.05	0.23	4.85E-01	7.91E-01	MTP18	mitochondrial protein 18 kDa	chr22q	223172_s_at	NM_001003704 /// NM_016498																				
2.80	2.67	0.14	4.85E-01	7.91E-01	PRG3	proteoglycan 3	chr11q12	220811_at	NM_006093																				
2.93	2.83	0.10	4.85E-01	7.91E-01	FOXP2	forkhead box P2	chr7q31	1564876_s_at	NM_014491 /// NM_148898 /// NM_148899																				
5.02	4.84	0.18	4.85E-01	7.91E-01	HOXC4	homeobox C4	chr12q13.3	206194_at	NM_014620 /// NM_153633																				
2.87	2.77	0.10	4.85E-01	7.91E-01	PAX2	paired box 2	chr10q24	206229_x_at	NM_000278 /// NM_003987 /// NM_003988 /// NM_003989 /// NM_003990																				
2.36	2.28	0.07	4.86E-01	7.91E-01	C20orf152	chromosome 20 open reading frame 152	chr20q11.23	1569466_at	NM_080834																				
2.45	2.35	0.10	4.86E-01	7.91E-01	LOC375010	hypothetical LOC375010	chr1q12	1558982_at	XR_041271																				
2.29	2.21	0.09	4.86E-01	7.91E-01	---	---	---	240177_at	---																				
4.92	4.83	0.09	4.86E-01	7.91E-01	ELL	elongation factor RNA polymerase II	chr19p13.1	204096_s_at	NM_006532																				
4.65	4.36	0.29	4.86E-01	7.91E-01	RWDD2A	RWD domain containing 2A	chr6q14.2	213555_at	NM_033411																				
2.38	2.26	0.12	4.86E-01	7.91E-01	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	chr8p21-p11.2	235540_at	NM_000825 /// NM_001083111																				
2.30	2.20	0.10	4.86E-01	7.91E-01	LOC100130468	hypothetical protein LOC100130468	chr18p11.22	240211_at	XM_001720765 /// XM_001721438 /// XM_001723029																				
3.16	3.06	0.11	4.86E-01	7.91E-01	DSCR10	Down syndrome critical region gene 10	chr21q22.13	1552467_at	NM_148676																				

5.48	5.27	0.21	4.86E-01	7.91E-01	AMACR /// C1QTNF3	alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein 3	chr5p13	209426_s_at	NM_014324 /// NM_030945 /// NM_181435 /// NM_203382
2.43	2.30	0.13	4.86E-01	7.91E-01	ZNF677	zinc finger protein 677	chr19q13.41	1569039_s_at	NM_182609
4.93	4.62	0.31	4.86E-01	7.91E-01	PTPRG	protein tyrosine phosphatase, receptor type, G	chr3p21-p14	204944_at	NM_002841
3.02	2.94	0.08	4.86E-01	7.91E-01	LOC389834	hypothetical LOC389834	---	241624_at	NM_001013655 /// XM_001726968
5.90	5.71	0.18	4.86E-01	7.91E-01	NCKIPSD	NCK interacting protein with SH3 domain	chr3p21	218697_at	NM_016453 /// NM_184231
5.45	5.31	0.14	4.86E-01	7.91E-01	ITSN2	intersectin 2	chr2pter-p25.1	209907_s_at	NM_006277 /// NM_019595 /// NM_147152
2.27	2.17	0.11	4.86E-01	7.91E-01	---	---	---	1562091_at	---
8.02	7.89	0.14	4.86E-01	7.91E-01	ACP1	acid phosphatase 1, soluble	chr2p25	215227_x_at	NM_001040649 /// NM_004300 /// NM_007099 /// NR_024080
2.12	2.03	0.09	4.86E-01	7.91E-01	KIAA0087	KIAA0087	chr7p15.2	207161_at	NR_022006 /// XM_001722166 /// XM_001723668 /// XM_001723724
4.22	4.12	0.11	4.86E-01	7.92E-01	C20orf134	chromosome 20 open reading frame 134	chr20q11.22	232619_at	NM_001024675
3.01	2.88	0.13	4.86E-01	7.92E-01	HACE1	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	chr6q21	227471_at	NM_020771
2.39	2.28	0.12	4.86E-01	7.92E-01	LMNA	Lamin A/C	chr1q21.2-q21.3	244225_x_at	NM_005572 /// NM_170707 /// NM_170708
11.07	10.56	0.52	4.86E-01	7.92E-01	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	chr16p13.3	209458_x_at	NM_000517 /// NM_000558
5.37	5.22	0.15	4.86E-01	7.92E-01	C9orf85	chromosome 9 open reading frame 85	chr9q21.13	238912_x_at	NM_182505
2.39	2.28	0.10	4.86E-01	7.92E-01	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	chrXq21	220738_s_at	NM_014496
8.28	8.04	0.24	4.86E-01	7.92E-01	FHL2	four and a half LIM domains 2	chr2q12-q14	202949_s_at	NM_001039492 /// NM_001450 /// NM_201555 /// NM_201557
7.04	6.78	0.26	4.87E-01	7.92E-01	MXD4	MAX dimerization protein 4	chr4p16.3	210778_s_at	NM_006454
7.40	7.17	0.24	4.87E-01	7.92E-01	RNASE6	ribonuclease, RNase A family, k6	chr14q11.2	213566_at	NM_005615
7.52	7.36	0.16	4.87E-01	7.92E-01	TMEM161A	transmembrane protein 161A	chr19p13.11	43977_at	NM_017814
2.89	2.77	0.12	4.87E-01	7.92E-01	ZSWIM1	Zinc finger, SWIM-type containing 1	chr20q13.12	217592_at	NM_080603
3.90	3.79	0.11	4.87E-01	7.92E-01	OSM	oncostatin M	chr22q12.2	214637_at	NM_020530
5.16	4.93	0.23	4.87E-01	7.92E-01	CRLF3	cytokine receptor-like factor 3	chr17q11.2	205474_at	NM_015986
4.35	4.20	0.14	4.88E-01	7.92E-01	---	---	---	238576_at	---
2.47	2.35	0.12	4.88E-01	7.92E-01	---	---	---	235696_at	---
4.95	4.77	0.18	4.88E-01	7.93E-01	U2AF2	U2 small nuclear RNA auxiliary factor 2	chr19q13.42	218382_s_at	NM_001012478 /// NM_007279
6.32	6.19	0.13	4.88E-01	7.93E-01	MKKS	McKusick-Kaufman syndrome	chr20p12	222530_s_at	NM_018848 /// NM_170784
3.07	2.73	0.33	4.88E-01	7.93E-01	---	---	---	240138_at	---
5.33	5.12	0.21	4.88E-01	7.93E-01	---	---	---	1557270_at	---
3.39	3.26	0.13	4.88E-01	7.93E-01	C9orf96	chromosome 9 open reading frame 96	chr9q34.2	236805_at	NM_153710

5.68	5.54	0.14	4.88E-01	7.93E-01	SPPL2B	signal peptide peptidase-like 2B	chr19p13.3	225248_at	NM_001077238 /// NM_152988
9.46	9.31	0.15	4.88E-01	7.93E-01	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	chr19q13.42	218563_at	NM_004542
4.47	4.24	0.23	4.88E-01	7.93E-01	DCUN1D3 /// EXOD1	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) /// exonuclease domain containing 1	chr16p12.2	213365_at	NM_080663 /// NM_173475
5.08	4.95	0.13	4.88E-01	7.93E-01	CROCCL1	ciliary rootlet coiled-coil, rootletin-like 1	chr1p36.13	1569291_at	XR_039823 /// XR_039824
8.29	8.10	0.19	4.88E-01	7.93E-01	LOC442497 /// SLC3A2	hypothetical protein LOC442497 /// solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	chr11q13 /// chr7p22	200924_s_at	NM_001012661 /// NM_001012662 /// NM_001012663 /// NM_001012664 /// NM_001013251 /// NM_002394
5.26	5.11	0.16	4.88E-01	7.93E-01	MORN4	MORN repeat containing 4	chr10q24.1	228354_at	NM_001098831 /// NM_178832
2.36	2.27	0.09	4.88E-01	7.93E-01	RNASEH2B	ribonuclease H2, subunit B	chr13q14.3	233156_at	NM_024570
2.68	2.59	0.09	4.88E-01	7.93E-01	---	---	---	239180_at	---
2.03	1.95	0.08	4.88E-01	7.93E-01	LOC100128692	Hypothetical protein LOC100128692	chr8q13.1	232314_at	XM_001720291 /// XM_001720298 /// XM_001720315
2.43	2.24	0.20	4.88E-01	7.93E-01	C16orf52	Chromosome 16 open reading frame 52	chr16p12.1	244835_at	NR_024104 /// XM_001126460 /// XM_001132387 /// XM_001724381
4.11	3.99	0.12	4.88E-01	7.93E-01	ADAT3	adenosine deaminase, tRNA-specific 3, TAD3 homolog (S. cerevisiae)	chr19p13.3	1553967_at	NM_138422
2.35	2.24	0.11	4.89E-01	7.93E-01	---	---	---	1566979_at	---
2.23	2.14	0.09	4.89E-01	7.93E-01	---	---	---	1563265_at	---
3.39	3.29	0.10	4.89E-01	7.93E-01	PIGV	Phosphatidylinositol glycan anchor biosynthesis, class V	chr1p36.11	240375_at	NM_017837
5.57	5.40	0.17	4.89E-01	7.93E-01	NTHL1	nth endonuclease III-like 1 (E. coli)	chr16p13.3	209731_at	NM_002528
4.96	4.71	0.24	4.89E-01	7.93E-01	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	chr1q44	216855_s_at	NM_004501 /// NM_031844
6.00	5.81	0.20	4.89E-01	7.93E-01	NUDT14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	chr14q32.33	231914_at	NM_177533
2.13	2.04	0.08	4.89E-01	7.93E-01	---	---	---	232791_at	---
2.00	1.91	0.09	4.89E-01	7.93E-01	---	---	---	234375_x_at	---
2.20	2.07	0.12	4.89E-01	7.93E-01	---	---	---	244517_x_at	---
11.74	11.65	0.09	4.89E-01	7.93E-01	ACTG1	actin, gamma 1	chr17q25	212988_x_at	NM_001614
2.86	2.75	0.12	4.89E-01	7.93E-01	LOXL4	lysyl oxidase-like 4	chr10q24	1570219_at	NM_032211
5.46	5.28	0.18	4.89E-01	7.93E-01	BTBD14B	BTB (POZ) domain containing 14B	chr19p13.13	227651_at	NM_052876
5.73	5.57	0.17	4.89E-01	7.93E-01	CHST10	carbohydrate sulfotransferase 10	chr2q11.2	204065_at	NM_004854
4.23	3.98	0.26	4.89E-01	7.93E-01	---	---	---	233271_at	---
2.61	2.53	0.08	4.89E-01	7.93E-01	WRNIP1	Werner helicase interacting protein 1	chr6p25.2	227619_at	NM_020135 /// NM_130395
5.03	4.90	0.13	4.89E-01	7.93E-01	---	---	---	237768_x_at	---
6.38	6.10	0.28	4.89E-01	7.94E-01	LYNX1	Ly6/neurotoxin 1	chr8q24.3	226305_at	NM_023946 /// NM_177457 /// NM_177458 /// NM_177476 /// NM_177477
7.27	7.08	0.19	4.89E-01	7.94E-01	RAD1	RAD1 homolog (S. pombe)	chr5p13.2	210216_x_at	NM_002853 /// NM_133377
2.19	2.11	0.08	4.89E-01	7.94E-01	---	---	---	1561618_at	---

3.36	3.27	0.09	4.89E-01	7.94E-01	GLT1D1	glycosyltransferase 1 domain containing 1	chr12q24.32	229770_at	NM_144669
2.21	2.11	0.10	4.89E-01	7.94E-01	C10orf118	chromosome 10 open reading frame 118	chr10q25.3	229399_at	NM_018017
2.66	2.57	0.09	4.90E-01	7.94E-01	SEMA3F	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	chr3p21.3	206832_s_at	NM_004186
3.41	3.31	0.10	4.90E-01	7.94E-01	FOXRED2	FAD-dependent oxidoreductase domain containing 2	chr22q12.3	233250_x_at	NM_001102371 /// NM_024955
2.72	2.58	0.13	4.90E-01	7.94E-01	---	---	---	238188_at	---
2.48	2.37	0.11	4.90E-01	7.94E-01	---	---	---	236468_at	---
2.74	2.56	0.17	4.90E-01	7.94E-01	FMNL3	formin-like 3	chr12q13.12	227844_at	NM_175736 /// NM_198900
5.29	5.08	0.21	4.90E-01	7.94E-01	SNX8	sorting nexin 8	chr7p22.2	223241_at	NM_013321
2.15	2.05	0.09	4.90E-01	7.94E-01	GUCA1A	guanylate cyclase activator 1A (retina)	chr6p21.1	1255_g_at	NM_000409
5.03	4.86	0.16	4.90E-01	7.94E-01	GPER	G protein-coupled estrogen receptor 1	chr7p22.3	210640_s_at	NM_001039966 /// NM_001098201 /// NM_001505
2.73	2.63	0.10	4.90E-01	7.94E-01	APOC3	apolipoprotein C-III	chr11q23.1-q23.2	205820_s_at	NM_000040
3.26	3.06	0.21	4.90E-01	7.94E-01	---	---	---	229705_at	---
2.18	2.09	0.10	4.90E-01	7.94E-01	SLC25A27	solute carrier family 25, member 27	chr6p11.2-q12	230624_at	NM_004277
4.23	4.09	0.14	4.90E-01	7.94E-01	GLDN	gliomedin	chr15q21.2	232649_at	NM_181789
4.63	4.38	0.25	4.90E-01	7.94E-01	COQ9	coenzyme Q9 homolog (S. cerevisiae)	chr16q13	235822_at	NM_020312
2.19	2.11	0.08	4.90E-01	7.94E-01	LOC731779	hypothetical protein LOC731779	---	1569297_at	XM_001725826
6.66	6.27	0.39	4.90E-01	7.94E-01	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	chr3p21.1	217850_at	NM_014366 /// NM_206825 /// NM_206826
3.38	3.27	0.11	4.90E-01	7.94E-01	---	---	---	1570124_at	---
5.65	5.33	0.31	4.90E-01	7.94E-01	KIAA1377	KIAA1377	chr11q22.1	235956_at	NM_020802
2.45	2.35	0.10	4.91E-01	7.94E-01	FLJ39639	hypothetical protein FLJ39639	chr16p13.3	243547_at	XM_001715751 /// XM_370932 /// XM_940089
2.07	1.98	0.09	4.91E-01	7.94E-01	---	---	---	1562656_at	---
2.11	2.03	0.08	4.91E-01	7.94E-01	IFIH1	Interferon induced with helicase C domain 1	chr2q24	216020_at	NM_022168
3.45	3.30	0.15	4.91E-01	7.94E-01	---	---	---	240271_at	---
6.14	5.95	0.19	4.91E-01	7.94E-01	GLE1	GLE1 RNA export mediator homolog (yeast)	chr9q34.11	225371_at	NM_001003722 /// NM_001499
2.64	2.57	0.08	4.91E-01	7.94E-01	C19orf15	chromosome 19 open reading frame 15	chr19q13.1	221316_at	NM_021185
4.69	4.56	0.13	4.91E-01	7.94E-01	GOLGA2	golgi autoantigen, golgin subfamily a, 2	chr9q34.11	204384_at	NM_004486
6.95	6.80	0.16	4.91E-01	7.94E-01	ZNF32	zinc finger protein 32	chr10q22-q25	209538_at	NM_001005368 /// NM_006973
2.07	1.98	0.09	4.91E-01	7.94E-01	GCM2	glial cells missing homolog 2 (Drosophila)	chr6p23	220799_at	NM_004752
2.24	2.13	0.11	4.91E-01	7.94E-01	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	chr15q15.1	237145_at	NM_001013703
2.79	2.66	0.13	4.91E-01	7.94E-01	SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	chr10q25	1553328_a_at	NM_003054
2.12	2.04	0.08	4.91E-01	7.94E-01	---	---	---	237192_at	---
4.88	4.77	0.11	4.91E-01	7.94E-01	PHF20	PHD finger protein 20	chr20q11.22-q11.23	1569906_s_at	NM_016436
4.02	3.90	0.12	4.91E-01	7.94E-01	IPO9	importin 9	chr1q32.1	213785_at	NM_018085
2.78	2.63	0.15	4.91E-01	7.95E-01	---	---	---	237904_at	---
2.30	2.20	0.10	4.92E-01	7.95E-01	---	---	---	1560559_at	---
2.06	1.97	0.08	4.92E-01	7.95E-01	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	chr19p13.2	206515_at	NM_000896
3.07	2.94	0.13	4.92E-01	7.95E-01	C6orf125	Chromosome 6 open reading frame 125	chr6p21.31	229443_at	NM_032340
2.63	2.52	0.10	4.92E-01	7.95E-01	TMEM111	Transmembrane protein 111	chr3p25.3	215250_at	NM_018447
2.59	2.50	0.09	4.92E-01	7.95E-01	FANCM	Fanconi anemia, complementation group M	chr14q21.3	242711_x_at	NM_020937
3.80	3.66	0.14	4.92E-01	7.95E-01	---	---	---	216366_x_at	---
2.04	1.95	0.09	4.92E-01	7.95E-01	C10orf136	chromosome 10 open reading frame 136	chr10q11.21	1560851_at	XM_001717004 /// XM_926383 /// XM_936868
2.53	2.45	0.07	4.92E-01	7.95E-01	---	---	---	1566586_at	---
1.98	1.87	0.11	4.92E-01	7.95E-01	MIER3	mesoderm induction early response 1, family member 3	chr5q11.2	1554449_at	NM_152622
2.73	2.53	0.20	4.92E-01	7.95E-01	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	chr1q41	214764_at	NM_016052
2.31	2.22	0.09	4.92E-01	7.95E-01	---	---	---	1556814_a_at	---
4.32	4.05	0.27	4.92E-01	7.95E-01	DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	chr7q22-q31	205761_s_at	NM_181581
5.20	5.09	0.11	4.92E-01	7.95E-01	TRAFD1	TRAF-type zinc finger domain containing 1	chr12q	202837_at	NM_006700

3.99	3.87	0.12	4.92E-01	7.95E-01	CCRL2 /// LOC727811	chemokine (C-C motif) receptor-like 2 /// similar to chemokine (C-C motif) receptor-like 2	chr3p21	211434_s_at	NM_001097632 /// NM_001130910 /// NM_003965 /// XM_001717282																				
4.28	4.03	0.25	4.92E-01	7.95E-01	---	---	---	1563431_x_at	---																				
2.62	2.50	0.12	4.93E-01	7.95E-01	---	---	---	236513_at	---																				
4.30	4.15	0.16	4.93E-01	7.95E-01	C1orf91	chromosome 1 open reading frame 91	chr1p36.11-p34.2	223656_s_at	NM_019118																				
4.52	4.31	0.21	4.93E-01	7.95E-01	AKNA	AT-hook transcription factor	chr9q32	225701_at	NM_030767																				
6.75	6.57	0.17	4.93E-01	7.95E-01	TSC22D3	TSC22 domain family, member 3	chrXq22.3	207001_x_at	NM_001015881 /// NM_004089 /// NM_198057																				
3.59	3.47	0.12	4.93E-01	7.95E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	241896_at	NM_012090 /// NM_033044																				
4.43	4.25	0.18	4.93E-01	7.95E-01	---	---	---	241798_at	---																				
2.42	2.33	0.09	4.93E-01	7.95E-01	USP26	ubiquitin specific peptidase 26	chrXq26.2	224532_at	NM_031907																				
2.21	2.12	0.09	4.93E-01	7.95E-01	TRHDE	thyrotropin-releasing hormone degrading enzyme	chr12q15-q21	219937_at	NM_013381																				
4.78	4.64	0.14	4.93E-01	7.95E-01	SPTBN4	spectrin, beta, non-erythrocytic 4	chr19q13.13	224297_s_at	NM_020971 /// NM_025213																				
2.05	1.97	0.08	4.93E-01	7.95E-01	---	---	---	237617_at	---																				
2.69	2.59	0.10	4.93E-01	7.95E-01	---	---	---	217247_at	---																				
3.76	3.57	0.19	4.93E-01	7.95E-01	SLC25A35	solute carrier family 25, member 35	chr17p13.1	236064_at	NM_201520																				
2.24	2.14	0.10	4.93E-01	7.95E-01	---	---	---	241591_at	---																				
4.19	4.03	0.16	4.93E-01	7.96E-01	CLCNKB	chloride channel Kb	chr1p36	1554748_at	NM_000085																				
1.95	1.87	0.08	4.93E-01	7.96E-01	---	---	---	1565614_at	---																				
4.28	4.15	0.13	4.93E-01	7.96E-01	---	---	---	236109_at	---																				
5.82	5.54	0.27	4.93E-01	7.96E-01	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	chr7q21.3	228494_at	NM_017650																				
7.91	7.58	0.33	4.94E-01	7.96E-01	CTGF	connective tissue growth factor	chr6q23.1	209101_at	NM_001901																				
3.62	3.44	0.18	4.94E-01	7.96E-01	41518	septin 1	chr16p11.1	227552_at	NM_052838																				
2.76	2.61	0.16	4.94E-01	7.96E-01	---	---	---	242478_at	---																				
7.47	7.32	0.15	4.94E-01	7.96E-01	CISD3	CDGSH iron sulfur domain 3	chr17q12	226727_at	XM_001714917 /// XM_001716624 /// XM_001718346																				
2.96	2.84	0.12	4.94E-01	7.96E-01	ATP10B	ATPase, class V, type 10B	chr5q34	214070_s_at	NM_025153																				
3.30	3.21	0.09	4.94E-01	7.96E-01	OAF	OAF homolog (Drosophila)	chr11q23.3	228939_at	NM_178507																				
2.84	2.67	0.17	4.94E-01	7.96E-01	FLJ10661 /// LOC100129420	similar to CG7889-PA /// similar to hCG1990547	chr8p23.1	1562904_s_at	XM_001720857 /// XM_001721359 /// XM_001721781 /// XR_015342 /// XR_015555 /// XR_040164																				
4.68	4.57	0.11	4.94E-01	7.96E-01	---	---	---	242857_at	---																				
3.92	3.78	0.14	4.94E-01	7.96E-01	NEK8	NIMA (never in mitosis gene a)- related kinase 8	chr17q11.1	1557170_at	NM_178170																				
2.31	2.24	0.07	4.94E-01	7.96E-01	---	---	---	1566221_at	---																				
2.97	2.89	0.09	4.94E-01	7.96E-01	---	---	---	243615_at	---																				
4.18	4.01	0.17	4.94E-01	7.96E-01	TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	chr1q23.2	228619_x_at	NM_001031800 /// NM_152902																				
2.53	2.44	0.09	4.94E-01	7.96E-01	---	---	---	243941_at	---																				
3.81	3.67	0.14	4.94E-01	7.96E-01	FAM166A	family with sequence similarity 166, member A	chr9q34.3	1562778_at	NM_001001710																				
2.10	2.01	0.09	4.94E-01	7.96E-01	---	---	---	1564807_at	---																				
2.59	2.48	0.11	4.94E-01	7.96E-01	---	---	---	235939_at	---																				
2.31	2.22	0.09	4.94E-01	7.96E-01	LOC126147	hypothetical protein BC018697	chr19q13.33	1558247_s_at	NM_145807																				
3.44	3.34	0.10	4.95E-01	7.96E-01	ZNF345	zinc finger protein 345	chr19q13.12	240199_x_at	NM_003419																				
5.44	5.21	0.23	4.95E-01	7.97E-01	---	---	---	239901_at	---																				
2.39	2.32	0.07	4.95E-01	7.97E-01	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	chr15q11.2-q12	1569689_s_at	NM_000814 /// NM_021912																				
3.27	3.17	0.09	4.95E-01	7.97E-01	RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	chr12q13-q14	236291_at	NM_002905																				

4.14	4.02	0.11	4.95E-01	7.97E-01	PRF1	perforin 1 (pore forming protein)	chr10q22	1553681_a_at	NM_001083116 /// NM_005041
2.67	2.56	0.12	4.95E-01	7.97E-01	---	---	---	1558760_at	---
2.82	2.71	0.11	4.95E-01	7.97E-01	BMP2K	BMP2 inducible kinase	chr4q21.21	59644_at	NM_017593 /// NM_198892
2.75	2.60	0.15	4.95E-01	7.97E-01	---	---	---	243560_at	---
2.00	1.92	0.08	4.95E-01	7.97E-01	---	---	---	237066_at	---
9.65	9.55	0.09	4.95E-01	7.97E-01	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	chr8q13.3	222992_s_at	NM_005005
3.38	3.23	0.15	4.95E-01	7.97E-01	CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	chr22q11|22q11.21	206184_at	NM_005207
2.49	2.38	0.11	4.95E-01	7.97E-01	---	---	---	1560792_at	---
6.82	6.65	0.17	4.95E-01	7.97E-01	EHBP1	EH domain binding protein 1	chr2p15	212653_s_at	NM_015252
2.73	2.60	0.13	4.95E-01	7.97E-01	---	---	---	241497_at	---
4.09	3.72	0.37	4.95E-01	7.97E-01	KLHL13	kelch-like 13 (Drosophila)	chrXq23-q24	227875_at	NM_033495
3.25	3.14	0.12	4.95E-01	7.97E-01	---	---	---	1563485_at	---
5.04	4.92	0.12	4.95E-01	7.97E-01	RDH13	retinol dehydrogenase 13 (all-trans/9-cis)	chr19q13.42	225449_at	NM_138412
2.10	2.02	0.08	4.96E-01	7.97E-01	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	chr10q24	217558_at	NM_000771
7.29	7.07	0.22	4.96E-01	7.97E-01	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	chr7q32	217799_x_at	NM_003344 /// NM_182697
2.16	2.07	0.09	4.96E-01	7.97E-01	CLEC12A	C-type lectin domain family 12, member A	chr12p13.2	1569401_at	NM_138337 /// NM_201623
6.86	6.69	0.17	4.96E-01	7.97E-01	SLC35E1	solute carrier family 35, member E1	chr19p13.11	229410_at	NM_024881
3.16	3.00	0.16	4.96E-01	7.97E-01	C1GALT1C1	C1GALT1-specific chaperone 1	chrXq24	238989_at	NM_001011551 /// NM_152692
2.23	2.15	0.08	4.96E-01	7.97E-01	TFG	TRK-fused gene	chr3q12.2	244614_at	NM_001007565 /// NM_006070
5.24	5.11	0.13	4.96E-01	7.97E-01	ADCK5	aarF domain containing kinase 5	chr8q24.3	228524_at	NM_174922
2.17	2.07	0.10	4.96E-01	7.97E-01	---	---	---	243996_at	---
2.40	2.31	0.09	4.96E-01	7.98E-01	GPR85	G protein-coupled receptor 85	chr7q31	234303_s_at	NM_018970
6.54	6.25	0.29	4.96E-01	7.98E-01	CDK6	cyclin-dependent kinase 6	chr7q21-q22	224847_at	NM_001259
2.84	2.71	0.12	4.96E-01	7.98E-01	---	---	---	239814_at	---
3.51	3.34	0.17	4.96E-01	7.98E-01	APOA5	apolipoprotein A-V	chr11q23	224244_s_at	NM_052968
3.53	3.38	0.15	4.96E-01	7.98E-01	ZSCAN16	zinc finger and SCAN domain containing 16	chr6p22.1	219676_at	NM_025231
4.97	4.85	0.12	4.96E-01	7.98E-01	XPO5	exportin 5	chr6p21.1	223057_s_at	NM_020750
3.21	3.06	0.16	4.96E-01	7.98E-01	METTL4	methyltransferase like 4	chr18p11.32	219698_s_at	NM_022840
2.37	2.27	0.10	4.96E-01	7.98E-01	---	---	---	243443_at	---
5.24	5.00	0.23	4.97E-01	7.98E-01	FAM120AOS	family with sequence similarity 120A opposite strand	chr9q22.31	1558761_a_at	NM_198841
2.57	2.47	0.09	4.97E-01	7.98E-01	---	---	---	1564451_at	---
2.29	2.22	0.08	4.97E-01	7.98E-01	---	---	---	1566964_at	---
5.65	5.47	0.18	4.97E-01	7.98E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	209153_s_at	NM_003200
5.16	4.98	0.18	4.97E-01	7.98E-01	SIGLEC10	sialic acid binding Ig-like lectin 10	chr19q13.3	1552807_a_at	NM_033130
5.48	5.31	0.17	4.97E-01	7.98E-01	C9orf75	chromosome 9 open reading frame 75	chr9q34.3	225891_at	NM_001128228 /// NM_173691
3.47	3.34	0.14	4.97E-01	7.98E-01	STK10	serine/threonine kinase 10	chr5q35.1	228394_at	NM_005990
2.80	2.69	0.11	4.97E-01	7.98E-01	CAPN13	calpain 13	chr2p22-p21	1552801_at	NM_144575
4.92	4.70	0.22	4.97E-01	7.98E-01	AXIN1	axin 1	chr16p13.3	212849_at	NM_003502 /// NM_181050
8.04	7.91	0.14	4.97E-01	7.98E-01	C17orf37	chromosome 17 open reading frame 37	chr17q12	224447_s_at	NM_032339
2.12	2.03	0.08	4.97E-01	7.98E-01	---	---	---	240575_at	---
3.84	3.68	0.15	4.97E-01	7.99E-01	---	---	---	231262_at	---
6.30	6.01	0.30	4.97E-01	7.99E-01	LPGAT1	lysophosphatidylglycerol acyltransferase 1	chr1q32	202651_at	NM_014873
3.40	3.27	0.14	4.97E-01	7.99E-01	LOC646891 /// SDCCAG3	similar to serologically defined colon cancer antigen 3 /// serologically defined colon cancer antigen 3	chr1q25.1 /// chr9q34.3	230058_at	NM_001039707 /// NM_001039708 /// NM_006643 /// XR_017348 /// XR_018947 /// XR_039660
2.39	2.30	0.09	4.97E-01	7.99E-01	ANKH	ankylosis, progressive homolog (mouse)	chr5p15.1	220076_at	NM_054027
5.92	5.74	0.18	4.98E-01	7.99E-01	TNKS1BP1	tankyrase 1 binding protein 1, 182kDa	chr11q12.1	224792_at	NM_033396
5.53	5.31	0.22	4.98E-01	7.99E-01	---	---	---	235766_x_at	---
5.32	5.20	0.12	4.98E-01	7.99E-01	FBXO42	F-box protein 42	chr1p36.23-p36.11	47773_at	NM_018994

3.71	3.55	0.17	4.98E-01	7.99E-01	---	---	---	230460_at	---
3.15	3.03	0.13	4.98E-01	7.99E-01	---	---	---	222334_at	---
6.22	6.08	0.14	4.98E-01	7.99E-01	CROT	carnitine O-octanoyltransferase	chr7q21.1	204573_at	NM_021151
8.38	8.26	0.12	4.98E-01	7.99E-01	SERINC3	serine incorporator 3	chr20q13.1-q13.3	221471_at	NM_006811 /// NM_198941
5.89	5.69	0.20	4.98E-01	7.99E-01	SPINT2	serine peptidase inhibitor, Kunitz type, 2	chr19q13.1	210715_s_at	NM_021102 /// XM_001720755 /// XM_001720786 /// XM_001722917
3.26	3.13	0.13	4.98E-01	7.99E-01	BRWD1	bromodomain and WD repeat domain containing 1	chr21q22.2	231960_at	NM_001007246 /// NM_018963 /// NM_033656
4.84	4.69	0.16	4.98E-01	7.99E-01	UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	chr2q14.3	218257_s_at	NM_001025777 /// NM_020120
4.72	4.50	0.22	4.98E-01	7.99E-01	RPS27L	ribosomal protein S27-like	chr15q22.2	238935_at	NM_015920
3.89	3.74	0.16	4.98E-01	7.99E-01	SUSD3	sushi domain containing 3	chr9q22.31	227182_at	NM_145006
3.17	3.09	0.08	4.98E-01	7.99E-01	TUBGCP6	tubulin, gamma complex associated protein 6	chr22q13.31-q13.33	234308_at	NM_020461
7.18	7.02	0.17	4.99E-01	7.99E-01	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)	chr19q13.11	212132_at	NM_001114093 /// NM_015578
5.30	5.14	0.16	4.99E-01	7.99E-01	PAQR4	progestin and adipoQ receptor family member IV	chr16p13.3	212858_at	NM_152341
2.60	2.45	0.16	4.99E-01	7.99E-01	LIMA1	LIM domain and actin binding 1	chr12q13	222456_s_at	NM_001113546 /// NM_001113547 /// NM_016357
6.66	6.45	0.21	4.99E-01	7.99E-01	BCL3	B-cell CLL/lymphoma 3	chr19q13.1-q13.2	204908_s_at	NM_005178
4.84	4.55	0.28	4.99E-01	7.99E-01	CENTD3	centaurin, delta 3	chr5q31.3	218950_at	NM_022481
2.11	2.02	0.09	4.99E-01	7.99E-01	LOC286370	hypothetical protein LOC286370	chr9q22.2	1561289_at	---
2.57	2.48	0.09	4.99E-01	7.99E-01	WDR33	WD repeat domain 33	chr2q14.3	218851_s_at	NM_001006622 /// NM_001006623 /// NM_018383
2.51	2.43	0.08	4.99E-01	8.00E-01	FAM123C	family with sequence similarity 123C	chr2q21.1	1553350_at	NM_001105193 /// NM_001105194 /// NM_001105195 /// NM_152698
6.37	6.17	0.20	4.99E-01	8.00E-01	TMEM160	transmembrane protein 160	chr19q13.32	219219_at	NM_017854
4.24	3.79	0.45	4.99E-01	8.00E-01	C12orf60	chromosome 12 open reading frame 60	chr12p12.3	229888_at	NM_175874
2.89	2.80	0.09	4.99E-01	8.00E-01	---	---	---	242226_at	---
2.87	2.77	0.10	4.99E-01	8.00E-01	---	---	---	232285_at	---
2.07	1.94	0.13	4.99E-01	8.00E-01	LOC100132181	Hypothetical protein LOC100132181	---	236181_at	XM_001722051
4.03	3.72	0.31	4.99E-01	8.00E-01	---	---	---	1558444_at	---
5.59	5.42	0.17	4.99E-01	8.00E-01	FLJ22222	hypothetical protein FLJ22222	chr17q25.3	219254_at	NM_024648 /// NM_175902
7.97	7.85	0.12	5.00E-01	8.00E-01	STIP1	stress-induced-phosphoprotein 1	chr11q13	213330_s_at	NM_006819
4.55	4.40	0.15	5.00E-01	8.00E-01	ZNF434	zinc finger protein 434	chr16p13.3	218937_at	NM_017810
3.81	3.72	0.10	5.00E-01	8.00E-01	KPNA6	karyopherin alpha 6 (importin alpha 7)	chr1p35.1-p34.3	212102_s_at	NM_012316
8.51	8.42	0.09	5.00E-01	8.00E-01	OS9	amplified in osteosarcoma	chr12q13	200714_x_at	NM_001017956 /// NM_001017957 /// NM_001017958 /// NM_006812
3.39	3.28	0.11	5.00E-01	8.00E-01	C22orf30	chromosome 22 open reading frame 30	chr22q12.2-q12.3	1553761_at	NM_173566
3.98	3.79	0.19	5.00E-01	8.00E-01	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	chr2p21	202552_s_at	NM_016441
2.56	2.45	0.11	5.00E-01	8.00E-01	---	---	---	241171_at	---
2.50	2.41	0.09	5.00E-01	8.00E-01	---	---	---	1556699_at	---
2.33	2.23	0.10	5.00E-01	8.00E-01	PIK3R4	Phosphoinositide-3-kinase, regulatory subunit 4	chr3q22.1	216436_at	NM_014602

4.90	4.13	0.77	5.00E-01	8.00E-01	---	---	---	242836_at	---
3.96	3.85	0.11	5.00E-01	8.00E-01	BCDIN3D	BCDIN3 domain containing	chr12q13.13	234979_at	NM_181708
2.34	2.25	0.08	5.00E-01	8.00E-01	---	---	---	236716_at	---
5.41	5.22	0.19	5.00E-01	8.00E-01	GIGYF1	GRB10 interacting GYF protein 1	chr7q22	228755_at	NM_022574
4.02	3.70	0.32	5.00E-01	8.00E-01	PDE5A	phosphodiesterase 5A, cGMP-specific	chr4q25-q27	227088_at	NM_001083 /// NM_033430 /// NM_033437
2.83	2.73	0.10	5.00E-01	8.00E-01	---	---	---	1569732_at	---
4.47	4.33	0.14	5.00E-01	8.00E-01	NCAPD2	non-SMC condensin I complex, subunit D2	chr12p13.3	201774_s_at	NM_014865
7.38	7.10	0.27	5.00E-01	8.00E-01	FAM102A	family with sequence similarity 102, member A	chr9q34.11	212400_at	NM_001035254 /// NM_203305
2.66	2.48	0.18	5.00E-01	8.01E-01	---	---	---	236220_at	---
2.35	2.26	0.09	5.00E-01	8.01E-01	---	---	---	237820_at	---
2.47	2.38	0.09	5.00E-01	8.01E-01	---	---	---	1561313_at	---
3.63	3.51	0.12	5.00E-01	8.01E-01	MRPS11	mitochondrial ribosomal protein S11	chr15q25	215919_s_at	NM_022839 /// NM_176805
4.34	4.17	0.16	5.01E-01	8.01E-01	RHOF	ras homolog gene family, member F (in filopodia)	chr12q24.31	222812_s_at	NM_019034
2.19	2.09	0.09	5.01E-01	8.01E-01	---	---	---	1561780_at	---
2.74	2.64	0.10	5.01E-01	8.01E-01	---	---	---	240006_at	---
3.79	3.66	0.13	5.01E-01	8.01E-01	KIR2DL2	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	chr19q13.4	211397_x_at	NM_014219
3.23	3.11	0.13	5.01E-01	8.01E-01	RGS11	regulator of G-protein signaling 11	chr16p13.3	211872_s_at	NM_003834 /// NM_183337
3.46	3.33	0.13	5.01E-01	8.01E-01	RILPL1	Rab interacting lysosomal protein-like 1	chr12q24.31	1554017_at	NM_178314
8.44	8.31	0.13	5.01E-01	8.01E-01	TSG101	tumor susceptibility gene 101	chr11p15	201758_at	NM_006292
2.57	2.47	0.10	5.01E-01	8.01E-01	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	chr9q13	217477_at	NM_003558
4.74	4.62	0.12	5.01E-01	8.01E-01	---	---	---	233412_x_at	---
3.07	2.94	0.13	5.01E-01	8.01E-01	---	---	---	1568804_at	---
2.72	2.61	0.10	5.01E-01	8.01E-01	HAS3	hyaluronan synthase 3	chr16q22.1	223541_at	NM_005329 /// NM_138612
2.11	2.02	0.09	5.01E-01	8.01E-01	LOC645591	hypothetical protein LOC645591	chr7q22.1	1554301_at	XM_934971
2.17	2.09	0.08	5.01E-01	8.01E-01	FAM54A	family with sequence similarity 54, member A	chr6q23.3	228069_at	NM_001099286 /// NM_138419
4.89	4.76	0.13	5.01E-01	8.01E-01	SFI1	Sfi1 homolog, spindle assembly associated (yeast)	chr22q12.2	213431_x_at	NM_001007467 /// NM_014775
4.59	4.25	0.34	5.01E-01	8.01E-01	C16orf52	chromosome 16 open reading frame 52	chr16p12.1	227351_at	NR_024104 /// XM_001126460 /// XM_001132387 /// XM_001724381
7.86	7.68	0.19	5.01E-01	8.01E-01	BSDC1	BSD domain containing 1	chr1p35.1	222200_s_at	NM_018045
2.91	2.75	0.17	5.01E-01	8.01E-01	ADAT2	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)	chr6q24.2	227213_at	NM_182503
2.54	2.45	0.09	5.01E-01	8.01E-01	OR1C1	olfactory receptor, family 1, subfamily C, member 1	chr1q44	1567055_at	NM_012353
3.64	3.51	0.13	5.01E-01	8.01E-01	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	chr19q13.2	211883_x_at	NM_001024912 /// NM_001712
6.95	6.84	0.11	5.02E-01	8.01E-01	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	chrXq13	214224_s_at	NM_006223
3.29	3.18	0.11	5.02E-01	8.01E-01	SPTBN5	spectrin, beta, non-erythrocytic 5	chr15q21	220067_at	NM_016642
1.99	1.90	0.08	5.02E-01	8.01E-01	---	---	---	241060_x_at	---
6.16	6.08	0.08	5.02E-01	8.01E-01	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	chr20q11.23	233056_x_at	NM_001042486 /// NM_014902 /// NM_183006
4.25	4.15	0.10	5.02E-01	8.01E-01	---	---	---	243377_at	---

2.83	2.73	0.10	5.02E-01	8.01E-01	KIAA1875	KIAA1875	chr8q24.3	233344_x_at	XM_001714043 /// XM_001714583 /// XM_001714586 /// XM_001714972 /// XM_001714978 /// XM_001717214																			
2.91	2.79	0.12	5.02E-01	8.01E-01	LOC170082	TFIIS central domain-containing protein 1	chrXp22.2	1563862_at	NM_152634																			
2.33	2.24	0.09	5.02E-01	8.01E-01	C21orf89	chromosome 21 open reading frame 89	chr21q22.3	1552876_at	XR_040130 /// XR_040131 /// XR_040132																			
5.85	5.67	0.18	5.02E-01	8.01E-01	PHKA1	phosphorylase kinase, alpha 1 (muscle)	chrXq12-q13	205450_at	NM_001122670 /// NM_002637																			
2.36	2.24	0.11	5.02E-01	8.01E-01	RBM45	RNA binding motif protein 45	chr2q31.2	237702_at	NM_152945																			
4.46	4.24	0.22	5.02E-01	8.01E-01	C9orf114	chromosome 9 open reading frame 114	chr9q34.11	218565_at	NM_016390																			
3.26	3.10	0.16	5.02E-01	8.01E-01	---	---	---	1555664_at	---																			
8.29	8.05	0.24	5.02E-01	8.01E-01	RABGGTB	Rab geranylgeranyltransferase, beta subunit	chr1p31	209181_s_at	NM_004582																			
6.45	6.32	0.13	5.02E-01	8.01E-01	CCDC101	coiled-coil domain containing 101	chr16p11.2	221822_at	NM_138414																			
2.31	2.22	0.09	5.02E-01	8.01E-01	LOC100131496	hypothetical protein LOC100131496	chr20q13.12	1558477_at	XM_001722187 /// XM_001722223 /// XM_001722594																			
4.54	4.37	0.17	5.02E-01	8.01E-01	---	---	---	217135_x_at	---																			
2.02	1.95	0.07	5.02E-01	8.02E-01	---	---	---	241673_x_at	---																			
9.95	9.82	0.13	5.03E-01	8.02E-01	PRDX5	peroxiredoxin 5	chr11q13	222994_at	NM_012094 /// NM_181651 /// NM_181652																			
5.90	5.74	0.16	5.03E-01	8.02E-01	FIZ1	FLT3-interacting zinc finger 1	chr19q13.42	226967_at	NM_032836																			
5.67	5.51	0.16	5.03E-01	8.02E-01	RBM17	RNA binding motif protein 17	chr10p15.1	224780_at	NM_032905																			
3.47	3.02	0.45	5.03E-01	8.02E-01	SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	chr4q13.1	219934_s_at	NM_005420																			
2.02	1.91	0.11	5.03E-01	8.02E-01	MTRF1L	Mitochondrial translational release factor 1-like	chr6q25-q26	217204_at	NM_001114184 /// NM_019041																			
4.81	4.60	0.21	5.03E-01	8.02E-01	ZNF598	zinc finger protein 598	chr16p13.3	225104_at	NM_178167																			
2.56	2.47	0.09	5.03E-01	8.02E-01	C4orf19	chromosome 4 open reading frame 19	chr4p14	219450_at	NM_001104629 /// NM_018302																			
2.67	2.56	0.11	5.03E-01	8.02E-01	C6orf26 /// MSH5	chromosome 6 open reading frame 26 /// mutS homolog 5 (E. coli)	chr6p21.3 /// chr6p21.33	221406_s_at	NM_001039651 /// NM_002441 /// NM_025259 /// NM_172165 /// NM_172166																			
3.29	3.19	0.10	5.03E-01	8.02E-01	---	---	---	244543_s_at	---																			
6.04	5.93	0.11	5.03E-01	8.02E-01	---	---	---	229293_at	---																			
3.79	3.67	0.13	5.03E-01	8.02E-01	IL23A	interleukin 23, alpha subunit p19	chr12q13.2	220054_at	NM_016584																			
4.11	3.86	0.25	5.03E-01	8.02E-01	ESR1	estrogen receptor 1	chr6q25.1	205225_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742																			
3.35	3.16	0.19	5.03E-01	8.02E-01	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene	chr7q11-q22	214757_at	NR_003614 /// XR_042144 /// XR_042161 /// XR_042167																			

3.91	3.80	0.11	5.03E-01	8.02E-01	---	---	---	223358_s_at	---
3.32	3.17	0.15	5.04E-01	8.03E-01	ANKRD34A	ankyrin repeat domain 34A	chr1q21.1	232735_at	NM_001039888
2.33	2.25	0.08	5.04E-01	8.03E-01	CASP2	caspase 2, apoptosis-related cysteine peptidase	chr7q34-q35	34449_at	NM_032982 /// NM_032983
3.20	3.03	0.17	5.04E-01	8.03E-01	SMG7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr1q25	217189_s_at	NM_173156 /// NM_201568 /// NM_201569
2.67	2.57	0.10	5.04E-01	8.03E-01	LOC349114	hypothetical LOC349114	chr7p14.1	1558423_at	XR_040227 /// XR_040228 /// XR_040229 /// XR_040230
4.07	3.98	0.09	5.04E-01	8.03E-01	ZNF805	zinc finger protein 805	chr19q13.43	235398_at	XM_001718504 /// XM_001718548 /// XM_001719150
1.90	1.80	0.10	5.04E-01	8.03E-01	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	chr7q31.2	234706_x_at	NM_000492
2.55	2.47	0.08	5.04E-01	8.03E-01	DISC1	disrupted in schizophrenia 1	chr1q42.1	217330_at	NM_001012957 /// NM_001012958 /// NM_001012959 /// NM_018662
4.73	4.58	0.15	5.04E-01	8.03E-01	POLG2	polymerase (DNA directed), gamma 2, accessory subunit	chr17q	205811_at	NM_007215
2.33	2.24	0.09	5.04E-01	8.03E-01	LOC401068	hypothetical gene supported by BC028186	chr3p21.1	1557754_at	XR_041577 /// XR_041578 /// XR_041579
2.89	2.74	0.15	5.04E-01	8.03E-01	FAM78B	family with sequence similarity 78, member B	chr1q24.1	1558113_at	NM_001017961
2.85	2.73	0.13	5.04E-01	8.03E-01	TMPRSS13	transmembrane protease, serine 13	chr11q23	223659_at	NM_001077263
4.38	4.18	0.20	5.04E-01	8.03E-01	DOK4	docking protein 4	chr16q13	209691_s_at	NM_018110
2.58	2.49	0.10	5.04E-01	8.03E-01	---	---	---	1560706_at	---
2.55	2.45	0.10	5.04E-01	8.03E-01	GPR19	G protein-coupled receptor 19	chr12p12.3	207183_at	NM_006143
2.06	1.98	0.08	5.04E-01	8.03E-01	GRIK2	glutamate receptor, ionotropic, kainate 2	chr6q16.3-q21	1563754_at	NM_021956 /// NM_175768
8.75	8.56	0.19	5.04E-01	8.03E-01	PTOV1	prostate tumor overexpressed gene 1	chr19q13.33	212032_s_at	NM_017432
2.97	2.88	0.08	5.04E-01	8.03E-01	RAB25	RAB25, member RAS oncogene family	chr1q22	218186_at	NM_020387
2.23	2.15	0.07	5.04E-01	8.03E-01	---	---	---	1569205_at	---
5.14	4.98	0.17	5.04E-01	8.03E-01	ABHD6 /// LOC643635	abhydrolase domain containing 6 /// similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11	chr1p36.33 /// chr3p14.3	221679_s_at	NM_020676 /// XM_926939
2.34	2.26	0.08	5.04E-01	8.03E-01	LOC339468	hypothetical protein LOC339468	chr1p31.1	1562908_at	---
3.57	3.46	0.10	5.04E-01	8.03E-01	---	---	---	1566548_at	---
2.11	1.98	0.13	5.04E-01	8.03E-01	ANKRD7	ankyrin repeat domain 7	chr7q31	206112_at	NM_001077708 /// NM_019644
7.77	7.53	0.24	5.05E-01	8.03E-01	---	---	---	213158_at	---
4.85	4.46	0.38	5.05E-01	8.03E-01	CH25H	cholesterol 25-hydroxylase	chr10q23	206932_at	NM_003956
8.34	8.19	0.15	5.05E-01	8.03E-01	COMMD3	COMM domain containing 3	chr10pter-q22.1	218048_at	NM_012071
5.61	5.29	0.33	5.05E-01	8.03E-01	FASTKD3	FAST kinase domains 3	chr5p15.3-p15.2	219200_at	NM_024091
4.05	3.87	0.18	5.05E-01	8.03E-01	LOC90835	hypothetical protein LOC90835	chr16p11.2	231300_at	NM_001014979
2.19	2.10	0.09	5.05E-01	8.03E-01	---	---	---	243861_at	---
2.38	2.25	0.13	5.05E-01	8.03E-01	PRSS16	protease, serine, 16 (thymus)	chr6p21	208165_s_at	NM_005865
2.66	2.55	0.10	5.05E-01	8.03E-01	IRX2	iroquois homeobox 2	chr5p15.33	228462_at	NM_001134222 /// NM_033267
2.90	2.80	0.10	5.05E-01	8.03E-01	---	---	---	241549_at	---
7.11	6.96	0.16	5.05E-01	8.03E-01	PIM3	pim-3 oncogene	chr22q13	224739_at	NM_001001852
2.90	2.79	0.11	5.05E-01	8.03E-01	FAM129C	family with sequence similarity 129, member C	chr19p13.11	1553369_at	NM_001098524 /// NM_173544

3.06	2.93	0.14	5.05E-01	8.03E-01	ATXN7L1	ataxin 7-like 1	chr7q22.2	232265_at	NM_020725 /// NM_152749																				
3.60	3.50	0.10	5.05E-01	8.03E-01	TPCN2	two pore segment channel 2	chr11q13.2	235194_at	NM_139075																				
2.49	2.40	0.09	5.05E-01	8.03E-01	MCM3APAS	minichromosome maintenance complex component 3 associated protein antisense	chr21q22.3	232740_at	NR_002776																				
3.17	3.06	0.10	5.05E-01	8.03E-01	CUGBP2	CUG triplet repeat, RNA binding protein 2	chr10p13	202158_s_at	NM_001025076 /// NM_001025077 /// NM_001083591 /// NM_006561																				
2.78	2.69	0.10	5.05E-01	8.03E-01	LOC100129803	Hypothetical protein LOC100129803	chr22q11.21	236145_at	XM_001715297 /// XM_001717354 /// XM_001719131																				
4.63	4.50	0.14	5.05E-01	8.03E-01	FBXL18	F-box and leucine-rich repeat protein 18	chr7p22.2	1553361_x_at	NM_024963																				
2.63	2.55	0.08	5.05E-01	8.03E-01	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	chr1p34-p33	1560657_at	NM_005424																				
2.84	2.73	0.11	5.05E-01	8.03E-01	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	chr20q12-q13.1	230687_at	NM_001011554 /// NM_022829																				
4.98	4.83	0.15	5.05E-01	8.03E-01	KRT6B	keratin 6B	chr12q12-q13	209126_x_at	NM_005555																				
4.69	4.47	0.22	5.05E-01	8.03E-01	tcag7.1177	opposite strand transcription unit to STAG3	chr7q22.1	1553971_a_at	NM_178831																				
2.16	2.08	0.08	5.05E-01	8.03E-01	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	chr8q21.11	1555217_at	NM_001001481 /// NM_018299																				
2.45	2.35	0.10	5.05E-01	8.03E-01	TMEM213	transmembrane protein 213	chr7q34	239593_at	NM_001085429																				
3.73	3.65	0.07	5.05E-01	8.03E-01	GATA6	GATA binding protein 6	chr18q11.1-q11.2	229282_at	NM_005257																				
4.51	4.29	0.22	5.06E-01	8.03E-01	HSPA12B	heat shock 70kD protein 12B	chr20p13	229172_at	NM_052970																				
3.46	3.36	0.10	5.06E-01	8.03E-01	PFTK2	PFTAIRE protein kinase 2	chr2q33.2	1552559_a_at	NM_139158																				
3.45	3.33	0.11	5.06E-01	8.03E-01	NUP210	nucleoporin 210kDa	chr3p25.1	212316_at	NM_024923																				
4.01	3.79	0.22	5.06E-01	8.03E-01	---	---	---	230305_at	---																				
4.73	4.61	0.12	5.06E-01	8.03E-01	EIF4E2	eukaryotic translation initiation factor 4E family member 2	chr2q37.1	226734_at	NM_004846																				
3.36	3.02	0.34	5.06E-01	8.03E-01	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	chr6q15	236796_at	NM_021813																				
2.24	2.11	0.13	5.06E-01	8.03E-01	---	---	---	1566631_at	---																				
2.71	2.47	0.23	5.06E-01	8.03E-01	MTF2	metal response element binding transcription factor 2	chr1p22.1	203347_s_at	NM_007358																				
4.28	4.11	0.17	5.06E-01	8.03E-01	BATF3	basic leucine zipper transcription factor, ATF-like 3	chr1q32.3	220358_at	NM_018664																				
3.41	3.28	0.13	5.06E-01	8.03E-01	FARS2	Phenylalanyl-tRNA synthetase 2, mitochondrial	chr6p25.1	215414_at	NM_006567																				
2.21	2.13	0.08	5.06E-01	8.03E-01	---	---	---	240893_at	---																				
2.83	2.72	0.11	5.06E-01	8.03E-01	LONRF1	LON peptidase N-terminal domain and ring finger 1	chr8p23.1	236556_s_at	NM_152271																				
2.70	2.61	0.09	5.06E-01	8.03E-01	RNF219	Ring finger protein 219	chr13q31.1	237686_at	NM_024546																				
5.11	4.96	0.14	5.06E-01	8.03E-01	C10orf114	chromosome 10 open reading frame 114	chr10p12.31	1555922_at	NM_001010911																				
2.21	2.13	0.09	5.06E-01	8.04E-01	CCDC147	coiled-coil domain containing 147	chr10q25.1	1557544_at	NM_001008723																				
1.97	1.89	0.07	5.06E-01	8.04E-01	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	chr7q31.2	215703_at	NM_000492																				
3.98	3.89	0.09	5.06E-01	8.04E-01	ARSI	arylsulfatase family, member I	chr5q33.1	230275_at	NM_001012301																				

2.31	2.17	0.14	5.07E-01	8.04E-01	CD46	CD46 molecule, complement regulatory protein	chr1q32	237126_at	NM_002389 /// NM_153826 /// NM_172350 /// NM_172351 /// NM_172352 /// NM_172353 /// NM_172354 /// NM_172355 /// NM_172356 /// NM_172357 /// NM_172358 /// NM_172359 /// NM_172360 /// NM_172361																			
4.50	4.35	0.15	5.07E-01	8.04E-01	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	chr17q12	1553048_a_at	NM_003559																				
3.62	3.42	0.20	5.07E-01	8.04E-01	C2orf55	chromosome 2 open reading frame 55	chr2q11.2	228067_at	NM_207362																				
2.32	2.21	0.10	5.07E-01	8.04E-01	CHRNA9	cholinergic receptor, nicotinic, alpha 9	chr4p14	221107_at	NM_017581																				
2.87	2.75	0.12	5.07E-01	8.04E-01	GRIA3	glutamate receptor, ionotrophic, AMPA 3	chrXq25-q26	230144_at	NM_000828 /// NM_007325																				
3.74	3.59	0.16	5.07E-01	8.04E-01	ZNF180	zinc finger protein 180	chr19q13.2	219495_s_at	NM_013256																				
2.26	2.19	0.08	5.07E-01	8.04E-01	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6	chr2q37	232654_s_at	NM_001072 /// NM_205862																				
6.03	5.89	0.14	5.07E-01	8.04E-01	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	chr8q22.2	202634_at	NM_005034																				
9.64	9.44	0.20	5.07E-01	8.04E-01	TUBA1A	tubulin, alpha 1a	chr12q12-q14.3	209118_s_at	NM_006009																				
3.32	3.08	0.24	5.07E-01	8.04E-01	MAP9	microtubule-associated protein 9	chr4q32.1	228423_at	NM_001039580																				
2.67	2.59	0.08	5.07E-01	8.04E-01	C1orf21	chromosome 1 open reading frame 21	chr1q25	223127_s_at	NM_030806																				
6.54	6.34	0.20	5.07E-01	8.04E-01	ALDOA	aldolase A, fructose-bisphosphate	chr16p11.2	238996_x_at	NM_000034 /// NM_001127617 /// NM_184041 /// NM_184043																				
2.19	2.06	0.13	5.07E-01	8.04E-01	---	---	---	232840_at	---																				
2.52	2.42	0.10	5.07E-01	8.04E-01	---	---	---	244223_at	---																				
3.24	3.11	0.13	5.07E-01	8.04E-01	INCENP	inner centromere protein antigens 135/155kDa	chr11q12-q13	219769_at	NM_001040694 /// NM_020238																				
2.15	2.06	0.09	5.07E-01	8.04E-01	KRTAP9-3	keratin associated protein 9-3	chr17q12-q21	234679_at	NM_031962																				
4.05	3.89	0.16	5.08E-01	8.04E-01	TACC2	transforming, acidic coiled-coil containing protein 2	chr10q26	211382_s_at	NM_006997 /// NM_206860 /// NM_206861 /// NM_206862																				
6.21	5.95	0.26	5.08E-01	8.04E-01	COL12A1	collagen, type XII, alpha 1	chr6q12-q13	225664_at	NM_004370 /// NM_080645																				
4.72	4.55	0.17	5.08E-01	8.04E-01	---	---	---	229786_at	---																				
5.14	5.02	0.12	5.08E-01	8.04E-01	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	chr8p11.1	222491_at	NM_152419																				
7.37	7.13	0.24	5.08E-01	8.04E-01	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	chr20q13.13	202673_at	NM_003859																				
4.36	4.25	0.11	5.08E-01	8.04E-01	ZNF276	zinc finger protein 276	chr16q24.3	231922_at	NM_001113525 /// NM_152287																				
6.01	5.81	0.20	5.08E-01	8.04E-01	C3orf39	chromosome 3 open reading frame 39	chr3p22.1	225689_at	NM_032806																				
5.34	5.10	0.23	5.08E-01	8.04E-01	KCNE3	potassium voltage-gated channel, Isk-related family, member 3	chr11q13-q14	227647_at	NM_005472																				
3.44	3.23	0.21	5.08E-01	8.04E-01	ZNF507	zinc finger protein 507	chr19q13.11	235618_at	NM_014910																				

3.06	2.89	0.17	5.08E-01	8.04E-01	---	---	---	227655_at	---
7.58	7.26	0.32	5.08E-01	8.04E-01	LRRC58	leucine rich repeat containing 58	chr3q13.33	225479_at	NM_001099678
4.08	3.95	0.13	5.08E-01	8.04E-01	ETV2	ets variant gene 2	chr19q13.12	215510_at	NM_014209
2.44	2.36	0.09	5.08E-01	8.04E-01	LOC728137 /// LOC728395 /// LOC728412 /// TSPY1	similar to testis specific protein, Y-linked 1 /// similar to testis specific protein, Y-linked 1 /// similar to testis specific protein, Y-linked 1 /// testis specific protein, Y-linked 1	chrYp11.2	216374_at	NM_001077697 /// NM_003308 /// XM_001126990 /// XM_001127025
3.22	3.08	0.14	5.08E-01	8.05E-01	VAMP5	Vesicle-associated membrane protein 5 (myobrevin)	chr2p11.2	214115_at	NM_006634
6.44	6.27	0.18	5.08E-01	8.05E-01	CRY2	cryptochrome 2 (photolyase-like)	chr11p11.2	212695_at	NM_001127457 /// NM_021117
3.44	3.33	0.11	5.08E-01	8.05E-01	LOC90379	hypothetical protein BC002926	chr19p13.12	221851_at	NM_138353
2.62	2.51	0.11	5.08E-01	8.05E-01	SFRS17A	splicing factor, arginine/serine-rich 17A	chrXp22.32; Ypter-p11.2	228447_at	NM_005088
7.82	7.68	0.13	5.08E-01	8.05E-01	hCG_1776980 /// SDHC	hCG1776980 /// succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	chr17p13.3 /// chr1q23.3	216591_s_at	NM_001035511 /// NM_001035512 /// NM_001035513 /// NM_001089593 /// NM_003001 /// XM_001717960 /// XM_001723532 /// XM_001725207
3.52	3.39	0.13	5.08E-01	8.05E-01	POM121	POM121 membrane glycoprotein (rat)	chr7q11.23	205096_at	NM_172020
2.21	2.14	0.07	5.08E-01	8.05E-01	CD58	CD58 molecule	chr1p13	222061_at	NM_001779
2.17	2.08	0.10	5.08E-01	8.05E-01	SPATA5	spermatogenesis associated 5	chr4q28.1	229075_at	NM_145207
4.93	4.81	0.11	5.09E-01	8.05E-01	PCIF1	PDX1 C-terminal inhibiting factor 1	chr20q13.12	89948_at	NM_022104
2.12	2.05	0.07	5.09E-01	8.05E-01	KLHL14	kelch-like 14 (Drosophila)	chr18q12.1	228377_at	NM_020805
5.60	5.47	0.12	5.09E-01	8.05E-01	LOC171220	destrin-2 pseudogene	chr12p13	211325_x_at	---
2.64	2.54	0.10	5.09E-01	8.05E-01	---	---	---	1556148_s_at	---
2.46	2.35	0.10	5.09E-01	8.05E-01	LOC339766	hypothetical protein LOC339766	chr2q37.1	1556168_s_at	XM_001721240 /// XM_291007 /// XM_939706
5.95	5.84	0.10	5.09E-01	8.05E-01	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	chr1p36.22	212323_s_at	NM_015378 /// NM_018156
5.10	4.88	0.22	5.09E-01	8.05E-01	SFXN4	sideroflexin 4	chr10q26.11	230637_at	NM_213649
2.64	2.55	0.09	5.09E-01	8.05E-01	---	---	---	1560856_at	---
2.79	2.62	0.17	5.09E-01	8.05E-01	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	chrXq22.3	236760_at	NM_001025580 /// NM_015365
5.74	5.60	0.14	5.09E-01	8.05E-01	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	chr11p15.5	215764_x_at	NM_012305
2.16	2.08	0.08	5.09E-01	8.05E-01	FANCB	Fanconi anemia, complementation group B	chrXp22.2	1557218_s_at	NM_001018113 /// NM_152633
3.68	3.55	0.13	5.09E-01	8.05E-01	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	chr19q13.2	233986_s_at	NM_022835
5.42	5.30	0.12	5.09E-01	8.05E-01	---	---	---	227815_at	---
7.06	6.69	0.37	5.09E-01	8.05E-01	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	chr11p15.5	216894_x_at	NM_000076 /// NM_001122630 /// NM_001122631
7.66	7.54	0.12	5.09E-01	8.05E-01	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	chrXq28	214333_x_at	NM_004135 /// NM_174869
7.87	7.75	0.13	5.09E-01	8.05E-01	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	chr8p22-p21	201089_at	NM_001693
7.85	7.55	0.31	5.10E-01	8.05E-01	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	chr3p12	213194_at	NM_002941 /// NM_133631
2.48	2.40	0.07	5.10E-01	8.05E-01	LOC148987	hypothetical protein LOC148987	chr1p32.3	1557567_a_at	---

4.53	4.28	0.26	5.10E-01	8.05E-01	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	chr14q31.1	225994_at	NM_017437
2.65	2.55	0.10	5.10E-01	8.05E-01	C8orf59	chromosome 8 open reading frame 59	chr8q21.2	1555243_x_at	NM_001099670 /// NM_001099671 /// NM_001099672 /// NM_001099673
2.32	2.23	0.08	5.10E-01	8.05E-01	YPEL1	yippee-like 1 (Drosophila)	chr22q11.2	228788_at	NM_013313
2.07	1.99	0.08	5.10E-01	8.05E-01	DDX10 /// LOC401533	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 /// hypothetical gene supported by BC049217	chr11q22-q23 /// chr9q21.32	1563522_at	NM_004398 /// XR_016904 /// XR_018409 /// XR_038540
2.47	2.40	0.07	5.10E-01	8.05E-01	---	---	---	237877_at	---
6.09	5.90	0.19	5.10E-01	8.05E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	213049_at	NM_014990 /// NM_194301
2.58	2.49	0.09	5.10E-01	8.05E-01	GBP5	guanylate binding protein 5	chr1p22.2	238581_at	NM_001134486 /// NM_052942
3.32	3.20	0.12	5.10E-01	8.05E-01	ALG9	asparagine-linked glycosylation 9 homolog (S. cerevisiae, alpha-1,2-mannosyltransferase)	chr11q23	228817_at	NM_001077690 /// NM_001077691 /// NM_001077692 /// NM_024740
4.60	4.50	0.10	5.10E-01	8.05E-01	CEP250	centrosomal protein 250kDa	chr20q11.22-q12	209495_at	NM_001035518 /// NM_007186
2.49	2.39	0.09	5.10E-01	8.05E-01	STARD9	StAR-related lipid transfer (START) domain containing 9	chr15q15.2	227108_at	XM_001129290 /// XM_001129482 /// XM_001717505
7.61	7.43	0.17	5.10E-01	8.05E-01	PPT2	palmitoyl-protein thioesterase 2	chr6p21.3	209490_s_at	NM_005155 /// NM_138717
2.96	2.81	0.15	5.10E-01	8.05E-01	MAP3K1	mitogen-activated protein kinase kinase kinase 1	chr5q11.2	214786_at	NM_005921
2.96	2.81	0.15	5.10E-01	8.05E-01	---	---	---	234395_at	---
3.17	3.09	0.09	5.10E-01	8.06E-01	LOC100132625	hypothetical protein LOC100132625	chrXq26.3	242012_at	XM_001720431
2.46	2.37	0.09	5.10E-01	8.06E-01	BTBD9	BTB (POZ) domain containing 9	chr6p21	1553375_at	NM_001099272 /// NM_052893 /// NM_152733
2.99	2.84	0.15	5.10E-01	8.06E-01	---	---	---	229525_at	---
2.82	2.59	0.22	5.10E-01	8.06E-01	HBP1	HMG-box transcription factor 1	chr7q22-q31	207361_at	NM_012257
8.49	8.36	0.13	5.10E-01	8.06E-01	RNH1	ribonuclease/angiogenin inhibitor 1	chr11p15.5	206050_s_at	NM_002939 /// NM_203383 /// NM_203384 /// NM_203385 /// NM_203386 /// NM_203387 /// NM_203388 /// NM_203389
4.54	4.34	0.19	5.10E-01	8.06E-01	ANXA11	annexin A11	chr10q23	214783_s_at	NM_001157 /// NM_145868 /// NM_145869
2.19	2.10	0.09	5.11E-01	8.06E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	1567376_at	NM_015512
8.11	7.98	0.13	5.11E-01	8.06E-01	POLE4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	chr2p12	225844_at	NM_019896

2.47	2.38	0.09	5.11E-01	8.06E-01	ZNF599	zinc finger protein 599	chr19q13.11	1558390_at	NM_001007248																			
2.63	2.55	0.08	5.11E-01	8.06E-01	---	---	---	1561897_at	---																			
4.29	4.15	0.14	5.11E-01	8.06E-01	FAM131A	family with sequence similarity 131, member A	chr3q27.1	232807_at	NM_144635																			
4.90	4.68	0.22	5.11E-01	8.06E-01	LZTFL1	leucine zipper transcription factor-like 1	chr3p21.3	218437_s_at	NM_020347																			
2.87	2.78	0.09	5.11E-01	8.06E-01	---	---	---	220101_x_at	---																			
5.48	5.33	0.15	5.11E-01	8.06E-01	VPRBP	Vpr (HIV-1) binding protein	chr3p21.2	226477_at	NM_014703																			
6.75	6.63	0.12	5.11E-01	8.06E-01	PRMT2	protein arginine methyltransferase 2	chr21q22.3	228725_x_at	NM_001535 /// NM_206962																			
8.14	8.00	0.14	5.11E-01	8.06E-01	COPA	coatomer protein complex, subunit alpha	chr1q23-q25	208684_at	NM_001098398 /// NM_004371																			
7.92	7.74	0.19	5.11E-01	8.06E-01	---	---	---	226621_at	---																			
7.64	7.41	0.23	5.11E-01	8.06E-01	PRAF2	PRA1 domain family, member 2	chrXp11.23	203456_at	NM_007213																			
6.28	6.09	0.18	5.11E-01	8.06E-01	NDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	chr16p13.11	218414_s_at	NM_017668																			
9.17	8.95	0.22	5.11E-01	8.06E-01	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	chr1q21	200797_s_at	NM_021960 /// NM_182763																			
2.45	2.37	0.09	5.12E-01	8.06E-01	TTN	titin	chr2q31	241791_at	NM_003319 /// NM_133378 /// NM_133379 /// NM_133432 /// NM_133437																			
4.05	3.89	0.16	5.12E-01	8.06E-01	RNF144B	Ring finger 144B	chr6p22.3	239012_at	NM_182757																			
4.57	4.18	0.39	5.12E-01	8.06E-01	FZD7	frizzled homolog 7 (Drosophila)	chr2q33	203706_s_at	NM_003507																			
6.56	6.38	0.18	5.12E-01	8.07E-01	TNRC6A	trinucleotide repeat containing 6A	chr16p11.2	224704_at	NM_014494																			
2.25	2.16	0.09	5.12E-01	8.07E-01	---	---	---	243057_at	---																			
2.66	2.54	0.12	5.12E-01	8.07E-01	CDCA2	cell division cycle associated 2	chr8p21.2	236957_at	NM_152562																			
2.23	2.15	0.08	5.12E-01	8.07E-01	NUPL1	nucleoporin like 1	chr13q12.13	225047_at	NM_001008564 /// NM_001008565 /// NM_014089																			
9.65	9.41	0.24	5.12E-01	8.07E-01	C4orf18	chromosome 4 open reading frame 18	chr4q32.1	223204_at	NM_001031700 /// NM_001128424 /// NM_016613																			
8.39	8.21	0.18	5.12E-01	8.07E-01	KIAA0152	KIAA0152	chr12q24.31	200616_s_at	NM_014730																			
2.19	2.11	0.08	5.12E-01	8.07E-01	---	---	---	236654_s_at	---																			
8.44	8.17	0.27	5.12E-01	8.07E-01	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	chr11q12.1	224356_x_at	NM_022349 /// NM_152851 /// NM_152852																			
2.57	2.47	0.10	5.12E-01	8.07E-01	ANO2	anoctamin 2	chr12p13.3	234718_at	NM_020373																			
2.99	2.89	0.10	5.12E-01	8.07E-01	CSH1 /// CSH2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// growth hormone 1	chr17q24.2	206885_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645																			
9.56	9.24	0.32	5.12E-01	8.07E-01	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	chr18q11.2	203440_at	NM_001792																			
2.69	2.53	0.16	5.13E-01	8.07E-01	FIGN	fidgetin	chr2q24.3	239710_at	NM_018086																			

6.48	6.31	0.16	5.13E-01	8.07E-01	BRD4	bromodomain containing 4	chr19p13.1	202102_s_at	NM_014299 /// NM_058243																				
2.45	2.34	0.10	5.13E-01	8.07E-01	SMAD6	SMAD family member 6	chr15q21-q22	209887_at	NM_005585																				
9.36	9.24	0.12	5.13E-01	8.07E-01	ERGIC3	ERGIC and golgi 3	chr20pter-q12	216032_s_at	NM_015966 /// NM_198398																				
4.36	4.19	0.17	5.13E-01	8.07E-01	RRAGB	Ras-related GTP binding B	chrXp11.21	205540_s_at	NM_006064 /// NM_016656																				
5.46	5.29	0.17	5.13E-01	8.07E-01	NXT2	nuclear transport factor 2-like export factor 2	chrXq22.3	209628_at	NM_018698																				
5.49	5.28	0.21	5.13E-01	8.07E-01	PI4K2B	phosphatidylinositol 4-kinase type 2 beta	chr4p15.2	222631_at	NM_018323																				
4.08	3.99	0.09	5.13E-01	8.07E-01	---	---	---	242256_x_at	---																				
7.84	7.70	0.14	5.13E-01	8.07E-01	C16orf13	chromosome 16 open reading frame 13	chr16p13.3	228114_x_at	NM_001040160 /// NM_001040161 /// NM_001040162 /// NM_001040165 /// NM_032366																				
5.76	5.48	0.28	5.13E-01	8.07E-01	RNF138	ring finger protein 138	chr18q12.1	218738_s_at	NM_016271 /// NM_198128																				
5.16	5.00	0.16	5.13E-01	8.07E-01	C1orf77	chromosome 1 open reading frame 77	chr1q21.3	209927_s_at	NM_015607																				
4.17	4.03	0.14	5.13E-01	8.07E-01	---	---	---	217604_at	---																				
3.17	3.08	0.09	5.14E-01	8.07E-01	---	---	---	216859_x_at	---																				
3.70	3.52	0.18	5.14E-01	8.08E-01	---	---	---	244145_at	---																				
5.89	5.72	0.17	5.14E-01	8.08E-01	TOLLIP	toll interacting protein	chr11p15.5	222469_s_at	NM_019009																				
5.26	4.94	0.32	5.14E-01	8.08E-01	---	---	---	1559351_at	---																				
2.16	2.05	0.11	5.14E-01	8.08E-01	CNTNAP4	contactin associated protein-like 4	chr16q23.1	1553442_a_at	NM_033401 /// NM_138994																				
5.07	4.56	0.52	5.14E-01	8.08E-01	RGS4	regulator of G-protein signaling 4	chr1q23.3	204337_at	NM_001102445 /// NM_001113380 /// NM_001113381 /// NM_005613																				
6.29	6.14	0.16	5.14E-01	8.08E-01	CSNK1G2	casein kinase 1, gamma 2	chr19p13.3	202574_s_at	NM_001319																				
5.74	5.51	0.24	5.14E-01	8.08E-01	ZNF862	zinc finger protein 862	chr7q36.1	226808_at	NM_001099220																				
2.76	2.67	0.10	5.14E-01	8.08E-01	STAB2	stabilin 2	chr12q23.3	237567_at	NM_017564																				
4.43	4.13	0.30	5.14E-01	8.08E-01	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	chr18q11	206233_at	NM_004775																				
2.04	1.96	0.08	5.14E-01	8.08E-01	---	---	---	240776_at	---																				
4.89	4.73	0.17	5.14E-01	8.08E-01	CXorf52	Chromosome X open reading frame 52	chrXq28	244164_at	XR_040189 /// XR_040190 /// XR_040191																				
2.40	2.31	0.09	5.14E-01	8.08E-01	---	---	---	1566897_at	---																				
3.62	3.50	0.13	5.14E-01	8.08E-01	---	---	---	231238_at	---																				
4.97	4.85	0.12	5.14E-01	8.08E-01	---	---	---	227459_at	---																				
2.08	1.99	0.08	5.14E-01	8.08E-01	---	---	---	240815_at	---																				
4.08	3.96	0.12	5.14E-01	8.08E-01	RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr15q15.1	230832_at	NM_015138																				
5.25	4.98	0.27	5.14E-01	8.08E-01	LOC729678	hypothetical protein LOC729678	chr5q35.3	1556180_at	XR_040500 /// XR_040501 /// XR_040502																				
3.69	3.59	0.10	5.14E-01	8.08E-01	CASP2	caspase 2, apoptosis-related cysteine peptidase	chr7q34-q35	211140_s_at	NM_032982 /// NM_032983																				
4.09	3.88	0.22	5.14E-01	8.08E-01	LOC284276	hypothetical LOC284276	chr18q23	1558850_s_at	XR_041397 /// XR_041398 /// XR_041399																				
6.87	6.77	0.10	5.14E-01	8.08E-01	SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	chr21q22.3	200739_s_at	NM_006936																				
2.33	2.23	0.09	5.14E-01	8.08E-01	TRIM59	tripartite motif-containing 59	chr3q26.1	235476_at	NM_173084																				
3.08	2.99	0.09	5.14E-01	8.08E-01	TATDN2	TatD DNase domain containing 2	chr3p25.3	1565580_s_at	NM_014760																				

5.86	5.70	0.16	5.14E-01	8.08E-01	CD34	CD34 molecule	chr1q32	209543_s_at	NM_001025109 /// NM_001773
5.33	5.22	0.12	5.14E-01	8.08E-01	---	---	---	214076_at	---
3.96	3.88	0.08	5.14E-01	8.08E-01	NRXN1	neurexin 1	chr2p16.3	237535_x_at	NM_004801 /// NM_138735
4.11	3.98	0.13	5.14E-01	8.08E-01	---	---	---	228918_at	---
2.98	2.72	0.26	5.15E-01	8.08E-01	ACAD11 /// NPHP3	acyl-Coenzyme A dehydrogenase family, member 11 /// nephronophthisis 3 (adolescent)	chr3q22.1	235432_at	NM_032169 /// NM_153240
3.28	3.21	0.08	5.15E-01	8.08E-01	SFRS14	splicing factor, arginine/serine-rich 14	chr19p12	212000_at	NM_001017392 /// NM_014884
3.43	3.32	0.10	5.15E-01	8.08E-01	C8orf66	chromosome 8 open reading frame 66	chr8q24.3	1563654_at	---
3.01	2.92	0.09	5.15E-01	8.08E-01	TNRC6C	trinucleotide repeat containing 6C	chr17q25.3	227149_at	NM_018996
6.82	6.66	0.16	5.15E-01	8.08E-01	TSTA3	tissue specific transplantation antigen P35B	chr8q24.3	201644_at	NM_003313
6.94	6.74	0.20	5.15E-01	8.08E-01	CCDC90B	coiled-coil domain containing 90B	chr11q14.1	218288_s_at	NM_021825
5.72	5.52	0.20	5.15E-01	8.08E-01	KIAA1833	hypothetical protein KIAA1833	chr8q24.3	227778_at	NM_001099280 /// NM_001099281 /// NM_032450
4.10	3.88	0.22	5.15E-01	8.08E-01	FAM46C	family with sequence similarity 46, member C	chr1p12	226811_at	NM_017709
5.26	4.54	0.72	5.15E-01	8.08E-01	MCF2	MCF.2 cell line derived transforming sequence	chrXq27	1555313_a_at	NM_001099855 /// NM_005369
6.78	6.59	0.18	5.15E-01	8.08E-01	LOC645139 /// LOC651789 /// PAIP1	hypothetical LOC645139 /// similar to poly(A) binding protein interacting protein 1 isoform 1 /// poly(A) binding protein interacting protein 1	chr17p11.2 /// chr5p12	213754_s_at	NM_006451 /// NM_182789 /// NM_183323 /// XM_001718191 /// XM_001719017 /// XM_928169
4.20	4.06	0.14	5.15E-01	8.08E-01	ACAN	aggrecan	chr15q26.1	205679_x_at	NM_001135 /// NM_013227
4.70	4.45	0.25	5.15E-01	8.08E-01	TANK	TRAF family member-associated NFKB activator	chr2q24-q31	209451_at	NM_004180 /// NM_133484
3.19	2.99	0.20	5.15E-01	8.08E-01	---	---	---	232205_at	---
4.77	4.67	0.09	5.15E-01	8.08E-01	CCDC57	coiled-coil domain containing 57	chr17q25.3	227783_at	NM_198082
3.67	3.45	0.22	5.15E-01	8.09E-01	GABBR1	Gamma-aminobutyric acid (GABA) B receptor, 1	chr6p21.31	238569_at	NM_001470 /// NM_021903 /// NM_021904 /// NM_021905
2.35	2.27	0.07	5.15E-01	8.09E-01	---	---	---	243930_x_at	---
2.94	2.83	0.11	5.15E-01	8.09E-01	WFIKKN2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	chr17q21.33	241358_at	NM_175575
3.56	3.45	0.11	5.16E-01	8.09E-01	WIZ	widely interspaced zinc finger motifs	chr19p13.1	221785_at	NM_021241
4.62	4.48	0.14	5.16E-01	8.09E-01	---	---	---	238527_at	---
2.67	2.57	0.11	5.16E-01	8.09E-01	---	---	---	1556761_at	---
5.47	5.26	0.21	5.16E-01	8.09E-01	---	---	---	243966_at	---
8.41	8.05	0.36	5.16E-01	8.09E-01	RAB20	RAB20, member RAS oncogene family	chr13q34	219622_at	NM_017817
2.64	2.53	0.11	5.16E-01	8.09E-01	PAX8	paired box 8	chr2q12-q14	207924_x_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992
5.72	5.56	0.16	5.16E-01	8.09E-01	EBI3	Epstein-Barr virus induced gene 3	chr19p13.3	219424_at	NM_005755

6.16	6.09	0.07	5.16E-01	8.09E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	215529_x_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891
2.99	2.91	0.08	5.16E-01	8.09E-01	---	---	---	216770_at	---
2.89	2.68	0.21	5.16E-01	8.09E-01	INO80D	INO80 complex subunit D	chr2q33.3	231152_at	NM_017759
5.71	5.47	0.24	5.16E-01	8.09E-01	C16orf57	chromosome 16 open reading frame 57	chr16q13	1554016_a_at	NM_024598
2.24	2.14	0.10	5.16E-01	8.09E-01	---	---	---	1556815_at	---
3.08	2.91	0.16	5.16E-01	8.09E-01	MORN1	MORN repeat containing 1	chr1p36.33-p36.32	1563668_at	NM_024848
2.30	2.21	0.09	5.16E-01	8.09E-01	---	---	---	1563913_at	---
4.54	4.36	0.18	5.16E-01	8.09E-01	PARVB	parvin, beta	chr22q13.2-q13.33	37966_at	NM_001003828 /// NM_013327
2.86	2.76	0.10	5.16E-01	8.09E-01	CYP2B6 /// CYP2B7P1	cytochrome P450, family 2, subfamily B, polypeptide 6 /// cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1	chr19q13.2	206754_s_at	NM_000767 /// NR_001278
2.03	1.93	0.10	5.16E-01	8.09E-01	---	---	---	240474_x_at	---
8.70	8.48	0.22	5.16E-01	8.09E-01	PBX1	Pre-B-cell leukemia homeobox 1	chr1q23	212148_at	NM_002585
6.16	5.78	0.38	5.16E-01	8.09E-01	ATXN1	ataxin 1	chr6p23	203231_s_at	NM_000332 /// NM_001128164
3.77	3.65	0.12	5.16E-01	8.09E-01	SLC38A1	solute carrier family 38, member 1	chr12q13.11	242367_at	NM_001077484 /// NM_030674
3.17	3.06	0.11	5.16E-01	8.09E-01	LOC731139	Hypothetical LOC731139	chr1q42.13	236905_at	XM_001132048 /// XM_001722185 /// XM_001722376
2.48	2.37	0.11	5.16E-01	8.09E-01	---	---	---	237498_at	---
2.53	2.39	0.14	5.16E-01	8.09E-01	OR2B3P	olfactory receptor, family 2, subfamily B, member 3 pseudogene	chr6p22.1	234903_at	NM_001005226
9.34	9.17	0.18	5.17E-01	8.09E-01	C1QB	complement component 1, q subcomponent, B chain	chr1p36.12	202953_at	NM_000491
4.71	4.53	0.17	5.17E-01	8.09E-01	SOS1	son of sevenless homolog 1 (Drosophila)	chr2p22-p21	212780_at	NM_005633
2.48	2.23	0.25	5.17E-01	8.09E-01	FAM76B	family with sequence similarity 76, member B	chr11q21	1553750_a_at	NM_144664
3.35	3.25	0.11	5.17E-01	8.09E-01	RHEBL1	Ras homolog enriched in brain like 1	chr12q13.12	1553713_a_at	NM_144593
9.37	9.28	0.09	5.17E-01	8.09E-01	CHMP4B	chromatin modifying protein 4B	chr20q11.22	225498_at	NM_176812
6.55	6.41	0.13	5.17E-01	8.09E-01	SSSCA1	Sjogren syndrome/scleroderma autoantigen 1	chr11q13.1	203114_at	NM_006396
2.48	2.40	0.08	5.17E-01	8.09E-01	CD6	CD6 molecule	chr11q13	1566448_at	NM_006725
5.34	5.15	0.18	5.17E-01	8.09E-01	SIRT7	sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)	chr17q25	218797_s_at	NM_016538
6.20	6.03	0.17	5.17E-01	8.09E-01	VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)	chr18q21.32-q21.33	218171_at	NM_004869
6.53	6.31	0.22	5.17E-01	8.09E-01	UBA3	ubiquitin-like modifier activating enzyme 3	chr3p24.3-p13	209115_at	NM_003968 /// NM_198195
3.36	3.23	0.13	5.17E-01	8.09E-01	NUP88	Nucleoporin 88kDa	chr17p13.2	230274_s_at	NM_002532
6.78	6.66	0.12	5.17E-01	8.09E-01	CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	chr22q11|22q11.21	212180_at	NM_005207
2.29	2.20	0.09	5.17E-01	8.09E-01	PEX1	peroxisomal biogenesis factor 1	chr7q21.2	204873_at	NM_000466
2.12	2.03	0.08	5.17E-01	8.09E-01	FLJ20518	similar to FSHD region gene 2 protein	---	234830_at	XM_001720702 /// XM_001722211
2.69	2.59	0.10	5.17E-01	8.09E-01	KIAA0090	KIAA0090	chr1p36.13	215991_s_at	NM_015047
2.48	2.35	0.13	5.17E-01	8.09E-01	LOC100134081	similar to 3-phosphoinositide dependent protein kinase-1	---	244629_s_at	XM_001715304
2.07	1.96	0.11	5.17E-01	8.09E-01	---	---	---	241139_at	---
7.98	7.72	0.26	5.17E-01	8.09E-01	PTGR1	prostaglandin reductase 1	chr9q31.3	228824_s_at	NM_012212
2.06	1.97	0.09	5.18E-01	8.09E-01	FLJ31222	Hypothetical LOC388387	chr17q21.31	1570189_at	XR_041466 /// XR_041467 /// XR_041468
5.49	5.29	0.20	5.18E-01	8.09E-01	GRK6	G protein-coupled receptor kinase 6	chr5q35	210981_s_at	NM_001004105 /// NM_001004106 /// NM_002082
6.09	5.98	0.11	5.18E-01	8.09E-01	HDAC11	histone deacetylase 11	chr3p25.1	219847_at	NM_024827
2.66	2.57	0.09	5.18E-01	8.09E-01	---	---	---	204536_s_at	---

3.66	3.48	0.17	5.18E-01	8.09E-01	NFYA	nuclear transcription factor Y, alpha	chr6p21.3	204109_s_at	NM_002505 /// NM_021705 /// XM_001716589 /// XM_001717592 /// XM_001718396																				
3.69	3.59	0.10	5.18E-01	8.10E-01	ARIH2	Ariadne homolog 2 (Drosophila)	chr3p21.2-p21.3	238068_at	NM_006321																				
5.77	5.22	0.55	5.18E-01	8.10E-01	PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like	chr10q11	226623_at	NM_032439																				
11.03	10.57	0.46	5.18E-01	8.10E-01	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	chr16p13.3	204018_x_at	NM_000517 /// NM_000558																				
5.80	5.63	0.17	5.18E-01	8.10E-01	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	chr19q13.4	208071_s_at	NM_002287 /// NM_021706																				
2.41	2.28	0.13	5.18E-01	8.10E-01	---	---	---	237068_at	---																				
2.00	1.93	0.08	5.18E-01	8.10E-01	PUS10	Pseudouridylate synthase 10	chr2p16.1	232945_at	NM_144709																				
2.16	2.07	0.09	5.18E-01	8.10E-01	LOC442028	hypothetical LOC442028	chr2q11.1	1561197_at	XR_017781 /// XR_039935 /// XR_039936																				
2.25	2.16	0.09	5.18E-01	8.10E-01	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif, 17	chr15q24	1552726_at	NM_139057																				
2.53	2.43	0.10	5.18E-01	8.10E-01	---	---	---	234537_at	---																				
2.81	2.66	0.15	5.18E-01	8.10E-01	COQ10B	Coenzyme Q10 homolog B (S. cerevisiae)	chr2q33.1	1561948_at	NM_025147																				
2.60	2.45	0.15	5.18E-01	8.10E-01	LOC100134017	hypothetical protein LOC100134017	---	217328_at	XM_001717113																				
4.87	4.60	0.27	5.18E-01	8.10E-01	ZNF140	zinc finger protein 140	chr12q24.32-q24.33	204523_at	NM_003440																				
5.84	5.62	0.22	5.19E-01	8.10E-01	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1	chr2q24.2	226668_at	NM_001128212 /// NM_001128213 /// NM_152528																				
6.29	6.07	0.23	5.19E-01	8.10E-01	TMEM149	transmembrane protein 149	chr19q13.12	219690_at	NM_024660																				
6.56	6.38	0.19	5.19E-01	8.10E-01	MICALL2	MICAL-like 2	chr7p22.3	219332_at	NM_182924																				
6.17	5.90	0.27	5.19E-01	8.10E-01	FAM89A	family with sequence similarity 89, member A	chr1q42.2	226448_at	NM_198552																				
4.61	4.32	0.29	5.19E-01	8.10E-01	CD37	CD37 molecule	chr19q13.3	204192_at	NM_001040031 /// NM_001774																				
3.46	3.36	0.11	5.19E-01	8.10E-01	ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	chr1q21-q23	1555380_at	NM_005099																				
6.18	6.08	0.10	5.19E-01	8.10E-01	MED8	mediator complex subunit 8	chr1p34.2	213696_s_at	NM_052877 /// NM_201542																				
2.99	2.89	0.10	5.19E-01	8.10E-01	LRRC15	leucine rich repeat containing 15	chr3q29	1552960_at	NM_130830																				
8.00	7.72	0.28	5.19E-01	8.10E-01	RBM39	RNA binding motif protein 39	chr20q11.22	208720_s_at	NM_004902 /// NM_184234																				
4.83	4.67	0.16	5.19E-01	8.10E-01	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1	chr2p25.1-p24.1	203763_at	NM_001012665 /// NM_015522 /// NM_016008																				
5.87	5.69	0.18	5.19E-01	8.10E-01	TP53BP2	tumor protein p53 binding protein, 2	chr1q42.1	203120_at	NM_001031685 /// NM_005426																				
2.58	2.48	0.10	5.19E-01	8.10E-01	KSR2	kinase suppressor of ras 2	chr12q24.22-q24.23	1553491_at	NM_173598																				
3.50	3.25	0.26	5.19E-01	8.10E-01	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	chr18p11.32	212569_at	NM_015295																				
3.10	3.02	0.08	5.19E-01	8.10E-01	---	---	---	1568754_at	---																				
2.19	2.12	0.08	5.19E-01	8.11E-01	C20orf66	chromosome 20 open reading frame 66	chr20q13.32	234798_x_at	XM_001716673 /// XM_001723936 /// XM_293121																				
5.14	4.97	0.17	5.19E-01	8.11E-01	PPCDC	phosphopantothenoylcysteine decarboxylase	chr15q24.2	219066_at	NM_021823																				
3.20	3.01	0.19	5.19E-01	8.11E-01	STX3	syntaxin 3	chr11q12.1	216985_s_at	NM_004177																				
6.37	6.12	0.25	5.20E-01	8.11E-01	PDE8A	phosphodiesterase 8A	chr15q25.3	212522_at	NM_002605 /// NM_173454																				

2.29	2.18	0.10	5.20E-01	8.11E-01	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	chr1p21	210441_at	NM_003672 /// NM_033312 /// NM_033313																				
3.97	3.84	0.13	5.20E-01	8.11E-01	---	---	---	1561619_at	---																				
5.82	5.64	0.18	5.20E-01	8.11E-01	SRPK1	SFRS protein kinase 1	chr6p21.3-p21.2	202200_s_at	NM_003137																				
4.57	4.45	0.11	5.20E-01	8.11E-01	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	chr17p13.2	1552768_at	NM_032294 /// NM_172206 /// NM_172207																				
4.27	4.13	0.14	5.20E-01	8.11E-01	FLJ31715	hypothetical protein FLJ31715	chr3p22.1	1553775_at	---																				
6.81	6.63	0.18	5.20E-01	8.11E-01	NCK2	NCK adaptor protein 2	chr2q12	203315_at	NM_001004720 /// NM_001004722 /// NM_003581																				
2.20	2.12	0.08	5.20E-01	8.11E-01	---	---	---	240989_at	---																				
5.53	5.39	0.15	5.20E-01	8.11E-01	ZNF579	zinc finger protein 579	chr19q13.42	229140_at	NM_152600																				
3.59	3.36	0.23	5.20E-01	8.11E-01	DEFA1 /// DEFA3 /// LOC728358	defensin, alpha 1 /// defensin, alpha 3, neutrophil-specific /// defensin, alpha 1	chr8p23.1 /// chr8pter-p23.3	205033_s_at	NM_001042500 /// NM_004084 /// NM_005217																				
2.35	2.25	0.09	5.20E-01	8.11E-01	---	---	---	232573_at	---																				
3.69	3.54	0.15	5.20E-01	8.11E-01	CASP8AP2	CASP8 associated protein 2	chr6q15	222201_s_at	NM_012115																				
4.66	4.54	0.12	5.20E-01	8.11E-01	TTPAL	tocopherol (alpha) transfer protein-like	chr20q13.12	219633_at	NM_001039199 /// NM_024331																				
2.65	2.54	0.11	5.20E-01	8.11E-01	TTC6	tetratricopeptide repeat domain 6	chr14q21.1	1556665_at	NM_001007795																				
4.45	4.24	0.21	5.20E-01	8.11E-01	LOC729810	hypothetical protein LOC729810	chr1q44	229200_at	XR_040839 /// XR_040840 /// XR_040841																				
2.66	2.54	0.12	5.20E-01	8.11E-01	ING2	Inhibitor of growth family, member 2	chr4q35.1	213544_at	NM_001564																				
2.42	2.35	0.07	5.20E-01	8.11E-01	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2	chr12q24.31	217603_at	NM_012463																				
2.32	2.24	0.08	5.20E-01	8.11E-01	---	---	---	1560946_at	---																				
3.00	2.87	0.12	5.20E-01	8.11E-01	hCG_17324	primary ciliary dyskinesia protein 1	chr2q14.2	231043_at	NM_001029996																				
2.27	2.18	0.09	5.20E-01	8.11E-01	CALCB	calcitonin-related polypeptide beta	chr11p15.2-p15.1	214636_at	NM_000728																				
3.80	3.68	0.12	5.20E-01	8.11E-01	KLHL22	kelch-like 22 (Drosophila)	chr22q11.21	221837_at	NM_032775																				
8.22	8.01	0.21	5.21E-01	8.11E-01	TSPAN7	tetraspanin 7	chrXp11.4	202242_at	NM_004615																				
1.98	1.89	0.09	5.21E-01	8.11E-01	---	---	---	1567281_at	---																				
6.90	6.67	0.23	5.21E-01	8.11E-01	PDE8A	phosphodiesterase 8A	chr15q25.3	212521_s_at	NM_002605 /// NM_173454																				
3.03	2.89	0.14	5.21E-01	8.11E-01	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	chr10q11.21	49306_at	NM_032023																				
2.34	2.22	0.12	5.21E-01	8.11E-01	---	---	---	1556239_a_at	---																				
4.00	3.88	0.12	5.21E-01	8.11E-01	---	---	---	236369_at	---																				
4.65	4.46	0.19	5.21E-01	8.11E-01	DLG5	discs, large homolog 5 (Drosophila)	chr10q23	210469_at	NM_004747																				
2.54	2.46	0.08	5.21E-01	8.11E-01	---	---	---	244664_at	---																				
3.36	3.21	0.14	5.21E-01	8.11E-01	HDAC4	histone deacetylase 4	chr2q37.3	1554322_a_at	NM_006037																				
3.56	3.41	0.15	5.21E-01	8.12E-01	---	---	---	240677_at	---																				
5.21	4.95	0.26	5.21E-01	8.12E-01	RBM25	RNA binding motif protein 25	chr14q24.3	212030_at	NM_021239																				
2.25	2.16	0.10	5.21E-01	8.12E-01	RYR3	ryanodine receptor 3	chr15q14-q15	206306_at	NM_001036																				
2.87	2.77	0.10	5.21E-01	8.12E-01	FGF18	fibroblast growth factor 18	chr5q34	206987_x_at	NM_003862																				
2.57	2.46	0.11	5.21E-01	8.12E-01	---	---	---	241873_at	---																				
2.40	2.29	0.12	5.21E-01	8.12E-01	C13orf38 /// SOHLH2	chromosome 13 open reading frame 38 /// spermatogenesis and oogenesis specific basic helix-loop-helix 2	chr13q13.3	233298_at	NM_017826 /// XM_001130109 /// XM_001133689 /// XM_001719885																				
2.97	2.84	0.12	5.22E-01	8.12E-01	RPUSD3	RNA pseudouridylate synthase domain containing 3	chr3p25.3	1566603_s_at	NM_173659																				
2.76	2.65	0.11	5.22E-01	8.12E-01	DHRS7	Dehydrogenase/reductase (SDR family) member 7	chr14q23.1	213868_s_at	NM_016029																				
2.09	2.01	0.07	5.22E-01	8.12E-01	GTPBP10	GTP-binding protein 10 (putative)	chr7q21.13	216619_at	NM_001042717 /// NM_033107																				
3.16	3.01	0.15	5.22E-01	8.12E-01	ZAN	zonadhesin	chr7q22	224263_x_at	NM_003386 /// NM_173059																				
2.40	2.30	0.10	5.22E-01	8.12E-01	SRrp35	serine-arginine repressor protein (35 kDa)	chr6q15	239295_at	NM_080743																				

2.04	1.96	0.07	5.22E-01	8.12E-01	CASC5	cancer susceptibility candidate 5	chr15q14	1552680_a_at	NM_144508 /// NM_170589																				
2.77	2.66	0.11	5.22E-01	8.12E-01	C6orf123	chromosome 6 open reading frame 123	chr6q27	207698_at	XR_039813 /// XR_039814 /// XR_039815																				
5.21	5.05	0.16	5.22E-01	8.12E-01	CDCA4	cell division cycle associated 4	chr14q32.33	218399_s_at	NM_017955 /// NM_145701																				
8.54	8.25	0.29	5.22E-01	8.12E-01	---	---	---	AFFX-M27830_5_at	---																				
9.11	9.00	0.11	5.22E-01	8.12E-01	GLTSCR2	glioma tumor suppressor candidate region gene 2	chr19q13.3	234339_s_at	NM_015710																				
6.61	6.49	0.12	5.22E-01	8.12E-01	---	---	---	225405_at	---																				
4.72	4.61	0.11	5.22E-01	8.12E-01	PMS2 /// PMS2CL	PMS2 postmeiotic segregation increased 2 (S. cerevisiae) /// PMS2 C-terminal like pseudogene	chr7p22.1 /// chr7p22.2	209805_at	NM_000535 /// NR_002217 /// NR_003085																				
6.28	6.06	0.22	5.22E-01	8.12E-01	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	chr12q23	221773_at	NM_005230																				
4.21	4.02	0.19	5.22E-01	8.12E-01	GLT25D2	glycosyltransferase 25 domain containing 2	chr1q25	209883_at	NM_015101																				
4.83	4.65	0.18	5.22E-01	8.12E-01	BIN3	bridging integrator 3	chr8p21.3	1557582_at	NM_018688																				
3.57	3.41	0.16	5.22E-01	8.12E-01	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	chr18q22.3	234977_at	NM_175907																				
6.70	6.50	0.20	5.22E-01	8.12E-01	TMEM38B	transmembrane protein 38B	chr9q31.2	222735_at	NM_018112																				
2.06	1.99	0.07	5.22E-01	8.12E-01	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4	deleted in azoospermia 1 /// deleted in azoospermia 2 /// deleted in azoospermia 3 /// deleted in azoospermia 4	chrYq11.223	216351_x_at	NM_001005375 /// NM_001005785 /// NM_001005786 /// NM_004081 /// NM_020363 /// NM_020364 /// NM_020420 /// XM_001718583																				
12.15	12.09	0.06	5.22E-01	8.12E-01	RPS13	ribosomal protein S13	chr11p15	200018_at	NM_001017																				
5.75	5.25	0.50	5.22E-01	8.12E-01	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	chr14q32	202510_s_at	NM_006291																				
2.62	2.53	0.09	5.22E-01	8.12E-01	---	---	---	240560_at	---																				
3.30	3.18	0.12	5.22E-01	8.12E-01	GRLF1	glucocorticoid receptor DNA binding factor 1	chr19q13.3	202046_s_at	NM_004491																				
2.36	2.27	0.09	5.23E-01	8.12E-01	ZNF670	zinc finger protein 670	chr1q44	223898_at	NM_033213																				
2.37	2.28	0.09	5.23E-01	8.12E-01	CUL2	cullin 2	chr10p11.21	203078_at	NM_003591																				
2.05	1.94	0.11	5.23E-01	8.12E-01	ZSWIM2	zinc finger, SWIM-type containing 2	chr2q32.1	1554932_at	NM_182521																				
5.81	5.62	0.19	5.23E-01	8.12E-01	C18orf55	chromosome 18 open reading frame 55	chr18q22.3	223181_at	NM_014177																				
2.45	2.36	0.09	5.23E-01	8.12E-01	---	---	---	1563118_at	---																				
12.45	12.36	0.09	5.23E-01	8.12E-01	RPS4X	ribosomal protein S4, X-linked	chrXq13.1	200933_x_at	NM_001007																				
3.50	3.28	0.22	5.23E-01	8.12E-01	---	---	---	237413_at	---																				
3.98	3.69	0.29	5.23E-01	8.12E-01	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	chr4q12	212853_at	NM_001040402 /// NM_015115																				
3.16	3.05	0.11	5.23E-01	8.12E-01	---	---	---	1566903_at	---																				
2.54	2.42	0.12	5.23E-01	8.12E-01	UBR4	ubiquitin protein ligase E3 component n-recognin 4	chr1p36.13	1563113_at	NM_020765																				
6.46	6.26	0.19	5.23E-01	8.12E-01	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	chr19q13.4	210644_s_at	NM_002287 /// NM_021706																				
2.80	2.63	0.16	5.23E-01	8.12E-01	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	chr2p22.1	1554453_at	NM_138394																				
2.23	2.15	0.09	5.23E-01	8.12E-01	---	---	---	241660_at	---																				
2.42	2.32	0.10	5.23E-01	8.12E-01	PARK2	Parkinson disease (autosomal recessive, juvenile) 2, parkin	chr6q25.2-q27	1554855_at	NM_004562 /// NM_013987 /// NM_013988																				
3.50	3.40	0.10	5.23E-01	8.12E-01	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	chr20p13	235993_at	NM_006814 /// NM_178578																				

2.28	2.21	0.07	5.23E-01	8.12E-01	DKFZp547E087 /// LOC100132247 /// LOC23117 /// LOC348162 /// LOC440345 /// LOC440350 /// LOC641298 /// LOC642799 /// LOC729602 /// LOC729978 /// LOC730153	hypothetical gene LOC283846 /// similar to Uncharacterized protein KIAA0220 /// KIAA0220-like protein /// hypothetical protein 348162 /// hypothetical protein LOC440345 /// similar to nuclear pore complex interacting protein /// PI-3-kinase-related kinase SMG-1 /// hypothetical LOC642799 /// similar to nuclear pore complex interacting protein /// NPIP-like protein 2 /// hypothetical LOC730153	chr16p11.2 /// chr16p12.1 /// chr16p12.2 /// chr16p13.11 /// chr16p13.13 /// chr18p11.21	215002_at	NM_001018122 /// NM_130464 /// XM_001713614 /// XM_001717235 /// XM_001717676 /// XM_001720898 /// XM_001720909 /// XM_001720910 /// XM_001723013 /// XM_001723016 /// XM_001724791 /// XM_001732844 /// XM_001732845 /// XM_496136 /// XM_931802 /// XM_931808 /// XM_931814 /// XM_931818 /// XM_931827 /// XM_931837 /// XM_931840 /// XR_015786 /// XR_016550 /// XR_041850																					
4.00	3.58	0.42	5.23E-01	8.12E-01	SOX9	SRY (sex determining region Y)-box 9	chr17q24.3-q25.1	202935_s_at	NM_000346																				
2.33	2.23	0.11	5.23E-01	8.13E-01	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	chr2p15	224154_at	NM_006577																				
3.05	2.98	0.08	5.23E-01	8.13E-01	LOC100128079	Hypothetical protein LOC100128079	chr16p11.2	243053_x_at	XM_001720212 /// XM_001724906 /// XM_001725467																				
2.73	2.62	0.11	5.23E-01	8.13E-01	LOC100127983	hypothetical protein LOC100127983	chr8q21.3	1557961_s_at	XM_001722508 /// XM_001722530 /// XM_001722571																				
4.72	4.59	0.13	5.23E-01	8.13E-01	SPAG16	sperm associated antigen 16	chr2q34	219109_at	NM_001025436 /// NM_024532																				
2.01	1.92	0.09	5.23E-01	8.13E-01	LOC441666	similar to zinc finger protein 99	chr10q11.21	1559503_a_at	XR_036880 /// XR_036934 /// XR_037702																				
7.64	7.51	0.13	5.23E-01	8.13E-01	ASNA1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	chr19q13.3	202024_at	NM_004317																				

2.19	2.10	0.09	5.23E-01	8.13E-01	FAM149B1	family with sequence similarity 149, member B1	chr10q22.2	213458_at	NM_173348 /// XM_001721910 /// XM_001722273 /// XM_001723052																			
7.19	6.97	0.22	5.23E-01	8.13E-01	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	chr12p13.1-p12	209112_at	NM_004064																			
7.11	6.98	0.13	5.24E-01	8.13E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	214894_x_at	NM_012090 /// NM_033044																			
7.45	7.29	0.15	5.24E-01	8.13E-01	UNC84B	unc-84 homolog B (C. elegans)	chr22q13.1	212144_at	NM_015374																			
4.93	4.75	0.18	5.24E-01	8.13E-01	HABP4	hyaluronan binding protein 4	chr9q22.3-q31	232341_x_at	NM_014282																			
2.31	2.24	0.07	5.24E-01	8.13E-01	---	---	---	1561545_at	---																			
2.62	2.53	0.09	5.24E-01	8.13E-01	FLJ42957	FLJ42957 protein	chr12q24.22	1563369_at	NM_207436																			
3.12	3.02	0.10	5.24E-01	8.13E-01	---	---	---	1562589_at	---																			
2.36	2.27	0.09	5.24E-01	8.13E-01	A2ML1	alpha-2-macroglobulin-like 1	chr12p13.31	1564307_a_at	NM_144670																			
2.68	2.56	0.12	5.24E-01	8.13E-01	FCAR	Fc fragment of IgA, receptor for	chr19q13.2-q13.4	211307_s_at	NM_002000 /// NM_133269 /// NM_133271 /// NM_133272 /// NM_133273 /// NM_133274 /// NM_133277 /// NM_133278 /// NM_133279																			
6.17	6.01	0.16	5.24E-01	8.13E-01	PRELP	proline/arginine-rich end leucine-rich repeat protein	chr1q32	37022_at	NM_002725 /// NM_201348																			
1.84	1.77	0.07	5.24E-01	8.13E-01	---	---	---	1561765_at	---																			
2.83	2.75	0.08	5.24E-01	8.13E-01	KCNK15	Potassium channel, subfamily K, member 15	chr20q12-q13	1560620_at	NM_022358																			
4.54	4.11	0.43	5.24E-01	8.13E-01	HOXB6	homeobox B6	chr17q21.3	205366_s_at	NM_018952																			
7.15	6.98	0.17	5.24E-01	8.13E-01	CPNE1	copine I	chr20q11.22	206918_s_at	NM_003915 /// NM_152925 /// NM_152926 /// NM_152927 /// NM_152928 /// NM_152929 /// NM_152930 /// NM_152931																			
2.14	2.04	0.10	5.24E-01	8.13E-01	---	---	---	237673_at	---																			
3.84	3.68	0.16	5.24E-01	8.13E-01	EHBP1L1	EH domain binding protein 1-like 1	chr11q13.1	91703_at	NM_001099409																			
7.11	6.95	0.16	5.24E-01	8.13E-01	CORO1C	coronin, actin binding protein, 1C	chr12q24.1	222409_at	NM_014325																			
3.07	2.97	0.10	5.24E-01	8.13E-01	IL19	interleukin 19	chr1q32.2	220745_at	NM_013371 /// NM_153758																			
2.45	2.37	0.08	5.24E-01	8.13E-01	---	---	---	1557398_at	---																			
6.80	6.64	0.16	5.24E-01	8.13E-01	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	chr10q24.32	200721_s_at	NM_005736																			
3.60	3.47	0.13	5.24E-01	8.13E-01	BEX5	BEX family member 5	chrXq22.1	229963_at	NM_001012978																			
5.51	5.29	0.22	5.24E-01	8.13E-01	SYK	spleen tyrosine kinase	chr9q22	226068_at	NM_003177																			
5.36	5.02	0.34	5.24E-01	8.13E-01	PNKD	paroxysmal nonkinesigenic dyskinesia	chr2q35	233177_s_at	NM_001077399 /// NM_015488 /// NM_022572																			
2.70	2.58	0.12	5.25E-01	8.13E-01	LOC339894	hypothetical protein LOC339894	chr3q25.31	1561402_at	---																			
2.83	2.72	0.10	5.25E-01	8.13E-01	---	---	---	234449_at	---																			

4.96	4.83	0.14	5.25E-01	8.13E-01	---	---	---	238887_at	---
4.78	4.61	0.17	5.25E-01	8.13E-01	---	---	---	240478_at	---
5.54	5.22	0.32	5.25E-01	8.14E-01	GIMAP1	GTPase, IMAP family member 1	chr7q36.1	1552316_a_at	NM_130759
3.97	3.85	0.13	5.25E-01	8.14E-01	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	chr7q36	211534_x_at	NM_002847 /// NM_130842 /// NM_130843
2.93	2.79	0.14	5.25E-01	8.14E-01	C3orf22	chromosome 3 open reading frame 22	chr3q21.3	237894_at	NM_152533
5.54	5.41	0.12	5.25E-01	8.14E-01	KLHDC4	kelch domain containing 4	chr16q24.3	221219_s_at	NM_017566
3.47	3.32	0.14	5.25E-01	8.14E-01	GDF11	growth differentiation factor 11	chr12q13.2	216860_s_at	NM_005811
2.34	2.23	0.11	5.25E-01	8.14E-01	---	---	---	1557522_x_at	---
2.83	2.74	0.09	5.25E-01	8.14E-01	MGC12916	hypothetical protein MGC12916	chr17p11.2	238664_s_at	---
3.36	3.18	0.17	5.25E-01	8.14E-01	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	chr22q13.1	205159_at	NM_000395
2.87	2.59	0.27	5.25E-01	8.14E-01	C8orf4	chromosome 8 open reading frame 4	chr8p11.2	218541_s_at	NM_020130
2.02	1.94	0.07	5.25E-01	8.14E-01	STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	chr15q24.1	1569334_at	NM_022369
3.34	3.24	0.10	5.25E-01	8.14E-01	---	---	---	1556075_at	---
3.96	3.84	0.13	5.25E-01	8.14E-01	---	---	---	242651_at	---
7.08	6.95	0.13	5.25E-01	8.14E-01	RHOT2	ras homolog gene family, member T2	chr16p13.3	222131_x_at	NM_138769
3.00	2.88	0.12	5.25E-01	8.14E-01	AZU1	azurocidin 1	chr19p13.3	214575_s_at	NM_001700
2.21	2.14	0.07	5.26E-01	8.14E-01	---	---	---	1564802_at	---
4.49	4.35	0.14	5.26E-01	8.14E-01	IQCG	IQ motif containing G	chr3q29	229161_at	NM_001134435 /// NM_032263
2.04	1.96	0.08	5.26E-01	8.14E-01	ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	chr5q35.1-q35.2	224024_at	NM_001031711 /// NM_020462
6.92	6.67	0.24	5.26E-01	8.14E-01	SPON2	spondin 2, extracellular matrix protein	chr4p16.3	218638_s_at	NM_001128325 /// NM_012445
2.05	1.98	0.07	5.26E-01	8.14E-01	---	---	---	243979_at	---
5.34	5.22	0.12	5.26E-01	8.14E-01	TPCN2	two pore segment channel 2	chr11q13.2	229251_s_at	NM_139075
7.20	7.01	0.19	5.26E-01	8.14E-01	CIDEB	cell death-inducing DFFA-like effector b	chr14q12	221188_s_at	NM_014430
3.53	3.44	0.09	5.26E-01	8.14E-01	GAFA2	FGF-2 activity-associated protein 2	chr16q23.2	1555645_at	XM_001725248 /// XM_001725329 /// XM_001726850
4.00	3.85	0.15	5.26E-01	8.14E-01	GOSR2	Golgi SNAP receptor complex member 2	chr17q21	239159_at	NM_001012511 /// NM_004287 /// NM_054022
2.14	2.06	0.07	5.26E-01	8.14E-01	---	---	---	243319_at	---
4.64	4.31	0.33	5.26E-01	8.14E-01	MAN1A1	mannosidase, alpha, class 1A, member 1	chr6q22	208116_s_at	NM_005907
6.50	6.39	0.11	5.26E-01	8.14E-01	MAP2K3	mitogen-activated protein kinase kinase 3	chr17q11.2	207667_s_at	NM_002756 /// NM_145109
2.50	2.40	0.09	5.26E-01	8.14E-01	ARSE	arylsulfatase E (chondrodysplasia punctata 1)	chrXp22.3	205894_at	NM_000047
6.85	6.71	0.14	5.26E-01	8.14E-01	41523	septin 6	chrXq24	212413_at	NM_015129 /// NM_145799 /// NM_145800 /// NM_145802
3.13	3.02	0.12	5.26E-01	8.14E-01	---	---	---	237892_at	---
4.21	4.04	0.18	5.26E-01	8.14E-01	DIS3L2	DIS3 mitotic control homolog (S. cerevisiae)-like 2	chr2q37.1	238602_at	NM_152383
2.48	2.39	0.09	5.26E-01	8.14E-01	---	---	---	240378_at	---
5.03	4.81	0.22	5.26E-01	8.14E-01	NAIF1	nuclear apoptosis inducing factor 1	chr9q34.11	227825_at	NM_197956
5.58	5.45	0.13	5.26E-01	8.14E-01	PRMT7	protein arginine methyltransferase 7	chr16q22.1	219408_at	NM_019023
2.35	2.27	0.08	5.26E-01	8.14E-01	NSBP1	nucleosomal binding protein 1	chrXq13.3	221238_at	NM_030763
3.37	3.20	0.17	5.27E-01	8.14E-01	---	---	---	241735_at	---
2.88	2.74	0.14	5.27E-01	8.14E-01	---	---	---	240295_at	---
2.29	2.19	0.10	5.27E-01	8.14E-01	ROBO2	roundabout, axon guidance receptor, homolog 2 (Drosophila)	chr3p12.3	226709_at	NM_001128929 /// NM_002942
6.20	5.95	0.25	5.27E-01	8.14E-01	RYK	RYK receptor-like tyrosine kinase	chr3q22	216976_s_at	NM_001005861 /// NM_002958
5.89	5.72	0.17	5.27E-01	8.14E-01	LDLRAP1	low density lipoprotein receptor adaptor protein 1	chr1p36-p35	221790_s_at	NM_015627
6.43	6.28	0.15	5.27E-01	8.14E-01	UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	chr14q32.12	218108_at	NM_001100417 /// NM_175748
2.57	2.48	0.09	5.27E-01	8.14E-01	---	---	---	239817_at	---

2.56	2.49	0.07	5.27E-01	8.14E-01	ANUBL1	AN1, ubiquitin-like, homolog (Xenopus laevis)	chr10q11.21	244206_at	NM_001128324 /// NM_174890
5.16	5.03	0.13	5.27E-01	8.14E-01	MPDZ	multiple PDZ domain protein	chr9p24-p22	213306_at	NM_003829
5.28	5.07	0.21	5.27E-01	8.14E-01	SPIRE1	spire homolog 1 (Drosophila)	chr18p11.21	1554807_a_at	NM_001128626 /// NM_001128627 /// NM_020148
2.64	2.55	0.09	5.27E-01	8.14E-01	PDE10A	phosphodiesterase 10A	chr6q26	211171_s_at	NM_001130690 /// NM_006661
4.58	4.42	0.16	5.27E-01	8.14E-01	LRRC20	leucine rich repeat containing 20	chr10q22.1	218550_s_at	NM_018205 /// NM_018239 /// NM_207119
2.35	2.25	0.10	5.27E-01	8.14E-01	---	---	---	1563015_at	---
2.41	2.29	0.12	5.27E-01	8.14E-01	---	---	---	215934_at	---
3.73	3.58	0.15	5.27E-01	8.14E-01	BMS1P5 /// CTGLF1 /// CTGLF6 /// CTGLF7	BMS1 pseudogene 5 /// centaurin, gamma-like family, member 1 /// centaurin, gamma-like family, member 6 /// centaurin, gamma-like family, member 7	chr10q11.21 /// chr10q11.22	242393_x_at	NM_133446 /// NR_003611 /// XM_001714786 /// XM_001716810
5.36	5.18	0.18	5.27E-01	8.14E-01	STK10	serine/threonine kinase 10	chr5q35.1	203047_at	NM_005990
2.37	2.28	0.09	5.27E-01	8.14E-01	SOX11	SRY (sex determining region Y)-box 11	chr2p25	204914_s_at	NM_003108
2.12	2.02	0.10	5.27E-01	8.14E-01	---	---	---	242544_x_at	---
2.04	1.96	0.08	5.27E-01	8.15E-01	LOC57399	uncharacterized gastric protein ZA52P	chr5q12.1	220893_at	XM_926542 /// XM_938963
2.64	2.56	0.08	5.27E-01	8.15E-01	---	---	---	1557025_a_at	---
4.62	4.41	0.21	5.27E-01	8.15E-01	DCHS1	dachsous 1 (Drosophila)	chr11p15.4	222101_s_at	NM_003737
5.97	5.63	0.35	5.27E-01	8.15E-01	JUN	jun oncogene	chr1p32-p31	201465_s_at	NM_002228
5.11	4.91	0.21	5.27E-01	8.15E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	212262_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855
2.84	2.75	0.09	5.28E-01	8.15E-01	ZBTB37	zinc finger and BTB domain containing 37	chr1q25.1	231547_at	NM_001122770 /// NM_032522
10.45	10.25	0.20	5.28E-01	8.15E-01	NAP1L1	nucleosome assembly protein 1-like 1	chr12q21.2	213864_s_at	NM_004537 /// NM_139207
2.86	2.74	0.11	5.28E-01	8.15E-01	C7orf16	Chromosome 7 open reading frame 16	chr7p15	231509_at	NM_006658
2.61	2.52	0.09	5.28E-01	8.15E-01	ARHGAP26	Rho GTPase activating protein 26	chr5q31	215955_x_at	NM_015071
8.98	8.89	0.09	5.28E-01	8.15E-01	H2AFY	H2A histone family, member Y	chr5q31.3-q32	207168_s_at	NM_001040158 /// NM_004893 /// NM_138609 /// NM_138610
3.05	2.93	0.12	5.28E-01	8.15E-01	ZNF540	zinc finger protein 540	chr19q13.12	238454_at	NM_152606
8.79	8.64	0.15	5.28E-01	8.15E-01	ARF4	ADP-ribosylation factor 4	chr3p21.2-p21.1	201096_s_at	NM_001660
4.24	4.16	0.08	5.28E-01	8.15E-01	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	chr20q13.33	232787_at	NM_001037335 /// NM_033405
3.26	3.16	0.09	5.28E-01	8.15E-01	---	---	---	232255_at	---
7.24	7.11	0.13	5.28E-01	8.15E-01	RNF38	ring finger protein 38	chr9p13	218528_s_at	NM_022781 /// NM_194328 /// NM_194329 /// NM_194330 /// NM_194332

4.35	4.24	0.11	5.28E-01	8.15E-01	TNNT3	troponin T type 3 (skeletal, fast)	chr11p15.5	1569986_x_at	NM_001042780 /// NM_001042781 /// NM_001042782 /// NM_006757																				
2.31	2.22	0.10	5.28E-01	8.15E-01	KIAA0748	KIAA0748	chr12q13.2	219724_s_at	NM_001098815																				
6.10	5.94	0.16	5.28E-01	8.15E-01	LOC100134190 /// LRP1	similar to low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) /// low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	chr12q13-q14	200785_s_at	NM_002332 /// XR_037669																				
2.10	2.01	0.09	5.28E-01	8.15E-01	C1orf145	chromosome 1 open reading frame 145	chr1q42.13	1560130_at	NM_001025495																				
3.71	3.51	0.20	5.28E-01	8.15E-01	NINJ2	ninjurin 2	chr12p13	219594_at	NM_016533																				
2.26	2.18	0.08	5.28E-01	8.15E-01	---	---	---	243932_at	---																				
6.80	6.53	0.27	5.28E-01	8.15E-01	PDHX	pyruvate dehydrogenase complex, component X	chr11p13	203067_at	NM_003477																				
2.37	2.26	0.11	5.29E-01	8.15E-01	---	---	---	220682_s_at	---																				
2.79	2.69	0.10	5.29E-01	8.15E-01	---	---	---	234222_at	---																				
4.48	4.33	0.15	5.29E-01	8.15E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	210984_x_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284																				
12.28	12.21	0.06	5.29E-01	8.15E-01	RPL34	ribosomal protein L34	chr4q25	200026_at	NM_000995 /// NM_033625																				
2.38	2.30	0.08	5.29E-01	8.16E-01	---	---	---	1556221_a_at	---																				
2.70	2.60	0.10	5.29E-01	8.16E-01	BCL10	B-cell CLL/lymphoma 10	chr1p22	1557258_a_at	NM_003921																				
2.63	2.52	0.11	5.29E-01	8.16E-01	TMEM144	transmembrane protein 144	chr4q32.1	219750_at	NM_018342																				
2.59	2.47	0.11	5.29E-01	8.16E-01	PIGG	Phosphatidylinositol glycan anchor biosynthesis, class G	chr4p16.3	231692_at	NM_001127178 /// NM_017733																				
3.21	3.10	0.12	5.29E-01	8.16E-01	---	---	---	229979_x_at	---																				
2.33	2.24	0.08	5.29E-01	8.16E-01	EPHA4	EPH receptor A4	chr2q36.1	238671_at	NM_004438																				
9.22	9.09	0.12	5.29E-01	8.16E-01	KRTCAP2	keratinocyte associated protein 2	chr1q22	224885_s_at	NM_173852																				
4.18	4.03	0.15	5.29E-01	8.16E-01	TBC1D2	TBC1 domain family, member 2	chr9q22.33	222173_s_at	NM_018421																				
6.81	6.68	0.13	5.29E-01	8.16E-01	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	chr12q13.11-q13.3	223684_s_at	NM_014311																				
7.08	6.93	0.15	5.29E-01	8.16E-01	EDNRB	endothelin receptor type B	chr13q22	204271_s_at	NM_000115 /// NM_001122659 /// NM_003991																				
2.05	1.98	0.07	5.29E-01	8.16E-01	LOC100133572 /// LOC650293 /// OR7E87P /// UNC93B2	similar to seven transmembrane helix receptor /// seven transmembrane helix receptor /// olfactory receptor, family 7, subfamily E, member 87 pseudogene /// unc-93 homolog B2 pseudogene (C. elegans)	chr11q13 /// chr7p22.1	215770_at	NM_001040071 /// XR_037209 /// XR_037560 /// XR_037638 /// XR_038242																				
9.00	8.78	0.22	5.29E-01	8.16E-01	VCAM1	vascular cell adhesion molecule 1	chr1p32-p31	203868_s_at	NM_001078 /// NM_080682																				
2.28	2.18	0.10	5.29E-01	8.16E-01	---	---	---	1561462_at	---																				
2.55	2.43	0.12	5.30E-01	8.16E-01	FAM118B	family with sequence similarity 118, member B	chr11q24.2	239318_at	NM_024556																				
3.36	3.26	0.10	5.30E-01	8.16E-01	ARHGAP5	Rho GTPase activating protein 5	chr14q12	235635_at	NM_001030055 /// NM_001173																				
6.69	6.49	0.20	5.30E-01	8.16E-01	STYXL1	serine/threonine/tyrosine interacting-like 1	chr7q11.23	232353_s_at	NM_016086																				
3.93	3.77	0.16	5.30E-01	8.16E-01	RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	chr12q13.1	210051_at	NM_001098531 /// NM_001098532 /// NM_006105																				
2.39	2.28	0.11	5.30E-01	8.16E-01	---	---	---	238620_at	---																				
2.13	2.06	0.07	5.30E-01	8.16E-01	---	---	---	244507_at	---																				

1.82	1.75	0.07	5.30E-01	8.16E-01	GRIA4	glutamate receptor, ionotrophic, AMPA 4	chr11q22	1569178_at	NM_000829 /// NM_001077243 /// NM_001077244 /// NM_001112812																				
4.19	4.09	0.10	5.30E-01	8.16E-01	ZMIZ2	zinc finger, MIZ-type containing 2	chr7p13	236309_x_at	NM_031449 /// NM_174929																				
1.93	1.86	0.07	5.30E-01	8.16E-01	TMPO	thymopoietin	chr12q22	237863_at	NM_001032283 /// NM_001032284 /// NM_003276																				
4.25	4.15	0.10	5.30E-01	8.16E-01	KIF18B	kinesin family member 18B	chr17q21.31	222039_at	NM_001080443																				
3.29	3.18	0.11	5.30E-01	8.16E-01	EPHB3	EPH receptor B3	chr3q21-qter	1438_at	NM_004443																				
2.21	2.14	0.07	5.30E-01	8.16E-01	UBXN4	UBX domain protein 4	chr2q21.3	1562741_at	NM_014607																				
8.62	8.41	0.21	5.30E-01	8.16E-01	C1R	complement component 1, r subcomponent	chr12p13	212067_s_at	NM_001733																				
2.14	2.04	0.10	5.30E-01	8.16E-01	KIAA1632	KIAA1632	chr18q12.3-q21.1	232030_at	NM_020964																				
3.12	3.00	0.13	5.30E-01	8.16E-01	---	---	---	1561749_at	---																				
2.29	2.22	0.07	5.30E-01	8.16E-01	NLRP11	NLR family, pyrin domain containing 11	chr19q13.42	1552531_a_at	NM_145007																				
2.22	2.15	0.07	5.30E-01	8.16E-01	---	---	---	1556678_a_at	---																				
2.99	2.86	0.13	5.30E-01	8.16E-01	ZNF678	Zinc finger protein 678	chr1q42.13	242923_at	NM_178549																				
5.73	5.47	0.26	5.30E-01	8.16E-01	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	chr3q29	202166_s_at	NM_006241																				
3.47	3.34	0.13	5.31E-01	8.16E-01	LOC100130417	similar to hCG1995469	---	1555980_a_at	XM_001714163 /// XM_001718964																				
3.84	3.74	0.10	5.31E-01	8.16E-01	DKFZp547J222	hypothetical LOC84237	chr4p15.33	234769_at	---																				
5.29	5.19	0.10	5.31E-01	8.16E-01	SF3B3	splicing factor 3b, subunit 3, 130kDa	chr16q22.1	200688_at	NM_012426																				
7.16	6.96	0.19	5.31E-01	8.16E-01	FUSIP1 /// LOC642558	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1	chr1p36.11	206095_s_at	NM_006625 /// NM_054016 /// XM_001713958 /// XM_001713979																				
3.46	3.32	0.13	5.31E-01	8.16E-01	STK33	serine/threonine kinase 33	chr11p15.3	228035_at	NM_030906																				
1.95	1.87	0.07	5.31E-01	8.16E-01	---	---	---	240433_x_at	---																				
2.16	2.09	0.07	5.31E-01	8.16E-01	---	---	---	1559009_at	---																				
2.93	2.81	0.11	5.31E-01	8.16E-01	---	---	---	242990_at	---																				
6.07	5.95	0.11	5.31E-01	8.17E-01	C18orf10	chromosome 18 open reading frame 10	chr18q12.2	213616_at	NM_015476																				
6.55	6.46	0.10	5.31E-01	8.17E-01	SLC25A26	solute carrier family 25, member 26	chr3p14.1	225862_at	NM_173471																				
2.77	2.71	0.06	5.31E-01	8.17E-01	LOC100101118 /// TTTY8	testis-specific transcript, Y-linked 8-like /// testis-specific transcript, Y-linked 8	chrYp11.2	224143_at	NR_001533 /// NR_003591																				
2.92	2.82	0.10	5.31E-01	8.17E-01	---	---	---	237789_at	---																				
2.13	2.06	0.08	5.31E-01	8.17E-01	---	---	---	239486_at	---																				
2.08	2.01	0.07	5.31E-01	8.17E-01	LOC254312	hypothetical LOC254312	chr10p14	231421_at	XM_001720442 /// XM_001723502 /// XM_001725214																				
6.07	5.87	0.20	5.31E-01	8.17E-01	GFPT1	glutamine-fructose-6-phosphate transaminase 1	chr2p13	202722_s_at	NM_002056																				
7.19	7.04	0.15	5.31E-01	8.17E-01	SNN	stannin	chr16p13	218032_at	NM_003498																				
3.93	3.79	0.15	5.31E-01	8.17E-01	MBTD1	mbt domain containing 1	chr17q21.33	226797_at	NM_017643																				
3.55	3.39	0.16	5.31E-01	8.17E-01	SLC2A11	solute carrier family 2 (facilitated glucose transporter), member 11	chr22q11.2	221262_s_at	NM_001024938 /// NM_001024939 /// NM_030807																				
4.88	4.70	0.18	5.31E-01	8.17E-01	SIPA1L1	Signal-induced proliferation-associated 1 like 1	chr14q24.2	202254_at	NM_015556																				
6.87	6.68	0.19	5.31E-01	8.17E-01	EFHA1	EF-hand domain family, member A1	chr13q12.11	212410_at	NM_152726																				
5.99	5.76	0.22	5.31E-01	8.17E-01	KIAA0515	KIAA0515	chr9q34.13	212069_s_at	NM_013318																				
2.05	1.97	0.08	5.31E-01	8.17E-01	---	---	---	238537_at	---																				
4.61	4.40	0.21	5.31E-01	8.17E-01	FRMD4A	FERM domain containing 4A	chr10p13	225168_at	NM_018027																				
2.38	2.29	0.08	5.32E-01	8.17E-01	---	---	---	241002_at	---																				
1.79	1.73	0.06	5.32E-01	8.17E-01	UBE2CBP	ubiquitin-conjugating enzyme E2C binding protein	chr6q14.1	1569262_x_at	NM_198920																				
11.89	11.82	0.07	5.32E-01	8.17E-01	ACTG1	actin, gamma 1	chr17q25	201550_x_at	NM_001614																				
5.50	5.30	0.19	5.32E-01	8.17E-01	DUSP3	dual specificity phosphatase 3	chr17q21	201537_s_at	NM_004090																				

3.35	3.23	0.11	5.32E-01	8.17E-01	DKFZP434B2016 /// LOC643313	similar to hypothetical protein LOC284701 /// similar to hypothetical protein LOC284701	chr16q24.3 /// chr1p36.33	211050_x_at	XM_932064 /// XM_932068 /// XM_932075 /// XM_933030 /// XM_933033 /// XM_933038 /// XM_933043																				
3.17	3.06	0.11	5.32E-01	8.17E-01	HIST1H1D	histone cluster 1, H1d	chr6p21.3	214537_at	NM_005320																				
2.32	2.21	0.10	5.32E-01	8.17E-01	MRPS18C	mitochondrial ribosomal protein S18C	chr4q21.23	220103_s_at	NM_016067																				
2.36	2.27	0.09	5.32E-01	8.17E-01	---	---	---	1559151_at	---																				
6.65	6.54	0.11	5.32E-01	8.17E-01	SSNA1	Sjogren syndrome nuclear autoantigen 1	chr9q34.3	210378_s_at	NM_003731																				
3.97	3.80	0.17	5.32E-01	8.17E-01	LOC90379	hypothetical protein BC002926	chr19p13.12	221849_s_at	NM_138353																				
3.89	3.75	0.14	5.32E-01	8.17E-01	GJB3	gap junction protein, beta 3, 31kDa	chr1p34	205490_x_at	NM_001005752 /// NM_024009																				
2.51	2.40	0.11	5.32E-01	8.17E-01	PSG4	pregnancy specific beta-1-glycoprotein 4	chr19q13.2	1568999_at	NM_002780 /// NM_213633																				
2.01	1.93	0.07	5.32E-01	8.17E-01	---	---	---	237435_at	---																				
3.61	3.53	0.08	5.32E-01	8.17E-01	C6orf106	chromosome 6 open reading frame 106	chr6p21.31	205457_at	NM_022758 /// NM_024294																				
3.24	3.08	0.16	5.32E-01	8.17E-01	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	chr8q21.11	222656_at	NM_001001481 /// NM_018299																				
3.01	2.86	0.15	5.33E-01	8.18E-01	FLJ40292	hypothetical LOC643210	chr9q34.3	1559311_at	XR_041801 /// XR_041802 /// XR_041803																				
4.20	4.07	0.13	5.33E-01	8.18E-01	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	chr15q22	206081_at	NM_004727																				
3.03	2.92	0.10	5.33E-01	8.18E-01	ATP11B	ATPase, class VI, type 11B	chr3q27	1554556_a_at	NM_014616																				
5.16	4.92	0.24	5.33E-01	8.18E-01	KSR1	Kinase suppressor of ras 1	chr17q11.1	235252_at	NM_014238																				
2.32	2.20	0.12	5.33E-01	8.18E-01	OFD1	oral-facial-digital syndrome 1	chrXp22	241751_at	NM_003611																				
6.80	6.62	0.18	5.33E-01	8.18E-01	TMEM41B	transmembrane protein 41B	chr11p15.4	212622_at	NM_015012																				
2.52	2.45	0.07	5.33E-01	8.18E-01	FARP2	FERM, RhoGEF and pleckstrin domain protein 2	chr2q37.3	1558855_at	NM_014808																				
2.00	1.91	0.09	5.33E-01	8.18E-01	BTF3	Basic transcription factor 3	chr5q13.2	243165_at	NM_001037637 /// NM_001207																				
3.07	2.97	0.11	5.33E-01	8.18E-01	PRB3	proline-rich protein BstNI subfamily 3	chr12p13.2	206998_x_at	NM_006249																				
7.36	7.24	0.11	5.33E-01	8.18E-01	PDPK1	3-phosphoinositide dependent protein kinase-1	chr16p13.3	224986_s_at	NM_002613 /// NM_031268																				
3.57	3.47	0.10	5.33E-01	8.18E-01	---	---	---	236546_at	---																				
4.80	4.64	0.16	5.33E-01	8.18E-01	ESPNL	espin-like	chr2q37.3	1557000_at	NM_194312																				
2.15	2.06	0.09	5.33E-01	8.18E-01	CXorf58	chromosome X open reading frame 58	chrXp22.11	1553391_at	NM_152761																				
7.05	6.87	0.18	5.33E-01	8.18E-01	WIBG	within bgcn homolog (Drosophila)	chr12q13.2	224465_s_at	NM_032345																				
8.80	8.62	0.18	5.34E-01	8.18E-01	ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	chrXp11.4	201443_s_at	NM_005765																				
3.20	3.09	0.11	5.34E-01	8.18E-01	OPRL1	opiate receptor-like 1	chr20q13.33	206563_s_at	NM_000913 /// NM_182647																				
2.39	2.32	0.07	5.34E-01	8.18E-01	---	---	---	234615_at	---																				
4.69	4.60	0.10	5.34E-01	8.18E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	1569073_x_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072																				
2.41	2.32	0.09	5.34E-01	8.18E-01	ZMYND17	zinc finger, MYND-type containing 17	chr10q22.2	241793_at	NM_001024593																				
2.35	2.28	0.07	5.34E-01	8.18E-01	MSRA	Methionine sulfoxide reductase A	chr8p23.1	240031_at	NM_012331																				

2.80	2.68	0.13	5.34E-01	8.18E-01	ZMYM5	zinc finger, MYM-type 5	chr13q12	206652_at	NM_001039649 /// NM_001039650
2.32	2.23	0.09	5.34E-01	8.18E-01	CYLC1	cylicin, basic protein of sperm head cytoskeleton 1	chrXq21.1	216809_at	NM_021118
7.41	7.24	0.17	5.34E-01	8.18E-01	BRD4	bromodomain containing 4	chr19p13.1	226052_at	NM_014299 /// NM_058243
2.91	2.83	0.09	5.34E-01	8.18E-01	---	---	---	1560952_at	---
2.09	2.00	0.10	5.34E-01	8.18E-01	STOM	stomatin	chr9q34.1	201062_at	NM_004099 /// NM_198194
1.86	1.80	0.06	5.34E-01	8.18E-01	---	---	---	1556220_at	---
2.38	2.24	0.14	5.34E-01	8.18E-01	EFHA2	EF-hand domain family, member A2	chr8p22	238458_at	NM_181723
2.35	2.27	0.07	5.34E-01	8.18E-01	C1orf187	chromosome 1 open reading frame 187	chr1p36.22	1556826_s_at	NM_198545
4.12	4.01	0.12	5.34E-01	8.18E-01	BCAN	Brevican	chr1q31	242843_at	NM_021948 /// NM_198427
2.42	2.34	0.08	5.34E-01	8.18E-01	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	chr1p36.21	1563961_at	NM_052929 /// XM_001714211 /// XM_934889 /// XM_946265
2.48	2.42	0.07	5.34E-01	8.18E-01	PMCHL1	pro-melanin-concentrating hormone-like 1	chr5p14.3	224418_x_at	NR_003921
6.34	6.14	0.20	5.34E-01	8.18E-01	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	chr16q22.1	224902_at	NM_017990
3.40	3.31	0.08	5.34E-01	8.18E-01	---	---	---	243331_at	---
2.02	1.94	0.08	5.34E-01	8.18E-01	DKFZp434L192	hypothetical protein DKFZp434L192	chr7p11.2	1553898_a_at	---
2.47	2.40	0.07	5.34E-01	8.18E-01	---	---	---	240679_at	---
8.74	8.63	0.10	5.34E-01	8.18E-01	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	chr2q36.1	213513_x_at	NM_005731 /// NM_152862
6.77	6.61	0.16	5.35E-01	8.19E-01	GDI1	GDP dissociation inhibitor 1	chrXq28	201864_at	NM_001493
4.06	3.94	0.12	5.35E-01	8.19E-01	---	---	---	243682_at	---
2.15	2.07	0.08	5.35E-01	8.19E-01	DMRT2	doublesex and mab-3 related transcription factor 2	chr9p24.3	223704_s_at	NM_001130865 /// NM_006557 /// NM_181872
2.64	2.54	0.10	5.35E-01	8.19E-01	CSDA	Cold shock domain protein A	chr12p13.1	228634_s_at	NM_003651
2.52	2.44	0.08	5.35E-01	8.19E-01	---	---	---	240182_at	---
2.34	2.27	0.06	5.35E-01	8.19E-01	MRGPRX3	MAS-related GPR, member X3	chr11p15.1	1553293_at	NM_054031
2.39	2.32	0.07	5.35E-01	8.19E-01	---	---	---	237938_at	---
2.43	2.35	0.09	5.35E-01	8.19E-01	LUZPP1	leucine zipper protein pseudogene 1	chr3p21.3	236731_at	---
2.80	2.70	0.10	5.35E-01	8.19E-01	---	---	---	210717_at	---
2.08	2.02	0.06	5.35E-01	8.19E-01	ASCL2	achaete-scute complex homolog 2 (Drosophila)	chr11p15.5	207607_at	NM_005170
2.13	2.06	0.07	5.35E-01	8.19E-01	---	---	---	238270_x_at	---
2.99	2.90	0.09	5.35E-01	8.19E-01	---	---	---	242597_at	---
2.32	2.24	0.08	5.35E-01	8.19E-01	---	---	---	1553208_s_at	---
2.18	2.10	0.08	5.36E-01	8.19E-01	---	---	---	1561762_s_at	---
4.54	4.31	0.23	5.36E-01	8.19E-01	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	chr2q33.1	226291_at	NM_020919
2.46	2.35	0.11	5.36E-01	8.19E-01	---	---	---	241534_at	---
5.20	5.00	0.20	5.36E-01	8.19E-01	CUTC	cutC copper transporter homolog (E. coli)	chr10q24.2	218970_s_at	NM_015960
2.25	2.18	0.07	5.36E-01	8.20E-01	---	---	---	243771_at	---
5.55	5.14	0.40	5.36E-01	8.20E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	213411_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723
3.01	2.85	0.17	5.36E-01	8.20E-01	FAM175A	family with sequence similarity 175, member A	chr4q21.21-q21.23	233543_s_at	NM_139076
3.20	3.12	0.08	5.36E-01	8.20E-01	EHMT1	euchromatic histone-lysine N-methyltransferase 1	chr9q34.3	222873_s_at	NM_024757
7.74	7.62	0.12	5.36E-01	8.20E-01	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	chr3p21	201040_at	NM_002070
2.48	2.40	0.08	5.36E-01	8.20E-01	APLP2	Amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	208701_at	NM_001642
6.02	5.90	0.11	5.36E-01	8.20E-01	ZFPL1	zinc finger protein-like 1	chr11q13	209428_s_at	NM_006782
2.56	2.47	0.09	5.37E-01	8.20E-01	HOXD3	homeobox D3	chr2q31.1	206602_s_at	NM_006898
3.90	3.76	0.14	5.37E-01	8.20E-01	SNED1	sushi, nidogen and EGF-like domains 1	chr2q37.3	213493_at	NM_001080437
2.76	2.66	0.09	5.37E-01	8.20E-01	TMEM39A	Transmembrane protein 39A	chr3q13.33	241392_at	NM_018266

6.81	6.67	0.14	5.37E-01	8.20E-01	RAB5C	RAB5C, member RAS oncogene family	chr17q21.2	201156_s_at	NM_004583 /// NM_201434
3.31	3.21	0.10	5.37E-01	8.20E-01	LOC100144604	hypothetical LOC100144604	---	1556768_at	NR_021493
5.94	5.67	0.27	5.37E-01	8.20E-01	HOXB7	homeobox B7	chr17q21.3	204778_x_at	NM_004502
7.75	7.58	0.17	5.37E-01	8.21E-01	EIF3A	eukaryotic translation initiation factor 3, subunit A	chr10q26	200595_s_at	NM_003750
2.99	2.88	0.11	5.37E-01	8.21E-01	CENTG2	centaurin, gamma 2	chr2q37	235968_at	NM_001037131 /// NM_014914
2.69	2.58	0.11	5.37E-01	8.21E-01	USP49	ubiquitin specific peptidase 49	chr6p21	244133_at	NM_018561
3.29	3.17	0.11	5.37E-01	8.21E-01	LARGE	like-glycosyltransferase	chr22q12.3	215538_at	NM_004737 /// NM_133642
2.72	2.63	0.09	5.37E-01	8.21E-01	---	---	---	236500_at	---
2.05	1.98	0.06	5.37E-01	8.21E-01	---	---	---	216443_at	---
2.36	2.27	0.09	5.37E-01	8.21E-01	---	---	---	242986_at	---
1.93	1.86	0.07	5.38E-01	8.21E-01	---	---	---	241332_at	---
7.87	7.70	0.16	5.38E-01	8.21E-01	BRP44	brain protein 44	chr1q24	202427_s_at	NM_015415
3.45	3.31	0.14	5.38E-01	8.21E-01	OAZ3	ornithine decarboxylase antizyme 3	chr1q21.3	222075_s_at	NM_016178
8.27	8.04	0.23	5.38E-01	8.21E-01	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	chr4p15.3	201385_at	NM_001358
2.55	2.43	0.12	5.38E-01	8.21E-01	SP3	Sp3 transcription factor	chr2q31	232529_at	NM_001017371 /// NM_003111
2.25	2.19	0.07	5.38E-01	8.21E-01	APOBEC4	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 4 (putative)	chr1q25.3	1554545_at	NM_203454
2.40	2.33	0.07	5.38E-01	8.21E-01	---	---	---	1561003_at	---
6.66	6.48	0.17	5.38E-01	8.21E-01	BRD4	bromodomain containing 4	chr19p13.1	226054_at	NM_014299 /// NM_058243
2.36	2.28	0.08	5.38E-01	8.21E-01	DKFZP434P211	POM121-like protein	chr22q11.22	222253_s_at	NR_003714
4.33	4.19	0.14	5.38E-01	8.21E-01	---	---	---	1569154_a_at	---
3.92	3.79	0.13	5.38E-01	8.21E-01	ACSS1	acyl-CoA synthetase short-chain family member 1	chr20p11.23-p11.21	234801_s_at	NM_032501
4.14	4.03	0.11	5.38E-01	8.21E-01	---	---	---	1559924_at	---
5.80	5.35	0.45	5.38E-01	8.21E-01	---	---	---	226345_at	---
4.98	4.85	0.13	5.38E-01	8.21E-01	ASB10	ankyrin repeat and SOCS box-containing 10	chr7q36.1	1553039_a_at	NM_080871
8.30	8.15	0.15	5.38E-01	8.21E-01	CAPZB	capping protein (actin filament) muscle Z-line, beta	chr1p36.1	37012_at	NM_004930
2.39	2.29	0.10	5.39E-01	8.21E-01	---	---	---	240860_at	---
5.40	5.23	0.17	5.39E-01	8.21E-01	CCDC59	coiled-coil domain containing 59	chr12q21.31	218936_s_at	NM_014167
9.70	9.51	0.19	5.39E-01	8.21E-01	TIMP2	TIMP metallopeptidase inhibitor 2	chr17q25	231579_s_at	NM_003255
2.36	2.27	0.10	5.39E-01	8.22E-01	BECN1	Beclin 1, autophagy related	chr17q21	1561652_at	NM_003766
7.98	7.84	0.14	5.39E-01	8.22E-01	RBPMS	RNA binding protein with multiple splicing	chr8p12-p11	209488_s_at	NM_001008710 /// NM_001008711 /// NM_001008712 /// NM_006867
2.88	2.79	0.09	5.39E-01	8.22E-01	H2AFJ	H2A histone family, member J	chr12p12	220936_s_at	NM_177925
2.87	2.79	0.09	5.39E-01	8.22E-01	---	---	---	215972_at	---
5.42	5.22	0.21	5.39E-01	8.22E-01	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	chr15q26.1	210046_s_at	NM_002168
3.38	3.28	0.10	5.39E-01	8.22E-01	C10orf110	chromosome 10 open reading frame 110	chr10p15.3	220703_at	XR_039896 /// XR_039897 /// XR_039898
1.97	1.90	0.07	5.39E-01	8.22E-01	PRSS7	protease, serine, 7 (enterokinase)	chr21q21|21q21.1	207638_at	NM_002772
2.85	2.72	0.13	5.39E-01	8.22E-01	CEP97	centrosomal protein 97kDa	chr3q12.3	235918_x_at	NM_024548
2.54	2.46	0.08	5.39E-01	8.22E-01	LOC100132080 /// LOC100132964 /// LOC100134695	hypothetical LOC100132080 /// hypothetical protein LOC100132964 /// hypothetical protein LOC100134695	chr7p22.3	1564472_at	XM_001720487 /// XM_001722092 /// XM_001722249
3.14	3.05	0.10	5.39E-01	8.22E-01	KIF5A	kinesin family member 5A	chr12q13.13	205318_at	NM_004984
3.08	3.01	0.07	5.40E-01	8.22E-01	OPN1LW /// OPN1MW /// OPN1MW2	opsin 1 (cone pigments), long-wave-sensitive /// opsin 1 (cone pigments), medium-wave-sensitive /// opsin 1 (cone pigments), medium-wave-sensitive 2	chrXq28	221327_s_at	NM_000513 /// NM_001048181 /// NM_020061
4.91	4.70	0.21	5.40E-01	8.22E-01	GAPVD1	GTPase activating protein and VPS9 domains 1	chr9q33.3	212804_s_at	NM_015635
2.43	2.33	0.10	5.40E-01	8.22E-01	---	---	---	240519_at	---
2.97	2.85	0.12	5.40E-01	8.22E-01	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	chr12q13	34726_at	NM_000725
2.28	2.21	0.08	5.40E-01	8.22E-01	---	---	---	1560898_at	---
2.35	2.25	0.09	5.40E-01	8.22E-01	ZNF425	Zinc finger protein 425	chr7q36.1	235565_at	NM_001001661

4.51	4.30	0.21	5.40E-01	8.22E-01	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	chr2p13	1554890_a_at	NM_022037 /// NM_022173
2.85	2.69	0.15	5.40E-01	8.22E-01	---	---	---	210824_at	---
2.98	2.88	0.10	5.40E-01	8.22E-01	GYPB /// GYPE	glycophorin B (MNS blood group) /// glycophorin E	chr4q28-q31 /// chr4q31.1	216833_x_at	NM_002100 /// NM_002102 /// NM_198682
2.17	2.10	0.07	5.40E-01	8.22E-01	CCDC67	coiled-coil domain containing 67	chr11q21	1558894_a_at	NM_181645
9.18	8.75	0.43	5.40E-01	8.22E-01	ZFAND5	zinc finger, AN1-type domain 5	chr9q13-q21	217741_s_at	NM_001102420 /// NM_001102421 /// NM_006007
2.07	1.97	0.09	5.40E-01	8.22E-01	---	---	---	1562389_at	---
5.26	5.11	0.14	5.40E-01	8.22E-01	ZNRF1	zinc and ring finger 1	chr16q23.1	223383_at	NM_032268
2.08	2.00	0.08	5.40E-01	8.22E-01	PSMD6	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	chr3p14.1	1555884_at	NM_014814
4.00	3.87	0.12	5.40E-01	8.22E-01	LLGL2	lethal giant larvae homolog 2 (Drosophila)	chr17q24-q25	1554006_a_at	NM_001015002 /// NM_001031803 /// NM_004524
2.63	2.52	0.12	5.40E-01	8.22E-01	LOC283404	hypothetical protein LOC283404	chr12q13.13	1558195_at	---
2.31	2.19	0.12	5.40E-01	8.22E-01	ZNF230	Zinc finger protein 230	chr19q13.31	1570135_at	NM_006300
2.07	1.98	0.08	5.40E-01	8.22E-01	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	chr2q31.1	219106_s_at	NM_006063
2.98	2.79	0.19	5.40E-01	8.22E-01	ZHX2	zinc fingers and homeoboxes 2	chr8q24.13	1557706_at	NM_014943
5.89	5.76	0.13	5.40E-01	8.22E-01	FLYWCH2	FLYWCH family member 2	chr16p13.3	226079_at	NM_138439
7.33	7.18	0.15	5.40E-01	8.22E-01	ACP2	acid phosphatase 2, lysosomal	chr11p11.2-p11.11|11p12-p11	202767_at	NM_001131064 /// NM_001610
3.99	3.85	0.15	5.41E-01	8.22E-01	RANBP17	RAN binding protein 17	chr5q34	219661_at	NM_022897
7.27	7.13	0.14	5.41E-01	8.22E-01	UBAP2	ubiquitin associated protein 2	chr9p13.3	221839_s_at	NM_018449
6.20	5.95	0.24	5.41E-01	8.22E-01	ZC3H7A	zinc finger CCCH-type containing 7A	chr16p13-p12	218348_s_at	NM_014153
1.86	1.80	0.06	5.41E-01	8.22E-01	DEFB126	defensin, beta 126	chr20p13	233166_at	NM_030931
2.25	2.15	0.09	5.41E-01	8.22E-01	SLC22A16	solute carrier family 22 (organic cation/carnitine transporter), member 16	chr6q22.1|6q21-q22.1	232233_at	NM_033125
6.34	6.10	0.24	5.41E-01	8.22E-01	TMEM158	transmembrane protein 158	chr3p21.3	213338_at	NM_015444
2.65	2.52	0.14	5.41E-01	8.23E-01	---	---	---	238808_at	---
2.53	2.44	0.09	5.41E-01	8.23E-01	IFNB1	interferon, beta 1, fibroblast	chr9p21	208173_at	NM_002176
4.94	4.79	0.15	5.41E-01	8.23E-01	---	---	---	214001_x_at	---
5.35	5.15	0.20	5.41E-01	8.23E-01	PARP3	poly (ADP-ribose) polymerase family, member 3	chr3p21.31-p21.1	209940_at	NM_001003931 /// NM_001003935 /// NM_005485
2.14	2.07	0.08	5.41E-01	8.23E-01	LOC100128590	hypothetical protein LOC100128590	chr2p22.1	244620_at	XM_001723678 /// XM_001726900
6.06	5.91	0.15	5.41E-01	8.23E-01	ZNF768	zinc finger protein 768	chr16p11.2	218916_at	NM_024671
3.90	3.79	0.11	5.41E-01	8.23E-01	---	---	---	1562254_at	---
6.81	6.60	0.21	5.41E-01	8.23E-01	BTBD3	BTB (POZ) domain containing 3	chr20p12.2	202946_s_at	NM_014962 /// NM_181443
2.45	2.36	0.09	5.41E-01	8.23E-01	NAIF1	nuclear apoptosis inducing factor 1	chr9q34.11	1554664_at	NM_197956
4.35	4.24	0.11	5.41E-01	8.23E-01	---	---	---	244884_at	---
3.22	3.14	0.09	5.41E-01	8.23E-01	CDC14B /// CDC14C	CDC14 cell division cycle 14 homolog B (S. cerevisiae) /// CDC14 cell division cycle 14 homolog C (S. cerevisiae)	chr7p12.3 /// chr9q22.33	230887_at	NM_001077181 /// NM_003671 /// NM_033331 /// NR_003595
2.27	2.18	0.09	5.42E-01	8.23E-01	---	---	---	1562507_at	---
2.94	2.80	0.14	5.42E-01	8.23E-01	LOC100131551	hypothetical LOC100131551	chr3q29	1564485_at	XM_001720505 /// XM_001726671 /// XM_001726778
5.37	5.25	0.12	5.42E-01	8.23E-01	hCG_2003956 /// LYPLA2 /// LYPLA2P1	hCG2003956 /// lysophospholipase II /// lysophospholipase II pseudogene 1	chr19p13.2 /// chr1p36.12-p35.1 /// chr6p21.32	215568_x_at	NM_007260 /// NR_001444

6.11	5.88	0.23	5.42E-01	8.23E-01	LYSMD3	LysM, putative peptidoglycan-binding, domain containing 3	chr5q14.3	226321_at	NM_198273																				
4.74	4.59	0.16	5.42E-01	8.23E-01	USP37	ubiquitin specific peptidase 37	chr2q35	226729_at	NM_020935																				
6.39	6.28	0.12	5.42E-01	8.23E-01	CMIP	c-Maf-inducing protein	chr16q23	224992_s_at	NM_030629 /// NM_198390																				
2.86	2.76	0.10	5.42E-01	8.23E-01	---	---	---	237317_at	---																				
9.36	9.09	0.27	5.42E-01	8.23E-01	AADAC	arylacetamide deacetylase (esterase)	chr3q21.3-q25.2	205969_at	NM_001086																				
2.37	2.28	0.08	5.42E-01	8.23E-01	---	---	---	234535_at	---																				
4.33	4.19	0.14	5.42E-01	8.23E-01	MPRIP	myosin phosphatase Rho interacting protein	chr17p11.2	238328_at	NM_015134 /// NM_201274																				
1.97	1.89	0.08	5.42E-01	8.23E-01	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	chr18q21.3-q22	211361_s_at	NM_012397																				
3.19	2.95	0.24	5.42E-01	8.23E-01	ZNF10	zinc finger protein 10	chr12q24.33	235366_at	NM_015394																				
2.84	2.73	0.11	5.42E-01	8.23E-01	C21orf89	chromosome 21 open reading frame 89	chr21q22.3	1552877_s_at	XR_040130 /// XR_040131 /// XR_040132																				
5.19	5.04	0.15	5.42E-01	8.23E-01	SSR1	signal sequence receptor, alpha	chr6p24.3	226712_at	NM_003144																				
2.79	2.63	0.16	5.42E-01	8.23E-01	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	chr12p12.1	208562_s_at	NM_005691 /// NM_020297 /// NM_020298																				
4.03	3.88	0.15	5.42E-01	8.23E-01	DNHD1	dynein heavy chain domain 1	chr11p15.4	229631_at	NM_144666																				
2.38	2.28	0.10	5.42E-01	8.23E-01	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	chrXp11.23	211425_x_at	NM_001034832 /// NM_001040612 /// NM_005636 /// NM_175729 /// XM_001725018																				
2.33	2.25	0.08	5.42E-01	8.23E-01	---	---	---	232468_at	---																				
2.87	2.80	0.07	5.43E-01	8.23E-01	---	---	---	235824_at	---																				
6.42	6.33	0.09	5.43E-01	8.23E-01	AURKAIP1	aurora kinase A interacting protein 1	chr1p36.33	227546_x_at	NM_001127229 /// NM_001127230 /// NM_017900																				
8.09	7.95	0.14	5.43E-01	8.23E-01	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	chrXp22.2-p22.1	224936_at	NM_001415																				
2.72	2.59	0.13	5.43E-01	8.23E-01	MTSS1	metastasis suppressor 1	chr8p22	210359_at	NM_014751																				
9.15	8.65	0.50	5.43E-01	8.23E-01	PCP4	Purkinje cell protein 4	chr21q22.2	205549_at	NM_006198																				
4.95	4.78	0.18	5.43E-01	8.23E-01	---	---	---	217152_at	---																				
2.04	1.97	0.06	5.43E-01	8.23E-01	---	---	---	243241_at	---																				
2.39	2.30	0.09	5.43E-01	8.23E-01	KIAA1731	KIAA1731	chr11q21	1565829_at	NM_033395																				
3.56	3.44	0.11	5.43E-01	8.23E-01	PI3	peptidase inhibitor 3, skin-derived (SKALP)	chr20q12-q13	203691_at	NM_002638																				
3.71	3.59	0.12	5.43E-01	8.23E-01	MGC16703	tubulin, alpha pseudogene	chr22q11.21	1552698_at	NR_003608																				
2.82	2.71	0.11	5.43E-01	8.23E-01	---	---	---	1556899_at	---																				
5.09	4.90	0.19	5.43E-01	8.23E-01	---	---	---	236194_at	---																				
4.97	4.64	0.33	5.43E-01	8.23E-01	RANBP2	RAN binding protein 2	chr2q12.3	201712_s_at	NM_006267																				
10.22	10.12	0.10	5.43E-01	8.23E-01	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	chr16p12.3	200085_s_at	NM_007108 /// NM_207013																				
3.36	3.29	0.07	5.43E-01	8.23E-01	MRPL38	mitochondrial ribosomal protein L38	chr17q25.3	1561508_at	NM_032478																				
5.10	4.96	0.14	5.43E-01	8.23E-01	AIFM2	apoptosis-inducing factor, mitochondrion-associated, 2	chr10q22.1	228445_at	NM_032797																				
5.50	5.31	0.19	5.43E-01	8.23E-01	RIPK2	receptor-interacting serine-threonine kinase 2	chr8q21	209545_s_at	NM_003821																				
5.40	5.28	0.12	5.43E-01	8.23E-01	C18orf19	chromosome 18 open reading frame 19	chr18p11.21	230739_at	NM_001098801 /// NM_152352																				
6.90	6.79	0.10	5.43E-01	8.23E-01	CIRH1A	cirrhosis, autosomal recessive 1A (cirhin)	chr16q22.1	224903_at	NM_032830																				
4.07	3.95	0.12	5.43E-01	8.23E-01	U2AF2	U2 small nuclear RNA auxiliary factor 2	chr19q13.42	229508_at	NM_001012478 /// NM_007279																				
2.82	2.70	0.12	5.43E-01	8.23E-01	PSRC1	proline/serine-rich coiled-coil 1	chr1p13.3	201896_s_at	NM_001005290 /// NM_001032290 /// NM_001032291 /// NM_032636																				

10.27	9.81	0.46	5.43E-01	8.23E-01	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	chr16p13.3	211699_x_at	NM_000517 /// NM_000558																				
5.62	5.44	0.18	5.43E-01	8.23E-01	BPTF	bromodomain PHD finger transcription factor	chr17q24.3	209271_at	NM_004459 /// NM_182641																				
3.61	3.53	0.08	5.44E-01	8.23E-01	MAP7D3	MAP7 domain containing 3	chrXq26.3	219626_at	NM_024597																				
3.04	2.95	0.09	5.44E-01	8.23E-01	FAM174B	Family with sequence similarity 174, member B	chr15q26.1	222085_at	NM_207446																				
2.72	2.64	0.07	5.44E-01	8.24E-01	HNMT	histamine N-methyltransferase	chr2q22.1	1554303_at	NM_001024074 /// NM_001024075 /// NM_006895																				
2.04	1.97	0.07	5.44E-01	8.24E-01	ZFYVE16	zinc finger, FYVE domain containing 16	chr5q14	1555011_at	NM_001105251 /// NM_014733																				
2.48	2.38	0.10	5.44E-01	8.24E-01	NSUN4	NOL1/NOP2/Sun domain family, member 4	chr1p34	1559848_at	NM_199044																				
2.67	2.58	0.09	5.44E-01	8.24E-01	---	---	---	242381_x_at	---																				
2.35	2.28	0.06	5.44E-01	8.24E-01	---	---	---	238559_at	---																				
5.95	5.84	0.11	5.44E-01	8.24E-01	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	chr1q22	226447_at	NM_018489																				
3.63	3.52	0.11	5.44E-01	8.24E-01	SYNJ2	Synaptojanin 2	chr6q25.3	216181_at	NM_003898																				
4.44	4.34	0.10	5.44E-01	8.24E-01	SPTBN1	Spectrin, beta, non-erythrocytic 1	chr2p21	226765_at	NM_003128 /// NM_178313																				
3.98	3.87	0.11	5.44E-01	8.24E-01	---	---	---	1556928_at	---																				
4.81	4.62	0.18	5.44E-01	8.24E-01	NARG1	NMDA receptor regulated 1	chr4q31.1	226998_at	NM_057175																				
4.08	4.00	0.08	5.44E-01	8.24E-01	---	---	---	241270_at	---																				
2.97	2.81	0.15	5.44E-01	8.24E-01	COMP	cartilage oligomeric matrix protein	chr19p13.1	205713_s_at	NM_000095																				
2.29	2.21	0.08	5.44E-01	8.24E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	215769_at	---																				
10.20	10.10	0.09	5.45E-01	8.24E-01	ATP5E	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	chr20q13.32	217801_at	NM_001001977 /// NM_006886																				
7.21	7.04	0.16	5.45E-01	8.24E-01	CLDND1	claudin domain containing 1	chr3q12.1	1554149_at	NM_001040181 /// NM_001040182 /// NM_001040183 /// NM_001040199 /// NM_001040200 /// NM_019895																				
2.36	2.24	0.12	5.45E-01	8.24E-01	---	---	---	1570600_at	---																				
2.84	2.75	0.09	5.45E-01	8.24E-01	GAS7	growth arrest-specific 7	chr17p13.1	207704_s_at	NM_001130831 /// NM_003644 /// NM_201432 /// NM_201433																				
8.58	8.41	0.16	5.45E-01	8.24E-01	N-PAC /// SEPT6	cytokine-like nuclear factor n-pac /// septin 6	chr16p13.3 /// chrXq24	212414_s_at	NM_015129 /// NM_032569 /// NM_145799 /// NM_145800 /// NM_145802																				
3.27	3.19	0.08	5.45E-01	8.24E-01	DNAH9	dynein, axonemal, heavy chain 9	chr17p12	210345_s_at	NM_001372 /// NM_004662																				
8.19	8.03	0.16	5.45E-01	8.24E-01	PRKAR2A	Protein kinase, cAMP-dependent, regulatory, type II, alpha	chr3p21.3-p21.2	213052_at	NM_004157																				
5.89	5.75	0.14	5.45E-01	8.24E-01	TICAM2 /// TMED7	toll-like receptor adaptor molecule 2 /// transmembrane emp24 protein transport domain containing 7	chr5q22.3 /// chr5q23.1	228234_at	NM_021649 /// NM_181836																				
1.95	1.89	0.07	5.45E-01	8.24E-01	---	---	---	1559172_at	---																				
3.09	2.98	0.11	5.45E-01	8.24E-01	SPINK4	serine peptidase inhibitor, Kazal type 4	chr9p13.3	207214_at	NM_014471																				
3.22	3.03	0.20	5.45E-01	8.24E-01	INTS2	integrator complex subunit 2	chr17q23.2	224308_s_at	NM_020748																				
2.85	2.77	0.08	5.45E-01	8.24E-01	---	---	---	1557555_at	---																				
2.34	2.24	0.10	5.45E-01	8.24E-01	LOC100134937	Hypothetical LOC100134937	---	240408_at	---																				
8.75	8.56	0.19	5.45E-01	8.24E-01	ABHD2	abhydrolase domain containing 2	chr15q26.1	225337_at	NM_007011 /// NM_152924																				

2.16	2.06	0.10	5.45E-01	8.24E-01	VPS8	Vacuolar protein sorting 8 homolog (S. cerevisiae)	chr3q27.2	236937_at	NM_001009921 /// NM_015303
2.59	2.50	0.10	5.45E-01	8.24E-01	---	---	---	1569727_at	---
1.88	1.81	0.07	5.45E-01	8.24E-01	---	---	---	1562866_at	---
5.54	5.27	0.27	5.45E-01	8.24E-01	INO80D	INO80 complex subunit D	chr2q33.3	226555_at	NM_017759
2.36	2.28	0.08	5.46E-01	8.24E-01	KIR2DL1	Killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	chr19q13.4	217296_at	NM_014218
3.29	3.16	0.13	5.46E-01	8.24E-01	---	---	---	238749_at	---
3.38	3.21	0.17	5.46E-01	8.24E-01	LOC731484	hypothetical LOC731484	chr2q37.1	244304_at	XR_015492 /// XR_037119 /// XR_037952
1.90	1.83	0.07	5.46E-01	8.24E-01	C14orf53	chromosome 14 open reading frame 53	chr14q23.3	237205_at	XR_041746 /// XR_041747 /// XR_041748
2.62	2.54	0.08	5.46E-01	8.24E-01	WAPAL	wings apart-like homolog (Drosophila)	chr10q23.2	217218_at	NM_015045
5.42	5.21	0.21	5.46E-01	8.24E-01	MED1	mediator complex subunit 1	chr17q12-q21.1	225456_at	NM_004774
6.42	6.29	0.13	5.46E-01	8.24E-01	TP53TG1	TP53 target 1 (non-protein coding)	chr7q21.1	210241_s_at	NM_007233 /// NR_015381
3.92	3.62	0.30	5.46E-01	8.24E-01	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	chr2q36-q37	214641_at	NM_000091 /// NM_031362 /// NM_031365 /// NM_031366
4.08	3.97	0.11	5.46E-01	8.24E-01	ESR1	estrogen receptor 1	chr6q25.1	211234_x_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742
5.49	5.24	0.24	5.46E-01	8.25E-01	---	---	---	1556568_a_at	---
2.54	2.48	0.06	5.46E-01	8.25E-01	SLAMF9	SLAM family member 9	chr1q23.2	1553769_at	NM_033438
2.19	2.12	0.07	5.46E-01	8.25E-01	PSG1 /// PSG3	pregnancy specific beta-1-glycoprotein 1 /// pregnancy specific beta-1-glycoprotein 3	chr19q13.2	203399_x_at	NM_006905 /// NM_021016
3.92	3.82	0.11	5.46E-01	8.25E-01	PSTPIP1	proline-serine-threonine phosphatase interacting protein 1	chr15q24-q25.1	211178_s_at	NM_003978
3.49	3.37	0.12	5.46E-01	8.25E-01	MED23	mediator complex subunit 23	chr6q22.33-q24.1	242707_at	NM_004830 /// NM_015979
1.97	1.90	0.07	5.46E-01	8.25E-01	H2AFY	H2A histone family, member Y	chr5q31.3-q32	1558779_at	NM_001040158 /// NM_004893 /// NM_138609 /// NM_138610
6.85	6.73	0.12	5.46E-01	8.25E-01	PACS2	phosphofurin acidic cluster sorting protein 2	chr14q32.33	1555823_at	NM_001100913 /// NM_015197
1.98	1.92	0.06	5.46E-01	8.25E-01	---	---	---	1570213_at	---
10.69	10.62	0.07	5.46E-01	8.25E-01	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	chr19q13.2	200826_at	NM_004597 /// NM_177542
2.47	2.39	0.09	5.46E-01	8.25E-01	IFNG	interferon, gamma	chr12q14	210354_at	NM_000619
3.04	2.93	0.10	5.46E-01	8.25E-01	SRR	Serine racemase	chr17p13	235677_at	NM_021947
6.63	6.34	0.29	5.47E-01	8.25E-01	CASD1	CAS1 domain containing 1	chr7q21.3	219342_at	NM_022900
2.06	1.98	0.08	5.47E-01	8.25E-01	GABRA2	gamma-aminobutyric acid (GABA) A receptor, alpha 2	chr4p12	207014_at	NM_000807 /// NM_001114175
2.55	2.42	0.13	5.47E-01	8.25E-01	ZMYM2	zinc finger, MYM-type 2	chr13q11-q12	210282_at	NM_003453 /// NM_197968
2.06	2.00	0.06	5.47E-01	8.25E-01	MGA	MAX gene associated	chr15q14	1564640_at	NM_001080541
4.32	4.21	0.11	5.47E-01	8.25E-01	GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	chr22q11.2	220762_s_at	NM_053004
1.88	1.81	0.07	5.47E-01	8.25E-01	CPXCR1	CPX chromosome region, candidate 1	chrXq21.3	1560494_a_at	NM_033048

2.18	2.10	0.08	5.47E-01	8.25E-01	SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	chr17p13.2	239805_at	NM_003984
2.77	2.65	0.11	5.47E-01	8.25E-01	---	---	---	1569099_at	---
2.28	2.18	0.09	5.47E-01	8.25E-01	IQUB	IQ motif and ubiquitin domain containing	chr7q31.32	1568924_a_at	NM_178827
5.61	5.48	0.13	5.47E-01	8.25E-01	MPND	MPN domain containing	chr19p13.3	233651_s_at	NM_032868
2.96	2.84	0.12	5.47E-01	8.25E-01	---	---	---	229388_at	---
4.22	4.10	0.12	5.47E-01	8.25E-01	TDRD10	tudor domain containing 10	chr1q21.3	231371_at	NM_001098475 /// NM_182499
6.88	6.72	0.16	5.47E-01	8.25E-01	KCTD1	potassium channel tetramerisation domain containing 1	chr18q11.2	226245_at	NM_198991
4.72	4.49	0.23	5.47E-01	8.25E-01	SLC25A40	solute carrier family 25, member 40	chr7q21.12	227012_at	NM_018843
3.19	3.10	0.09	5.48E-01	8.25E-01	---	---	---	1557702_at	---
2.51	2.40	0.11	5.48E-01	8.25E-01	---	---	---	237694_at	---
7.81	7.30	0.51	5.48E-01	8.25E-01	TFRC	transferrin receptor (p90, CD71)	chr3q29	208691_at	NM_001128148 /// NM_003234
3.30	3.20	0.10	5.48E-01	8.26E-01	ACTN3	actinin, alpha 3	chr11q13.1	206891_at	NM_001104
2.59	2.51	0.08	5.48E-01	8.26E-01	PCDH19	protocadherin 19	chrXq13.3	227282_at	NM_001105243 /// NM_020766
2.24	2.17	0.07	5.48E-01	8.26E-01	---	---	---	1564131_a_at	---
3.24	3.09	0.14	5.48E-01	8.26E-01	---	---	---	236712_at	---
2.41	2.32	0.09	5.48E-01	8.26E-01	---	---	---	1569728_at	---
3.60	3.46	0.15	5.48E-01	8.26E-01	---	---	---	239706_x_at	---
8.30	8.14	0.16	5.48E-01	8.26E-01	WASF2	WAS protein family, member 2	chr1p36.11-p34.3	224562_at	NM_006990
7.41	7.25	0.16	5.48E-01	8.26E-01	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	chr2p12-p11.2	202546_at	NM_003761
2.81	2.67	0.13	5.49E-01	8.26E-01	---	---	---	240566_at	---
2.10	2.02	0.08	5.49E-01	8.26E-01	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	chr8p21.1	235178_x_at	NM_001017420
2.52	2.42	0.10	5.49E-01	8.26E-01	GPSN2	glycoprotein, synaptic 2	chr19p13.12	1569392_at	NM_138501
5.47	5.22	0.25	5.49E-01	8.26E-01	LOXL3	lysyl oxidase-like 3	chr2p13	228253_at	NM_032603
7.05	6.95	0.10	5.49E-01	8.26E-01	PIGV	phosphatidylinositol glycan anchor biosynthesis, class V	chr1p36.11	219238_at	NM_017837
3.45	3.31	0.14	5.49E-01	8.27E-01	COL5A3	collagen, type V, alpha 3	chr19p13.2	218975_at	NM_015719
4.39	4.23	0.15	5.49E-01	8.27E-01	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	chr9p12	222793_at	NM_014314
2.19	2.11	0.08	5.49E-01	8.27E-01	GRM1	glutamate receptor, metabotropic 1	chr6q24	207299_s_at	NM_000838 /// NM_001114329
7.84	7.66	0.18	5.49E-01	8.27E-01	FBN1	fibrillin 1	chr15q21.1	202766_s_at	NM_000138
2.02	1.95	0.07	5.49E-01	8.27E-01	C2orf21	chromosome 2 open reading frame 21	chr2q35	237660_at	NM_032504 /// NM_182587 /// XM_001715588 /// XM_001717212 /// XM_001717654
3.05	2.96	0.09	5.49E-01	8.27E-01	---	---	---	244034_at	---
10.89	10.81	0.08	5.49E-01	8.27E-01	BTF3	basic transcription factor 3	chr5q13.2	211939_x_at	NM_001037637 /// NM_001207
4.75	4.69	0.06	5.49E-01	8.27E-01	---	---	---	222329_x_at	---
2.48	2.40	0.09	5.49E-01	8.27E-01	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)	chr6p21.3	217323_at	NR_001298
2.62	2.47	0.15	5.49E-01	8.27E-01	LOC645513	hypothetical LOC645513	chr4q26-q27	242305_at	XM_001714125 /// XM_001714854 /// XM_001717939
2.39	2.32	0.07	5.49E-01	8.27E-01	ABHD5	Abhydrolase domain containing 5	chr3p21	232862_at	NM_016006
3.20	3.08	0.12	5.50E-01	8.27E-01	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	chr9q13	239761_at	NM_001097633 /// NM_001097634 /// NM_001097635 /// NM_001097636 /// NM_001490
2.96	2.88	0.09	5.50E-01	8.27E-01	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	chr7q32	227950_at	NM_003344 /// NM_182697
2.76	2.62	0.14	5.50E-01	8.27E-01	NLRP8	NLR family, pyrin domain containing 8	chr19q13.42	1553526_at	NM_176811

6.37	6.16	0.21	5.50E-01	8.27E-01	ZNF639	zinc finger protein 639	chr3q26.32	222623_s_at	NM_016331																				
2.67	2.59	0.08	5.50E-01	8.27E-01	MGC26718	Similar to ankyrin repeat domain 20A	chr18p11.21	1559170_at	NM_001029999																				
9.33	9.18	0.14	5.50E-01	8.27E-01	TSC22D3	TSC22 domain family, member 3	chrXq22.3	208763_s_at	NM_001015881 /// NM_004089 /// NM_198057																				
5.41	5.23	0.18	5.50E-01	8.27E-01	XPO7	exportin 7	chr8p21	208459_s_at	NM_001100161 /// NM_001100162 /// NM_015024																				
2.20	2.13	0.07	5.50E-01	8.27E-01	---	---	---	236068_s_at	---																				
3.03	2.86	0.17	5.50E-01	8.27E-01	RBBP9	retinoblastoma binding protein 9	chr20p11.2	232751_at	NM_006606																				
2.81	2.69	0.12	5.50E-01	8.27E-01	WBSCR19	Williams Beuren syndrome chromosome region 19	chr7p13	232964_at	NM_175064																				
2.12	2.05	0.07	5.50E-01	8.27E-01	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	chr11p15.3	235906_at	NM_006284																				
2.13	2.06	0.07	5.50E-01	8.27E-01	---	---	---	1566892_at	---																				
2.52	2.42	0.10	5.50E-01	8.27E-01	TCERG1L	transcription elongation regulator 1-like	chr10q26.3	231257_at	NM_174937																				
9.43	9.32	0.11	5.50E-01	8.27E-01	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	chr16p13.3	223112_s_at	NM_004548																				
7.69	7.45	0.24	5.50E-01	8.27E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	225116_at	NM_001113239 /// NM_022740																				
2.04	1.96	0.08	5.51E-01	8.27E-01	---	---	---	241804_at	---																				
3.00	2.90	0.10	5.51E-01	8.27E-01	C18orf15	chromosome 18 open reading frame 15	chr18p11.21	1553435_at	XR_040983 /// XR_040984 /// XR_040985																				
3.54	3.37	0.17	5.51E-01	8.27E-01	---	---	---	240128_at	---																				
3.29	3.21	0.08	5.51E-01	8.27E-01	RAB40A	RAB40A, member RAS oncogene family	chrXq22.1	217589_at	NM_080879																				
6.01	5.73	0.28	5.51E-01	8.27E-01	KIAA0430	KIAA0430	chr16p13.11	202386_s_at	NM_014647																				
2.62	2.53	0.08	5.51E-01	8.27E-01	C6orf164	chromosome 6 open reading frame 164	chr6q15-q16.1	230506_at	---																				
7.26	7.15	0.11	5.51E-01	8.28E-01	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	chr1p36.33	200744_s_at	NM_002074																				
1.99	1.90	0.09	5.51E-01	8.28E-01	SPOCK3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	chr4q32.3	206434_at	NM_001040159 /// NM_016950																				
4.90	4.68	0.22	5.51E-01	8.28E-01	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	chr21q22.11	204194_at	NM_001011545 /// NM_001186 /// NM_206866																				
6.59	6.48	0.12	5.51E-01	8.28E-01	MED16	mediator complex subunit 16	chr19p13.3	221938_x_at	NM_005481																				
3.62	3.48	0.14	5.51E-01	8.28E-01	KIF21B	kinesin family member 21B	chr1pter-q31.3	204411_at	NM_017596																				
2.40	2.33	0.07	5.51E-01	8.28E-01	ZNF568	zinc finger protein 568	chr19q13.12	1562282_at	NM_198539																				
4.25	4.16	0.09	5.51E-01	8.28E-01	SIRPA	signal-regulatory protein alpha	chr20p13	202895_s_at	NM_001040022 /// NM_001040023 /// NM_080792																				
7.41	7.30	0.11	5.51E-01	8.28E-01	DOCK5 /// PPP2R2A	dedicator of cytokinesis 5 /// protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	chr8p21.2	202313_at	NM_002717 /// NM_024940																				
2.83	2.72	0.11	5.52E-01	8.28E-01	ALLC	allantoicase	chr2q35	220365_at	NM_018436																				
2.84	2.74	0.11	5.52E-01	8.28E-01	TTN	Titin	chr2q31	240793_at	NM_003319 /// NM_133378 /// NM_133379 /// NM_133432 /// NM_133437																				
6.11	5.92	0.20	5.52E-01	8.28E-01	C10orf119	chromosome 10 open reading frame 119	chr10q26.11	222464_s_at	NM_024834																				
5.87	5.75	0.12	5.52E-01	8.28E-01	PPP1R13B	protein phosphatase 1, regulatory (inhibitor) subunit 13B	chr14q32.33	216347_s_at	NM_015316																				
2.62	2.48	0.13	5.52E-01	8.28E-01	TRIM13	tripartite motif-containing 13	chr13q14	1569142_at	NM_001007278 /// NM_005798 /// NM_052811 /// NM_213590																				

2.80	2.71	0.09	5.52E-01	8.28E-01	LOC376693	hypothetical LOC376693	chr1q32.1	1566720_at	XR_017819 /// XR_017832 /// XR_040066
2.73	2.62	0.11	5.52E-01	8.28E-01	---	---	---	1566498_at	---
2.55	2.44	0.11	5.52E-01	8.28E-01	---	---	---	241702_at	---
2.34	2.26	0.08	5.52E-01	8.28E-01	---	---	---	243776_at	---
5.07	4.93	0.14	5.52E-01	8.28E-01	WDFY3	WD repeat and FYVE domain containing 3	chr4q21.23	212598_at	NM_014991 /// NM_178583 /// NM_178585
4.24	4.14	0.10	5.52E-01	8.28E-01	DIRAS1	DIRAS family, GTP-binding RAS-like 1	chr19p13.3	226573_at	NM_145173
3.45	3.32	0.13	5.52E-01	8.28E-01	ARHGAP21	Rho GTPase activating protein 21	chr10p12.1|10p12.3	241701_at	NM_020824
2.42	2.34	0.07	5.52E-01	8.28E-01	---	---	---	1563681_at	---
1.97	1.90	0.07	5.52E-01	8.28E-01	FAM12A	family with sequence similarity 12, member A	chr14q11.2	208143_s_at	NM_006683
2.37	2.27	0.10	5.53E-01	8.28E-01	SPANXA1 /// SPANXA2 /// SPANXB1 /// SPANXB2 /// SPANXC /// SPANXF1	sperm protein associated with the nucleus, X-linked, family member A1 /// SPANX family, member A2 /// SPANX family, member B1 /// SPANX family, member B2 /// SPANX family, member C /// SPANX family, member F1	chrXq27.1	220922_s_at	NM_013453 /// NM_022661 /// NM_032461 /// NM_139019 /// NM_145662 /// NM_145664 /// XM_001713741 /// XM_001713760
6.24	6.13	0.11	5.53E-01	8.28E-01	DMWD	dystrophia myotonica, WD repeat containing	chr19q13.3	33768_at	NM_004943
5.10	4.95	0.16	5.53E-01	8.28E-01	PTAFR	platelet-activating factor receptor	chr1p35-p34.3	211661_x_at	NM_000952
2.90	2.79	0.10	5.53E-01	8.28E-01	---	---	---	1556434_at	---
2.17	2.08	0.09	5.53E-01	8.29E-01	---	---	---	1560282_at	---
2.09	2.00	0.09	5.53E-01	8.29E-01	WDR26	WD repeat domain 26	chr1q42.11	223863_at	NM_001115113 /// NM_025160
2.49	2.41	0.08	5.53E-01	8.29E-01	---	---	---	234269_at	---
2.76	2.67	0.09	5.53E-01	8.29E-01	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	chr17p12-p11.2	221062_at	NM_006041
2.40	2.29	0.11	5.53E-01	8.29E-01	SLAMF1	signaling lymphocytic activation molecule family member 1	chr1q22-q23	206181_at	NM_003037
11.45	11.34	0.11	5.53E-01	8.29E-01	PRDX2	peroxiredoxin 2	chr19p13.2	39729_at	NM_005809 /// NM_181738
5.26	5.18	0.08	5.53E-01	8.29E-01	DIAPH1	diaphanous homolog 1 (Drosophila)	chr5q31	213514_s_at	NM_001079812 /// NM_005219
2.06	1.99	0.08	5.53E-01	8.29E-01	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	chr21q22.1|21q22.11	216990_at	NM_000819 /// NM_175085
2.06	1.96	0.09	5.53E-01	8.29E-01	BHLHB9	Basic helix-loop-helix domain containing, class B, 9	chrXq23	1569674_at	NM_030639
2.17	2.11	0.06	5.53E-01	8.29E-01	GLS	glutaminase	chr2q32-q34	211414_at	NM_014905
6.29	6.07	0.22	5.53E-01	8.29E-01	CTGLF6	centaurin, gamma-like family, member 6	chr10q11.22	239151_at	XM_001716810
2.24	2.16	0.08	5.53E-01	8.29E-01	---	---	---	1559568_at	---
3.06	2.97	0.09	5.53E-01	8.29E-01	---	---	---	1561360_at	---
4.28	4.04	0.24	5.53E-01	8.29E-01	IRF5	interferon regulatory factor 5	chr7q32	239412_at	NM_001098627 /// NM_001098628 /// NM_001098629 /// NM_001098630 /// NM_001098631 /// NM_002200 /// NM_032643
6.73	6.51	0.22	5.53E-01	8.29E-01	PGM5	phosphoglucomutase 5	chr9q13	208491_s_at	NM_021965
5.55	5.38	0.17	5.53E-01	8.29E-01	PACS1	phosphofurin acidic cluster sorting protein 1	chr11q13.1	224658_x_at	NM_018026
3.39	3.29	0.10	5.53E-01	8.29E-01	ARMCX4	armadillo repeat containing, X-linked 4	chrXq22.1	1564399_a_at	NM_152583
8.29	8.15	0.14	5.53E-01	8.29E-01	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	chr6p21.3	201500_s_at	NM_021959
3.25	3.13	0.12	5.54E-01	8.29E-01	UPB1	ureidopropionase, beta	chr22q11.2	224042_at	NM_016327

6.54	6.35	0.19	5.54E-01	8.29E-01	DDAH2	dimethylarginine dimethylaminohydrolase 2	chr6p21.3	215537_x_at	NM_013974																			
3.29	3.20	0.10	5.54E-01	8.29E-01	ARNT	aryl hydrocarbon receptor nuclear translocator	chr1q21	210828_s_at	NM_001668 /// NM_178426 /// NM_178427																			
2.39	2.28	0.11	5.54E-01	8.29E-01	STON2	stonin 2	chr14q31.1	1552543_a_at	NM_033104																			
8.07	7.51	0.57	5.54E-01	8.29E-01	VCAN	versican	chr5q14.3	211571_s_at	NM_001126336 /// NM_004385																			
5.80	5.51	0.29	5.54E-01	8.29E-01	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	214693_x_at	NM_001037675 /// NM_001039703 /// NM_001101663 /// NM_001102663 /// NM_015383 /// NM_017940 /// NM_173638 /// NM_183372 /// XM_001717398 /// XM_001717802 /// XM_001721345 /// XM_001721349 /// XM_001722184 /// XM_001723523 /// XM_001726946																			
2.11	2.03	0.08	5.54E-01	8.30E-01	---	---	---	243573_at	---																			
2.87	2.70	0.17	5.54E-01	8.30E-01	THADA	thyroid adenoma associated	chr2p21	1554493_s_at	NM_001083953 /// NM_022065																			
2.59	2.51	0.07	5.54E-01	8.30E-01	VIL1	villin 1	chr2q35-q36	1554943_at	NM_007127																			
3.19	3.08	0.11	5.54E-01	8.30E-01	---	---	---	231130_at	---																			
2.90	2.81	0.09	5.54E-01	8.30E-01	LOC100129166	hypothetical protein LOC100129166	chr2q37.1	1570090_at	XM_001720687 /// XM_001723639 /// XM_001726227																			
4.00	3.85	0.15	5.54E-01	8.30E-01	ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	chr16q22.1	205346_at	NM_006927																			
3.54	3.41	0.12	5.54E-01	8.30E-01	---	---	---	1557685_at	---																			
5.35	5.20	0.15	5.54E-01	8.30E-01	IPPK	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	chr9q21.33-q22.31	219092_s_at	NM_022755																			
4.44	4.32	0.11	5.54E-01	8.30E-01	---	---	---	225722_at	---																			
5.81	5.68	0.13	5.54E-01	8.30E-01	ANAPC1	anaphase promoting complex subunit 1	chr2q12.1	218575_at	NM_022662																			
4.14	3.98	0.15	5.55E-01	8.30E-01	ZNF582	zinc finger protein 582	chr19q13.43	241602_at	NM_144690																			
6.76	6.55	0.21	5.55E-01	8.30E-01	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	chr6p25.2	202126_at	NM_003913																			
6.49	6.22	0.26	5.55E-01	8.30E-01	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	chr4q12	201014_s_at	NM_001079524 /// NM_001079525 /// NM_006452																			
2.87	2.78	0.08	5.55E-01	8.30E-01	---	---	---	1563086_at	---																			
7.58	7.42	0.16	5.55E-01	8.30E-01	SLC39A6	solute carrier family 39 (zinc transporter), member 6	chr18q12.2	202088_at	NM_001099406 /// NM_012319																			
4.10	3.93	0.17	5.55E-01	8.30E-01	DKFZP434B0335	DKFZP434B0335 protein	chr7q21.3	231912_s_at	NM_015395																			

2.74	2.65	0.09	5.55E-01	8.30E-01	CSH1 /// CSH2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// growth hormone 1	chr17q24.2	206886_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645
7.35	7.24	0.12	5.55E-01	8.30E-01	RANBP3	RAN binding protein 3	chr19p13.3	202640_s_at	NM_003624 /// NM_007320 /// NM_007322
2.29	2.19	0.10	5.55E-01	8.30E-01	---	---	---	237512_at	---
7.46	7.20	0.26	5.55E-01	8.30E-01	---	---	---	226438_at	---
5.38	5.20	0.17	5.55E-01	8.30E-01	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	chr1p36.3	226929_at	NM_005957
3.40	3.31	0.09	5.55E-01	8.30E-01	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	chr3q27-q28	210680_s_at	NM_001031849 /// NM_001879 /// NM_139125
2.53	2.45	0.08	5.55E-01	8.30E-01	---	---	---	229425_at	---
2.36	2.30	0.06	5.55E-01	8.30E-01	C3orf65	Chromosome 3 open reading frame 65	chr3q27.2	1562832_at	NM_001039788
2.05	1.98	0.06	5.55E-01	8.30E-01	LOC100129673	Similar to hCG2042915	chr17p13.2	236074_at	XM_001715544 /// XM_001717297
4.05	3.91	0.14	5.55E-01	8.30E-01	LOC729234	fumarylacetoacetate hydrolase domain containing 2 pseudogene	chr2q11.2	228198_s_at	NR_003698
2.15	2.08	0.08	5.56E-01	8.30E-01	OR2F2	olfactory receptor, family 2, subfamily F, member 2	chr7q35	217302_at	NM_001004685
5.53	5.36	0.17	5.56E-01	8.30E-01	TP53TG1	TP53 target 1 (non-protein coding)	chr7q21.1	209917_s_at	NM_007233 /// NR_015381
2.66	2.58	0.08	5.56E-01	8.30E-01	---	---	---	236680_at	---
3.31	3.22	0.09	5.56E-01	8.30E-01	---	---	---	216715_at	---
2.31	2.24	0.07	5.56E-01	8.30E-01	---	---	---	1561572_at	---
3.67	3.54	0.14	5.56E-01	8.30E-01	---	---	---	236809_at	---
2.05	1.98	0.07	5.56E-01	8.30E-01	GAN	gigaxonin	chr16q24.1	220124_at	NM_022041
4.91	4.74	0.17	5.56E-01	8.30E-01	---	---	---	229593_at	---
4.06	3.97	0.09	5.56E-01	8.30E-01	C11orf1	Chromosome 11 open reading frame 1	chr11q13-q22	231538_at	NM_022761
10.42	10.23	0.19	5.56E-01	8.30E-01	TPD52L1	tumor protein D52-like 1	chr6q22-q23	203786_s_at	NM_001003395 /// NM_001003396 /// NM_001003397 /// NM_003287
2.24	2.14	0.10	5.56E-01	8.30E-01	---	---	---	234805_at	---
3.87	3.71	0.16	5.56E-01	8.30E-01	CA4	carbonic anhydrase IV	chr17q23	206208_at	NM_000717
5.99	5.87	0.13	5.56E-01	8.30E-01	OXER1	oxoeicosanoid (OXE) receptor 1	chr2p21	1553222_at	NM_148962
3.05	2.96	0.09	5.56E-01	8.30E-01	JRKL	Jerky homolog-like (mouse)	chr11q21	1557790_at	NM_003772
6.46	6.30	0.16	5.56E-01	8.31E-01	RAB32	RAB32, member RAS oncogene family	chr6q24.3	204214_s_at	NM_006834
3.62	3.47	0.15	5.56E-01	8.31E-01	GK3P	glycerol kinase 3 pseudogene	chr4q32.1	215966_x_at	---
5.87	5.69	0.17	5.56E-01	8.31E-01	SNX11	sorting nexin 11	chr17q21.32	220140_s_at	NM_013323 /// NM_152244
2.30	2.16	0.14	5.56E-01	8.31E-01	RFXAP	regulatory factor X-associated protein	chr13q14	229431_at	NM_000538
3.36	3.24	0.11	5.56E-01	8.31E-01	CHAF1A	chromatin assembly factor 1, subunit A (p150)	chr19p13.3	203975_s_at	NM_005483
4.38	4.23	0.15	5.56E-01	8.31E-01	C1orf107	chromosome 1 open reading frame 107	chr1q32.2	220251_at	NM_014388
3.21	3.08	0.12	5.57E-01	8.31E-01	---	---	---	1565677_at	---
2.22	2.16	0.06	5.57E-01	8.31E-01	---	---	---	242604_at	---
3.01	2.91	0.10	5.57E-01	8.31E-01	C1orf56	Chromosome 1 open reading frame 56	chr1q21.2	230468_s_at	NM_017860

5.93	5.84	0.09	5.57E-01	8.31E-01	C1orf144	chromosome 1 open reading frame 144	chr1p36.13	212003_at	NM_001114600 /// NM_015609																				
4.46	4.34	0.12	5.57E-01	8.31E-01	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	chr1q23	204007_at	NM_000570																				
5.47	5.35	0.12	5.57E-01	8.31E-01	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	chr11p15.5	217182_at	NM_017511 /// XM_001134429 /// XM_001714104 /// XM_001714774																				
3.27	3.17	0.10	5.57E-01	8.31E-01	S1PR5	sphingosine-1-phosphate receptor 5	chr19p13.2	230464_at	NM_030760																				
2.32	2.23	0.09	5.57E-01	8.31E-01	DMRT1	doublesex and mab-3 related transcription factor 1	chr9p24.3	220493_at	NM_021951																				
2.11	2.03	0.08	5.57E-01	8.31E-01	FAM80B	Family with sequence similarity 80, member B	chr12p13.31	236911_at	NM_020734																				
2.86	2.78	0.08	5.57E-01	8.31E-01	ADD2	adducin 2 (beta)	chr2p14-p13	237336_at	NM_001617 /// NM_017482 /// NM_017483 /// NM_017484 /// NM_017488																				
2.60	2.47	0.14	5.57E-01	8.31E-01	---	---	---	1562760_at	---																				
2.62	2.51	0.12	5.57E-01	8.31E-01	VRK3	vaccinia related kinase 3	chr19q13	1566700_at	NM_001025778 /// NM_016440																				
3.66	3.52	0.14	5.57E-01	8.31E-01	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	chr11q13	214369_s_at	NM_001098670 /// NM_001098671 /// NM_153819																				
6.43	6.32	0.10	5.57E-01	8.31E-01	TRAPPC9	trafficking protein particle complex 9	chr8q24.3	56829_at	NM_031466																				
3.78	3.65	0.13	5.57E-01	8.31E-01	LOC440350 /// LOC729602 /// LOC729978 /// PDXDC2	similar to nuclear pore complex interacting protein /// similar to nuclear pore complex interacting protein /// NPIP-like protein 2 /// pyridoxal-dependent decarboxylase domain containing 2	chr16p11.2 /// chr16p13.13 /// chr16q22.1 /// chr18p11.21	215920_s_at	NM_001018122 /// NR_003610 /// XM_001713614 /// XM_001717235 /// XM_001720898 /// XM_001720909 /// XM_001720910 /// XM_001723013 /// XM_001723016 /// XM_001732844 /// XM_001732845																				
2.24	2.17	0.07	5.57E-01	8.31E-01	---	---	---	1561469_at	---																				
4.28	4.17	0.11	5.57E-01	8.31E-01	MED20	mediator complex subunit 20	chr6p21.1	206961_s_at	NM_004275																				
5.82	5.53	0.28	5.57E-01	8.31E-01	GART	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	chr21q22.1|21q22.11	230097_at	NM_000819 /// NM_175085																				
3.89	3.78	0.11	5.57E-01	8.31E-01	---	---	---	1566456_at	---																				
3.45	3.33	0.12	5.57E-01	8.31E-01	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	chr1p21.1-p13.2	224315_at	NM_007204																				
4.06	3.90	0.16	5.57E-01	8.31E-01	ANTXR1	anthrax toxin receptor 1	chr2p13.1	220092_s_at	NM_018153 /// NM_032208 /// NM_053034																				
4.21	4.07	0.14	5.57E-01	8.31E-01	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	chr13q14	218653_at	NM_014252																				
4.27	4.15	0.12	5.57E-01	8.31E-01	GLTSCR1	glioma tumor suppressor candidate region gene 1	chr19q13.3	219445_at	NM_015711																				
2.09	2.02	0.07	5.58E-01	8.31E-01	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	chr3q26.3	242428_at	NM_020640																				
4.17	4.01	0.15	5.58E-01	8.31E-01	---	---	---	240854_x_at	---																				
5.78	5.51	0.28	5.58E-01	8.31E-01	ZBTB1	zinc finger and BTB domain containing 1	chr14q23.3	213376_at	NM_001123329 /// NM_014950																				

3.17	3.03	0.14	5.58E-01	8.31E-01	FBLN7	fibulin 7	chr2q13	229247_at	NM_001128165 /// NM_153214																			
4.84	4.65	0.19	5.58E-01	8.31E-01	WDR1	WD repeat domain 1	chr4p16.1	210935_s_at	NM_005112 /// NM_017491																			
5.41	5.28	0.13	5.58E-01	8.31E-01	C8orf41	chromosome 8 open reading frame 41	chr8p12	219124_at	NM_001102401 /// NM_025115																			
3.44	3.34	0.10	5.58E-01	8.31E-01	LOC158376	hypothetical LOC158376	chr9p13.3	1557371_a_at	XM_001129749 /// XM_001130949 /// XM_001721058																			
3.78	3.70	0.08	5.58E-01	8.31E-01	OR10H1	olfactory receptor, family 10, subfamily H, member 1	chr19p13.1	208558_at	NM_013940																			
2.32	2.24	0.08	5.58E-01	8.31E-01	FAR1	fatty acyl CoA reductase 1	chr11p15.2	234767_at	NM_032228																			
2.43	2.34	0.09	5.58E-01	8.31E-01	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	chr1p31.3	240227_at	NM_001077700 /// NM_001077701 /// NM_001077702 /// NM_001077703 /// NM_001077704 /// NM_020948																			
1.94	1.87	0.07	5.58E-01	8.31E-01	---	---	---	1556439_at	---																			
2.12	2.04	0.08	5.58E-01	8.31E-01	---	---	---	1562083_at	---																			
2.39	2.31	0.08	5.58E-01	8.31E-01	C8orf46	chromosome 8 open reading frame 46	chr8q13.1	229430_at	NM_152765																			
3.59	3.45	0.14	5.58E-01	8.31E-01	SIRT4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	chr12q	222248_s_at	NM_012240																			
3.99	3.83	0.17	5.58E-01	8.31E-01	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	chr19q13.3	214017_s_at	NM_014681																			
7.47	7.35	0.12	5.58E-01	8.31E-01	UBAP1	ubiquitin associated protein 1	chr9p13.3	221490_at	NM_016525																			
3.29	3.06	0.23	5.58E-01	8.31E-01	PTBP2	polypyrimidine tract binding protein 2	chr1p22.1-p21.3	218683_at	NM_021190																			
2.13	2.06	0.08	5.58E-01	8.31E-01	LOC401312	LOC401318	chr7p15.3	1557604_at	---																			
3.64	3.52	0.12	5.58E-01	8.31E-01	RBM26	RNA binding motif protein 26	chr13q31.1	222626_at	NM_022118																			
5.75	5.65	0.10	5.58E-01	8.31E-01	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	chr8q24.2	209781_s_at	NM_006558																			
2.34	2.27	0.07	5.58E-01	8.31E-01	---	---	---	1562038_at	---																			
4.74	4.64	0.10	5.58E-01	8.32E-01	FLJ20433	hypothetical protein FLJ20433	chr9q34.3	220838_at	NM_017820																			
4.04	3.89	0.16	5.59E-01	8.32E-01	NFXL1	nuclear transcription factor, X-box binding-like 1	chr4p12	227220_at	NM_152995																			
2.76	2.64	0.12	5.59E-01	8.32E-01	ZMYM6	zinc finger, MYM-type 6	chr1p34.2	219925_at	NM_007167																			
3.15	3.05	0.10	5.59E-01	8.32E-01	SAFB	Scaffold attachment factor B	chr19p13.3-p13.2	213635_s_at	NM_002967																			
3.86	3.78	0.08	5.59E-01	8.32E-01	BTF3L4	basic transcription factor 3-like 4	chr1p32.3	238675_x_at	NM_152265																			
2.42	2.34	0.08	5.59E-01	8.32E-01	---	---	---	224398_at	---																			
2.16	2.09	0.07	5.59E-01	8.32E-01	---	---	---	241297_at	---																			
3.19	3.06	0.13	5.59E-01	8.32E-01	---	---	---	242312_x_at	---																			
3.46	3.36	0.09	5.59E-01	8.32E-01	---	---	---	230119_at	---																			
3.40	3.24	0.16	5.59E-01	8.32E-01	ARHGAP22	Rho GTPase activating protein 22	chr10q11.22	206298_at	NM_021226																			
2.03	1.94	0.09	5.59E-01	8.32E-01	---	---	---	1564220_a_at	---																			
2.79	2.69	0.09	5.59E-01	8.32E-01	---	---	---	243367_at	---																			
3.05	2.97	0.08	5.59E-01	8.32E-01	KIAA1632	KIAA1632	chr18q12.3-q21.1	236108_at	NM_020964																			
5.72	5.54	0.18	5.59E-01	8.32E-01	ZNF274	zinc finger protein 274	chr19qter	204937_s_at	NM_016324 /// NM_016325 /// NM_133502																			
2.84	2.74	0.09	5.59E-01	8.32E-01	CKM	creatine kinase, muscle	chr19q13.2-q13.3	204810_s_at	NM_001824																			
4.57	4.42	0.15	5.59E-01	8.32E-01	PPP1R3E	protein phosphatase 1, regulatory (inhibitor) subunit 3E	chr14q11.2	229001_at	XR_040048 /// XR_040049 /// XR_040050																			
4.05	3.97	0.08	5.59E-01	8.32E-01	---	---	---	1561918_at	---																			
2.03	1.94	0.08	5.59E-01	8.32E-01	ERICH1	glutamate-rich 1	chr8p23.3	1556357_s_at	NM_207332																			
4.73	4.53	0.20	5.59E-01	8.32E-01	RGNEF	Rho-guanine nucleotide exchange factor	chr5q13.2	1554004_a_at	NM_001080479																			
2.82	2.73	0.09	5.59E-01	8.32E-01	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	chr19p13.3-p13.2	234035_at	NM_005968 /// NM_031203																			
6.66	6.43	0.23	5.59E-01	8.32E-01	NDFIP2	Nedd4 family interacting protein 2	chr13q31.1	224799_at	NM_019080																			
4.37	4.27	0.10	5.59E-01	8.32E-01	C1orf182	chromosome 1 open reading frame 182	chr1q22	230608_at	NM_144627																			
5.77	5.63	0.15	5.59E-01	8.32E-01	ELMOD3	ELMO/CED-12 domain containing 3	chr2p11.2	226286_at	NM_032213																			

3.05	2.92	0.13	5.59E-01	8.32E-01	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	chr1q42-q44	205306_x_at	NM_003679
4.84	4.70	0.14	5.59E-01	8.32E-01	ADO	2-aminoethanethiol (cysteamine) dioxygenase	chr10q21.2	212500_at	NM_032804
2.08	2.01	0.07	5.59E-01	8.32E-01	KLHL23	kelch-like 23 (Drosophila)	chr2q31.1	217505_at	NM_144711
6.37	6.26	0.12	5.60E-01	8.32E-01	AK1	adenylate kinase 1	chr9q34.1	202588_at	NM_000476
5.73	5.57	0.17	5.60E-01	8.32E-01	LRRC16A	leucine rich repeat containing 16A	chr6p22.2	219573_at	NM_017640
3.18	3.04	0.13	5.60E-01	8.32E-01	LOC100130275	hypothetical protein LOC100130275	chr6p24.3	1560503_a_at	XM_001720213 /// XM_001724910 /// XM_001725291
6.64	6.48	0.17	5.60E-01	8.32E-01	YIPF2	Yip1 domain family, member 2	chr19p13.2	221939_at	NM_024029
2.87	2.80	0.07	5.60E-01	8.32E-01	---	---	---	210920_x_at	---
4.63	4.50	0.14	5.60E-01	8.32E-01	---	---	---	235819_at	---
6.52	6.42	0.10	5.60E-01	8.32E-01	TRAK1	trafficking protein, kinesin binding 1	chr3p25.3-p24.1	214924_s_at	NM_001042646 /// NM_014965
7.44	7.27	0.18	5.60E-01	8.32E-01	RAN	RAN, member RAS oncogene family	chr12q24.3	200749_at	NM_006325
4.38	4.21	0.16	5.60E-01	8.32E-01	CIDEC	cell death-inducing DFFA-like effector c	chr3p25.3	219398_at	NM_022094
7.68	7.55	0.13	5.60E-01	8.32E-01	MRPS25	mitochondrial ribosomal protein S25	chr3p25	224869_s_at	NM_022497
9.35	9.27	0.08	5.60E-01	8.32E-01	ITM2B	integral membrane protein 2B	chr13q14.3	217731_s_at	NM_021999
2.04	1.97	0.07	5.60E-01	8.33E-01	G30	putative protein LG30	chr13q33.2|13q34	1553024_at	---
4.53	4.42	0.11	5.61E-01	8.33E-01	ANKRD13D	ankyrin repeat domain 13 family, member D	chr11q13.1	244756_at	NM_207354
3.36	3.24	0.12	5.61E-01	8.33E-01	---	---	---	243383_at	---
7.35	7.25	0.11	5.61E-01	8.33E-01	C19orf42	chromosome 19 open reading frame 42	chr19p13.11	224717_s_at	NM_024104
3.95	3.84	0.11	5.61E-01	8.33E-01	C9orf114	chromosome 9 open reading frame 114	chr9q34.11	222674_at	NM_016390
3.91	3.73	0.18	5.61E-01	8.33E-01	---	---	---	230406_at	---
3.61	3.50	0.11	5.61E-01	8.33E-01	TEPP	testis/prostate/placenta-expressed protein	chr16q13	240119_at	NM_199046 /// NM_199456
5.52	5.39	0.13	5.61E-01	8.33E-01	USP3	ubiquitin specific peptidase 3	chr15q22.3	226652_at	NM_006537
2.22	2.15	0.07	5.61E-01	8.33E-01	---	---	---	1561479_at	---
2.43	2.35	0.09	5.61E-01	8.33E-01	OR2M4	olfactory receptor, family 2, subfamily M, member 4	chr1q44	1566289_at	NM_017504
2.10	2.02	0.07	5.61E-01	8.33E-01	---	---	---	237771_s_at	---
3.49	3.39	0.10	5.61E-01	8.33E-01	---	---	---	213569_at	---
2.90	2.70	0.20	5.61E-01	8.33E-01	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	chr15q15.3	1555106_a_at	NM_016396
4.25	4.16	0.09	5.61E-01	8.33E-01	---	---	---	1560047_s_at	---
2.07	1.99	0.08	5.61E-01	8.33E-01	ANKFN1	Ankyrin-repeat and fibronectin type III domain containing 1	chr17q22	1559640_at	NM_153228
2.12	2.05	0.07	5.61E-01	8.33E-01	---	---	---	1561025_at	---
9.64	9.51	0.13	5.61E-01	8.33E-01	NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	chrXp11.3	218320_s_at	NM_019056
2.26	2.18	0.08	5.61E-01	8.33E-01	---	---	---	1558343_at	---
2.89	2.72	0.16	5.61E-01	8.33E-01	---	---	---	235928_at	---
2.98	2.88	0.10	5.62E-01	8.33E-01	KIAA1217	KIAA1217	chr10p12.2-p12.1	1560115_a_at	NM_001098500 /// NM_001098501 /// NM_019590
2.54	2.45	0.08	5.62E-01	8.33E-01	---	---	---	1569449_a_at	---
2.27	2.18	0.10	5.62E-01	8.33E-01	---	---	---	1562481_at	---
4.40	4.28	0.12	5.62E-01	8.33E-01	SLC45A4	solute carrier family 45, member 4	chr8q24.3	225598_at	NM_001080431
3.89	3.80	0.09	5.62E-01	8.33E-01	---	---	---	213739_at	---
2.04	1.98	0.06	5.62E-01	8.33E-01	---	---	---	244386_at	---
2.71	2.61	0.10	5.62E-01	8.33E-01	ZBED4	zinc finger, BED-type containing 4	chr22q13.33	204799_at	NM_014838
7.55	7.43	0.11	5.62E-01	8.33E-01	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	chr10q23.3	218228_s_at	NM_025235
1.89	1.82	0.07	5.62E-01	8.33E-01	---	---	---	1563185_at	---
5.59	5.43	0.16	5.62E-01	8.34E-01	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	chr12q24.13	222727_s_at	NM_024959
2.46	2.35	0.10	5.62E-01	8.34E-01	---	---	---	240511_at	---
6.44	6.34	0.10	5.62E-01	8.34E-01	SS18L2	synovial sarcoma translocation gene on chromosome 18-like 2	chr3p21	218283_at	NM_016305
5.48	5.20	0.28	5.62E-01	8.34E-01	FLJ10357	hypothetical protein FLJ10357	chr14q11.2	227855_at	NM_018071
3.84	3.67	0.17	5.62E-01	8.34E-01	PKP4	plakophilin 4	chr2q23-q31	201927_s_at	NM_001005476 /// NM_003628
4.41	4.24	0.17	5.62E-01	8.34E-01	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	chr12q24.13	224433_s_at	NM_001111322 /// NM_024072
2.06	1.99	0.07	5.62E-01	8.34E-01	THEX1	three prime histone mRNA exonuclease 1	chr8p23.1	231852_at	NM_153332
7.02	6.92	0.09	5.62E-01	8.34E-01	SEPHS2	selenophosphate synthetase 2	chr16p11.2	200961_at	NM_012248
3.47	3.41	0.06	5.63E-01	8.34E-01	TMEM143	transmembrane protein 143	chr19q13.32	219589_s_at	NM_018273

2.61	2.53	0.08	5.63E-01	8.34E-01	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	chr8p11.23	1570042_a_at	NM_001005845 /// NM_003816																				
4.74	4.58	0.16	5.63E-01	8.34E-01	CLCC1	chloride channel CLIC-like 1	chr1p13.3	207855_s_at	NM_001048210 /// NM_015127																				
2.17	2.10	0.07	5.63E-01	8.34E-01	---	---	---	1562311_at	---																				
2.89	2.75	0.14	5.63E-01	8.34E-01	ZNF333	zinc finger protein 333	chr19p13	1559674_at	NM_032433																				
2.30	2.24	0.06	5.63E-01	8.34E-01	DENND4C	DENN/MADD domain containing 4C	chr9p22.1	234968_at	NM_017925																				
3.18	3.05	0.14	5.63E-01	8.34E-01	LOC643837	hypothetical LOC643837	chr1p36.33	235497_at	NR_015368 /// XM_927114																				
6.15	5.89	0.26	5.63E-01	8.34E-01	ATR	ataxia telangiectasia and Rad3 related	chr3q22-q24	209903_s_at	NM_001184																				
4.41	4.31	0.10	5.63E-01	8.34E-01	GATA1	GATA binding protein 1 (globin transcription factor 1)	chrXp11.23	1555590_a_at	NM_002049																				
5.97	5.89	0.08	5.63E-01	8.34E-01	---	---	---	233757_x_at	---																				
2.43	2.36	0.07	5.63E-01	8.34E-01	ZNF587	zinc finger protein 587	chr19q13.43	1558251_a_at	NM_032828																				
5.00	4.89	0.11	5.63E-01	8.34E-01	RP9	retinitis pigmentosa 9 (autosomal dominant)	chr7p14.3	227852_at	NM_203288																				
2.81	2.70	0.11	5.63E-01	8.34E-01	---	---	---	1565002_at	---																				
4.36	4.26	0.10	5.63E-01	8.34E-01	CYTH4	cytohesin 4	chr22q12.3-q13.1	211521_s_at	NM_013385																				
6.92	6.78	0.13	5.63E-01	8.34E-01	MED25	mediator complex subunit 25	chr19q13.3	208110_x_at	NM_030973																				
2.34	2.20	0.14	5.64E-01	8.34E-01	ZNF597	zinc finger protein 597	chr16p13.3	230542_at	NM_152457																				
2.18	2.08	0.10	5.64E-01	8.34E-01	---	---	---	216518_at	---																				
3.22	3.14	0.08	5.64E-01	8.34E-01	KLK2	kallikrein-related peptidase 2	chr19q13.41	210339_s_at	NM_001002231 /// NM_005551																				
2.34	2.28	0.07	5.64E-01	8.34E-01	---	---	---	1569833_at	---																				
4.47	4.36	0.11	5.64E-01	8.34E-01	PPHLN1	periphilin 1	chr12q12	227025_at	NM_016488 /// NM_201438 /// NM_201439 /// NM_201440 /// NM_201515																				
7.27	7.10	0.17	5.64E-01	8.35E-01	41523	septin 6	chrXq24	214298_x_at	NM_015129 /// NM_145799 /// NM_145800 /// NM_145802																				
5.07	5.00	0.07	5.64E-01	8.35E-01	HDAC10	histone deacetylase 10	chr22q13.31	226672_s_at	NM_032019																				
6.17	6.02	0.15	5.64E-01	8.35E-01	BRMS1L	breast cancer metastasis-suppressor 1-like	chr14q13.2	226580_at	NM_032352																				
2.19	2.11	0.08	5.64E-01	8.35E-01	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	chr12q12-q14	211790_s_at	NM_003482																				
2.44	2.33	0.11	5.64E-01	8.35E-01	PKHD1L1	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	chr8q23.1-q23.2	230673_at	NM_177531																				
2.09	2.02	0.07	5.64E-01	8.35E-01	MAGEA4	melanoma antigen family A, 4	chrXq28	214254_at	NM_001011548 /// NM_001011549 /// NM_001011550 /// NM_002362																				
2.23	2.16	0.07	5.64E-01	8.35E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	216573_at	---																				
2.20	2.10	0.10	5.64E-01	8.35E-01	C2orf65	Chromosome 2 open reading frame 65	chr2p13.1	234325_at	NM_138804																				
5.82	5.70	0.12	5.64E-01	8.35E-01	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	chr5q33.1-qter	205270_s_at	NM_005565																				
2.85	2.74	0.11	5.64E-01	8.35E-01	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	chr1p36.1	214230_at	NM_001039802 /// NM_001791 /// NM_044472																				
4.24	4.15	0.10	5.64E-01	8.35E-01	C8orf74	chromosome 8 open reading frame 74	chr8p23.1	1569245_at	NM_001040032																				

2.53	2.47	0.07	5.64E-01	8.35E-01	LOC100132894	hypothetical protein LOC100132894	chr18q23	241821_at	XM_001715252 /// XM_001715267 /// XM_001715273 /// XM_001715281 /// XM_001721389 /// XM_001721391 /// XM_001721392 /// XM_001721394 /// XM_001721411 /// XM_001721413 /// XM_001721414 /// XM_001721415																		
2.93	2.84	0.09	5.64E-01	8.35E-01	---	---	---	1560621_at	---																			
1.86	1.80	0.06	5.65E-01	8.35E-01	---	---	---	243991_at	---																			
1.98	1.91	0.07	5.65E-01	8.35E-01	RECQL5	RecQ protein-like 5	chr17q25.2-q25.3	1561720_at	NM_001003715 /// NM_001003716 /// NM_004259																			
2.81	2.74	0.07	5.65E-01	8.35E-01	MSMB	microseminoprotein, beta-	chr10q11.2	210297_s_at	NM_002443 /// NM_138634																			
7.81	7.54	0.27	5.65E-01	8.35E-01	RSRC2	arginine/serine-rich coiled-coil 2	chr12q24.31	202302_s_at	NM_023012 /// NM_198261 /// NM_198262																			
2.80	2.71	0.09	5.65E-01	8.35E-01	---	---	---	237421_at	---																			
4.70	4.29	0.41	5.65E-01	8.35E-01	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	chr1q21	200796_s_at	NM_021960 /// NM_182763																			
5.53	5.32	0.21	5.65E-01	8.35E-01	GCC2	GRIP and coiled-coil domain containing 2	chr2q12.3	202832_at	NM_014635 /// NM_181453																			
5.25	5.06	0.19	5.65E-01	8.35E-01	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	chr17q25	202856_s_at	NM_001042422 /// NM_001042423 /// NM_004207																			
2.02	1.96	0.06	5.65E-01	8.35E-01	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	chr3p14.1	1559256_at	NM_001033057 /// NM_004742 /// NM_015520																			
6.27	6.13	0.13	5.65E-01	8.35E-01	RGNEF	Rho-guanine nucleotide exchange factor	chr5q13.2	219610_at	NM_001080479																			
5.10	4.98	0.12	5.65E-01	8.35E-01	APTX	aprataxin	chr9p13.3	222658_s_at	NM_017692 /// NM_175069 /// NM_175071 /// NM_175072 /// NM_175073																			
4.72	4.60	0.11	5.65E-01	8.35E-01	KLK4	kallikrein-related peptidase 4	chr19q13.41	1555697_at	NM_004917																			
3.24	3.15	0.09	5.65E-01	8.35E-01	B4GALT4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	chr3q13.3	210540_s_at	NM_003778 /// NM_212543																			
12.10	12.02	0.08	5.65E-01	8.35E-01	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	chr12p13	217398_x_at	NM_002046																			
6.18	6.03	0.14	5.65E-01	8.35E-01	INO80B /// WBP1	INO80 complex subunit B /// WW domain binding protein 1	chr2p12 /// chr2p13.1	222093_s_at	NM_012477 /// NM_031288																			
3.42	3.30	0.12	5.65E-01	8.35E-01	MED14	mediator complex subunit 14	chrXp11.4-p11.2	202611_s_at	NM_004229																			

8.11	7.85	0.26	5.66E-01	8.35E-01	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	chr2q31	201146_at	NM_006164
2.21	2.14	0.07	5.66E-01	8.35E-01	LOC100132077	Hypothetical protein LOC100132077	chr9q22.32	1559514_at	XM_001724121
3.54	3.45	0.09	5.66E-01	8.35E-01	CLDN19	claudin 19	chr1p34.2	1554805_at	NM_001123395 /// NM_148960
2.86	2.74	0.11	5.66E-01	8.35E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	1559052_s_at	NM_002577
6.31	6.16	0.15	5.66E-01	8.36E-01	MTMR4	myotubularin related protein 4	chr17q22-q23	212277_at	NM_004687
3.27	3.15	0.12	5.66E-01	8.36E-01	LOC391142	hypothetical gene supported by AJ249778; NM_001531	chr1q25.3	1565671_a_at	XM_001131151 /// XM_001132552 /// XM_001718634
5.75	5.54	0.21	5.66E-01	8.36E-01	RHOQ	ras homolog gene family, member Q	chr2p21	1559582_at	NM_012249
2.03	1.96	0.07	5.66E-01	8.36E-01	---	---	---	1569528_at	---
7.87	7.71	0.17	5.66E-01	8.36E-01	C2orf18	chromosome 2 open reading frame 18	chr2p23.3	225695_at	NM_017877
3.68	3.53	0.15	5.66E-01	8.36E-01	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	chr20p12	213973_at	NM_001042576 /// NM_004587
3.25	2.84	0.41	5.66E-01	8.36E-01	PGAP1	post-GPI attachment to proteins 1	chr2q33.1	220576_at	NM_024989
2.40	2.29	0.11	5.66E-01	8.36E-01	---	---	---	1561895_at	---
2.43	2.33	0.10	5.66E-01	8.36E-01	CCL23	chemokine (C-C motif) ligand 23	chr17q12	210548_at	NM_005064 /// NM_145898
2.66	2.58	0.09	5.66E-01	8.36E-01	KIAA0754	hypothetical LOC643314	chr1p34.2	239009_at	NM_015038
6.34	6.22	0.12	5.66E-01	8.36E-01	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	chr1p13.3	204342_at	NM_013386 /// NM_213651
2.56	2.49	0.07	5.66E-01	8.36E-01	---	---	---	1556812_a_at	---
2.79	2.67	0.11	5.66E-01	8.36E-01	ZNF649	zinc finger protein 649	chr19q13.33	223616_at	NM_023074
6.93	6.78	0.14	5.66E-01	8.36E-01	C11orf24	chromosome 11 open reading frame 24	chr11q13	218299_at	NM_022338
2.85	2.70	0.15	5.67E-01	8.36E-01	---	---	---	237496_at	---
2.37	2.30	0.08	5.67E-01	8.36E-01	LOC100131600	hypothetical protein LOC100131600	chr20p13	234742_at	XM_001722993 /// XM_001724766 /// XM_001724813
1.88	1.81	0.07	5.67E-01	8.36E-01	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1	chr7q31-q32	220502_s_at	NM_022444
7.70	7.40	0.30	5.67E-01	8.36E-01	CTBP1	C-terminal binding protein 1	chr4p16	213979_s_at	NM_001012614 /// NM_001328
3.47	3.37	0.10	5.67E-01	8.36E-01	MAPK1	mitogen-activated protein kinase 1	chr22q11.2|22q11.21	1552263_at	NM_002745 /// NM_138957
1.96	1.89	0.07	5.67E-01	8.36E-01	IGFBP1	insulin-like growth factor binding protein 1	chr7p13-p12	205302_at	NM_000596
2.25	2.18	0.07	5.67E-01	8.36E-01	UGT1A10 /// UGT1A6 /// UGT1A7 /// UGT1A8	UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A7 /// UDP glucuronosyltransferase 1 family, polypeptide A8	chr2q37	221304_at	NM_001072 /// NM_019075 /// NM_019076 /// NM_019077 /// NM_205862
2.22	2.15	0.07	5.67E-01	8.36E-01	LOC100128993	Similar to hCG2036572	chr8p22	1560595_at	XM_001715896 /// XM_001716686 /// XM_001717417
2.54	2.45	0.09	5.67E-01	8.36E-01	RHCE /// RHD	Rh blood group, CcEe antigens /// Rh blood group, D antigen	chr1p36.11	215819_s_at	NM_001127691 /// NM_016124 /// NM_020485 /// NM_138616 /// NM_138617 /// NM_138618
2.74	2.66	0.09	5.67E-01	8.36E-01	NUDT9P1	nudix (nucleoside diphosphate linked moiety X)-type motif 9 pseudogene 1	chr10q23.32	1552564_at	NR_002779
1.97	1.91	0.06	5.67E-01	8.36E-01	---	---	---	1557012_a_at	---

7.82	7.71	0.11	5.67E-01	8.36E-01	TBL2	transducin (beta)-like 2	chr7q11.23	212685_s_at	NM_012453
2.92	2.78	0.14	5.67E-01	8.36E-01	---	---	---	239610_at	---
6.75	6.62	0.13	5.67E-01	8.36E-01	UBAP1	ubiquitin associated protein 1	chr9p13.3	46270_at	NM_016525
2.28	2.21	0.07	5.67E-01	8.36E-01	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	chr2p13-p12	206035_at	NM_002908
6.54	6.43	0.11	5.67E-01	8.36E-01	TNIP2	TNFAIP3 interacting protein 2	chr4p16.3	232160_s_at	NM_024309
5.03	4.93	0.10	5.67E-01	8.36E-01	COL7A1	collagen, type VII, alpha 1	chr3p21.1	217312_s_at	NM_000094
5.21	4.98	0.23	5.67E-01	8.36E-01	CD3EAP	CD3e molecule, epsilon associated protein	chr19q13.3	205264_at	NM_012099
6.48	6.34	0.15	5.67E-01	8.37E-01	MED28	Mediator complex subunit 28	chr4p16	228992_at	NM_025205
3.55	3.44	0.11	5.67E-01	8.37E-01	ELA3B	elastase 3B, pancreatic	chr1p36.12	206151_x_at	NM_007352
2.32	2.24	0.08	5.68E-01	8.37E-01	---	---	---	216090_x_at	---
2.74	2.62	0.11	5.68E-01	8.37E-01	C20orf141	chromosome 20 open reading frame 141	chr20p13	1554041_at	NM_080739
2.51	2.38	0.13	5.68E-01	8.37E-01	RUFY2	RUN and FYVE domain containing 2	chr10q21.3	235345_at	NM_001042417 /// NM_017987
2.62	2.54	0.08	5.68E-01	8.37E-01	GRID2	glutamate receptor, ionotropic, delta 2	chr4q22	221364_at	NM_001510
7.38	7.22	0.15	5.68E-01	8.37E-01	C12orf52	chromosome 12 open reading frame 52	chr12q24.13	221777_at	NM_032848
2.13	2.06	0.07	5.68E-01	8.37E-01	---	---	---	1558750_a_at	---
8.74	8.60	0.14	5.68E-01	8.37E-01	APOA1BP	apolipoprotein A-I binding protein	chr1q22-q21.2	225427_s_at	NM_144772
2.02	1.96	0.06	5.68E-01	8.37E-01	HRH4	histamine receptor H4	chr18q11.2	221170_at	NM_021624
6.27	6.10	0.18	5.68E-01	8.37E-01	LOC402778	similar to RIKEN cDNA 6330512M04 gene (mouse)	---	1564573_at	---
5.41	5.25	0.16	5.68E-01	8.37E-01	STIM1	stromal interaction molecule 1	chr11p15.5	202764_at	NM_003156
2.36	2.28	0.08	5.68E-01	8.37E-01	XCR1	chemokine (C motif) receptor 1	chr3p21.3-p21.1|3p21.3	221468_at	NM_001024644 /// NM_005283
3.40	3.28	0.12	5.68E-01	8.37E-01	GTPBP1	GTP binding protein 1	chr22q13.1	226359_at	NM_004286
5.71	5.52	0.20	5.68E-01	8.37E-01	IPO4	importin 4	chr14q12	218305_at	NM_024658
11.36	11.29	0.07	5.68E-01	8.37E-01	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	chrXq22.2	217963_s_at	NM_014380 /// NM_206915 /// NM_206917
4.11	3.99	0.11	5.68E-01	8.37E-01	C1orf203	chromosome 1 open reading frame 203	chr1p12	1559376_at	---
4.49	4.30	0.19	5.68E-01	8.37E-01	PTN	pleiotrophin	chr7q33-q34	209466_x_at	NM_002825
5.51	5.33	0.17	5.68E-01	8.37E-01	TNS1	Tensin 1	chr2q35-q36	232750_at	NM_022648
2.20	2.11	0.09	5.68E-01	8.37E-01	---	---	---	234509_at	---
5.79	5.70	0.09	5.68E-01	8.37E-01	MORG1	mitogen-activated protein kinase organizer 1	chr19p13.13	224434_s_at	NM_001099737 /// NM_032332
2.69	2.62	0.07	5.68E-01	8.37E-01	---	---	---	1562145_at	---
2.99	2.91	0.08	5.68E-01	8.37E-01	---	---	---	1569305_a_at	---
6.37	6.01	0.36	5.68E-01	8.37E-01	GZF1	GDNF-inducible zinc finger protein 1	chr20p12.3-p11.21	225884_s_at	NM_022482
4.57	4.32	0.26	5.69E-01	8.37E-01	HBG1 /// HBG2	hemoglobin, gamma A /// hemoglobin, gamma G	chr11p15.5	204419_x_at	NM_000184 /// NM_000559
2.55	2.43	0.13	5.69E-01	8.37E-01	AGGF1	angiogenic factor with G patch and FHA domains 1	chr5q13.3	208042_at	NM_018046
4.12	4.01	0.10	5.69E-01	8.37E-01	---	---	---	229066_at	---
4.04	3.88	0.16	5.69E-01	8.37E-01	LOC650392	Hypothetical protein LOC650392	---	1569871_at	XM_944170
2.67	2.57	0.10	5.69E-01	8.37E-01	PSMD6	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	chr3p14.1	232284_at	NM_014814
2.93	2.87	0.07	5.69E-01	8.37E-01	---	---	---	238192_at	---
1.96	1.89	0.08	5.69E-01	8.37E-01	CDC14B /// CDC14C /// LOC100131447	CDC14 cell division cycle 14 homolog B (S. cerevisiae) /// CDC14 cell division cycle 14 homolog C (S. cerevisiae) /// hypothetical LOC100131447	chr7p12.3 /// chr9q22.33	1553320_s_at	NM_001077181 /// NM_003671 /// NM_033331 /// NR_003595 /// XR_036885 /// XR_037167
3.17	3.09	0.08	5.69E-01	8.37E-01	KIAA1009	KIAA1009	chr6q14.3	206005_s_at	NM_014895
6.48	6.27	0.20	5.69E-01	8.37E-01	DDAH2	dimethylarginine dimethylaminohydrolase 2	chr6p21.3	202262_x_at	NM_013974
5.23	5.09	0.14	5.69E-01	8.37E-01	ZNF142	zinc finger protein 142	chr2q34-q35	204474_at	NM_001105537 /// NM_005081
2.03	1.96	0.06	5.69E-01	8.37E-01	---	---	---	217470_at	---
9.35	9.25	0.10	5.69E-01	8.37E-01	SPCS1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	chr3p21.1	217927_at	NM_014041
9.02	8.86	0.16	5.69E-01	8.37E-01	SEC11A	SEC11 homolog A (S. cerevisiae)	chr15q25.3	216274_s_at	NM_014300
2.53	2.45	0.08	5.69E-01	8.37E-01	---	---	---	241021_at	---
11.88	11.82	0.07	5.69E-01	8.37E-01	ACTG1	actin, gamma 1	chr17q25	211983_x_at	NM_001614
3.28	3.14	0.14	5.69E-01	8.37E-01	CD84	CD84 molecule	chr1q24	211188_at	NM_003874
2.20	2.13	0.07	5.69E-01	8.37E-01	ZNF33A	zinc finger protein 33A	chr10p11.2	224276_at	NM_006954 /// NM_006974
2.44	2.36	0.09	5.69E-01	8.37E-01	---	---	---	1561298_at	---

5.08	4.97	0.11	5.70E-01	8.38E-01	AARS2	alanyl-tRNA synthetase 2, mitochondrial (putative)	chr6p21.1	230024_at	NM_020745
5.44	5.32	0.12	5.70E-01	8.38E-01	---	---	---	229798_s_at	---
2.08	2.02	0.07	5.70E-01	8.38E-01	---	---	---	235220_at	---
3.92	3.78	0.14	5.70E-01	8.38E-01	TYMS	thymidylate synthetase	chr18p11.32	1554696_s_at	NM_001071
2.05	1.99	0.06	5.70E-01	8.38E-01	---	---	---	242115_at	---
2.35	2.27	0.08	5.70E-01	8.38E-01	---	---	---	1561187_at	---
2.13	2.04	0.09	5.70E-01	8.38E-01	FAM5C	family with sequence similarity 5, member C	chr1q31.1	217562_at	NM_199051
2.29	2.14	0.15	5.70E-01	8.38E-01	AGTR2	angiotensin II receptor, type 2	chrXq22-q23	207294_at	NM_000686
2.76	2.65	0.11	5.70E-01	8.38E-01	CLTA	clathrin, light chain (Lca)	chr9p13	1560434_x_at	NM_001076677 /// NM_001833 /// NM_007096
4.07	3.97	0.09	5.70E-01	8.38E-01	C11orf35	chromosome 11 open reading frame 35	chr11p15.5	236050_at	NM_173573
2.72	2.59	0.13	5.70E-01	8.38E-01	CDH4	cadherin 4, type 1, R-cadherin (retinal)	chr20q13.3	220227_at	NM_001794
8.42	8.31	0.11	5.70E-01	8.38E-01	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	chr16p12.1	224666_at	NM_145080
3.25	3.13	0.12	5.70E-01	8.38E-01	WDR86	WD repeat domain 86	chr7q36.1	243526_at	NM_198285
3.30	3.20	0.11	5.70E-01	8.38E-01	LOC283902	hypothetical gene supported by BC019009	chr16q22.3	1570315_at	NM_001101347
2.79	2.72	0.07	5.70E-01	8.38E-01	---	---	---	1557623_at	---
4.83	4.72	0.12	5.71E-01	8.38E-01	PPP2R5B	protein phosphatase 2, regulatory subunit B', beta isoform	chr11q12-q13	635_s_at	NM_006244
2.55	2.45	0.11	5.71E-01	8.38E-01	DAND5	DAN domain family, member 5	chr19p13.13	1562772_a_at	NM_152654
2.83	2.75	0.08	5.71E-01	8.38E-01	C9orf4	chromosome 9 open reading frame 4	chr9q31	239097_at	NM_014334
2.09	2.00	0.09	5.71E-01	8.38E-01	---	---	---	216456_at	---
2.24	2.17	0.08	5.71E-01	8.38E-01	DAOA	D-amino acid oxidase activator	chr13q33.2|13q34	1555662_s_at	NM_172370
7.95	7.79	0.16	5.71E-01	8.38E-01	DST	dystonin	chr6p12.1	215016_x_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380
3.02	2.94	0.08	5.71E-01	8.38E-01	---	---	---	1560964_at	---
5.94	5.80	0.14	5.71E-01	8.38E-01	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	chr9q34.3	226389_s_at	NM_005312 /// NM_198679
2.29	2.21	0.08	5.71E-01	8.38E-01	MBD2	methyl-CpG binding domain protein 2	chr18q21	214396_s_at	NM_003927 /// NM_015832
2.77	2.65	0.12	5.71E-01	8.38E-01	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	chr5q22.2	235258_at	NM_152624
3.29	3.20	0.09	5.71E-01	8.38E-01	BTN2A2	butyrophilin, subfamily 2, member A2	chr6p22.1	205299_s_at	NM_006995 /// NM_181531
5.54	5.29	0.24	5.71E-01	8.38E-01	FPR1	formyl peptide receptor 1	chr19q13.4	205119_s_at	NM_002029
3.90	3.71	0.19	5.71E-01	8.38E-01	TBC1D24	TBC1 domain family, member 24	chr16p13.3	227632_at	NM_020705
2.18	2.11	0.07	5.71E-01	8.38E-01	ZNF334	zinc finger protein 334	chr20q13.12	220022_at	NM_018102 /// NM_199441
7.50	7.29	0.21	5.71E-01	8.38E-01	SLC2A3P1	Solute carrier family 2 (facilitated glucose transporter), member 3 pseudogene 1	chr5q35.1	221751_at	XR_037100 /// XR_037424 /// XR_037874
3.58	3.44	0.14	5.71E-01	8.38E-01	PEX16	peroxisomal biogenesis factor 16	chr11p11.2	221603_at	NM_004813 /// NM_057174
2.67	2.57	0.10	5.71E-01	8.38E-01	---	---	---	243486_at	---
7.59	7.41	0.18	5.72E-01	8.39E-01	SLCO2B1	solute carrier organic anion transporter family, member 2B1	chr11q13	203473_at	NM_007256
2.48	2.40	0.08	5.72E-01	8.39E-01	NPY2R	neuropeptide Y receptor Y2	chr4q31	208379_x_at	NM_000910
2.60	2.51	0.10	5.72E-01	8.39E-01	---	---	---	1561065_at	---
3.08	2.96	0.12	5.72E-01	8.39E-01	LOC283861	hypothetical locus LOC283861	chr16q24.3	1554520_at	---
2.09	2.02	0.07	5.72E-01	8.39E-01	---	---	---	1562839_at	---
2.25	2.16	0.09	5.72E-01	8.39E-01	---	---	---	1568663_a_at	---
5.31	5.14	0.17	5.72E-01	8.39E-01	SKI	v-ski sarcoma viral oncogene homolog (avian)	chr1q22-q24	229265_at	NM_003036

10.32	10.11	0.21	5.72E-01	8.39E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	209312_x_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447																			
3.04	2.89	0.15	5.72E-01	8.39E-01	LOC283551	hypothetical protein LOC283551	chr14q22.1	239777_at	NM_001012706																				
3.03	2.91	0.11	5.72E-01	8.39E-01	---	---	---	238397_at	---																				
2.72	2.65	0.07	5.72E-01	8.39E-01	---	---	---	235807_at	---																				
7.34	7.14	0.20	5.72E-01	8.39E-01	ACTN1	actinin, alpha 1	chr14q24.1-q24.2|14q24|14q22q24	208636_at	NM_001102 /// NM_001130004 /// NM_001130005																				
5.80	5.65	0.15	5.72E-01	8.39E-01	---	---	---	233116_at	---																				
3.52	3.44	0.08	5.72E-01	8.39E-01	---	---	---	244530_at	---																				
2.52	2.42	0.10	5.72E-01	8.39E-01	CEP70	Centrosomal protein 70kDa	chr3q22-q23	238154_at	NM_024491																				
7.42	7.26	0.15	5.72E-01	8.39E-01	SPIRE1	spire homolog 1 (Drosophila)	chr18p11.21	224995_at	NM_001128626 /// NM_001128627 /// NM_020148																				
2.28	2.22	0.06	5.73E-01	8.39E-01	LOC199899	hypothetical protein LOC199899	chr1p31.3	242284_at	XM_378866 /// XM_945515																				
3.71	3.57	0.14	5.73E-01	8.39E-01	---	---	---	236080_at	---																				
2.50	2.40	0.10	5.73E-01	8.39E-01	FKRP	fukutin related protein	chr19q13.32	219853_at	NM_001039885 /// NM_024301																				
4.40	4.27	0.13	5.73E-01	8.39E-01	KIAA1467	KIAA1467	chr12p13.1	213234_at	NM_020853																				

6.88	6.80	0.08	5.73E-01	8.39E-01	MAP4	microtubule-associated protein 4	chr3p21	212567_s_at	NM_001134364 /// NM_001134365 /// NM_002375 /// NM_030884 /// NM_030885
7.06	6.42	0.64	5.73E-01	8.39E-01	CCL21	chemokine (C-C motif) ligand 21	chr9p13	204606_at	NM_002989
7.23	7.11	0.12	5.73E-01	8.39E-01	WIPF2	WAS/WASL interacting protein family, member 2	chr17q21.2	212049_at	NM_133264
8.73	8.53	0.20	5.73E-01	8.39E-01	ANXA6	annexin A6	chr5q32-q34	200982_s_at	NM_001155 /// NM_004033
3.63	3.47	0.15	5.73E-01	8.40E-01	C4orf12	chromosome 4 open reading frame 12	chr4q21.3	238081_at	NR_015359 /// XR_042111 /// XR_042112 /// XR_042113
2.68	2.59	0.09	5.73E-01	8.40E-01	ZNF587	zinc finger protein 587	chr19q13.43	1558253_x_at	NM_032828
2.60	2.51	0.08	5.73E-01	8.40E-01	LOC158257	hypothetical protein LOC158257	chr9q22.32	1559129_a_at	XM_001715705 /// XM_001716287 /// XM_001717793
2.21	2.14	0.07	5.74E-01	8.40E-01	---	---	---	241183_at	---
5.64	5.51	0.12	5.74E-01	8.40E-01	TACC2	transforming, acidic coiled-coil containing protein 2	chr10q26	202289_s_at	NM_006997 /// NM_206860 /// NM_206861 /// NM_206862
4.13	4.04	0.09	5.74E-01	8.40E-01	USP28	ubiquitin specific peptidase 28	chr11q23	230623_x_at	NM_020886
4.78	4.69	0.09	5.74E-01	8.40E-01	CASZ1	castor zinc finger 1	chr1p36.22	220015_at	NM_001079843 /// NM_017766
3.60	3.51	0.09	5.74E-01	8.40E-01	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	chr4p15.1	219195_at	NM_013261
5.99	5.76	0.23	5.74E-01	8.40E-01	MBD4	methyl-CpG binding domain protein 4	chr3q21-q22	214047_s_at	NM_003925
5.71	5.60	0.11	5.74E-01	8.40E-01	LOC100129673	similar to hCG2042915	chr17p13.2	236611_at	XM_001715544 /// XM_001717297
7.66	6.65	1.01	5.74E-01	8.40E-01	XIST	X (inactive)-specific transcript (non-protein coding)	chrXq13.2	227671_at	NR_001564
3.75	3.64	0.11	5.74E-01	8.40E-01	DKFZP434K028	hypothetical LOC26070	chr11q12.3	1554880_at	---
6.52	6.31	0.21	5.74E-01	8.40E-01	IMPAD1	inositol monophosphatase domain containing 1	chr8q12.1	218516_s_at	NM_017813
5.32	5.21	0.11	5.74E-01	8.40E-01	WHSC1	Wolf-Hirschhorn syndrome candidate 1	chr4p16.3	209054_s_at	NM_001042424 /// NM_007331 /// NM_133330 /// NM_133331 /// NM_133334 /// NM_133335
2.03	1.95	0.08	5.74E-01	8.40E-01	AFF3 /// MLL	AF4/FMR2 family, member 3 /// myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23 /// chr2q11.2-q12	1565034_s_at	NM_001025108 /// NM_002285 /// NM_005933
2.04	1.96	0.08	5.74E-01	8.40E-01	C6orf62	Chromosome 6 open reading frame 62	chr6p22.2	222309_at	NM_030939
8.35	8.20	0.15	5.74E-01	8.40E-01	C5orf24	chromosome 5 open reading frame 24	chr5q31.1	224876_at	NM_152409
5.33	5.20	0.13	5.74E-01	8.40E-01	---	---	---	227116_at	---
3.37	3.25	0.12	5.75E-01	8.40E-01	A2M	alpha-2-macroglobulin	chr12p13.3-p12.3	1558450_at	NM_000014
7.73	7.56	0.17	5.75E-01	8.40E-01	TM4SF1	transmembrane 4 L six family member 1	chr3q21-q25	209386_at	NM_014220
5.01	4.80	0.21	5.75E-01	8.40E-01	C6orf154	chromosome 6 open reading frame 154	chr6p21.1	235935_at	NM_001012974
3.89	3.60	0.28	5.75E-01	8.40E-01	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	chr2q24.1	225447_at	NM_000408 /// NM_001083112

8.72	8.55	0.18	5.75E-01	8.41E-01	ACTR10	actin-related protein 10 homolog (S. cerevisiae)	chr14q23.1	222230_s_at	NM_018477
2.38	2.27	0.11	5.75E-01	8.41E-01	HPCAL4	hippocalcin like 4	chr1p34.2	219671_at	NM_016257
2.14	2.08	0.06	5.75E-01	8.41E-01	---	---	---	240605_at	---
6.06	5.90	0.15	5.75E-01	8.41E-01	TRIM26	tripartite motif-containing 26	chr6p21.3	202702_at	NM_003449
7.86	7.76	0.09	5.75E-01	8.41E-01	POP4	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	chr19q12	202868_s_at	NM_006627
2.06	1.98	0.09	5.75E-01	8.41E-01	---	---	---	1556395_at	---
2.30	2.21	0.09	5.75E-01	8.41E-01	---	---	---	1560012_at	---
3.32	3.20	0.11	5.75E-01	8.41E-01	---	---	---	233374_at	---
2.37	2.30	0.08	5.75E-01	8.41E-01	---	---	---	239674_at	---
8.08	7.92	0.16	5.75E-01	8.41E-01	CASC4	cancer susceptibility candidate 4	chr15q15.3	224619_at	NM_138423 /// NM_177974
2.10	2.03	0.07	5.75E-01	8.41E-01	---	---	---	237675_at	---
4.17	4.04	0.13	5.75E-01	8.41E-01	GPR6	G protein-coupled receptor 6	chr6q21	1553507_a_at	NM_005284
2.45	2.36	0.09	5.75E-01	8.41E-01	---	---	---	236727_at	---
2.09	2.02	0.07	5.75E-01	8.41E-01	---	---	---	240753_at	---
2.85	2.74	0.11	5.75E-01	8.41E-01	RNF40	ring finger protein 40	chr16p11.2-p11.1	217642_at	NM_014771
2.50	2.41	0.09	5.75E-01	8.41E-01	LOC100134109	similar to collagen, type XXII, alpha 1	---	242326_at	XM_001714227
2.43	2.35	0.08	5.75E-01	8.41E-01	CLEC3A	C-type lectin domain family 3, member A	chr16q23	231802_at	NM_005752
2.69	2.59	0.11	5.75E-01	8.41E-01	ATXN7L2	ataxin 7-like 2	chr1p13.3	230038_at	NM_153340
2.95	2.86	0.09	5.75E-01	8.41E-01	---	---	---	1558720_at	---
3.17	3.08	0.08	5.76E-01	8.41E-01	NLGN2	Neuroligin 2	chr17p13.1	235838_at	NM_020795
2.33	2.26	0.07	5.76E-01	8.41E-01	C4orf34	chromosome 4 open reading frame 34	chr4p14	222336_at	NM_174921
5.06	4.85	0.21	5.76E-01	8.41E-01	FLJ41484	hypothetical LOC650669	chr13q34	238127_at	XR_042106 /// XR_042107
6.56	6.09	0.47	5.76E-01	8.41E-01	HOXB2	homeobox B2	chr17q21-q22	205453_at	NM_002145
5.70	5.50	0.20	5.76E-01	8.41E-01	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	chr21q22.3	202086_at	NM_002462
2.30	2.23	0.07	5.76E-01	8.41E-01	SLC35F5	Solute carrier family 35, member F5	chr2q14.1	240335_at	NM_025181
2.18	2.11	0.07	5.76E-01	8.41E-01	---	---	---	234240_at	---
2.64	2.54	0.11	5.76E-01	8.41E-01	---	---	---	242784_at	---
2.22	2.16	0.06	5.76E-01	8.41E-01	---	---	---	1563331_at	---
8.33	8.08	0.25	5.76E-01	8.41E-01	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	chr11q12.1	223280_x_at	NM_022349 /// NM_152851 /// NM_152852
1.99	1.93	0.07	5.76E-01	8.41E-01	SYT16	synaptotagmin XVI	chr14q23.2	1554797_at	NM_031914
7.60	7.42	0.19	5.76E-01	8.41E-01	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	chr4q12	1555837_s_at	NM_000938
2.98	2.90	0.08	5.76E-01	8.41E-01	LRP5	Low density lipoprotein receptor-related protein 5	chr11q13.4	229591_at	NM_002335
4.24	4.08	0.16	5.76E-01	8.41E-01	MTAP	methylthioadenosine phosphorylase	chr9p21	216685_s_at	NM_002451
3.14	2.95	0.19	5.76E-01	8.42E-01	HS1BP3	HCLS1 binding protein 3	chr2p24.1	237407_at	NM_022460
2.51	2.39	0.12	5.76E-01	8.42E-01	PPAPDC1A	phosphatidic acid phosphatase type 2 domain containing 1A	chr10q26.12	236044_at	NM_001030059
4.37	4.15	0.21	5.76E-01	8.42E-01	SIPA1L2	signal-induced proliferation-associated 1 like 2	chr1q42.2	225056_at	NM_020808
2.05	1.99	0.06	5.77E-01	8.42E-01	tcag7.1188	hypothetical LOC340340	chr7q22.3	1561254_at	---
3.81	3.69	0.12	5.77E-01	8.42E-01	SFN	stratifin	chr1p36.11	209260_at	NM_006142
2.68	2.57	0.10	5.77E-01	8.42E-01	---	---	---	230713_at	---
2.23	2.16	0.08	5.77E-01	8.42E-01	SHOX2	short stature homeobox 2	chr3q25-q26.1	210135_s_at	NM_003030 /// NM_006884
2.67	2.57	0.10	5.77E-01	8.42E-01	C19orf26	chromosome 19 open reading frame 26	chr19p13.3	1552354_at	NM_152769
2.60	2.52	0.07	5.77E-01	8.42E-01	C3orf19	chromosome 3 open reading frame 19	chr3p25.1	1558094_s_at	NM_016474
9.06	8.89	0.16	5.77E-01	8.42E-01	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	chr3p24.3	201811_x_at	NM_001018009 /// NM_004844
2.53	2.45	0.08	5.77E-01	8.42E-01	C4orf47	chromosome 4 open reading frame 47	chr4q35.1	237585_at	NM_001114357 /// XM_001720135 /// XM_001723753 /// XM_001723780
3.54	3.43	0.11	5.77E-01	8.42E-01	C16orf55	chromosome 16 open reading frame 55	chr16q24.3	229660_at	NM_153025
5.15	4.94	0.22	5.77E-01	8.42E-01	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)	chr11q22.3	228916_at	NM_152434
6.12	5.92	0.19	5.77E-01	8.42E-01	---	---	---	227126_at	---

3.67	3.55	0.12	5.77E-01	8.42E-01	SPATS1 /// TMEM151B	spermatogenesis associated, serine-rich 1 /// transmembrane protein 151B	chr6p21.1	1564066_at	NM_145026 /// XM_001723534 /// XM_001723740 /// XM_001725716																				
3.25	3.03	0.23	5.77E-01	8.42E-01	ZBTB10	zinc finger and BTB domain containing 10	chr8q13-q21.1	233899_x_at	NM_001105539 /// NM_023929																				
2.19	2.12	0.07	5.77E-01	8.42E-01	---	---	---	239914_at	---																				
3.18	3.07	0.10	5.77E-01	8.42E-01	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	chr4q25-q27	222858_s_at	NM_014395																				
3.95	3.82	0.13	5.77E-01	8.42E-01	LRRC27	leucine rich repeat containing 27	chr10q26.3	228886_at	NM_030626																				
2.40	2.31	0.08	5.77E-01	8.42E-01	LOC221710	hypothetical protein LOC221710	chr6p24.1	1564651_at	XM_001720414 /// XM_001724989 /// XM_001725361																				
2.97	2.86	0.11	5.77E-01	8.42E-01	---	---	---	1565558_at	---																				
2.83	2.70	0.12	5.77E-01	8.42E-01	BTNL8 /// LOC653117	butyrophilin-like 8 /// similar to B7h.4	chr5q35.3	220421_at	NM_001040462 /// NM_024850 /// XM_001722839 /// XM_001722840																				
2.74	2.66	0.07	5.77E-01	8.42E-01	LOC730102	hypothetical protein LOC730102	chr1q25.2	239279_at	XR_015609 /// XR_015793 /// XR_041281																				
1.94	1.88	0.06	5.78E-01	8.42E-01	NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	chr4q25-q26	1570222_at	NM_022569																				
2.32	2.25	0.07	5.78E-01	8.42E-01	NFE2	nuclear factor (erythroid-derived 2), 45kDa	chr12q13	209930_s_at	NM_006163																				
3.17	3.08	0.10	5.78E-01	8.42E-01	FLJ35390	hypothetical LOC255031	chr7p13	1558123_at	---																				
3.43	3.32	0.11	5.78E-01	8.42E-01	ZNF182 /// ZNF630	zinc finger protein 182 /// zinc finger protein 630	chrXp11.3-p11.1 /// chrXp22.11-p11.23	233082_at	NM_001007088 /// NM_001037735 /// NM_006962																				
4.26	4.16	0.10	5.78E-01	8.42E-01	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	chr14q11.2	216603_at	NM_012244 /// NM_182728																				
3.88	3.80	0.08	5.78E-01	8.42E-01	---	---	---	232948_at	---																				
3.05	2.92	0.13	5.78E-01	8.42E-01	GART	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	chr21q22.1|21q22.11	244822_at	NM_000819 /// NM_175085																				
7.48	7.38	0.10	5.78E-01	8.42E-01	INSR	insulin receptor	chr19p13.3-p13.2	213792_s_at	NM_000208 /// NM_001079817																				
1.91	1.85	0.06	5.78E-01	8.42E-01	PAX4	paired box 4	chr7q32	207867_at	NM_006193																				
2.86	2.77	0.09	5.78E-01	8.42E-01	C9orf93	chromosome 9 open reading frame 93	chr9p22.3	1559672_a_at	NM_173550																				
2.77	2.67	0.10	5.78E-01	8.43E-01	WDR4	WD repeat domain 4	chr21q22.3	235551_at	NM_018669 /// NM_033661																				
2.41	2.31	0.10	5.78E-01	8.43E-01	---	---	---	243433_at	---																				
6.02	5.77	0.25	5.78E-01	8.43E-01	ARRDC4	arrestin domain containing 4	chr15q26.3	225283_at	NM_183376																				
3.72	3.62	0.10	5.78E-01	8.43E-01	ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	chr17p13.2	207189_s_at	NM_015113 /// XM_001127649 /// XM_001719617 /// XM_001723898																				
3.04	2.95	0.09	5.79E-01	8.43E-01	CLDN17	claudin 17	chr21q22.11	221328_at	NM_012131																				
6.22	6.04	0.18	5.79E-01	8.43E-01	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	chr22q13.2-q13.31	33307_at	NM_015703																				
3.25	3.15	0.10	5.79E-01	8.43E-01	FLJ42627	Hypothetical LOC645644	chr16p13.3	221944_at	NM_001039907																				
3.47	3.35	0.12	5.79E-01	8.43E-01	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	chr3p22-p21	228499_at	NM_004567																				

5.68	5.57	0.10	5.79E-01	8.43E-01	POU2F1	POU class 2 homeobox 1	chr1q22-q23	227254_at	NM_002697
3.57	3.41	0.16	5.79E-01	8.43E-01	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	chr12q13.13	207056_s_at	NM_001039960 /// NM_004858
2.06	1.99	0.07	5.79E-01	8.43E-01	TRPC3	transient receptor potential cation channel, subfamily C, member 3	chr4q27	206425_s_at	NM_001130698 /// NM_003305
2.17	2.08	0.09	5.79E-01	8.43E-01	---	---	---	1570146_at	---
2.49	2.42	0.07	5.79E-01	8.43E-01	LOC400581	GRB2-related adaptor protein-like	chr17p11.2	1559689_a_at	NM_001129778 /// XM_001720657 /// XM_001723190
2.04	1.98	0.05	5.79E-01	8.43E-01	---	---	---	1556789_a_at	---
2.22	2.13	0.09	5.79E-01	8.43E-01	UBE2CBP	ubiquitin-conjugating enzyme E2C binding protein	chr6q14.1	233327_at	NM_198920
4.79	4.47	0.32	5.79E-01	8.43E-01	LOC154761	hypothetical LOC154761	chr7q34	227868_at	---
4.79	4.58	0.21	5.79E-01	8.43E-01	LOC283357	hypothetical protein LOC283357	chr12p13.33	235151_at	---
2.60	2.53	0.08	5.79E-01	8.43E-01	FABP1	Fatty acid binding protein 1, liver	chr2p11	231693_at	NM_001443
4.47	4.27	0.19	5.79E-01	8.43E-01	MANEAL	mannosidase, endo-alpha-like	chr1p34.3	226132_s_at	NM_001031740 /// NM_001113482 /// NM_152496
3.11	2.98	0.13	5.79E-01	8.43E-01	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta	chr1p|1p36.3	230255_at	NM_000815
7.23	7.07	0.16	5.79E-01	8.43E-01	CD320	CD320 molecule	chr19p13.3-p13.2	218529_at	NM_016579
5.25	5.11	0.14	5.79E-01	8.43E-01	AP3M2	adaptor-related protein complex 3, mu 2 subunit	chr8p11.2	203410_at	NM_001134296 /// NM_006803
3.11	2.98	0.13	5.79E-01	8.43E-01	LOC100128439	hypothetical protein LOC100128439	chr19p13.3	1558448_a_at	XM_001723279 /// XM_001726335 /// XM_001726390
7.97	7.75	0.22	5.79E-01	8.43E-01	SREBF1	sterol regulatory element binding transcription factor 1	chr17p11.2	202308_at	NM_001005291 /// NM_004176
3.17	3.06	0.10	5.79E-01	8.43E-01	---	---	---	1566580_at	---
5.52	5.43	0.08	5.79E-01	8.43E-01	---	---	---	1556540_a_at	---
6.83	6.64	0.19	5.79E-01	8.43E-01	TOP2B	topoisomerase (DNA) II beta 180kDa	chr3p24	211987_at	NM_001068
3.73	3.62	0.11	5.80E-01	8.43E-01	EFCAB6	EF-hand calcium binding domain 6	chr22q13.1-q13.33	220271_x_at	NM_022785 /// NM_198856
2.82	2.73	0.10	5.80E-01	8.43E-01	---	---	---	233044_at	---
1.94	1.88	0.07	5.80E-01	8.43E-01	C9orf93	chromosome 9 open reading frame 93	chr9p22.3	1553433_at	NM_173550
5.24	5.14	0.10	5.80E-01	8.43E-01	THOP1	thimet oligopeptidase 1	chr19q13.3	203235_at	NM_003249
2.84	2.72	0.12	5.80E-01	8.43E-01	HIST1H3E	histone cluster 1, H3e	chr6p21.3	214616_at	NM_003532
4.71	4.56	0.15	5.80E-01	8.43E-01	INTS7	integrator complex subunit 7	chr1p36.13-q42.3	218783_at	NM_015434
2.05	1.98	0.07	5.80E-01	8.43E-01	LOC286189	hypothetical protein LOC286189	chr8q13.1	1556421_at	---
5.42	5.35	0.08	5.80E-01	8.43E-01	ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)	chr3p25.3-p25.2	218673_s_at	NM_006395
2.40	2.31	0.08	5.80E-01	8.43E-01	---	---	---	1561712_at	---
2.90	2.82	0.08	5.80E-01	8.43E-01	ARS2	Arsenate resistance protein 2	chr7q21	214127_s_at	NM_001128852 /// NM_001128853 /// NM_001128854 /// NM_015908 /// NM_182800
3.75	3.63	0.13	5.80E-01	8.43E-01	SPHK1	sphingosine kinase 1	chr17q25.2	219257_s_at	NM_021972 /// NM_182965
6.71	6.62	0.09	5.80E-01	8.43E-01	GIT1	G protein-coupled receptor kinase interactor 1	chr17p11.2	218030_at	NM_001085454 /// NM_014030
3.01	2.86	0.15	5.80E-01	8.43E-01	OTUD6B	OTU domain containing 6B	chr8q21.3	222825_at	NM_016023
2.89	2.82	0.07	5.80E-01	8.43E-01	---	---	---	229861_at	---
2.97	2.88	0.09	5.80E-01	8.43E-01	TEX28	testis expressed 28	chrXq28	207364_at	NM_001586
4.40	4.24	0.16	5.80E-01	8.43E-01	---	---	---	229342_at	---
5.11	4.99	0.12	5.81E-01	8.43E-01	ZNF446	zinc finger protein 446	chr19q13.43	1554160_a_at	NM_017908
3.14	3.04	0.10	5.81E-01	8.43E-01	SNX19	sorting nexin 19	chr11q25	1554986_a_at	NM_014758

2.25	2.20	0.05	5.81E-01	8.43E-01	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	chr9p22.3	228926_s_at	NM_003070 /// NM_139045																				
2.26	2.20	0.06	5.81E-01	8.43E-01	LOC285735	hypothetical protein LOC285735	chr6q23.2	1561691_at	XR_040023 /// XR_040024 /// XR_040025																				
6.45	6.21	0.24	5.81E-01	8.43E-01	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	chr7q31|14q24.2-q24.3	1554462_a_at	NM_012328																				
4.48	4.25	0.23	5.81E-01	8.43E-01	C17orf48	chromosome 17 open reading frame 48	chr17p13.1	220606_s_at	NM_020233																				
2.55	2.44	0.11	5.81E-01	8.43E-01	GLS	Glutaminase	chr2q32-q34	223080_at	NM_014905																				
4.05	3.87	0.18	5.81E-01	8.43E-01	41525	septin 8	chr5q31	209000_s_at	NM_001098811 /// NM_001098812 /// NM_001098813 /// NM_015146																				
2.39	2.33	0.06	5.81E-01	8.43E-01	PRKDC	Protein kinase, DNA-activated, catalytic polypeptide	chr8q11	215757_at	NM_001081640 /// NM_006904																				
5.70	5.56	0.14	5.81E-01	8.43E-01	DUSP22 /// LOC100134371	dual specificity phosphatase 22 /// similar to dual specificity phosphatase 22	chr6p25.3	226440_at	NM_020185 /// XM_001717801																				
4.45	4.31	0.15	5.81E-01	8.43E-01	HCG18	HLA complex group 18	chr6p21.3	225577_at	NR_024052 /// NR_024053 /// XM_933653 /// XM_936164 /// XM_944855																				
7.46	7.33	0.13	5.81E-01	8.43E-01	---	---	---	235964_x_at	---																				
3.76	3.65	0.11	5.81E-01	8.43E-01	---	---	---	204552_at	---																				
3.94	3.80	0.14	5.81E-01	8.43E-01	NCOA5	nuclear receptor coactivator 5	chr20q12-q13.12	234471_s_at	NM_020967																				
2.90	2.79	0.11	5.81E-01	8.43E-01	---	---	---	236780_at	---																				
3.39	3.29	0.10	5.81E-01	8.43E-01	NHSL1	NHS-like 1	chr6q23.3	234321_x_at	XM_001723403 /// XM_496826 /// XM_941807																				
3.58	3.47	0.12	5.81E-01	8.43E-01	BXDC2	brix domain containing 2	chr5p13.2	219177_at	NM_018321																				
2.86	2.76	0.10	5.81E-01	8.44E-01	LYK5	Protein kinase LYK5	chr17q23.3	1557528_at	NM_001003786 /// NM_001003787 /// NM_001003788 /// NM_153335																				
3.51	3.38	0.12	5.81E-01	8.44E-01	NRP2	neuropilin 2	chr2q33.3	211844_s_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279																				
1.96	1.89	0.07	5.81E-01	8.44E-01	CCDC132	coiled-coil domain containing 132	chr7q21.3	1554216_at	NM_017667 /// NM_024553																				
2.80	2.70	0.10	5.81E-01	8.44E-01	---	---	---	1561037_a_at	---																				
3.61	3.47	0.15	5.81E-01	8.44E-01	---	---	---	1566146_x_at	---																				
7.58	7.38	0.20	5.81E-01	8.44E-01	FAM21A /// FAM21B	family with sequence similarity 21, member A /// family with sequence similarity 21, member B	chr10q11.22 /// chr10q11.23	212370_x_at	NM_001005751 /// NM_018232																				
3.70	3.63	0.08	5.81E-01	8.44E-01	CALML4	Calmodulin-like 4	chr15q23	1566149_at	NM_001031733 /// NM_033429																				

3.27	3.16	0.11	5.81E-01	8.44E-01	RIPPLY2	ripply2 homolog (zebrafish)	chr6q26	223740_at	XR_017853 /// XR_017956 /// XR_040210																				
4.85	4.75	0.10	5.81E-01	8.44E-01	---	---	---	228037_at	---																				
2.38	2.30	0.08	5.82E-01	8.44E-01	LOC648232	Hypothetical protein LOC100128757	---	1557919_a_at	XM_937280																				
2.39	2.32	0.07	5.82E-01	8.44E-01	ATP13A4	ATPase type 13A4	chr3q29	1557136_at	NM_032279																				
2.95	2.85	0.10	5.82E-01	8.44E-01	TBX21	T-box 21	chr17q21.32	220684_at	NM_013351																				
3.68	3.56	0.12	5.82E-01	8.44E-01	C21orf63	chromosome 21 open reading frame 63	chr21q22.11	227188_at	NM_058187																				
2.49	2.41	0.08	5.82E-01	8.44E-01	---	---	---	237982_at	---																				
2.08	2.00	0.08	5.82E-01	8.44E-01	---	---	---	233046_at	---																				
2.42	2.35	0.06	5.82E-01	8.44E-01	C15orf54	chromosome 15 open reading frame 54	chr15q14	1562367_at	NM_207445																				
6.87	6.72	0.15	5.82E-01	8.44E-01	---	---	---	225356_at	---																				
3.11	3.04	0.07	5.82E-01	8.44E-01	SYT9	synaptotagmin IX	chr11p15.4	1555053_at	NM_175733																				
7.47	7.36	0.12	5.82E-01	8.44E-01	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	chr3p21.3	203071_at	NM_001005914 /// NM_004636																				
2.32	2.25	0.08	5.82E-01	8.44E-01	---	---	---	240269_at	---																				
7.52	7.44	0.08	5.82E-01	8.44E-01	CHMP4A	chromatin modifying protein 4A	chr14q12	218571_s_at	NM_014169																				
2.59	2.50	0.09	5.82E-01	8.44E-01	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	chr11q23.2	202885_s_at	NM_002716 /// NM_181699																				
2.22	2.12	0.10	5.82E-01	8.44E-01	---	---	---	241033_at	---																				
4.93	4.78	0.15	5.82E-01	8.44E-01	UNC93B1	unc-93 homolog B1 (C. elegans)	chr11q13	225869_s_at	NM_030930																				
3.13	3.03	0.10	5.82E-01	8.44E-01	C6orf208	chromosome 6 open reading frame 208	chr6q27	220904_at	XR_041373 /// XR_041374 /// XR_041375																				
2.26	2.19	0.07	5.83E-01	8.44E-01	RP6-213H19.1	serine/threonine protein kinase MST4	chrXq26.2	224407_s_at	NM_001042452 /// NM_001042453 /// NM_016542																				
7.75	7.59	0.16	5.83E-01	8.44E-01	SRA1	steroid receptor RNA activator 1	chr5q31.3	224864_at	NM_001035235																				
2.58	2.49	0.09	5.83E-01	8.44E-01	C7orf62	chromosome 7 open reading frame 62	chr7q21.13	231441_at	NM_152706																				
2.50	2.42	0.08	5.83E-01	8.44E-01	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	chr12q23.1	241794_at	NM_022496																				
8.09	8.01	0.08	5.83E-01	8.44E-01	CALR	calreticulin	chr19p13.3-p13.2	212953_x_at	NM_004343																				
3.41	3.29	0.12	5.83E-01	8.44E-01	---	---	---	239783_at	---																				
2.79	2.71	0.08	5.83E-01	8.45E-01	hCG_1815504	hCG1815504	chr13q12.3	239781_at	XM_001129572 /// XM_001717067 /// XM_498560																				
2.59	2.51	0.08	5.83E-01	8.45E-01	---	---	---	228659_at	---																				
2.18	2.12	0.06	5.83E-01	8.45E-01	---	---	---	237871_x_at	---																				
4.12	4.01	0.12	5.83E-01	8.45E-01	SRRM2	serine/arginine repetitive matrix 2	chr16p13.3	1554671_a_at	NM_016333																				
4.73	4.55	0.18	5.83E-01	8.45E-01	LOC253039	hypothetical LOC253039	chr9q33.2	1555892_s_at	XM_001715306 /// XM_001719409 /// XM_001725827																				
2.13	2.07	0.06	5.83E-01	8.45E-01	---	---	---	1566518_at	---																				
2.13	2.07	0.07	5.83E-01	8.45E-01	---	---	---	231630_at	---																				
5.21	5.09	0.12	5.83E-01	8.45E-01	---	---	---	226821_at	---																				
2.86	2.75	0.11	5.83E-01	8.45E-01	DOPEY2	dopey family member 2	chr21q22.2	205248_at	NM_005128																				
2.94	2.85	0.10	5.83E-01	8.45E-01	RCAN3	RCAN family member 3	chr1p35.3-p33	229064_s_at	NM_013441																				
2.81	2.74	0.07	5.83E-01	8.45E-01	---	---	---	237143_at	---																				
3.84	3.76	0.09	5.84E-01	8.45E-01	DCBLD1	discoidin, CUB and LCCL domain containing 1	chr6q22.2	226609_at	NM_173674																				
3.13	2.99	0.14	5.84E-01	8.45E-01	THAP9	THAP domain containing 9	chr4q21.22	230185_at	NM_024672																				
2.74	2.68	0.06	5.84E-01	8.45E-01	COL9A3	collagen, type IX, alpha 3	chr20q13.3	204724_s_at	NM_001853																				
4.10	3.94	0.16	5.84E-01	8.45E-01	CENPO	centromere protein O	chr2p23.3	226118_at	NM_024322																				
2.70	2.61	0.09	5.84E-01	8.45E-01	---	---	---	1555205_at	---																				
2.07	2.00	0.07	5.84E-01	8.45E-01	ELMOD2	ELMO/CED-12 domain containing 2	chr4q31.1	1557837_a_at	NM_153702																				
2.26	2.19	0.07	5.84E-01	8.45E-01	---	---	---	223860_at	---																				
3.38	3.27	0.11	5.84E-01	8.45E-01	---	---	---	1561607_at	---																				
2.52	2.45	0.08	5.84E-01	8.45E-01	EP400	E1A binding protein p400	chr12q24.33	230628_at	NM_015409																				
2.62	2.53	0.09	5.84E-01	8.45E-01	ENAM	enamelin	chr4q13.3	223893_at	NM_031889																				
5.53	5.44	0.09	5.84E-01	8.45E-01	ZNF432	zinc finger protein 432	chr19q13.33	219848_s_at	NM_014650																				
5.23	5.08	0.15	5.84E-01	8.45E-01	BRP44	Brain protein 44	chr1q24	227669_at	NM_015415																				
5.63	5.53	0.10	5.84E-01	8.45E-01	C14orf79	chromosome 14 open reading frame 79	chr14q32.33	213512_at	NM_174891																				

2.27	2.20	0.06	5.84E-01	8.45E-01	ACP1	acid phosphatase 1, soluble	chr2p25	1554808_at	NM_001040649 /// NM_004300 /// NM_007099 /// NR_024080																				
7.35	7.22	0.13	5.84E-01	8.45E-01	UBXN6	UBX domain protein 6	chr19p13	220757_s_at	NM_025241																				
2.82	2.75	0.07	5.84E-01	8.45E-01	CHAT	choline acetyltransferase	chr10q11.2	221197_s_at	NM_020549 /// NM_020984 /// NM_020985 /// NM_020986																				
4.21	4.08	0.13	5.84E-01	8.45E-01	C1orf91	chromosome 1 open reading frame 91	chr1p36.11-p34.2	223676_at	NM_019118																				
8.84	8.72	0.12	5.84E-01	8.45E-01	G6PC3	glucose 6 phosphatase, catalytic, 3	chr17q21.31	44654_at	NM_138387																				
2.92	2.82	0.10	5.84E-01	8.45E-01	CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)	chr3p21.3	205344_at	NM_006574																				
3.96	3.85	0.10	5.84E-01	8.45E-01	BICD1	bicaudal D homolog 1 (Drosophila)	chr12p11.2-p11.1	214806_at	NM_001003398 /// NM_001714																				
7.78	7.63	0.15	5.85E-01	8.45E-01	SYPL1	synaptophysin-like 1	chr7q22.2	201259_s_at	NM_006754 /// NM_182715																				
6.71	6.52	0.19	5.85E-01	8.45E-01	GCAT	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	chr22q13.1	205164_at	NM_014291																				
2.36	2.29	0.06	5.85E-01	8.45E-01	HNRNPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	227744_s_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370																				
4.53	4.45	0.08	5.85E-01	8.45E-01	HCN3	hyperpolarization activated cyclic nucleotide-gated potassium channel 3	chr1q22	228741_s_at	NM_020897																				
2.34	2.25	0.09	5.85E-01	8.45E-01	CLDN23	claudin 23	chr8p23.1	228707_at	NM_194284																				
2.79	2.73	0.06	5.85E-01	8.45E-01	C19orf29	Chromosome 19 open reading frame 29	chr19p13.3	237990_x_at	NM_001080543 /// NM_021231																				
8.14	8.02	0.12	5.85E-01	8.45E-01	LRP10	low density lipoprotein receptor-related protein 10	chr14q11.2	201412_at	NM_014045																				
2.61	2.52	0.10	5.85E-01	8.45E-01	NEK9	NIMA (never in mitosis gene a)- related kinase 9	chr14q24.3	230153_at	NM_033116																				
10.44	10.34	0.10	5.85E-01	8.45E-01	METTL7A	methyltransferase like 7A	chr12q13.13	207761_s_at	NM_014033																				
2.51	2.43	0.08	5.85E-01	8.45E-01	GFI1B	growth factor independent 1B transcription repressor	chr9q34.13	208501_at	NM_004188																				
2.07	2.01	0.07	5.85E-01	8.45E-01	CAPN10	calpain 10	chr2q37.3	221040_at	NM_021251 /// NM_023083 /// NM_023085 /// NM_023089																				
4.08	3.96	0.13	5.85E-01	8.45E-01	---	---	---	228560_at	---																				
2.74	2.66	0.08	5.85E-01	8.45E-01	---	---	---	239119_at	---																				
1.94	1.88	0.06	5.85E-01	8.45E-01	SYNJ1	Synaptojanin 1	chr21q22.2	232993_at	NM_003895 /// NM_203446																				
2.12	2.04	0.08	5.85E-01	8.45E-01	---	---	---	1566096_x_at	---																				
2.80	2.72	0.09	5.85E-01	8.45E-01	CDH16	cadherin 16, KSP-cadherin	chr16q22.1	206517_at	NM_004062																				
11.20	11.10	0.10	5.85E-01	8.45E-01	HLA-A	major histocompatibility complex, class I, A	chr6p21.3	213932_x_at	NM_002116 /// XM_001713645																				
5.25	5.14	0.11	5.85E-01	8.45E-01	HDLBP	high density lipoprotein binding protein	chr2q37.3	222916_s_at	NM_005336 /// NM_203346																				

3.98	3.78	0.20	5.85E-01	8.46E-01	OPA1	optic atrophy 1 (autosomal dominant)	chr3q28-q29|3q28-q29	214306_at	NM_015560 /// NM_130831 /// NM_130832 /// NM_130833 /// NM_130834 /// NM_130835 /// NM_130836 /// NM_130837
2.86	2.74	0.12	5.85E-01	8.46E-01	FAM118A	family with sequence similarity 118, member A	chr22q13	219629_at	NM_001104595 /// NM_017911
4.96	4.84	0.13	5.85E-01	8.46E-01	GK	glycerol kinase	chrXp21.3	217167_x_at	NM_000167 /// NM_001128127 /// NM_203391
4.27	4.17	0.09	5.86E-01	8.46E-01	---	---	---	221181_at	---
2.28	2.22	0.07	5.86E-01	8.46E-01	PLSCR2	phospholipid scramblase 2	chr3q24	207374_at	NM_020359
6.24	6.11	0.13	5.86E-01	8.46E-01	VPS26B	vacuolar protein sorting 26 homolog B (S. pombe)	chr11q25	230306_at	NM_052875
3.48	3.34	0.14	5.86E-01	8.46E-01	MED13	mediator complex subunit 13	chr17q22-q23	223780_s_at	NM_005121
4.18	4.08	0.10	5.86E-01	8.46E-01	STX4	Syntaxin 4	chr16p11.2	236232_at	NM_004604
3.34	3.23	0.12	5.86E-01	8.46E-01	SPP2	secreted phosphoprotein 2, 24kDa	chr2q37-qter	214478_at	NM_006944
5.61	5.47	0.14	5.86E-01	8.46E-01	SORBS1	sorbin and SH3 domain containing 1	chr10q23.3-q24.1	222513_s_at	NM_001034954 /// NM_001034955 /// NM_001034956 /// NM_001034957 /// NM_006434 /// NM_015385 /// NM_024991
5.30	5.18	0.11	5.86E-01	8.46E-01	ZNF43	zinc finger protein 43	chr19p13.1-p12	222136_x_at	NM_003423
1.96	1.89	0.07	5.86E-01	8.46E-01	PTPN2	protein tyrosine phosphatase, non-receptor type 2	chr18p11.3-p11.2	204935_at	NM_002828 /// NM_080422 /// NM_080423
6.70	6.47	0.24	5.86E-01	8.46E-01	MEIS1	Meis homeobox 1	chr2p14-p13	1559477_s_at	NM_002398
6.20	6.08	0.12	5.86E-01	8.46E-01	SLC35B4	solute carrier family 35, member B4	chr7q33	225881_at	NM_032826
2.40	2.33	0.07	5.86E-01	8.46E-01	---	---	---	234205_at	---
6.96	6.88	0.08	5.87E-01	8.46E-01	---	---	---	225141_at	---
1.97	1.91	0.07	5.87E-01	8.46E-01	---	---	---	1564351_at	---
2.69	2.61	0.08	5.87E-01	8.46E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	211399_at	NM_000141 /// NM_022970
2.00	1.93	0.07	5.87E-01	8.46E-01	PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	chr2q21.1	1569552_at	NM_014369
2.82	2.67	0.14	5.87E-01	8.46E-01	AOF1	amine oxidase (flavin containing) domain 1	chr6p22.3	227021_at	NM_153042
6.08	5.85	0.23	5.87E-01	8.46E-01	CCL13	chemokine (C-C motif) ligand 13	chr17q11.2	206407_s_at	NM_005408
5.17	5.08	0.10	5.87E-01	8.46E-01	---	---	---	1566178_x_at	---
3.26	3.01	0.25	5.87E-01	8.46E-01	---	---	---	242137_at	---
3.44	3.36	0.08	5.87E-01	8.46E-01	---	---	---	1569127_at	---
7.53	7.35	0.18	5.87E-01	8.46E-01	ZMYND8	zinc finger, MYND-type containing 8	chr20q13.12	209048_s_at	NM_012408 /// NM_183047 /// NM_183048
4.89	4.75	0.14	5.87E-01	8.46E-01	ESAM	endothelial cell adhesion molecule	chr11q24.2	225369_at	NM_138961
4.10	4.01	0.09	5.87E-01	8.46E-01	---	---	---	242240_at	---
4.00	3.75	0.25	5.87E-01	8.46E-01	GPR183	G protein-coupled receptor 183	chr13q32.3	205419_at	NM_004951
2.32	2.25	0.07	5.87E-01	8.46E-01	---	---	---	239113_at	---
2.44	2.37	0.07	5.87E-01	8.46E-01	SH2D1B	SH2 domain containing 1B	chr1q23.3	1553177_at	NM_053282
4.71	4.28	0.44	5.87E-01	8.46E-01	KLF4	Kruppel-like factor 4 (gut)	chr9q31	220266_s_at	NM_004235
6.21	6.04	0.17	5.88E-01	8.47E-01	RBM7	RNA binding motif protein 7	chr11q23.1-q23.2	218379_at	NM_016090

2.62	2.54	0.08	5.88E-01	8.47E-01	SSX1	synovial sarcoma, X breakpoint 1	chrXp11.23-p11.22	206626_x_at	NM_005635																				
2.03	1.96	0.06	5.88E-01	8.47E-01	TSGA10	testis specific, 10	chr2q11.2	223838_at	NM_025244 /// NM_182911																				
3.03	2.91	0.13	5.88E-01	8.47E-01	NANOS1	Nanos homolog 1 (Drosophila)	chr10q26.11	228526_at	NM_199461																				
2.26	2.19	0.07	5.88E-01	8.47E-01	---	---	---	217155_at	---																				
2.41	2.34	0.07	5.88E-01	8.47E-01	LOC728377 /// OR2A4 /// OR2A7	similar to rho guanine nucleotide exchange factor 5 /// olfactory receptor, family 2, subfamily A, member 4 /// olfactory receptor, family 2, subfamily A, member 7	chr6q23 /// chr7q35	233492_s_at	NM_001005328 /// NM_030908 /// XR_041051 /// XR_041052																			
2.36	2.29	0.08	5.88E-01	8.47E-01	HOOK3	hook homolog 3 (Drosophila)	chr8p11.21	1558315_s_at	NM_032410																				
4.47	4.35	0.12	5.88E-01	8.47E-01	DCUN1D3 /// EXOD1	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) /// exonuclease domain containing 1	chr16p12.2	239648_at	NM_080663 /// NM_173475																				
3.24	3.17	0.07	5.88E-01	8.47E-01	GPR3	G protein-coupled receptor 3	chr1p36.1-p35	214613_at	NM_005281																				
4.52	4.44	0.07	5.88E-01	8.47E-01	EZH1	enhancer of zeste homolog 1 (Drosophila)	chr17q21.1-q21.3	239197_s_at	NM_001991																				
7.36	7.25	0.11	5.88E-01	8.47E-01	MGC9913	hypothetical protein MGC9913	chr19q13.43	244740_at	---																				
2.26	2.18	0.09	5.88E-01	8.47E-01	C22orf32	chromosome 22 open reading frame 32	chr22q13.2	227648_at	NM_033318																				
5.98	5.84	0.15	5.88E-01	8.47E-01	WIZ	widely interspaced zinc finger motifs	chr19p13.1	52005_at	NM_021241																				
3.08	2.99	0.09	5.88E-01	8.47E-01	SCHIP1	schwannomin interacting protein 1	chr3q25.33	204030_s_at	NM_014575																				
2.54	2.44	0.10	5.88E-01	8.47E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	209637_s_at	NM_002926 /// NM_198227 /// NM_198229																				
4.00	3.92	0.09	5.89E-01	8.47E-01	---	---	---	242389_at	---																				
3.07	2.95	0.12	5.89E-01	8.47E-01	RTBDN	retbindin	chr19p12	223719_s_at	NM_001080997 /// NM_031429																				
4.11	4.02	0.08	5.89E-01	8.47E-01	XAF1	XIAP associated factor 1	chr17p13.2	206133_at	NM_017523 /// NM_199139																				
2.62	2.55	0.07	5.89E-01	8.47E-01	NHLRC2	NHL repeat containing 2	chr10q25.3	236185_at	NM_198514																				
7.93	7.80	0.13	5.89E-01	8.47E-01	UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)	chr3p24.2	212519_at	NM_003341 /// NM_182666																				
4.16	4.08	0.08	5.89E-01	8.47E-01	CLDN19	claudin 19	chr1p34.2	1554804_a_at	NM_001123395 /// NM_148960																				
7.34	7.08	0.27	5.89E-01	8.47E-01	C12orf11	chromosome 12 open reading frame 11	chr12p11.23	221652_s_at	NM_018164																				
2.51	2.44	0.07	5.89E-01	8.47E-01	LOC100130716 /// MUC12	similar to mucin 11 /// mucin 12, cell surface associated	chr7q22	231814_at	XM_001713845 /// XM_001714400 /// XM_001720551 /// XM_001724943 /// XM_379904 /// XM_936315																				
3.13	2.99	0.14	5.89E-01	8.47E-01	ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	chr11p15.1	210246_s_at	NM_000352																				
3.72	3.66	0.07	5.89E-01	8.47E-01	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	chr5q33.1	222187_x_at	NM_005754 /// NM_198395																				
3.02	2.89	0.13	5.89E-01	8.47E-01	TRIP6	thyroid hormone receptor interactor 6	chr7q22	214262_at	NM_003302																				
3.32	3.22	0.10	5.89E-01	8.48E-01	---	---	---	238256_at	---																				
2.53	2.43	0.10	5.89E-01	8.48E-01	---	---	---	1560498_at	---																				
4.58	4.48	0.10	5.89E-01	8.48E-01	DIXDC1	DIX domain containing 1	chr11q23.1	1558340_at	NM_001037954 /// NM_033425																				
5.90	5.77	0.13	5.89E-01	8.48E-01	SBF2	SET binding factor 2	chr11p15.4	226169_at	NM_030962																				
3.35	3.24	0.11	5.89E-01	8.48E-01	LOC100130389	hypothetical LOC100130389	chrXq26.3	236914_at	XR_038316 /// XR_038539 /// XR_038549																				
2.76	2.66	0.09	5.89E-01	8.48E-01	PRKX	protein kinase, X-linked	chrXp22.3	204061_at	NM_005044																				

7.51	7.36	0.15	5.89E-01	8.48E-01	LOC729580	hypothetical LOC729580	chr20q11.22	78047_s_at	XM_001126751 /// XM_001130700 /// XM_001714754																			
6.78	6.64	0.14	5.89E-01	8.48E-01	HDLBP	high density lipoprotein binding protein	chr2q37.3	225012_at	NM_005336 /// NM_203346																			
2.03	1.97	0.07	5.89E-01	8.48E-01	---	---	---	1569784_at	---																			
7.29	6.98	0.31	5.90E-01	8.48E-01	FCN3	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	chr1p36.11	205866_at	NM_003665 /// NM_173452																			
2.51	2.44	0.07	5.90E-01	8.48E-01	FBXO36	F-box protein 36	chr2q36.3	1555195_at	NM_174899																			
2.37	2.29	0.08	5.90E-01	8.48E-01	ANGEL2	angel homolog 2 (Drosophila)	chr1q32.3	217630_at	NM_144567																			
4.01	3.94	0.07	5.90E-01	8.48E-01	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	chr11p15.5	212161_at	NM_012305																			
2.76	2.68	0.08	5.90E-01	8.48E-01	FAM182B /// RP13-401N8.2	family with sequence similarity 182, member B /// hypothetical gene supported by BC042812	chr20p11.1 /// chr20p11.21-p11.1	222205_x_at	XM_001132551 /// XM_001133521 /// XM_001718365 /// XM_933752																			
4.76	4.66	0.10	5.90E-01	8.48E-01	PIGX	phosphatidylinositol glycan anchor biosynthesis, class X	chr3q29	1563111_a_at	NM_017861																			
2.25	2.18	0.06	5.90E-01	8.48E-01	ADAM32	ADAM metallopeptidase domain 32	chr8p11.23	1552266_at	NM_145004																			
6.66	6.58	0.09	5.90E-01	8.48E-01	GNL1	guanine nucleotide binding protein-like 1	chr6p21.3	203307_at	NM_005275																			
2.32	2.24	0.08	5.90E-01	8.48E-01	---	---	---	238386_x_at	---																			
4.33	4.22	0.11	5.90E-01	8.48E-01	NECAB2	N-terminal EF-hand calcium binding protein 2	chr16q23.3	215005_at	NM_019065																			
3.42	3.34	0.08	5.90E-01	8.48E-01	FZD9	frizzled homolog 9 (Drosophila)	chr7q11.23	207639_at	NM_003508																			
5.35	5.17	0.18	5.90E-01	8.48E-01	SEC23IP	SEC23 interacting protein	chr10q25-q26	209175_at	NM_007190																			
4.07	3.94	0.13	5.90E-01	8.48E-01	IKZF4	IKAROS family zinc finger 4 (Eos)	chr12q13	229752_at	NM_022465																			
3.81	3.75	0.07	5.90E-01	8.48E-01	MAP1LC3C	microtubule-associated protein 1 light chain 3 gamma	chr1q43	221697_at	NM_001004343																			
2.45	2.36	0.09	5.90E-01	8.48E-01	PCDHB4	protocadherin beta 4	chr5q31	240317_at	NM_018938																			
2.50	2.42	0.08	5.90E-01	8.48E-01	---	---	---	1564154_at	---																			
2.15	2.08	0.07	5.90E-01	8.48E-01	LOC283352	hypothetical protein LOC283352	chr12q24.33	1569454_a_at	---																			
9.24	9.13	0.11	5.91E-01	8.48E-01	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	chr11q13	203189_s_at	NM_002496																			
5.10	4.84	0.26	5.91E-01	8.48E-01	YOD1	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	chr1q32.1	227309_at	NM_018566																			
4.66	4.52	0.13	5.91E-01	8.48E-01	SLC39A5	solute carrier family 39 (metal ion transporter), member 5	chr12q13.2	1552281_at	NM_173596																			
2.31	2.24	0.07	5.91E-01	8.48E-01	---	---	---	1570283_at	---																			
3.42	3.33	0.09	5.91E-01	8.48E-01	KCNG2	potassium voltage-gated channel, subfamily G, member 2	chr18q22-q23	208550_x_at	NM_012283																			
3.49	3.39	0.09	5.91E-01	8.48E-01	---	---	---	229673_at	---																			
5.26	5.15	0.11	5.91E-01	8.48E-01	TRIOBP	TRIO and F-actin binding protein	chr22q13.1	1552332_at	NM_001039141 /// NM_007032 /// NM_138632																			
5.30	5.04	0.26	5.91E-01	8.48E-01	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	chr1p11.2	214511_x_at	NM_001004340 /// NM_001017986																			
3.53	3.45	0.08	5.91E-01	8.48E-01	CD109	CD109 molecule	chr6q13	229900_at	NM_133493																			
1.99	1.93	0.06	5.91E-01	8.48E-01	---	---	---	207465_at	---																			
4.20	4.09	0.11	5.91E-01	8.48E-01	MEGF8	multiple EGF-like-domains 8	chr19q12	214778_at	NM_001410																			
6.84	6.75	0.09	5.91E-01	8.48E-01	MED11	mediator complex subunit 11	chr17p13.2	226958_s_at	NM_001001683																			
4.35	4.21	0.14	5.91E-01	8.49E-01	TEAD3	TEA domain family member 3	chr6p21.2	209454_s_at	NM_003214																			
6.26	6.15	0.11	5.91E-01	8.49E-01	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	chr17q11.2	208420_x_at	NM_003170																			
10.33	10.11	0.22	5.91E-01	8.49E-01	C4A /// C4B	complement component 4A (Rodgers blood group) /// complement component 4B (Childo blood group)	chr6p21.3	208451_s_at	NM_000592 /// NM_001002029 /// NM_007293																			
3.02	2.93	0.09	5.91E-01	8.49E-01	---	---	---	226681_at	---																			
6.31	6.16	0.15	5.91E-01	8.49E-01	MMP24	Matrix metallopeptidase 24 (membrane-inserted)	chr20q11.2	49679_s_at	NM_006690																			

2.74	2.65	0.09	5.91E-01	8.49E-01	LOC220729 /// SDHALP1 /// SDHALP2	succinate dehydrogenase complex, subunit A, flavoprotein pseudogene /// succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1 /// succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	chr3q29	243293_at	NR_003264 /// NR_003265 /// NR_003266 /// XR_015171 /// XR_042153 /// XR_042171 /// XR_042174																				
2.27	2.19	0.07	5.91E-01	8.49E-01	---	---	---	1558273_a_at	---																				
5.48	5.26	0.22	5.91E-01	8.49E-01	SAC3D1	SAC3 domain containing 1	chr11q13.1	205449_at	NM_013299																				
3.93	3.66	0.27	5.91E-01	8.49E-01	---	---	---	243431_at	---																				
2.35	2.28	0.07	5.91E-01	8.49E-01	LOC285422	hypothetical protein LOC285422	chr4q31.21	1563685_at	---																				
4.29	4.06	0.23	5.92E-01	8.49E-01	ZBTB44	zinc finger and BTB domain containing 44	chr11q24.3	1554470_s_at	NM_014155																				
2.27	2.19	0.08	5.92E-01	8.49E-01	DNAH6 /// DNHL1 /// LOC200383	dynein, axonemal, heavy chain 6 /// dynein heavy chain-like 1 /// similar to Dynein heavy chain at 16F	chr2p11.2	1552957_at	NM_001370 /// NM_173645																				
6.75	6.66	0.09	5.92E-01	8.49E-01	HDGF2	hepatoma-derived growth factor-related protein 2	chr19p13.3	223252_at	NM_001001520 /// NM_032631																				
3.65	3.57	0.08	5.92E-01	8.49E-01	---	---	---	215594_at	---																				
7.88	7.82	0.06	5.92E-01	8.49E-01	ENSA	endosulfine alpha	chr1q21.2	202596_at	NM_004436 /// NM_207042 /// NM_207043 /// NM_207044 /// NM_207045 /// NM_207046 /// NM_207047 /// NM_207168																				
2.12	2.04	0.08	5.92E-01	8.49E-01	C4orf28	chromosome 4 open reading frame 28	chr4p15.31	235517_at	NM_001130727 /// NM_145048																				
3.20	3.08	0.12	5.92E-01	8.49E-01	C9orf98	chromosome 9 open reading frame 98	chr9q34.13	1557666_s_at	NM_152572																				
2.75	2.67	0.08	5.92E-01	8.49E-01	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	chr6p22.3-p22.1	227789_at	NM_020662																				
6.54	6.43	0.11	5.92E-01	8.49E-01	LOC201229	hypothetical protein LOC201229	chr17q11.2	213195_at	NM_001076680																				
2.75	2.65	0.10	5.92E-01	8.49E-01	RFFL	ring finger and FYVE-like domain containing 1	chr17q12	1562603_at	NM_001017368 /// NM_057178																				
3.92	3.81	0.11	5.92E-01	8.49E-01	41529	septin 12	chr16p13.3	230947_at	NM_144605																				
2.57	2.50	0.07	5.92E-01	8.49E-01	---	---	---	244600_at	---																				
4.47	4.29	0.18	5.92E-01	8.49E-01	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)	chr10p14-p13	203519_s_at	NM_015542 /// NM_080599																				
2.91	2.84	0.07	5.92E-01	8.49E-01	HRASLS5	HRAS-like suppressor family, member 5	chr11q13.2	231452_at	NM_054108																				
5.14	5.04	0.09	5.92E-01	8.49E-01	APITD1	apoptosis-inducing, TAF9-like domain 1	chr1p36.22	213454_at	NM_198544 /// NM_199294 /// NM_199295																				
5.56	5.42	0.15	5.92E-01	8.49E-01	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	chr21q22.3	222492_at	NM_003681																				
3.47	3.30	0.16	5.92E-01	8.49E-01	LOC731484	hypothetical LOC731484	chr2q37.1	242539_at	XR_015492 /// XR_037119 /// XR_037952																				
2.37	2.31	0.06	5.92E-01	8.49E-01	LOC400622	hypothetical LOC400622	chr17q25.3	1556435_at	---																				
2.29	2.22	0.07	5.93E-01	8.49E-01	LOC440896	hypothetical gene LOC440896	chr9q12	1556883_a_at	NM_001039940 /// NR_015361																				

3.19	3.11	0.08	5.93E-01	8.49E-01	DIRC3	disrupted in renal carcinoma 3	chr2q35	232434_at	XM_001721776 /// XM_001725484 /// XM_001725524																			
3.51	3.45	0.06	5.93E-01	8.49E-01	ULK2	Unc-51-like kinase 2 (C. elegans)	chr17p11.2	215154_at	NM_014683																			
2.08	2.01	0.07	5.93E-01	8.49E-01	TP63	tumor protein p63	chr3q28	1555581_a_at	NM_001114978 /// NM_001114979 /// NM_001114980 /// NM_001114981 /// NM_001114982 /// NM_003722																			
2.53	2.36	0.17	5.93E-01	8.49E-01	LOC100131622 /// PABPC5	hypothetical protein LOC100131622 /// poly(A) binding protein, cytoplasmic 5	chrXq21.3	233136_at	NM_080832 /// XM_001713750																			
4.24	4.17	0.08	5.93E-01	8.49E-01	BTBD9	BTB (POZ) domain containing 9	chr6p21	229867_at	NM_001099272 /// NM_052893 /// NM_152733																			
8.05	7.91	0.14	5.93E-01	8.49E-01	SRA1	steroid receptor RNA activator 1	chr5q31.3	224130_s_at	NM_001035235																			
2.40	2.32	0.08	5.93E-01	8.49E-01	---	---	---	237353_at	---																			
5.60	5.30	0.30	5.93E-01	8.49E-01	C5orf33	chromosome 5 open reading frame 33	chr5p13.2	226946_at	NM_001085411 /// NM_153013																			
2.45	2.36	0.09	5.93E-01	8.49E-01	CSMD1	CUB and Sushi multiple domains 1	chr8p23.2	1562330_s_at	NM_033225																			
2.19	2.13	0.06	5.93E-01	8.49E-01	C20orf85	chromosome 20 open reading frame 85	chr20q13.32	229542_at	NM_178456																			
8.94	8.78	0.16	5.93E-01	8.49E-01	TNS1	tensin 1	chr2q35-q36	221748_s_at	NM_022648																			
3.74	3.66	0.08	5.93E-01	8.50E-01	TP53INP1	tumor protein p53 inducible nuclear protein 1	chr8q22	244721_at	NM_033285																			
2.08	2.03	0.06	5.93E-01	8.50E-01	---	---	---	241283_at	---																			
5.85	5.74	0.11	5.93E-01	8.50E-01	FBXO31	F-box protein 31	chr16q24.2	219784_at	NM_024735																			
4.28	4.15	0.13	5.93E-01	8.50E-01	NY-SAR-48	sarcoma antigen NY-SAR-48	chr19p13.11	226308_at	NM_001011699 /// NM_033417																			
2.47	2.39	0.08	5.94E-01	8.50E-01	---	---	---	242391_at	---																			
4.21	3.92	0.28	5.94E-01	8.50E-01	C20orf160	chromosome 20 open reading frame 160	chr20q11.2	231991_at	NM_080625																			
2.59	2.51	0.08	5.94E-01	8.50E-01	TLL2	tolloid-like 2	chr10q23-q24	215843_s_at	NM_012465																			
3.06	2.98	0.08	5.94E-01	8.50E-01	---	---	---	223052_x_at	---																			
2.25	2.16	0.09	5.94E-01	8.50E-01	KCNJ1	potassium inwardly-rectifying channel, subfamily J, member 1	chr11q24	210403_s_at	NM_000220 /// NM_153764 /// NM_153765 /// NM_153766 /// NM_153767																			
3.32	3.23	0.09	5.94E-01	8.50E-01	LOC100129722	hypothetical protein LOC100129722	chr9q34.3	1566906_at	XM_001720584 /// XM_001723078 /// XM_001723633																			
6.34	6.16	0.17	5.94E-01	8.50E-01	FKSG24	hypothetical protein MGC12972	chr19p13.11	223473_at	NM_032683																			
2.70	2.60	0.10	5.94E-01	8.50E-01	---	---	---	236211_at	---																			
2.50	2.44	0.07	5.94E-01	8.50E-01	SPG7	Spastic paraplegia 7 (pure and complicated autosomal recessive)	chr16q24.3	238286_at	NM_003119 /// NM_199367																			
8.52	8.29	0.22	5.94E-01	8.50E-01	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	chr7q22	203680_at	NM_002736																			
2.75	2.65	0.10	5.94E-01	8.50E-01	MDH1B	malate dehydrogenase 1B, NAD (soluble)	chr2q33.3	238721_at	NM_001039845																			

4.95	4.87	0.08	5.94E-01	8.50E-01	HFE	hemochromatosis	chr6p21.3	211329_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011																				
7.86	7.76	0.10	5.94E-01	8.50E-01	AKIRIN2	akirin 2	chr6q15	223145_s_at	NM_018064																				
3.98	3.75	0.23	5.94E-01	8.50E-01	CDC42SE2	CDC42 small effector 2	chr5q31.1	1552613_s_at	NM_001038702 /// NM_020240																				
3.86	3.75	0.10	5.94E-01	8.50E-01	---	---	---	230463_at	---																				
2.59	2.47	0.12	5.94E-01	8.50E-01	AASS	aminoadipate-semialdehyde synthase	chr7q31.3	214829_at	NM_005763																				
6.80	6.71	0.09	5.94E-01	8.50E-01	RP11-529I10.4	deleted in a mouse model of primary ciliary dyskinesia	chr10q24.32	226009_at	NM_015448																				
6.39	6.29	0.10	5.94E-01	8.50E-01	CBR4	carbonyl reductase 4	chr4q32.3	244052_at	NM_032783																				
9.95	9.85	0.10	5.94E-01	8.50E-01	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	chr19p13.3	228690_s_at	NM_175614																				
4.55	4.42	0.13	5.94E-01	8.50E-01	---	---	---	239735_at	---																				
2.02	1.97	0.05	5.94E-01	8.50E-01	ANP32A /// ANP32C /// ANP32D /// LOC100128146 /// LOC723972	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A /// acidic (leucine-rich) nuclear phosphoprotein 32 family, member C /// acidic (leucine-rich) nuclear phosphoprotein 32 family, member D /// hypothetical protein LOC100128146 /// hepatopoietin PCn127	chr12q13.11 /// chr15q14 /// chr15q22.3-q23 /// chr15q23 /// chr4q32.3	208571_at	NM_006305 /// NM_012403 /// NM_012404 /// NR_003144 /// XM_001724880 /// XM_001725287 /// XM_001726740																				
2.40	2.32	0.08	5.94E-01	8.50E-01	PRDM15	PR domain containing 15	chr21q22.3	234524_at	NM_001040424 /// NM_022115																				
3.51	3.43	0.09	5.94E-01	8.50E-01	YIPF4	Yip1 domain family, member 4	chr2p22.3	213999_at	NM_032312																				
2.21	2.10	0.11	5.94E-01	8.50E-01	LOC283658	hypothetical protein LOC283658	chr15q21.1	239741_at	---																				
2.81	2.71	0.10	5.95E-01	8.50E-01	---	---	---	234460_at	---																				
3.28	3.20	0.09	5.95E-01	8.50E-01	TREML2	triggering receptor expressed on myeloid cells-like 2	chr6p21.1	219748_at	NM_024807																				
3.45	3.34	0.11	5.95E-01	8.50E-01	C7orf28B	chromosome 7 open reading frame 28B	chr7p22.1	215024_at	NM_198097 /// XM_001720226																				
3.23	3.12	0.11	5.95E-01	8.50E-01	---	---	---	242736_at	---																				
2.80	2.69	0.10	5.95E-01	8.50E-01	MXD1	MAX dimerization protein 1	chr2p13-p12	206877_at	NM_002357																				
3.90	3.77	0.13	5.95E-01	8.50E-01	MCART1	mitochondrial carrier triple repeat 1	chr9p13.3-p12	238574_at	NM_033412																				
6.82	6.69	0.13	5.95E-01	8.50E-01	OTUD4	OTU domain containing 4	chr4q31.21	203480_s_at	NM_001102653 /// NM_017493 /// NM_199324																				
2.55	2.48	0.07	5.95E-01	8.50E-01	SHROOM4	shroom family member 4	chrXp11.22	232404_at	NM_020717																				
5.29	5.08	0.21	5.95E-01	8.50E-01	C17orf42	Chromosome 17 open reading frame 42	---	238295_at	NM_024683																				
6.15	5.64	0.50	5.96E-01	8.51E-01	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	chr6p21.3	209823_x_at	NM_002123 /// XM_001722253 /// XM_001723447																				
4.12	3.93	0.19	5.96E-01	8.51E-01	HOOK1	hook homolog 1 (Drosophila)	chr1p32.1	225792_at	NM_015888																				
2.54	2.46	0.08	5.96E-01	8.51E-01	CDC7	cell division cycle 7 homolog (S. cerevisiae)	chr1p22	204510_at	NM_001134419 /// NM_001134420 /// NM_003503																				

2.16	2.09	0.07	5.96E-01	8.51E-01	C6orf50	chromosome 6 open reading frame 50	chr6p25.1	224183_at	XR_040722 /// XR_040723 /// XR_040724																				
3.57	3.44	0.14	5.96E-01	8.51E-01	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	chrXp11.22	46947_at	NM_019067																				
2.55	2.43	0.11	5.96E-01	8.51E-01	---	---	---	243591_at	---																				
3.12	3.05	0.08	5.96E-01	8.51E-01	CMTM1	CKLF-like MARVEL transmembrane domain containing 1	chr16q21	231219_at	NM_052999 /// NM_181268 /// NM_181269 /// NM_181270 /// NM_181271 /// NM_181272 /// NM_181283 /// NM_181296																				
2.51	2.44	0.07	5.96E-01	8.51E-01	BLVRA	Biliverdin reductase A	chr7p14-cen	229109_s_at	NM_000712																				
2.29	2.23	0.06	5.96E-01	8.51E-01	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	chr5q13	224227_s_at	NM_018429																				
2.94	2.80	0.13	5.96E-01	8.51E-01	MIB1	mindbomb homolog 1 (Drosophila)	chr18q11.2	224722_at	NM_020774																				
3.13	3.03	0.10	5.96E-01	8.51E-01	---	---	---	240720_at	---																				
3.85	3.74	0.11	5.96E-01	8.51E-01	PLEKHB2	pleckstrin homology domain containing, family B (evectins) member 2	chr2q21.1	224121_x_at	NM_001100623 /// NM_017958																				
6.75	6.65	0.10	5.96E-01	8.51E-01	KLC1	kinesin light chain 1	chr14q32.3	212878_s_at	NM_001130107 /// NM_005552 /// NM_182923																				
2.24	2.18	0.06	5.96E-01	8.51E-01	SFT2D1	SFT2 domain containing 1	chr6q27	232487_at	NM_145169																				
1.90	1.83	0.07	5.96E-01	8.51E-01	---	---	---	1562190_at	---																				
2.33	2.26	0.07	5.96E-01	8.51E-01	SPATA5	spermatogenesis associated 5	chr4q28.1	241546_at	NM_145207																				
6.54	6.44	0.10	5.96E-01	8.51E-01	ITSN1	intersectin 1 (SH3 domain protein)	chr21q22.1-q22.2	35776_at	NM_001001132 /// NM_003024																				
2.54	2.48	0.06	5.96E-01	8.51E-01	---	---	---	222097_at	---																				
2.38	2.31	0.07	5.96E-01	8.51E-01	IZUMO1	izumo sperm-egg fusion 1	chr19q13.33	1554196_at	NM_182575																				
7.03	6.79	0.25	5.96E-01	8.51E-01	PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15B	chr1q32.1	224692_at	NM_032833																				
5.59	5.45	0.14	5.96E-01	8.51E-01	HELZ	helicase with zinc finger	chr17q24.2	225910_at	NM_014877																				
2.25	2.17	0.09	5.96E-01	8.51E-01	OTP	orthopedia homeobox	chr5q13.3	223835_x_at	NM_032109																				
2.20	2.13	0.08	5.96E-01	8.51E-01	---	---	---	1554108_at	---																				
6.87	6.77	0.10	5.96E-01	8.51E-01	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	chr16q13	202697_at	NM_007006																				
2.86	2.74	0.11	5.96E-01	8.51E-01	---	---	---	1560263_at	---																				
6.08	5.99	0.09	5.96E-01	8.51E-01	PANX2	pannexin 2	chr22q13.33	1552944_a_at	NM_052839																				
1.97	1.92	0.05	5.97E-01	8.51E-01	ZNF407	zinc finger protein 407	chr18q23	220836_at	NM_017757																				
8.43	8.33	0.11	5.97E-01	8.51E-01	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	chrXq28	202471_s_at	NM_004135 /// NM_174869																				
3.39	3.25	0.14	5.97E-01	8.51E-01	RASL12	RAS-like, family 12	chr15q11.2-q22.33	219167_at	NM_016563																				
6.15	6.08	0.08	5.97E-01	8.51E-01	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	chr1p33-p32	225051_at	NM_004437 /// NM_203342 /// NM_203343																				
8.01	7.82	0.18	5.97E-01	8.51E-01	HSPC159	galectin-related protein	chr2p14	226188_at	NM_014181																				
5.63	5.55	0.08	5.97E-01	8.51E-01	CABP4	calcium binding protein 4	chr11q13.1	1554202_x_at	NM_145200																				
2.49	2.41	0.08	5.97E-01	8.51E-01	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	chr6q22-q23	204798_at	NM_001130172 /// NM_001130173 /// NM_005375																				
3.43	3.30	0.13	5.97E-01	8.51E-01	BIRC5	baculoviral IAP repeat-containing 5	chr17q25	202095_s_at	NM_001012270 /// NM_001012271 /// NM_001168																				
5.51	5.29	0.22	5.97E-01	8.51E-01	IRF6	interferon regulatory factor 6	chr1q32.3-q41	202597_at	NM_006147																				
2.83	2.74	0.08	5.97E-01	8.51E-01	---	---	---	237581_at	---																				

2.69	2.63	0.06	5.97E-01	8.51E-01	C10orf108	chromosome 10 open reading frame 108	chr10p15.3	1559000_at	XR_041941 /// XR_041942 /// XR_041943 /// XR_041945 /// XR_041946																				
3.81	3.62	0.18	5.97E-01	8.51E-01	---	---	---	228243_at	---																				
2.73	2.67	0.06	5.97E-01	8.51E-01	HRG	histidine-rich glycoprotein	chr3q27	31835_at	NM_000412																				
8.44	8.24	0.19	5.97E-01	8.51E-01	PTGR1	prostaglandin reductase 1	chr9q31.3	231897_at	NM_012212																				
2.59	2.52	0.07	5.97E-01	8.51E-01	CD276	CD276 molecule	chr15q23-q24	1559583_at	NM_001024736 /// NM_025240																				
6.33	5.93	0.39	5.97E-01	8.51E-01	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	chr7q21.1	207819_s_at	NM_000443 /// NM_018849 /// NM_018850																				
2.48	2.42	0.06	5.97E-01	8.51E-01	---	---	---	1562524_at	---																				
4.75	4.66	0.10	5.97E-01	8.51E-01	NKX6-3	NK6 homeobox 3	chr8p11.21	1552885_a_at	NM_152568																				
3.02	2.94	0.09	5.98E-01	8.51E-01	---	---	---	239857_at	---																				
2.31	2.23	0.08	5.98E-01	8.51E-01	HSPA9	heat shock 70kDa protein 9 (mortalin)	chr5q31.1	232200_at	NM_004134																				
2.96	2.84	0.12	5.98E-01	8.51E-01	AGGF1	angiogenic factor with G patch and FHA domains 1	chr5q13.3	210710_at	NM_018046																				
4.04	3.95	0.09	5.98E-01	8.51E-01	FGFR1	fibroblast growth factor receptor 1	chr8p11.2-p11.1	210973_s_at	NM_015850 /// NM_023105 /// NM_023106 /// NM_023107 /// NM_023108 /// NM_023110 /// NM_023111																				
4.88	4.72	0.16	5.98E-01	8.51E-01	C1orf21	chromosome 1 open reading frame 21	chr1q25	221272_s_at	NM_030806																				
2.97	2.83	0.14	5.98E-01	8.52E-01	LMO7	LIM domain 7	chr13q22.2	1556377_s_at	NM_005358																				
3.50	3.40	0.10	5.98E-01	8.52E-01	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	chr17q21.1	212834_at	NM_007010 /// NM_152300																				
2.16	2.07	0.09	5.98E-01	8.52E-01	---	---	---	236031_x_at	---																				
6.81	6.69	0.12	5.98E-01	8.52E-01	PNPLA6	patatin-like phospholipase domain containing 6	chr19p13.3-p13.2	203718_at	NM_006702																				
3.16	3.07	0.09	5.98E-01	8.52E-01	GNG3	guanine nucleotide binding protein (G protein), gamma 3	chr11p11	222005_s_at	NM_012202																				
2.49	2.41	0.07	5.98E-01	8.52E-01	---	---	---	239054_at	---																				
2.39	2.32	0.07	5.98E-01	8.52E-01	GRK7	G protein-coupled receptor kinase 7	chr3q21-q23	1552929_at	NM_139209																				
5.17	5.03	0.14	5.98E-01	8.52E-01	TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	chr6p21.31	1558136_s_at	NM_005643																				
2.23	2.16	0.07	5.98E-01	8.52E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	210834_s_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719																				

8.68	8.52	0.16	5.99E-01	8.52E-01	GSN	gelsolin (amyloidosis, Finnish type)	chr9q33	200696_s_at	NM_000177 /// NM_001127662 /// NM_001127663 /// NM_001127664 /// NM_001127665 /// NM_001127666 /// NM_001127667 /// NM_198252																				
5.10	4.94	0.16	5.99E-01	8.52E-01	BLVRA	biliverdin reductase A	chr7p14-cen	203771_s_at	NM_000712																				
4.27	4.13	0.14	5.99E-01	8.52E-01	---	---	---	240839_at	---																				
2.71	2.61	0.10	5.99E-01	8.52E-01	ADAT2	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)	chr6q24.2	236817_at	NM_182503																				
5.02	4.84	0.17	5.99E-01	8.52E-01	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	chr17q11.2-q12|17q21.1	216836_s_at	NM_001005862 /// NM_004448																				
3.15	3.07	0.09	5.99E-01	8.52E-01	PKNOX1	PBX/knotted 1 homeobox 1	chr21q22.3	216004_s_at	NM_004571																				
2.40	2.33	0.08	5.99E-01	8.52E-01	---	---	---	239995_at	---																				
5.40	5.19	0.21	5.99E-01	8.52E-01	---	---	---	239721_at	---																				
5.15	5.05	0.10	5.99E-01	8.52E-01	ATP8B1	ATPase, class I, type 8B, member 1	chr18q21-q22|18q21.31	214594_x_at	NM_005603																				
2.36	2.30	0.06	5.99E-01	8.52E-01	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	chr19q13.4	208426_x_at	NM_001080770 /// NM_001080772 /// NM_002255																				
2.24	2.17	0.07	5.99E-01	8.52E-01	---	---	---	1565585_at	---																				
4.84	4.66	0.19	5.99E-01	8.52E-01	SOCS3	suppressor of cytokine signaling 3	chr17q25.3	206359_at	NM_003955																				
2.63	2.51	0.12	5.99E-01	8.52E-01	ZNF654	zinc finger protein 654	chr3p11.2	219239_s_at	NM_018293																				
3.57	3.42	0.15	5.99E-01	8.52E-01	HRH3	histamine receptor H3	chr20q13.33	1555715_a_at	NM_007232																				
4.99	4.76	0.23	5.99E-01	8.52E-01	SETDB2	SET domain, bifurcated 2	chr13q14	235339_at	NM_031915																				
2.53	2.44	0.08	6.00E-01	8.53E-01	---	---	---	236169_at	---																				
2.40	2.32	0.08	6.00E-01	8.53E-01	---	---	---	234819_at	---																				
5.06	4.91	0.15	6.00E-01	8.53E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	201984_s_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284																				
2.51	2.42	0.08	6.00E-01	8.53E-01	---	---	---	239303_at	---																				
2.95	2.83	0.12	6.00E-01	8.53E-01	CD6	CD6 molecule	chr11q13	211893_x_at	NM_006725																				
2.99	2.92	0.07	6.00E-01	8.53E-01	---	---	---	214824_at	---																				
3.24	3.14	0.10	6.00E-01	8.53E-01	---	---	---	1566633_at	---																				
5.74	5.64	0.10	6.00E-01	8.53E-01	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	chr17q11.2	208830_s_at	NM_003170																				
3.01	2.93	0.08	6.00E-01	8.53E-01	---	---	---	242610_x_at	---																				
8.20	8.08	0.12	6.00E-01	8.53E-01	LSM3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr3p25.1	202209_at	NM_014463																				
2.12	2.04	0.08	6.00E-01	8.53E-01	---	---	---	242122_at	---																				
3.27	3.19	0.07	6.00E-01	8.53E-01	---	---	---	241076_at	---																				
5.23	5.13	0.10	6.00E-01	8.53E-01	NCR2	natural cytotoxicity triggering receptor 2	chr6p21.1	217045_x_at	NM_004828																				
2.28	2.20	0.07	6.00E-01	8.53E-01	---	---	---	1561211_at	---																				
5.77	5.65	0.12	6.00E-01	8.53E-01	---	---	---	231819_at	---																				
5.11	4.94	0.17	6.00E-01	8.53E-01	---	---	---	235513_at	---																				
2.75	2.67	0.07	6.00E-01	8.53E-01	TRIM33	tripartite motif-containing 33	chr1p13.1	214815_at	NM_015906 /// NM_033020																				
2.85	2.77	0.08	6.00E-01	8.53E-01	CHIC1	cysteine-rich hydrophobic domain 1	chrXq13-q21	1557786_s_at	NM_001039840																				
2.99	2.93	0.06	6.00E-01	8.53E-01	---	---	---	1570229_at	---																				
2.45	2.37	0.08	6.00E-01	8.53E-01	LOC100132815	hypothetical protein LOC100132815	chr19p12	1560446_at	XM_001720961 /// XM_001726067 /// XM_001726889																				

3.40	3.29	0.12	6.00E-01	8.53E-01	LOC285847	hypothetical protein LOC285847	chr6p21.31	1557723_at	XM_934928 /// XM_934929 /// XM_945988 /// XM_945990																				
2.11	2.03	0.09	6.00E-01	8.53E-01	---	---	---	239447_at	---																				
4.60	4.49	0.11	6.00E-01	8.53E-01	SAP30	Sin3A-associated protein, 30kDa	chr4q34.1	204899_s_at	NM_003864																				
2.21	2.14	0.07	6.00E-01	8.53E-01	MGC16142	hypothetical protein MGC16142	chr7q21.3	1553881_at	---																				
5.03	4.86	0.17	6.01E-01	8.53E-01	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	chr1p12	209900_s_at	NM_003051																				
5.78	5.60	0.18	6.01E-01	8.53E-01	VRK2	vaccinia related kinase 2	chr2p16-p15	205126_at	NM_001130480 /// NM_001130481 /// NM_001130482 /// NM_001130483 /// NM_006296																				
2.98	2.84	0.14	6.01E-01	8.53E-01	FLT3LG	fms-related tyrosine kinase 3 ligand	chr19q13.3	210607_at	NM_001459																				
3.07	2.97	0.10	6.01E-01	8.53E-01	TOP3B	topoisomerase (DNA) III beta	chr22q11.22	215781_s_at	NM_003935																				
5.02	4.83	0.19	6.01E-01	8.53E-01	GMNN	geminin, DNA replication inhibitor	chr6p22.2	218350_s_at	NM_015895																				
2.98	2.84	0.15	6.01E-01	8.53E-01	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	chr14q12	210278_s_at	NM_001128126 /// NM_007077																				
2.23	2.14	0.08	6.01E-01	8.53E-01	---	---	---	237873_s_at	---																				
5.28	5.18	0.10	6.01E-01	8.53E-01	EDNRB	endothelin receptor type B	chr13q22	204273_at	NM_000115 /// NM_001122659 /// NM_003991																				
4.54	4.35	0.19	6.01E-01	8.53E-01	---	---	---	225411_at	---																				
3.21	3.08	0.13	6.01E-01	8.53E-01	ANKRD32	ankyrin repeat domain 32	chr5q15	223542_at	NM_032290																				
4.15	4.04	0.11	6.01E-01	8.53E-01	MCC	mutated in colorectal cancers	chr5q21	206132_at	NM_001085377 /// NM_002387																				
2.22	2.17	0.05	6.01E-01	8.53E-01	ZNF677	zinc finger protein 677	chr19q13.41	238254_at	NM_182609																				
2.32	2.23	0.09	6.01E-01	8.53E-01	C2orf65	chromosome 2 open reading frame 65	chr2p13.1	1555148_a_at	NM_138804																				
3.82	3.73	0.09	6.01E-01	8.53E-01	MGC15613	hypothetical protein MGC15613	---	1561850_at	---																				
6.17	6.00	0.17	6.01E-01	8.53E-01	SFXN3	sideroflexin 3	chr10q24.31	217226_s_at	NM_030971																				
3.96	3.76	0.20	6.02E-01	8.54E-01	LOC100129673	similar to hCG2042915	chr17p13.2	236075_s_at	XM_001715544 /// XM_001717297																				
2.57	2.49	0.08	6.02E-01	8.54E-01	ACRV1	acrosomal vesicle protein 1	chr11q23-q24	207973_x_at	NM_001612 /// NM_020069 /// NM_020107 /// NM_020108 /// NM_020109 /// NM_020110 /// NM_020111 /// NM_020113 /// NM_020115																				
2.99	2.90	0.09	6.02E-01	8.54E-01	SCYE1	Small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	chr4q24	235594_at	NM_004757																				
2.98	2.87	0.11	6.02E-01	8.54E-01	NRAP	nebulin-related anchoring protein	chr10q24-q26	235312_s_at	NM_006175 /// NM_198060																				
2.85	2.78	0.07	6.02E-01	8.54E-01	---	---	---	234668_at	---																				
2.29	2.21	0.08	6.02E-01	8.54E-01	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	chr22q13.1-q13.2	206632_s_at	NM_004900																				
4.71	4.53	0.18	6.02E-01	8.54E-01	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	chr16p12.1	216908_x_at	XR_015784																				
11.93	11.85	0.07	6.02E-01	8.54E-01	PEBP1	phosphatidylethanolamine binding protein 1	chr12q24.23	211941_s_at	NM_002567																				
6.89	6.77	0.13	6.02E-01	8.54E-01	ATP5SL	ATP5S-like	chr19q13.2	45828_at	NM_018035																				

6.21	6.00	0.21	6.02E-01	8.54E-01	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	chr14q11.2	202752_x_at	NM_012244 /// NM_182728																				
4.11	3.70	0.41	6.02E-01	8.54E-01	AVPR1A	arginine vasopressin receptor 1A	chr12q14-q15	206251_s_at	NM_000706																				
2.99	2.92	0.07	6.02E-01	8.54E-01	ZNF107	zinc finger protein 107	chr7q11.2	1560854_s_at	NM_001013746 /// NM_016220																				
5.78	5.44	0.34	6.02E-01	8.54E-01	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	chr10q21.3	218878_s_at	NM_012238																				
3.89	3.80	0.09	6.02E-01	8.54E-01	GNL1 /// LOC285831	guanine nucleotide binding protein-like 1 /// hypothetical protein LOC285831	chr6p21.3 /// chr6p21.32	228857_at	NM_005275																				
3.21	3.13	0.08	6.02E-01	8.54E-01	ALOX15B	arachidonate 15-lipoxygenase, type B	chr17p13.1	1555416_a_at	NM_001039130 /// NM_001039131 /// NM_001141																				
2.65	2.55	0.10	6.02E-01	8.54E-01	---	---	---	239354_at	---																				
2.48	2.41	0.07	6.02E-01	8.54E-01	LOC285147	hypothetical protein LOC285147	chr2p25.2	236166_at	---																				
3.45	3.38	0.07	6.02E-01	8.54E-01	---	---	---	1559766_at	---																				
2.38	2.31	0.06	6.02E-01	8.54E-01	---	---	---	1561979_at	---																				
2.21	2.15	0.06	6.03E-01	8.54E-01	LOC646484	hypothetical LOC646484	chr4q31.1	244649_at	XM_933646 /// XM_943429																				
4.90	4.65	0.26	6.03E-01	8.54E-01	---	---	---	244447_at	---																				
3.02	2.90	0.11	6.03E-01	8.54E-01	LOC440149	hypothetical LOC440149	chr13q34	236366_at	---																				
3.60	3.52	0.08	6.03E-01	8.54E-01	SPNS3	spinster homolog 3 (Drosophila)	chr17p13.2	235900_at	NM_182538																				
2.58	2.43	0.16	6.03E-01	8.54E-01	SEC63	SEC63 homolog (S. cerevisiae)	chr6q21	235395_at	NM_007214																				
2.95	2.88	0.06	6.03E-01	8.54E-01	NFKBID	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	chr19q13.12	241889_at	NM_139239																				
3.62	3.49	0.13	6.03E-01	8.54E-01	BCAN	brevican	chr1q31	223632_s_at	NM_021948 /// NM_198427																				
6.36	6.26	0.10	6.03E-01	8.54E-01	REPS1	RALBP1 associated Eps domain containing 1	---	224366_s_at	NM_001128617 /// NM_031922																				
5.84	5.73	0.11	6.03E-01	8.54E-01	---	---	---	230449_x_at	---																				
2.63	2.54	0.09	6.03E-01	8.54E-01	---	---	---	1561705_at	---																				
2.58	2.50	0.08	6.03E-01	8.54E-01	FSD2	fibronectin type III and SPRY domain containing 2	chr15q25.2	237222_at	NM_001007122																				
4.29	4.16	0.13	6.03E-01	8.54E-01	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	chr5q31.1	228039_at	NM_014829																				
6.48	6.34	0.14	6.03E-01	8.54E-01	PLXND1	plexin D1	chr3q21.3	38671_at	NM_015103																				
4.97	4.86	0.12	6.03E-01	8.54E-01	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	chr7q35-q36	210036_s_at	NM_000238 /// NM_172056 /// NM_172057																				
4.83	4.68	0.15	6.03E-01	8.54E-01	---	---	---	237600_at	---																				
2.30	2.22	0.07	6.03E-01	8.54E-01	EYA3	eyes absent homolog 3 (Drosophila)	chr1p36	1554844_at	NM_001990																				
2.49	2.41	0.08	6.03E-01	8.54E-01	NPAL1	NIPA-like domain containing 1	chr4p12	232158_x_at	NM_207330																				
2.24	2.17	0.08	6.03E-01	8.54E-01	---	---	---	214416_at	---																				
3.13	3.04	0.09	6.03E-01	8.54E-01	USP42	ubiquitin specific peptidase 42	chr7p22.1	226174_at	NM_032172																				
3.57	3.47	0.10	6.04E-01	8.55E-01	PML	promyelocytic leukemia	chr15q22	210362_x_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250																				
3.99	3.87	0.12	6.04E-01	8.55E-01	SPATS2	spermatogenesis associated, serine-rich 2	chr12q13.12	222594_s_at	NM_023071																				

7.46	7.36	0.09	6.04E-01	8.55E-01	TSPAN4	tetraspanin 4	chr11p15.5	209263_x_at	NM_001025234 /// NM_001025235 /// NM_001025236 /// NM_001025237 /// NM_001025238 /// NM_001025239 /// NM_003271																				
1.97	1.92	0.05	6.04E-01	8.55E-01	---	---	---	237729_at	---																				
2.39	2.31	0.08	6.04E-01	8.55E-01	---	---	---	233984_at	---																				
2.12	2.05	0.07	6.04E-01	8.55E-01	---	---	---	1561863_a_at	---																				
2.40	2.32	0.08	6.04E-01	8.55E-01	FBXL21	F-box and leucine-rich repeat protein 21	chr5q31	1555413_s_at	NM_012159																				
5.84	5.69	0.14	6.04E-01	8.55E-01	PPP1R13L	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	chr19q13.32	218849_s_at	NM_006663																				
3.00	2.88	0.11	6.04E-01	8.55E-01	RFX7	regulatory factor X, 7	chr15q21.3	218430_s_at	NM_022841																				
8.37	8.20	0.17	6.04E-01	8.55E-01	---	---	---	202377_at	---																				
2.13	2.06	0.07	6.04E-01	8.55E-01	SIX4	SIX homeobox 4	chr14q23	231797_at	NM_017420																				
2.15	2.07	0.08	6.04E-01	8.55E-01	---	---	---	233906_at	---																				
2.67	2.58	0.09	6.04E-01	8.55E-01	C6orf195	chromosome 6 open reading frame 195	chr6p25.2	1553363_at	NM_152554																				
5.39	5.30	0.09	6.04E-01	8.55E-01	GATAD1	GATA zinc finger domain containing 1	chr7q21-q22	214718_at	NM_021167																				
2.33	2.27	0.06	6.04E-01	8.55E-01	BAGE	B melanoma antigen	chr21p11.1	1555369_at	NM_001187																				
2.12	2.06	0.06	6.04E-01	8.55E-01	---	---	---	234577_at	---																				
2.41	2.26	0.15	6.04E-01	8.55E-01	BCL2A1	BCL2-related protein A1	chr15q24.3	205681_at	NM_001114735 /// NM_004049																				
5.80	5.54	0.26	6.05E-01	8.55E-01	CSTA	cystatin A (stefin A)	chr3q21	204971_at	NM_005213																				
2.07	2.02	0.06	6.05E-01	8.55E-01	PLEKHA8	Pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	chr7p21-p11.2	1560556_a_at	NM_032639																				
8.34	8.23	0.11	6.05E-01	8.55E-01	GYG1	glycogenin 1	chr3q24-q25.1	201554_x_at	NM_004130																				
2.57	2.49	0.09	6.05E-01	8.55E-01	ITIH5	inter-alpha (globulin) inhibitor H5	chr10p14	1553243_at	NM_001001851 /// NM_030569 /// NM_032817																				
6.67	6.40	0.26	6.05E-01	8.55E-01	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	chr6q14-q15	217833_at	NM_006372																				
2.54	2.43	0.10	6.05E-01	8.55E-01	RP9	Retinitis pigmentosa 9 (autosomal dominant)	chr7p14.3	227849_at	NM_203288																				
4.11	4.05	0.07	6.05E-01	8.55E-01	UBE2O	ubiquitin-conjugating enzyme E2O	chr17q25.1	1554814_at	NM_022066																				
3.69	3.54	0.16	6.05E-01	8.55E-01	MAPK8	mitogen-activated protein kinase 8	chr10q11.22	226046_at	NM_002750 /// NM_139046 /// NM_139047 /// NM_139049																				
4.79	4.69	0.10	6.05E-01	8.55E-01	SULT1A3 /// SULT1A4	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	chr16p11.2	222094_at	NM_001017387 /// NM_001017389 /// NM_001017390 /// NM_001017391 /// NM_003166 /// NM_177552																				
4.77	4.59	0.18	6.05E-01	8.55E-01	---	---	---	231258_at	---																				
2.80	2.73	0.07	6.05E-01	8.55E-01	GLI2	GLI-Kruppel family member GLI2	chr2q14	208057_s_at	NM_005270																				
2.93	2.84	0.09	6.05E-01	8.55E-01	---	---	---	233706_at	---																				
2.00	1.94	0.06	6.05E-01	8.55E-01	---	---	---	240619_at	---																				
2.50	2.42	0.08	6.05E-01	8.55E-01	PTPRD	protein tyrosine phosphatase, receptor type, D	chr9p23-p24.3	205712_at	NM_001040712 /// NM_002839 /// NM_130391 /// NM_130392 /// NM_130393																				
2.87	2.76	0.11	6.05E-01	8.55E-01	---	---	---	216790_at	---																				
2.58	2.51	0.07	6.05E-01	8.55E-01	RPS6	ribosomal protein S6	chr9p21	211690_at	NM_001010																				

4.64	4.55	0.08	6.05E-01	8.55E-01	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	211465_x_at	NM_000150 /// NM_001040701																				
2.72	2.66	0.07	6.05E-01	8.55E-01	KIAA1107	KIAA1107	chr1p22.1	1558293_at	NM_015237 /// XM_034086 /// XM_937137																				
4.50	4.34	0.16	6.05E-01	8.55E-01	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	chr4q21.3	204201_s_at	NM_006264 /// NM_080683 /// NM_080684 /// NM_080685																				
3.58	3.47	0.11	6.05E-01	8.55E-01	LOC100133311 /// LOC100134764 /// LOC285944	similar to hCG1644697 /// similar to hCG1644697 /// hypothetical protein LOC285944	chr7p15.2	239915_at	XM_001717382 /// XM_001717666 /// XM_001718357																				
4.89	4.78	0.11	6.05E-01	8.55E-01	WDR21A	WD repeat domain 21A	chr14q24.3	226938_at	NM_015604 /// NM_181340 /// NM_181341																				
7.30	6.99	0.32	6.05E-01	8.55E-01	AMIGO2	adhesion molecule with Ig-like domain 2	chr12q13.11	222108_at	NM_181847																				
2.79	2.71	0.08	6.06E-01	8.56E-01	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14	chr19q13	220776_at	NM_013348 /// NM_170720																				
4.92	4.76	0.16	6.06E-01	8.56E-01	LOC339344	hypothetical protein LOC339344	chr19q13.32	227937_at	NM_001012643																				
3.21	3.12	0.09	6.06E-01	8.56E-01	SEC14L2	SEC14-like 2 (S. cerevisiae)	chr22q12.2	240024_at	NM_012429																				
2.34	2.23	0.11	6.06E-01	8.56E-01	FLJ77644 /// TMEM106A	similar to transmembrane protein 106A /// transmembrane protein 106A	chr17q21.31	1552302_at	NM_145041 /// XM_001133074 /// XM_001722626																				
3.75	3.65	0.10	6.06E-01	8.56E-01	PCDHB3	protocadherin beta 3	chr5q31	221410_x_at	NM_018937																				
2.30	2.22	0.09	6.06E-01	8.56E-01	ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	chr4q23-q24	210505_at	NM_000673																				
3.02	2.87	0.14	6.06E-01	8.56E-01	LOC642236	similar to FRG1 protein (FSHD region gene 1 protein)	chr9q12	242770_at	XR_041084 /// XR_041085 /// XR_041086 /// XR_041087																				
7.26	7.14	0.12	6.06E-01	8.56E-01	C11orf48	chromosome 11 open reading frame 48	chr11q12.3	221637_s_at	NM_024099																				
2.39	2.33	0.06	6.06E-01	8.56E-01	---	---	---	1564148_at	---																				
3.36	3.28	0.08	6.06E-01	8.56E-01	---	---	---	237067_at	---																				
2.83	2.77	0.06	6.06E-01	8.56E-01	WDR62	WD repeat domain 62	chr19q13.12	1553123_at	NM_001083961 /// NM_173636																				
1.98	1.92	0.06	6.06E-01	8.56E-01	---	---	---	238348_x_at	---																				
5.94	5.82	0.12	6.06E-01	8.56E-01	ANO10	anoctamin 10	chr3p22.1-p21.33	218910_at	NM_018075																				
6.64	6.53	0.11	6.06E-01	8.56E-01	PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	chr14q11-q24	209625_at	NM_004569																				
4.97	4.89	0.08	6.06E-01	8.56E-01	DNAH3	Dynein, axonemal, heavy chain 3	chr16p12.2	220725_x_at	NM_017539																				
2.28	2.22	0.06	6.06E-01	8.56E-01	---	---	---	237625_s_at	---																				
5.00	4.75	0.25	6.06E-01	8.56E-01	SLC39A14	solute carrier family 39 (zinc transporter), member 14	chr8p21.3	1555434_a_at	NM_001128431 /// NM_015359																				
3.23	3.09	0.14	6.06E-01	8.56E-01	---	---	---	241173_at	---																				
5.27	5.18	0.09	6.06E-01	8.56E-01	CLEC4E	C-type lectin domain family 4, member E	chr12p13.31	222934_s_at	NM_014358																				
2.19	2.10	0.09	6.06E-01	8.56E-01	---	---	---	1561062_a_at	---																				
2.48	2.39	0.09	6.06E-01	8.56E-01	DTNB	dystrobrevin, beta	chr2p24	215295_at	NM_021907 /// NM_033147 /// NM_033148 /// NM_183360 /// NM_183361																				

7.78	7.68	0.10	6.07E-01	8.56E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	205967_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054																			
3.26	3.14	0.12	6.07E-01	8.56E-01	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	chr4p15.2	1569634_at	NM_016955 /// NM_153825																				
3.91	3.73	0.18	6.07E-01	8.56E-01	LOC283345	RPL13-2 pseudogene	chr12p13.31	210822_at	NR_002803																				
4.40	4.25	0.15	6.07E-01	8.56E-01	SH3TC1	SH3 domain and tetratricopeptide repeats 1	chr4p16.1	219256_s_at	NM_018986																				
2.23	2.15	0.08	6.07E-01	8.56E-01	WDR52	WD repeat domain 52	chr3q13.2	221103_s_at	NM_018338																				
2.33	2.26	0.07	6.07E-01	8.56E-01	---	---	---	1559057_at	---																				
5.50	5.41	0.09	6.07E-01	8.56E-01	SYNPO	synaptopodin	chr5q33.1	235128_at	NM_001109974 /// NM_007286																				
5.60	5.47	0.13	6.07E-01	8.56E-01	RARG	retinoic acid receptor, gamma	chr12q13	204188_s_at	NM_000966 /// NM_001042728																				
3.31	3.22	0.08	6.07E-01	8.56E-01	CORT	cortistatin	chr1p36|1p36.22	210182_at	NM_001302																				
3.71	3.56	0.15	6.07E-01	8.56E-01	SNX14	Sorting nexin 14	chr6q14.3	230759_at	NM_020468 /// NM_153816																				
2.06	1.98	0.08	6.07E-01	8.56E-01	SPIN3	spindlin family, member 3	chrXp11.1	1554098_at	NM_001010862																				
5.64	5.50	0.14	6.07E-01	8.56E-01	H2AFY	H2A histone family, member Y	chr5q31.3-q32	214500_at	NM_001040158 /// NM_004893 /// NM_138609 /// NM_138610																				
4.57	4.42	0.16	6.07E-01	8.56E-01	C12orf43	chromosome 12 open reading frame 43	chr12q	219022_at	NM_022895																				
3.57	3.47	0.10	6.07E-01	8.56E-01	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	chr11q21	209893_s_at	NM_002033																				
3.50	3.41	0.09	6.07E-01	8.56E-01	MEIS3	Meis homeobox 3	chr19q13.32	1569402_at	NM_001009813 /// NM_020160																				
4.82	4.71	0.11	6.07E-01	8.56E-01	NPFF	neuropeptide FF-amide peptide precursor	chr12q13.13	206402_s_at	NM_003717																				
2.49	2.41	0.08	6.07E-01	8.56E-01	---	---	---	242316_at	---																				
2.64	2.56	0.08	6.08E-01	8.57E-01	LOC100130905	hypothetical protein LOC100130905	chr12q23.3	226526_s_at	XM_001715433 /// XM_001718747																				
2.20	2.12	0.08	6.08E-01	8.57E-01	TRPC7	transient receptor potential cation channel, subfamily C, member 7	chr5q31.2	234407_s_at	NM_020389																				
7.30	7.12	0.17	6.08E-01	8.57E-01	BIRC2	baculoviral IAP repeat-containing 2	chr11q22	202076_at	NM_001166																				
5.95	5.72	0.23	6.08E-01	8.57E-01	INTS8	integrator complex subunit 8	chr8q22.1	218905_at	NM_017864																				
5.18	5.07	0.11	6.08E-01	8.57E-01	ATP11B	ATPase, class VI, type 11B	chr3q27	212536_at	NM_014616																				
2.98	2.89	0.08	6.08E-01	8.57E-01	LOC286149	hypothetical protein LOC286149	chr8q22.1	1556755_s_at	---																				

1.85	1.79	0.07	6.08E-01	8.57E-01	ZNF852	zinc finger protein 852	chr3p21.32	1564662_at	XM_001717402 /// XM_001717544 /// XM_001725070																			
8.20	8.04	0.15	6.08E-01	8.57E-01	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	chr21q22.3	226616_s_at	NM_001001503 /// NM_021075																			
2.16	2.08	0.08	6.08E-01	8.57E-01	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	chr15q21.1	1566861_at	NM_001482																			
3.59	3.50	0.09	6.08E-01	8.57E-01	---	---	---	237703_at	---																			
7.23	7.10	0.13	6.08E-01	8.57E-01	PDE12	phosphodiesterase 12	chr3p14.3	231839_at	NM_177966																			
2.71	2.61	0.10	6.08E-01	8.57E-01	---	---	---	1556332_at	---																			
2.07	2.01	0.06	6.08E-01	8.57E-01	---	---	---	237499_at	---																			
6.67	6.47	0.20	6.08E-01	8.57E-01	DDEFL1	development and differentiation enhancing factor-like 1	chr1p36.12	219103_at	NM_017707																			
3.17	3.08	0.09	6.08E-01	8.57E-01	SLC15A4	Solute carrier family 15, member 4	chr12q24.32	229503_at	NM_145648																			
5.04	4.88	0.16	6.08E-01	8.57E-01	SHROOM4	shroom family member 4	chrXp11.22	244825_at	NM_020717																			
2.01	1.95	0.06	6.09E-01	8.57E-01	LOC645513	Hypothetical LOC645513	chr4q26-q27	1561760_s_at	XM_001714125 /// XM_001714854 /// XM_001717939																			
2.42	2.34	0.08	6.09E-01	8.57E-01	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	chr6q21	235226_at	NM_015076																			
4.00	3.92	0.08	6.09E-01	8.57E-01	MED26	mediator complex subunit 26	chr19p13.11	231724_at	NM_004831																			
4.08	3.87	0.21	6.09E-01	8.57E-01	---	---	---	228191_at	---																			
3.73	3.66	0.07	6.09E-01	8.57E-01	---	---	---	240547_at	---																			
3.10	3.03	0.07	6.09E-01	8.57E-01	---	---	---	236599_at	---																			
3.00	2.92	0.08	6.09E-01	8.57E-01	SH3GLP2	SH3-domain GRB2-like pseudogene 2	chr17q11.2	1567027_at	---																			
5.24	5.07	0.18	6.09E-01	8.57E-01	TRA2A	transformer-2 alpha	chr7p15.3	213575_at	NM_013293																			
2.66	2.55	0.11	6.09E-01	8.57E-01	---	---	---	1556914_at	---																			
4.69	4.56	0.13	6.09E-01	8.57E-01	---	---	---	229255_x_at	---																			
7.53	7.44	0.10	6.09E-01	8.57E-01	TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)	chr1p32.3	223017_at	NM_015913																			
8.87	8.80	0.07	6.09E-01	8.57E-01	RPN1	ribophorin I	chr3q21.3	201011_at	NM_002950																			
2.43	2.37	0.06	6.09E-01	8.57E-01	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	chr6p22.3-p22.2	206264_at	NM_001503 /// NM_177483																			
2.38	2.32	0.07	6.09E-01	8.57E-01	SLC10A7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	chr4q31.22	1555108_at	NM_001029998 /// NM_032128																			
2.53	2.45	0.08	6.09E-01	8.57E-01	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	chr1p22.3	203019_x_at	NM_014021																			
2.83	2.75	0.08	6.09E-01	8.57E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	210804_x_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097																			
2.17	2.10	0.07	6.09E-01	8.57E-01	---	---	---	1561924_at	---																			
3.35	3.26	0.08	6.09E-01	8.57E-01	---	---	---	241212_at	---																			
2.70	2.57	0.13	6.09E-01	8.57E-01	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	chr4q21	204470_at	NM_001511																			
2.67	2.60	0.07	6.09E-01	8.57E-01	CLCA1	CLCA family member 1, chloride channel regulator	chr1p31-p22	210107_at	NM_001285																			
2.47	2.37	0.09	6.09E-01	8.58E-01	TDH	L-threonine dehydrogenase	chr8p23.1	1555151_s_at	NR_001578																			
2.22	2.15	0.07	6.09E-01	8.58E-01	---	---	---	1562982_at	---																			
2.64	2.56	0.09	6.10E-01	8.58E-01	---	---	---	1561487_at	---																			
2.04	1.99	0.06	6.10E-01	8.58E-01	C20orf197	chromosome 20 open reading frame 197	chr20q13.33	1553311_at	NM_173644																			
3.91	3.79	0.12	6.10E-01	8.58E-01	ZNF142	zinc finger protein 142	chr2q34-q35	37586_at	NM_001105537 /// NM_005081																			
5.91	5.77	0.14	6.10E-01	8.58E-01	ATG12	ATG12 autophagy related 12 homolog (S. cerevisiae)	chr5q21-q22	204833_at	NM_004707																			
8.56	8.46	0.10	6.10E-01	8.58E-01	ADAR	adenosine deaminase, RNA-specific	chr1q21.1-q21.2	201786_s_at	NM_001025107 /// NM_001111 /// NM_015840 /// NM_015841																			
5.91	5.79	0.11	6.10E-01	8.58E-01	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	chr17q21	225628_s_at	NM_005937																			
3.17	3.08	0.09	6.10E-01	8.58E-01	---	---	---	235883_at	---																			
2.50	2.43	0.07	6.10E-01	8.58E-01	LOC284930	hypothetical protein LOC284930	chr22q13.32	1564446_at	---																			
2.26	2.20	0.06	6.10E-01	8.58E-01	ATP9B	ATPase, class II, type 9B	chr18q23	1564344_at	NM_198531																			
4.95	4.87	0.08	6.10E-01	8.58E-01	ALDH3B1	Aldehyde dehydrogenase 3 family, member B1	chr11q13	1565731_at	NM_000694 /// NM_001030010																			

3.08	3.02	0.06	6.10E-01	8.58E-01	LOC285178	hypothetical protein LOC285178	chr2q35	230057_at	---																			
3.95	3.80	0.15	6.10E-01	8.58E-01	SFRS4	splicing factor, arginine/serine-rich 4	chr1p35.3	239512_at	NM_005626																			
7.43	7.34	0.09	6.10E-01	8.58E-01	MRPS7	mitochondrial ribosomal protein S7	chr17q25	217932_at	NM_015971																			
2.58	2.50	0.08	6.10E-01	8.58E-01	IQGAP3	IQ motif containing GTPase activating protein 3	chr1q22-q23.1	229538_s_at	NM_178229																			
7.47	7.29	0.18	6.10E-01	8.58E-01	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	chr11q13.2	204158_s_at	NM_006019 /// NM_006053																			
3.27	3.16	0.12	6.11E-01	8.58E-01	TNIK	TRAF2 and NCK interacting kinase	chr3q26.2-q26.31	239288_at	NM_015028																			
3.45	3.35	0.10	6.11E-01	8.58E-01	HAS3	hyaluronan synthase 3	chr16q22.1	1552980_at	NM_005329 /// NM_138612																			
2.49	2.44	0.05	6.11E-01	8.58E-01	---	---	---	1562878_at	---																			
4.05	3.92	0.14	6.11E-01	8.58E-01	---	---	---	239049_at	---																			
2.30	2.23	0.07	6.11E-01	8.58E-01	---	---	---	1569193_at	---																			
2.17	2.10	0.07	6.11E-01	8.58E-01	SLCO1A2	solute carrier organic anion transporter family, member 1A2	chr12p12	211480_s_at	NM_005075 /// NM_021094 /// NM_134431																			
6.56	6.39	0.17	6.11E-01	8.58E-01	SLC37A2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	chr11q24.2	238638_at	NM_198277																			
4.00	3.88	0.12	6.11E-01	8.59E-01	ZBTB42	Zinc finger and BTB domain containing 42	chr14q32.33	229691_at	XM_001717198																			
4.39	4.31	0.07	6.11E-01	8.59E-01	BBS1	Bardet-Biedl syndrome 1	chr11q13.1	222643_s_at	NM_024649																			
2.03	1.96	0.06	6.11E-01	8.59E-01	FAM154B	family with sequence similarity 154, member B	chr15q25.2	1556158_at	NM_001008226																			
7.97	7.80	0.17	6.11E-01	8.59E-01	CSF1R	colony stimulating factor 1 receptor	chr5q33-q35	203104_at	NM_005211																			
8.16	8.01	0.15	6.11E-01	8.59E-01	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	chr5q23-q31	228588_s_at	NM_003337																			
4.04	3.85	0.19	6.11E-01	8.59E-01	---	---	---	242420_at	---																			
2.28	2.22	0.06	6.11E-01	8.59E-01	GAGE1	G antigen 1	chrXp11.4-p11.2	208283_at	NM_001040663 /// NM_001468																			
1.85	1.80	0.05	6.12E-01	8.59E-01	---	---	---	1567173_at	---																			
3.81	3.72	0.09	6.12E-01	8.59E-01	DOK4	docking protein 4	chr16q13	207747_s_at	NM_018110																			
1.86	1.80	0.07	6.12E-01	8.59E-01	TFB2M	transcription factor B2, mitochondrial	chr1q44	1566930_at	NM_022366																			
2.49	2.41	0.07	6.12E-01	8.59E-01	MRPL20	mitochondrial ribosomal protein L20	chr1p36.3-p36.2	220527_at	NM_017971																			
3.63	3.54	0.08	6.12E-01	8.59E-01	ANGPT4	angiopoietin 4	chr20p13	221134_at	NM_015985																			
5.04	4.91	0.14	6.12E-01	8.59E-01	---	---	---	239991_at	---																			
3.89	3.81	0.08	6.12E-01	8.59E-01	AP3D1	adaptor-related protein complex 3, delta 1 subunit	chr19p13.3	210974_s_at	NM_001077523 /// NM_003938																			
8.71	8.66	0.06	6.12E-01	8.59E-01	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	chr1p36.33	200746_s_at	NM_002074																			
3.92	3.81	0.12	6.12E-01	8.59E-01	PBLD	phenazine biosynthesis-like protein domain containing	chr10pter-q25.3	1555175_a_at	NM_001033083 /// NM_022129																			

2.40	2.31	0.09	6.12E-01	8.59E-01	GAGE1 /// GAGE12F /// GAGE12G /// GAGE12I /// GAGE12J /// GAGE2A /// GAGE2B /// GAGE2C /// GAGE2D /// GAGE2E /// GAGE3 /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7 /// GAGE8	G antigen 1 /// G antigen 12F /// G antigen 12G /// G antigen 12I /// G antigen 12J /// G antigen 2A /// G antigen 2B /// G antigen 2C /// G antigen 2D /// G antigen 2E /// G antigen 3 /// G antigen 4 /// G antigen 5 /// G antigen 6 /// G antigen 7 /// G antigen 8	chrXp11.23 /// chrXp11.4-p11.2	207739_s_at	NM_001040663 /// NM_001098405 /// NM_001098406 /// NM_001098407 /// NM_001098409 /// NM_001098411 /// NM_001127200 /// NM_001127212 /// NM_001468 /// NM_001472 /// NM_001474 /// NM_001475 /// NM_001476 /// NM_001477 /// NM_012196 /// NM_021123 /// XM_001130991
2.54	2.48	0.06	6.12E-01	8.59E-01	ZNF333	zinc finger protein 333	chr19p13	1569251_a_at	NM_032433
2.42	2.35	0.07	6.12E-01	8.59E-01	---	---	---	217298_at	---
8.11	7.99	0.12	6.12E-01	8.59E-01	MFSD1	major facilitator superfamily domain containing 1	chr3q25.33	218109_s_at	NM_022736
12.00	11.93	0.07	6.12E-01	8.59E-01	RPL24 /// SLC36A2	ribosomal protein L24 /// solute carrier family 36 (proton/amino acid symporter), member 2	chr3q12 /// chr5q33.1	214143_x_at	NM_000986 /// NM_181776
2.31	2.24	0.06	6.12E-01	8.59E-01	DKFZp686O1327	Similar to hCG2041586	chr2q22.3	216877_at	XM_379141
1.89	1.82	0.07	6.12E-01	8.59E-01	LOC148987	hypothetical protein LOC148987	chr1p32.3	1557566_at	---
4.20	4.10	0.10	6.12E-01	8.59E-01	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	chr11p15.5	221913_at	NM_001017524 /// NM_012239
3.33	3.25	0.08	6.13E-01	8.59E-01	CDC42SE1	CDC42 small effector 1	chr1q21.2	223674_s_at	NM_001038707 /// NM_020239
3.68	3.57	0.11	6.13E-01	8.59E-01	---	---	---	224260_at	---
3.82	3.74	0.08	6.13E-01	8.59E-01	LOC283859	hypothetical protein LOC283859	chr16q12.1	229481_at	---
2.28	2.21	0.07	6.13E-01	8.59E-01	---	---	---	1554649_at	---
2.51	2.42	0.09	6.13E-01	8.59E-01	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase	chr16q24.3	236866_at	NM_000512
4.91	4.84	0.08	6.13E-01	8.59E-01	SMYD2	SET and MYND domain containing 2	chr1q41	243288_at	NM_020197
3.25	3.15	0.10	6.13E-01	8.59E-01	ARMC4	armadillo repeat containing 4	chr10p12.1-p11.23	221077_at	NM_018076
2.56	2.49	0.07	6.13E-01	8.59E-01	C3orf47	chromosome 3 open reading frame 47	chr3q21.3	1558168_at	XR_040787 /// XR_040788 /// XR_040789
4.31	4.19	0.12	6.13E-01	8.59E-01	KIF22	kinesin family member 22	chr16p11.2	216969_s_at	NM_007317
10.21	10.03	0.18	6.13E-01	8.59E-01	HLA-DRB1	Major histocompatibility complex, class II, DR beta 3	chr6p21.3	208306_x_at	NM_002124
5.73	5.62	0.11	6.13E-01	8.59E-01	PSMG1	proteasome (prosome, macropain) assembly chaperone 1	chr21q22.3	203405_at	NM_003720 /// NM_203433
2.50	2.43	0.07	6.13E-01	8.59E-01	TKTL1	transketolase-like 1	chrXq28	214183_s_at	NM_012253
2.76	2.67	0.09	6.13E-01	8.59E-01	---	---	---	229413_s_at	---
2.59	2.53	0.06	6.13E-01	8.59E-01	---	---	---	240102_at	---
4.31	4.11	0.21	6.13E-01	8.59E-01	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	chr8p23	219341_at	NM_018941
2.98	2.90	0.08	6.13E-01	8.59E-01	GPR156	G protein-coupled receptor 156	chr3q13.33	1553028_at	NM_153002
3.09	2.99	0.10	6.13E-01	8.59E-01	CAMTA1	calmodulin binding transcription activator 1	chr1p36.31-p36.23	241882_at	NM_015215
2.99	2.90	0.08	6.14E-01	8.59E-01	---	---	---	234885_at	---
2.39	2.31	0.08	6.14E-01	8.59E-01	---	---	---	237113_at	---

6.60	6.48	0.12	6.14E-01	8.59E-01	MTMR14	myotubularin related protein 14	chr3p26	222143_s_at	NM_001077525 /// NM_001077526 /// NM_022485																				
2.38	2.29	0.09	6.14E-01	8.59E-01	---	---	---	222335_at	---																				
6.43	6.28	0.15	6.14E-01	8.59E-01	C8orf30A	chromosome 8 open reading frame 30A	chr8q24.3	219071_x_at	NM_016458																				
5.81	5.67	0.14	6.14E-01	8.59E-01	LOC100133072 /// LOC729991 /// MEF2B	hypothetical protein LOC100133072 /// hypothetical LOC729991 /// myocyte enhancer factor 2B	chr19p12 /// chr19p13.11	1553978_at	NM_005919 /// XM_001720164 /// XM_001725837 /// XM_001726862 /// XR_041227 /// XR_041228 /// XR_041229																				
2.82	2.73	0.10	6.14E-01	8.59E-01	C5orf28	chromosome 5 open reading frame 28	chr5p12	238635_at	NM_022483																				
2.68	2.63	0.05	6.14E-01	8.59E-01	HIST3H3	histone cluster 3, H3	chr1q42	208572_at	NM_003493																				
4.73	4.61	0.12	6.14E-01	8.60E-01	NAT6	N-acetyltransferase 6	chr3p21.3	210874_s_at	NM_012191																				
1.86	1.80	0.07	6.14E-01	8.60E-01	---	---	---	1562342_at	---																				
2.20	2.15	0.05	6.14E-01	8.60E-01	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)	chr6p21.3	239975_at	NR_001435																				
4.33	4.04	0.29	6.14E-01	8.60E-01	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	chr7p14.3	223584_s_at	NM_015483																				
2.25	2.20	0.06	6.14E-01	8.60E-01	---	---	---	241728_at	---																				
2.80	2.74	0.06	6.14E-01	8.60E-01	---	---	---	236396_at	---																				
4.89	4.70	0.19	6.14E-01	8.60E-01	MUM1	melanoma associated antigen (mutated) 1	chr19p13.3	229033_s_at	NM_032853																				
7.48	7.40	0.08	6.14E-01	8.60E-01	HM13	histocompatibility (minor) 13	chr20q11.21	232209_x_at	NM_030789 /// NM_178580 /// NM_178581 /// NM_178582																				
8.04	7.79	0.25	6.14E-01	8.60E-01	CFI	complement factor I	chr4q25	203854_at	NM_000204																				
2.36	2.29	0.07	6.14E-01	8.60E-01	---	---	---	215970_at	---																				
2.34	2.27	0.07	6.14E-01	8.60E-01	---	---	---	239971_at	---																				
8.34	8.24	0.11	6.15E-01	8.60E-01	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	chr12p13.2	207643_s_at	NM_001065																				
5.40	5.31	0.09	6.15E-01	8.60E-01	HAP1	huntingtin-associated protein 1	chr17q21.2-q21.3	211604_x_at	NM_001079870 /// NM_001079871 /// NM_003949 /// NM_177977																				
2.30	2.22	0.08	6.15E-01	8.60E-01	---	---	---	220814_at	---																				
2.58	2.50	0.08	6.15E-01	8.60E-01	EPHA10	EPH receptor A10	chr1p34.3	243717_at	NM_001099439 /// NM_173641																				
2.49	2.40	0.09	6.15E-01	8.60E-01	---	---	---	1561916_at	---																				
2.08	2.00	0.08	6.15E-01	8.60E-01	---	---	---	1568802_at	---																				
2.15	2.10	0.06	6.15E-01	8.60E-01	C21orf41	chromosome 21 open reading frame 41	chr21q22.11	1552401_a_at	NR_002214 /// NR_002215 /// XM_001720046 /// XM_001724646 /// XM_001725376																				
5.61	5.46	0.15	6.15E-01	8.60E-01	MON1A	MON1 homolog A (yeast)	chr3p21.31	224500_s_at	NM_032355																				
3.71	3.60	0.11	6.15E-01	8.60E-01	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	chr2q35	210423_s_at	NM_000578																				

2.67	2.57	0.09	6.15E-01	8.60E-01	hCG_2009921	hypothetical locus LOC441204	chr7p15.2	240423_at	NR_015364 /// XM_001722132 /// XM_001723644 /// XM_001723694 /// XM_499061 /// XM_943507																			
2.69	2.59	0.10	6.15E-01	8.60E-01	DOCK1	Dedicator of cytokinesis 1	chr10q26.13-q26.3	232973_at	NM_001380																			
3.27	3.19	0.09	6.15E-01	8.60E-01	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	chr2p16.1	219498_s_at	NM_018014 /// NM_022893 /// NM_138559																			
1.99	1.92	0.07	6.15E-01	8.60E-01	RAD9B	RAD9 homolog B (S. cerevisiae)	chr12q24.11	1564688_a_at	NM_152442																			
2.82	2.74	0.09	6.15E-01	8.60E-01	---	---	---	1562863_at	---																			
4.60	4.47	0.13	6.15E-01	8.60E-01	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	chr16q12.1	224839_s_at	NM_133443																			
3.04	2.90	0.14	6.15E-01	8.60E-01	MB	myoglobin	chr22q13.1	204179_at	NM_005368 /// NM_203377 /// NM_203378																			
3.29	3.19	0.09	6.15E-01	8.60E-01	ELL3	elongation factor RNA polymerase II-like 3	chr15q15.3	219518_s_at	NM_025165																			
2.06	1.99	0.07	6.15E-01	8.60E-01	---	---	---	1561754_at	---																			
3.24	3.05	0.19	6.16E-01	8.60E-01	C3orf64	chromosome 3 open reading frame 64	chr3p14.1	221935_s_at	NM_173654																			
3.08	2.96	0.12	6.16E-01	8.61E-01	METTL10	methyltransferase like 10	chr10q26.13	226634_at	NM_212554																			
3.03	2.95	0.08	6.16E-01	8.61E-01	---	---	---	237486_at	---																			
3.73	3.57	0.16	6.16E-01	8.61E-01	TET2	tet oncogene family member 2	chr4q24	227624_at	NM_001127208 /// NM_017628																			
2.38	2.31	0.06	6.16E-01	8.61E-01	---	---	---	234441_at	---																			
2.58	2.48	0.10	6.16E-01	8.61E-01	TTN	Titin	chr2q31	242771_at	NM_003319 /// NM_133378 /// NM_133379 /// NM_133432 /// NM_133437																			
2.15	2.08	0.07	6.16E-01	8.61E-01	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	chr9p13	229403_at	NM_001497																			
3.96	3.89	0.08	6.16E-01	8.61E-01	---	---	---	232834_at	---																			
5.79	5.59	0.20	6.16E-01	8.61E-01	FAM115A	family with sequence similarity 115, member A	chr7q35	212981_s_at	NM_014719																			
5.08	4.98	0.10	6.16E-01	8.61E-01	PRDM1	PR domain containing 1, with ZNF domain	chr6q21-q22.1	235668_at	NM_001198 /// NM_182907																			
2.44	2.37	0.08	6.16E-01	8.61E-01	UNQ9391	tryptophan/serine protease	chr8p23.1	1570274_at	NM_198464																			
2.79	2.71	0.09	6.16E-01	8.61E-01	KRT17	keratin 17	chr17q12-q21	205157_s_at	NM_000422																			
2.13	2.04	0.09	6.16E-01	8.61E-01	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	chrXp21.2	1552928_s_at	NM_152787																			
2.16	2.09	0.07	6.16E-01	8.61E-01	---	---	---	1563993_at	---																			
5.26	5.13	0.13	6.16E-01	8.61E-01	C14orf37	chromosome 14 open reading frame 37	chr14q23.1	1557176_a_at	NM_001001872																			
5.69	5.48	0.21	6.16E-01	8.61E-01	---	---	---	228116_at	---																			
2.56	2.44	0.13	6.16E-01	8.61E-01	CHORDC1	Cysteine and histidine-rich domain (CHORD)-containing 1	chr11q14.3	239436_at	NM_012124																			
2.25	2.18	0.06	6.16E-01	8.61E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	1566272_at	NM_014990 /// NM_194301																			
5.32	5.17	0.15	6.17E-01	8.61E-01	RB1CC1	RB1-inducible coiled-coil 1	chr8q11	202034_x_at	NM_001083617 /// NM_014781																			
4.23	4.04	0.19	6.17E-01	8.61E-01	ZEB2	zinc finger E-box binding homeobox 2	chr2q22	203603_s_at	NM_014795																			
5.28	5.19	0.09	6.17E-01	8.61E-01	RCE1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	chr11q13	205332_at	NM_001032279 /// NM_005133																			
2.25	2.19	0.05	6.17E-01	8.61E-01	CLEC4E	C-type lectin domain family 4, member E	chr12p13.31	219859_at	NM_014358																			
2.44	2.37	0.07	6.17E-01	8.61E-01	FOXK2	forkhead box K2	chr17q25	242937_at	NM_004514																			
6.00	5.82	0.18	6.17E-01	8.61E-01	ADSS	adenylosuccinate synthase	chr1cen-q12	221761_at	NM_001126																			
2.82	2.75	0.06	6.17E-01	8.61E-01	DLGAP1	discs, large (Drosophila) homolog-associated protein 1	chr18p11.3	210750_s_at	NM_001003809 /// NM_004746																			

2.73	2.66	0.07	6.17E-01	8.61E-01	---	---	---	1563147_at	---
5.40	5.30	0.10	6.17E-01	8.61E-01	SNAP29	synaptosomal-associated protein, 29kDa	chr22q11.21	222597_at	NM_004782
2.21	2.16	0.06	6.17E-01	8.61E-01	TRIM31	tripartite motif-containing 31	chr6p21.3	208170_s_at	NM_007028
2.31	2.25	0.07	6.17E-01	8.61E-01	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	chrXp21.2	1558518_at	NM_152787
2.12	2.05	0.07	6.17E-01	8.61E-01	ICEBERG	ICEBERG caspase-1 inhibitor	chr11q21-q22	231733_at	NM_021571
2.00	1.96	0.05	6.17E-01	8.61E-01	SPIC	Spi-C transcription factor (Spi-1/PU.1 related)	chr12q23.2	1553851_at	NM_152323
2.36	2.28	0.07	6.17E-01	8.61E-01	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	chr2q24-q32	211039_at	NM_000079 /// NM_001039523
2.42	2.33	0.09	6.17E-01	8.61E-01	CLPTM1L	CLPTM1-like	chr5pter-p15.3	229416_at	NM_030782 /// XM_001722978
7.23	7.08	0.15	6.17E-01	8.61E-01	STAG2	stromal antigen 2	chrXq25	209022_at	NM_001042749 /// NM_001042750 /// NM_001042751 /// NM_006603
2.03	1.97	0.06	6.17E-01	8.61E-01	---	---	---	1559284_at	---
3.37	3.21	0.16	6.17E-01	8.62E-01	STX16	syntaxin 16	chr20q13.32	221638_s_at	NM_001001433 /// NM_003763
7.11	6.99	0.12	6.17E-01	8.62E-01	LMF2	lipase maturation factor 2	chr22q13.33	31837_at	NM_033200
2.06	2.01	0.06	6.17E-01	8.62E-01	CATSPERB	cation channel, sperm-associated, beta	chr14q32.12	1570470_at	NM_024764
2.19	2.12	0.07	6.17E-01	8.62E-01	---	---	---	240253_at	---
2.36	2.28	0.08	6.18E-01	8.62E-01	XYLB	xylulokinase homolog (H. influenzae)	chr3p22-p21.3	208317_at	NM_005108
2.46	2.31	0.14	6.18E-01	8.62E-01	KLHL8	kelch-like 8 (Drosophila)	chr4q22.1	1561206_at	NM_020803
5.00	4.87	0.13	6.18E-01	8.62E-01	KCTD18	potassium channel tetramerisation domain containing 18	chr2q33.1	226493_at	NM_152387
1.90	1.83	0.07	6.18E-01	8.62E-01	LOC285326	hypothetical protein LOC285326	chr3p24.2	1556528_at	---
2.08	2.02	0.07	6.18E-01	8.62E-01	PCDHB15	protocadherin beta 15	chr5q31	231789_at	NM_018935
1.90	1.85	0.06	6.18E-01	8.62E-01	---	---	---	1567387_at	---
4.34	4.21	0.13	6.18E-01	8.62E-01	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	chr19q13.1-q13.4	206296_x_at	NM_001042600 /// NM_007181
2.58	2.50	0.09	6.18E-01	8.62E-01	---	---	---	233806_at	---
2.08	2.01	0.07	6.18E-01	8.62E-01	---	---	---	244560_at	---
2.96	2.89	0.07	6.18E-01	8.62E-01	---	---	---	1569067_at	---
7.85	7.74	0.11	6.18E-01	8.62E-01	AIF1	allograft inflammatory factor 1	chr6p21.3	209901_x_at	NM_001623 /// NM_032955
4.01	3.90	0.11	6.18E-01	8.62E-01	HDGFL1	hepatoma derived growth factor-like 1	chr6p22.3	232680_at	NM_138574
3.27	3.19	0.08	6.18E-01	8.62E-01	F7	coagulation factor VII (serum prothrombin conversion accelerator)	chr13q34	237414_at	NM_000131 /// NM_019616
6.14	5.89	0.26	6.18E-01	8.62E-01	---	---	---	241692_at	---
8.68	8.55	0.14	6.18E-01	8.62E-01	GM2A	GM2 ganglioside activator	chr5q31.3-q33.1	212737_at	NM_000405
1.99	1.93	0.06	6.18E-01	8.62E-01	LOC728449	hypothetical protein LOC728449	chr10q11.22	1557094_at	XM_001128973
6.00	5.83	0.17	6.18E-01	8.62E-01	NSMCE4A	non-SMC element 4 homolog A (S. cerevisiae)	chr10q26.13	211376_s_at	NM_017615
2.45	2.36	0.09	6.18E-01	8.62E-01	INTS6	integrator complex subunit 6	chr13q14.12-q14.2	235283_at	NM_001039937 /// NM_001039938 /// NM_012141
5.84	5.70	0.14	6.18E-01	8.62E-01	DDEF1	development and differentiation enhancing factor 1	chr8q24.1-q24.2	221039_s_at	NM_018482
3.59	3.51	0.08	6.18E-01	8.62E-01	---	---	---	241852_at	---
2.14	2.06	0.07	6.18E-01	8.62E-01	---	---	---	239822_at	---
2.53	2.45	0.08	6.18E-01	8.62E-01	BIVM	Basic, immunoglobulin-like variable motif containing	chr13q32-q33.1	229589_x_at	NM_017693
2.22	2.15	0.08	6.18E-01	8.62E-01	---	---	---	240055_at	---
4.41	4.34	0.07	6.18E-01	8.62E-01	MYCBP	c-myc binding protein	chr1p33-p32.2	203361_s_at	NM_012333
2.33	2.26	0.07	6.18E-01	8.62E-01	ASXL3	additional sex combs like 3 (Drosophila)	chr18q11	233536_at	NM_030632
3.32	3.24	0.08	6.18E-01	8.62E-01	RGS6	regulator of G-protein signaling 6	chr14q24.3	210270_at	NM_004296
4.14	4.03	0.11	6.18E-01	8.62E-01	NEK6	NIMA (never in mitosis gene a)-related kinase 6	chr9q33.3-q34.11	239267_at	NM_014397
2.20	2.13	0.07	6.19E-01	8.62E-01	SERP2	Stress-associated endoplasmic reticulum protein family member 2	chr13q14.11	239890_s_at	NM_001010897
3.12	3.02	0.09	6.19E-01	8.62E-01	APOL4	apolipoprotein L, 4	chr22q11.2-q13.2	224491_at	NM_030643 /// NM_145660

2.79	2.70	0.09	6.19E-01	8.62E-01	RGR	retinal G protein coupled receptor	chr10q23	1555219_at	NM_001012720 /// NM_001012722 /// NM_002921																				
1.99	1.94	0.05	6.19E-01	8.62E-01	SH3GLP3	SH3-domain GRB2-like pseudogene 3	chr17q24.2	1566251_at	---																				
3.80	3.66	0.14	6.19E-01	8.62E-01	TPM2	tropomyosin 2 (beta)	chr9p13.2-p13.1	229911_at	NM_003289 /// NM_213674																				
2.55	2.46	0.09	6.19E-01	8.62E-01	ZMYM6	zinc finger, MYM-type 6	chr1p34.2	1552970_s_at	NM_007167																				
6.35	6.04	0.31	6.19E-01	8.62E-01	KLF6	Kruppel-like factor 6	chr10p15	208960_s_at	NM_001300																				
4.56	4.48	0.08	6.19E-01	8.62E-01	MLH3	mutL homolog 3 (E. coli)	chr14q24.3	214525_x_at	NM_001040108 /// NM_014381																				
5.27	5.15	0.12	6.19E-01	8.62E-01	UNQ1887	signal peptide peptidase 3	chr12q24.31	224638_at	NM_139015																				
8.03	7.93	0.10	6.19E-01	8.62E-01	RAB2A	RAB2A, member RAS oncogene family	chr8q12.1	208730_x_at	NM_002865																				
2.38	2.32	0.06	6.19E-01	8.62E-01	---	---	---	216556_x_at	---																				
7.40	7.26	0.14	6.19E-01	8.62E-01	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19p13.3	213766_x_at	NM_002067																				
2.78	2.70	0.08	6.19E-01	8.62E-01	LOC654841	hypothetical LOC654841	chr2q36-q37	1557862_at	---																				
4.93	4.85	0.08	6.19E-01	8.62E-01	SFRS8	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	chr12q24.33	202773_s_at	NM_004592																				
4.64	4.38	0.26	6.19E-01	8.62E-01	SLAMF8	SLAM family member 8	chr1q23.2	219386_s_at	NM_020125																				
10.95	10.84	0.10	6.19E-01	8.62E-01	LDHA	lactate dehydrogenase A	chr11p15.4	200650_s_at	NM_005566																				
2.67	2.59	0.08	6.20E-01	8.62E-01	---	---	---	216704_at	---																				
7.23	7.06	0.16	6.20E-01	8.62E-01	COQ10B	coenzyme Q10 homolog B (S. cerevisiae)	chr2q33.1	219397_at	NM_025147																				
2.72	2.63	0.09	6.20E-01	8.63E-01	PRKG2	protein kinase, cGMP-dependent, type II	chr4q13.1-q21.1	207505_at	NM_006259																				
2.78	2.58	0.20	6.20E-01	8.63E-01	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	chr5p13	1569054_at	NM_004172																				
5.92	5.76	0.15	6.20E-01	8.63E-01	CPNE2	copine II	chr16q13	225129_at	NM_152727																				
7.09	6.95	0.14	6.20E-01	8.63E-01	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	chr10q26	201458_s_at	NM_001007793 /// NM_004725																				
1.90	1.85	0.05	6.20E-01	8.63E-01	DLEU2	Deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	1569600_at	NR_002612																				
2.20	2.14	0.07	6.20E-01	8.63E-01	---	---	---	243551_at	---																				
2.45	2.37	0.07	6.20E-01	8.63E-01	CSH1 /// CSH2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// growth hormone 1	chr17q24.2	211151_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645																				
2.36	2.30	0.06	6.20E-01	8.63E-01	MTNR1A	melatonin receptor 1A	chr4q35.1	221369_at	NM_005958																				
4.61	4.43	0.17	6.20E-01	8.63E-01	MGC33894	transcript expressed during hematopoiesis 2	chr17p11.2	226657_at	NM_152914																				
3.34	3.19	0.15	6.20E-01	8.63E-01	LOC255512	hypothetical protein LOC255512	chr11p15.5	1555865_at	---																				
2.78	2.68	0.09	6.20E-01	8.63E-01	---	---	---	239305_at	---																				
4.53	4.47	0.06	6.20E-01	8.63E-01	---	---	---	217191_x_at	---																				
2.08	2.01	0.07	6.20E-01	8.63E-01	TERF2	telomeric repeat binding factor 2	chr16q22.1	1555183_at	NM_005652																				
2.31	2.24	0.07	6.20E-01	8.63E-01	EFCAB2	EF-hand calcium binding domain 2	chr1q44	1557674_s_at	NM_032328																				
4.69	4.55	0.14	6.20E-01	8.63E-01	LOC648998	similar to Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH oxidase factor 1) (47 kDa neutrophil oxidase factor) (p47-phox) (NCF-47K) (47 kDa autosomal chronic granulomatous disease protein) (NOXO2)	---	214084_x_at	XM_001723264 /// XM_001725090																			
5.18	5.10	0.08	6.20E-01	8.63E-01	ZNF707	zinc finger protein 707	chr8q24.3	232076_at	NM_001100598 /// NM_001100599 /// NM_173831																				
4.79	4.70	0.09	6.20E-01	8.63E-01	ZNF589	zinc finger protein 589	chr3p21	219968_at	NM_016089																				
9.21	9.14	0.07	6.21E-01	8.63E-01	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	chr5p15.33	203606_at	NM_004553																				

7.30	7.11	0.19	6.21E-01	8.63E-01	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	chr21q22.13	209033_s_at	NM_001396 /// NM_101395 /// NM_130436 /// NM_130437 /// NM_130438																				
4.35	4.22	0.13	6.21E-01	8.63E-01	WNT4	wingless-type MMTV integration site family, member 4	chr1p36.23-p35.1	230751_at	NM_030761																				
4.39	4.26	0.12	6.21E-01	8.63E-01	CDCA3	cell division cycle associated 3	chr12p13	221436_s_at	NM_031299																				
3.86	3.73	0.13	6.21E-01	8.63E-01	PDLIM4	PDZ and LIM domain 4	chr5q31.1	214175_x_at	NM_001131027 /// NM_003687																				
4.21	4.07	0.14	6.21E-01	8.63E-01	---	---	---	229544_at	---																				
2.15	2.09	0.06	6.21E-01	8.63E-01	---	---	---	1568932_at	---																				
2.38	2.28	0.10	6.21E-01	8.63E-01	---	---	---	239881_at	---																				
6.84	6.69	0.15	6.21E-01	8.63E-01	FAM53B	family with sequence similarity 53, member B	chr10q26.13	203206_at	NM_014661																				
2.84	2.74	0.10	6.21E-01	8.63E-01	---	---	---	1557135_at	---																				
7.38	7.09	0.30	6.21E-01	8.63E-01	CREM	cAMP responsive element modulator	chr10p11.21	207630_s_at	NM_001881 /// NM_181571 /// NM_182717 /// NM_182718 /// NM_182719 /// NM_182720 /// NM_182721 /// NM_182722 /// NM_182723 /// NM_182724 /// NM_182725 /// NM_182769 /// NM_182770 /// NM_182771 /// NM_182772 /// NM_182850 /// NM_182853 /// NM_183011 /// NM_183012 /// NM_183013 /// NM_183060																				
5.00	4.89	0.11	6.21E-01	8.63E-01	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	chr11q21-q22.1	219469_at	NM_001080463																				
4.82	4.64	0.18	6.21E-01	8.63E-01	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	chr3q21.1	219284_at	NM_024610																				
4.41	4.22	0.19	6.21E-01	8.63E-01	ARMCX4	Armadillo repeat containing, X-linked 4	chrXq22.1	227444_at	NM_152583																				
5.98	5.91	0.08	6.21E-01	8.63E-01	PTCRA	pre T-cell antigen receptor alpha	chr6p21.3	215492_x_at	NM_138296																				
3.82	3.75	0.07	6.21E-01	8.63E-01	ESRRB	estrogen-related receptor beta	chr14q24.3	207726_at	NM_004452																				
5.97	5.84	0.13	6.21E-01	8.63E-01	RRN3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	chr16p12	222204_s_at	NM_018427																				
7.74	7.57	0.17	6.21E-01	8.63E-01	STAT1	signal transducer and activator of transcription 1, 91kDa	chr2q32.2	200887_s_at	NM_007315 /// NM_139266																				
7.84	7.76	0.08	6.21E-01	8.63E-01	TCF25	transcription factor 25 (basic helix-loop-helix)	chr16q24.3	213311_s_at	NM_014972																				
2.85	2.78	0.07	6.22E-01	8.63E-01	LOC144481	hypothetical protein LOC144481	chr12q22	1559315_s_at	XM_001128090 /// XM_001134139																				

2.90	2.76	0.14	6.22E-01	8.64E-01	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	chr2q36-q37	216893_s_at	NM_000091 /// NM_031362 /// NM_031365 /// NM_031366
8.08	7.97	0.11	6.22E-01	8.64E-01	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	chr19q13.32	206491_s_at	NM_003827
9.68	9.53	0.15	6.22E-01	8.64E-01	HIF1A	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	chr14q21-q24	200989_at	NM_001530 /// NM_181054
6.10	6.01	0.09	6.22E-01	8.64E-01	NADK	NAD kinase	chr1p36.33-p36.21	208917_x_at	NM_023018
2.53	2.47	0.06	6.22E-01	8.64E-01	---	---	---	244196_at	---
4.02	3.90	0.12	6.22E-01	8.64E-01	---	---	---	239154_at	---
2.77	2.71	0.06	6.22E-01	8.64E-01	---	---	---	232273_at	---
2.41	2.33	0.08	6.22E-01	8.64E-01	---	---	---	1564665_at	---
6.35	6.21	0.14	6.22E-01	8.64E-01	IRF8	interferon regulatory factor 8	chr16q24.1	204057_at	NM_002163
2.62	2.55	0.07	6.22E-01	8.64E-01	IRAK1BP1	interleukin-1 receptor-associated kinase 1 binding protein 1	chr6q14-q15	238599_at	NM_001010844
6.13	5.99	0.13	6.22E-01	8.64E-01	FAM122A	family with sequence similarity 122A	chr9q21.11	226443_at	NM_138333
3.55	3.47	0.08	6.22E-01	8.64E-01	POM121L2	POM121 membrane glycoprotein-like 2 (rat)	chr6p22.1	216582_at	XM_001715475 /// XM_001717703 /// XM_001718816
2.75	2.64	0.10	6.22E-01	8.64E-01	---	---	---	235422_at	---
3.30	3.14	0.15	6.22E-01	8.64E-01	SLMO2	slowmo homolog 2 (Drosophila)	chr20q13.32	217851_s_at	NM_016045
3.10	3.02	0.08	6.22E-01	8.64E-01	C21orf90	chromosome 21 open reading frame 90	chr21q22.3	1554954_at	XR_017894 /// XR_017992 /// XR_040133
2.72	2.64	0.08	6.22E-01	8.64E-01	CSH1	chorionic somatomammotropin hormone 1 (placental lactogen)	chr17q24.2	208356_x_at	NM_001317 /// NM_022640 /// NM_022641
5.49	5.39	0.10	6.22E-01	8.64E-01	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	chr17p13.1	201556_s_at	NM_014232
2.70	2.63	0.07	6.22E-01	8.64E-01	TBX10	T-box 10	chr11q13.2	207689_at	NM_005995
3.20	3.15	0.05	6.22E-01	8.64E-01	FIZ1	FLT3-interacting zinc finger 1	chr19q13.42	228663_x_at	NM_032836
2.21	2.13	0.07	6.22E-01	8.64E-01	---	---	---	234413_at	---
6.66	6.57	0.10	6.23E-01	8.64E-01	TSHZ1	teashirt zinc finger homeobox 1	chr18q22.3	223283_s_at	NM_005786
4.88	4.80	0.08	6.23E-01	8.64E-01	C4BPB	complement component 4 binding protein, beta	chr1q32	208209_s_at	NM_000716 /// NM_001017364 /// NM_001017365 /// NM_001017366 /// NM_001017367
6.80	6.63	0.17	6.23E-01	8.64E-01	PTCD3	Pentatricopeptide repeat domain 3	chr2p11.2	217895_at	NM_017952
2.77	2.46	0.31	6.23E-01	8.64E-01	LOC100130216 /// USP9Y	hypothetical protein LOC100130216 /// ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	chrYq11.2	206624_at	NM_004654 /// XM_001713696
2.46	2.39	0.07	6.23E-01	8.64E-01	LAYN	Layilin	chr11q23.1	1556886_a_at	NM_178834
4.68	4.44	0.24	6.23E-01	8.64E-01	SMC4	structural maintenance of chromosomes 4	chr3q26.1	201664_at	NM_001002800 /// NM_005496
6.24	6.14	0.10	6.23E-01	8.64E-01	APOL2	apolipoprotein L, 2	chr22q12	221653_x_at	NM_030882 /// NM_145637
8.13	8.05	0.08	6.23E-01	8.64E-01	OPHN1	oligophrenin 1	chrXq12	206323_x_at	NM_002547
2.72	2.63	0.09	6.23E-01	8.64E-01	---	---	---	1556542_a_at	---
2.86	2.76	0.10	6.23E-01	8.64E-01	LOC729173	hypothetical protein LOC729173	chr11q23.3	1564229_at	XM_001129552 /// XM_001725108 /// XM_001726309
2.18	2.13	0.05	6.23E-01	8.64E-01	---	---	---	1559737_at	---
4.09	3.97	0.12	6.23E-01	8.64E-01	---	---	---	239445_at	---

3.25	3.12	0.13	6.23E-01	8.64E-01	FAM87A /// FAM87B /// LOC100134357	family with sequence similarity 87, member A /// family with sequence similarity 87, member B /// similar to hCG1735895	chr1p36.33 /// chr8p23.3	1559141_s_at	XM_001713962 /// XM_001719631 /// XM_001719643 /// XM_001719709 /// XM_001719721 /// XM_001721137 /// XM_001721145
2.97	2.89	0.08	6.23E-01	8.64E-01	POU3F3	POU class 3 homeobox 3	chr2q12.1	208563_x_at	NM_006236
2.49	2.43	0.06	6.24E-01	8.64E-01	FLJ12825	hypothetical gene supported by AK022887; AK056417	chr12q13.13	1557296_at	---
3.13	3.00	0.13	6.24E-01	8.64E-01	CDC20	cell division cycle 20 homolog (S. cerevisiae)	chr1p34.1	202870_s_at	NM_001255
9.74	9.61	0.13	6.24E-01	8.64E-01	TMEM66	transmembrane protein 66	chr8p12	200847_s_at	NM_016127
4.95	4.78	0.17	6.24E-01	8.64E-01	EIF3J	eukaryotic translation initiation factor 3, subunit J	chr15q15.3	208264_s_at	NM_003758
5.20	5.08	0.12	6.24E-01	8.64E-01	TPP1	tripeptidyl peptidase I	chr11p15	214195_at	NM_000391
2.03	1.96	0.07	6.24E-01	8.64E-01	---	---	---	236399_at	---
2.60	2.45	0.14	6.24E-01	8.64E-01	ZBTB3	zinc finger and BTB domain containing 3	chr11q12.3	220391_at	NM_024784
7.02	6.92	0.10	6.24E-01	8.65E-01	---	---	---	1559436_x_at	---
2.39	2.32	0.07	6.24E-01	8.65E-01	SOX5	SRY (sex determining region Y)-box 5	chr12p12.1	1569638_at	NM_006940 /// NM_152989 /// NM_178010
4.04	3.93	0.10	6.24E-01	8.65E-01	RELL2	RELT-like 2	chr5q31.3	1564031_a_at	NM_001130029 /// NM_173828
2.58	2.47	0.11	6.24E-01	8.65E-01	---	---	---	243444_at	---
3.50	3.43	0.08	6.24E-01	8.65E-01	---	---	---	231493_at	---
4.05	3.95	0.11	6.24E-01	8.65E-01	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr19p13.11	212924_s_at	NM_012321
2.37	2.30	0.07	6.24E-01	8.65E-01	---	---	---	242678_at	---
2.33	2.26	0.07	6.24E-01	8.65E-01	TAAR9	trace amine associated receptor 9	chr6q23.2	1553066_at	NM_175057
4.68	4.58	0.10	6.24E-01	8.65E-01	HIPK4	homeodomain interacting protein kinase 4	chr19q13.2	1553238_a_at	NM_144685
3.40	3.25	0.15	6.24E-01	8.65E-01	SLC35E4	solute carrier family 35, member E4	chr22q12.2	1568623_a_at	NM_001001479
4.71	4.50	0.21	6.24E-01	8.65E-01	ZNF836	zinc finger protein 836	chr19q13.33	1569076_a_at	NM_001102657
3.39	3.32	0.07	6.24E-01	8.65E-01	MED14	mediator complex subunit 14	chrXp11.4-p11.2	215167_at	NM_004229
4.14	4.04	0.10	6.24E-01	8.65E-01	TMEM132A	transmembrane protein 132A	chr11q12.2	222758_s_at	NM_017870 /// NM_178031
3.39	3.22	0.17	6.25E-01	8.65E-01	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	chr21q11	220330_s_at	NM_022136
3.11	3.01	0.10	6.25E-01	8.65E-01	LOC127841	hypothetical protein LOC127841	chr1q32.1	1565556_at	---
2.41	2.33	0.08	6.25E-01	8.65E-01	PRIM2	primase, DNA, polypeptide 2 (58kDa)	chr6p12-p11.1	215708_s_at	NM_000947
2.54	2.42	0.11	6.25E-01	8.65E-01	---	---	---	236590_at	---
4.84	4.71	0.13	6.25E-01	8.65E-01	MPZL1	myelin protein zero-like 1	chr1q24.2	210087_s_at	NM_003953 /// NM_024569
3.25	3.17	0.08	6.25E-01	8.65E-01	DENND5B	DENN/MADD domain containing 5B	chr12p11.21	238917_s_at	NM_144973
2.83	2.76	0.07	6.25E-01	8.65E-01	GCLC	glutamate-cysteine ligase, catalytic subunit	chr6p12	1555330_at	NM_001498
2.24	2.16	0.08	6.25E-01	8.65E-01	---	---	---	235380_at	---
7.57	7.49	0.08	6.25E-01	8.65E-01	PGK1	phosphoglycerate kinase 1	chrXq13	200737_at	NM_000291
4.00	3.86	0.14	6.25E-01	8.65E-01	---	---	---	242490_at	---
1.91	1.87	0.05	6.25E-01	8.65E-01	TSPAN2	tetraspanin 2	chr1p13.2	227233_at	NM_005725
3.26	3.17	0.10	6.25E-01	8.65E-01	---	---	---	240054_at	---
2.12	2.06	0.06	6.25E-01	8.65E-01	---	---	---	1568939_at	---
5.94	5.69	0.25	6.25E-01	8.65E-01	PDGFC	platelet derived growth factor C	chr4q32	222719_s_at	NM_016205
3.60	3.54	0.06	6.25E-01	8.65E-01	HS3ST6	heparan sulfate (glucosamine) 3-O-sulfotransferase 6	chr16p13.3	239547_at	NM_001009606
2.68	2.59	0.09	6.25E-01	8.65E-01	GTDC1	glycosyltransferase-like domain containing 1	chr2q22.2-q22.3	220853_at	NM_001006636 /// NM_024659
2.06	2.00	0.06	6.25E-01	8.65E-01	GPR85	G protein-coupled receptor 85	chr7q31	219898_at	NM_018970
3.62	3.55	0.07	6.25E-01	8.65E-01	ZSCAN2	zinc finger and SCAN domain containing 2	chr15q25.2	220516_at	NM_001007072 /// NM_017894 /// NM_181877
4.20	4.09	0.11	6.25E-01	8.65E-01	WDR22	WD repeat domain 22	chr14q23-q24.1	227251_at	NM_003861
3.22	3.15	0.07	6.25E-01	8.65E-01	---	---	---	1559713_at	---
9.81	9.69	0.11	6.25E-01	8.65E-01	STUB1	STIP1 homology and U-box containing protein 1	chr16p13.3	227625_s_at	NM_005861

9.56	9.49	0.07	6.25E-01	8.65E-01	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	chr7q22.1	202961_s_at	NM_001003713 /// NM_001003714 /// NM_001039178 /// NM_004889																				
7.20	7.02	0.17	6.25E-01	8.65E-01	GIMAP5	GTPase, IMAP family member 5	chr7q36.1	218805_at	NM_018384																				
6.35	6.27	0.08	6.25E-01	8.65E-01	---	---	---	217329_x_at	---																				
2.24	2.19	0.05	6.25E-01	8.65E-01	KLRA1	killer cell lectin-like receptor subfamily A, member 1	chr12p13-p12	207229_at	NM_006611																				
4.81	4.71	0.11	6.26E-01	8.65E-01	---	---	---	1569895_at	---																				
2.45	2.38	0.06	6.26E-01	8.65E-01	C2CD2L	C2CD2-like	chr11q23.3	204758_s_at	NM_014807																				
5.44	5.36	0.07	6.26E-01	8.65E-01	LOC390705	similar to protein phosphatase 2A 48 kDa regulatory subunit isoform 1; serine/threonine protein phosphatase 2A, 48kDa regulatory subunit; PP2A, subunit B, PR48 isoform; PP2A B subunit PR48; NY-REN-8 antigen	chr16p11.2	237163_x_at	XR_015850																				
2.63	2.55	0.08	6.26E-01	8.65E-01	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	chr15q11.2	1552696_at	NM_144599																				
2.30	2.24	0.06	6.26E-01	8.65E-01	SCGB1A1	secretoglobin, family 1A, member 1 (uteroglobin)	chr11q12.3-q13.1	205725_at	NM_003357																				
1.96	1.90	0.05	6.26E-01	8.65E-01	LOC645513	Hypothetical LOC645513	chr4q26-q27	239556_at	XM_001714125 /// XM_001714854 /// XM_001717939																				
5.14	5.00	0.14	6.26E-01	8.65E-01	DPP8	dipeptidyl-peptidase 8	chr15q22	227018_at	NM_017743 /// NM_130434 /// NM_197960 /// NM_197961																				
3.40	3.28	0.12	6.26E-01	8.65E-01	MCM4	minichromosome maintenance complex component 4	chr8q11.2	222037_at	NM_005914 /// NM_182746																				
5.63	5.53	0.11	6.26E-01	8.65E-01	---	---	---	225139_at	---																				
4.34	4.25	0.09	6.26E-01	8.65E-01	C8orf37	chromosome 8 open reading frame 37	chr8q22.1	244569_at	NM_177965																				
10.46	10.37	0.09	6.26E-01	8.65E-01	H3F3A /// H3F3B	H3 histone, family 3A /// H3 histone, family 3B (H3.3B)	chr17q25 /// chr1q41	209069_s_at	NM_002107 /// NM_005324																				
5.48	5.37	0.11	6.26E-01	8.65E-01	PCF11	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	chr11q13	203378_at	NM_015885																				
2.47	2.40	0.08	6.26E-01	8.65E-01	RTN4RL2	reticulon 4 receptor-like 2	chr11q12.1	229345_at	NM_178570																				
2.31	2.23	0.07	6.26E-01	8.65E-01	RAB11FIP4	RAB11 family interacting protein 4 (class II)	chr17q11.2	225746_at	NM_032932																				
2.32	2.25	0.07	6.26E-01	8.65E-01	DGKE	diacylglycerol kinase, epsilon 64kDa	chr17q22	1554623_x_at	NM_003647																				
2.44	2.38	0.06	6.26E-01	8.65E-01	---	---	---	1565265_at	---																				
2.63	2.55	0.08	6.26E-01	8.65E-01	---	---	---	239856_at	---																				
2.84	2.75	0.10	6.26E-01	8.65E-01	KRT38	keratin 38	chr17q12-q21	207716_at	NM_006771																				
3.05	2.96	0.09	6.27E-01	8.65E-01	---	---	---	233176_at	---																				
2.25	2.18	0.07	6.27E-01	8.65E-01	---	---	---	1565599_at	---																				
8.09	7.69	0.40	6.27E-01	8.65E-01	NRCAM	neuronal cell adhesion molecule	chr7q31.1-q31.2	204105_s_at	NM_001037132 /// NM_001037133 /// NM_005010																				
6.69	6.58	0.11	6.27E-01	8.65E-01	ZBTB7A	zinc finger and BTB domain containing 7A	chr19p13.3	226554_at	NM_015898																				
1.97	1.92	0.05	6.27E-01	8.65E-01	C1orf67	chromosome 1 open reading frame 67	chr1q42.12	1554540_at	NM_144989																				
5.18	5.07	0.11	6.27E-01	8.65E-01	GABPA	GA binding protein transcription factor, alpha subunit 60kDa	chr21q21-q22.1|21q21.3	227428_at	NM_002040																				
2.85	2.77	0.08	6.27E-01	8.65E-01	HDAC2	histone deacetylase 2	chr6q21	242141_at	NM_001527																				
8.76	8.66	0.09	6.27E-01	8.65E-01	GTF2I /// GTF2IP1 /// LOC100093631	general transcription factor II, i /// general transcription factor II, i, pseudogene 1 /// general transcription factor II, i, pseudogene	chr7q11.23	210891_s_at	NM_001518 /// NM_032999 /// NM_033000 /// NM_033001 /// NR_002206 /// NR_003580																				
2.36	2.28	0.08	6.27E-01	8.65E-01	---	---	---	1569789_at	---																				
7.83	7.75	0.07	6.27E-01	8.66E-01	C9orf64	chromosome 9 open reading frame 64	chr9q21.32	223697_x_at	NM_032307																				
2.35	2.28	0.07	6.27E-01	8.66E-01	---	---	---	217519_at	---																				
2.67	2.57	0.10	6.27E-01	8.66E-01	---	---	---	216029_at	---																				
2.21	2.13	0.08	6.27E-01	8.66E-01	---	---	---	1570621_at	---																				
3.39	3.31	0.08	6.27E-01	8.66E-01	NBPF3	neuroblastoma breakpoint family, member 3	chr1p36.12	1558825_s_at	NM_032264																				
2.47	2.41	0.06	6.27E-01	8.66E-01	---	---	---	236839_at	---																				

2.35	2.30	0.06	6.27E-01	8.66E-01	SPATS2	spermatogenesis associated, serine-rich 2	chr12q13.12	1570130_at	NM_023071																			
2.04	1.98	0.06	6.27E-01	8.66E-01	DKFZp434G179	hypothetical protein DKFZp434G179	chr2p15	234847_at	---																			
2.89	2.68	0.21	6.27E-01	8.66E-01	TANK	TRAF family member-associated NFKB activator	chr2q24-q31	210458_s_at	NM_004180 /// NM_133484																			
5.18	5.04	0.14	6.27E-01	8.66E-01	TRAPPC2L	trafficking protein particle complex 2-like	chr16q24.3	238627_at	NM_016209																			
2.81	2.74	0.06	6.27E-01	8.66E-01	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	chr16p11.2	215744_at	NM_004960																			
4.61	4.49	0.12	6.27E-01	8.66E-01	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	chr13q14.3	223330_s_at	NM_001130912 /// NM_006704																			
7.67	7.56	0.11	6.28E-01	8.66E-01	MCTS1	malignant T cell amplified sequence 1	chrXq22-q24	218163_at	NM_014060 /// XM_001715103																			
2.98	2.86	0.13	6.28E-01	8.66E-01	GMCL1	germ cell-less homolog 1 (Drosophila)	chr2p13.3	218458_at	NM_178439																			
2.66	2.58	0.09	6.28E-01	8.66E-01	PCGEM1	prostate-specific transcript 1 (non-protein coding)	chr2q32	234515_at	NR_002769																			
2.14	2.07	0.06	6.28E-01	8.66E-01	VSX1	visual system homeobox 1	chr20p11.23-p11.22	222972_at	NM_014588 /// NM_199425																			
6.94	6.81	0.13	6.28E-01	8.66E-01	HMBS	hydroxymethylbilane synthase	chr11q23.3	203040_s_at	NM_000190 /// NM_001024382																			
2.48	2.43	0.06	6.28E-01	8.66E-01	---	---	---	243380_at	---																			
4.62	4.50	0.12	6.28E-01	8.66E-01	---	---	---	1558237_x_at	---																			
2.56	2.48	0.09	6.28E-01	8.66E-01	TTTY11	testis-specific transcript, Y-linked 11	chrYp11.2	224174_at	NR_001548																			
5.85	5.72	0.13	6.28E-01	8.66E-01	C6orf1	chromosome 6 open reading frame 1	chr6p21.31	226306_at	NM_001008703 /// NM_001008704 /// NM_178508																			
5.54	5.42	0.12	6.28E-01	8.66E-01	MED14	mediator complex subunit 14	chrXp11.4-p11.2	202610_s_at	NM_004229																			
4.55	4.47	0.08	6.28E-01	8.66E-01	LOC157627	hypothetical LOC157627	chr8p23.1	214839_at	---																			
3.30	3.20	0.10	6.28E-01	8.66E-01	TBCCD1	TBCC domain containing 1	chr3q27.3	206451_at	NM_001134415 /// NM_018138																			
4.90	4.78	0.13	6.28E-01	8.66E-01	MYO6	myosin VI	chr6q13	203216_s_at	NM_004999																			
5.42	5.33	0.09	6.28E-01	8.66E-01	ARNT	aryl hydrocarbon receptor nuclear translocator	chr1q21	218221_at	NM_001668 /// NM_178426 /// NM_178427																			
2.67	2.58	0.09	6.28E-01	8.66E-01	C1orf105	chromosome 1 open reading frame 105	chr1q24.3	214357_at	NM_139240																			
3.98	3.88	0.09	6.28E-01	8.66E-01	---	---	---	242066_at	---																			
2.13	2.08	0.05	6.28E-01	8.66E-01	---	---	---	237147_at	---																			
2.19	2.13	0.06	6.28E-01	8.66E-01	---	---	---	1557504_at	---																			
2.08	2.00	0.08	6.28E-01	8.66E-01	---	---	---	228724_at	---																			
3.80	3.71	0.09	6.28E-01	8.66E-01	ZNF821	zinc finger protein 821	chr16q22.3	41397_at	NM_017530																			
3.08	3.01	0.07	6.28E-01	8.66E-01	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	chr21q22.11	217633_at	NM_014825																			
4.89	4.75	0.13	6.28E-01	8.66E-01	DHFR	dihydrofolate reductase	chr5q11.2-q13.2	202534_x_at	NM_000791																			
2.53	2.47	0.06	6.28E-01	8.66E-01	SH3GLP2	SH3-domain GRB2-like pseudogene 2	chr17q11.2	1567028_s_at	---																			
6.92	6.72	0.20	6.29E-01	8.66E-01	C1orf198	chromosome 1 open reading frame 198	chr1q42.13-q43	223063_at	NM_032800																			
2.40	2.32	0.07	6.29E-01	8.66E-01	MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	chr11q22.3	205828_at	NM_002422																			
2.62	2.56	0.06	6.29E-01	8.66E-01	GRIA4	glutamate receptor, ionotrophic, AMPA 4	chr11q22	208464_at	NM_000829 /// NM_001077243 /// NM_001077244 /// NM_001112812																			
2.14	2.08	0.06	6.29E-01	8.66E-01	LOC51145	erythrocyte transmembrane protein	chr9q33.3	220752_at	XR_041655 /// XR_041656																			
5.78	5.66	0.12	6.29E-01	8.66E-01	---	---	---	225935_at	---																			
2.24	2.07	0.17	6.29E-01	8.66E-01	LOC100130829 /// ZFY	hypothetical protein LOC100130829 /// zinc finger protein, Y-linked	chrYp11.3	207246_at	NM_003411 /// XM_001713692																			
6.87	6.74	0.12	6.29E-01	8.66E-01	PGRMC2	progesterone receptor membrane component 2	chr4q26	201701_s_at	NM_006320																			
2.55	2.45	0.10	6.29E-01	8.66E-01	BAHCC1	BAH domain and coiled-coil containing 1	chr17q25.3	1559075_s_at	NM_001080519																			
6.03	5.94	0.09	6.29E-01	8.66E-01	EIF2C1	eukaryotic translation initiation factor 2C, 1	chr1p35-p34	218287_s_at	NM_012199																			
4.79	4.69	0.10	6.29E-01	8.66E-01	FAM18B2	family with sequence similarity 18, member B2	chr17p12	1552377_s_at	NM_145301																			
7.71	7.59	0.12	6.29E-01	8.66E-01	SURF4	surfeit 4	chr9q34.2	222979_s_at	NM_033161																			
6.74	6.65	0.09	6.29E-01	8.66E-01	WDR61	WD repeat domain 61	chr15q25.1	221531_at	NM_025234																			

4.57	4.27	0.30	6.29E-01	8.66E-01	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	chr10q21	206385_s_at	NM_001149 /// NM_020987
3.32	3.10	0.22	6.30E-01	8.66E-01	IL6	interleukin 6 (interferon, beta 2)	chr7p21	205207_at	NM_000600
2.54	2.46	0.08	6.30E-01	8.66E-01	C3orf42	chromosome 3 open reading frame 42	chr3p26-p25	223725_at	XR_040160 /// XR_040161 /// XR_040162
2.27	2.21	0.06	6.30E-01	8.66E-01	LRP1B	low density lipoprotein-related protein 1B (deleted in tumors)	chr2q21.2	219643_at	NM_018557
2.72	2.63	0.08	6.30E-01	8.66E-01	NADSYN1	NAD synthetase 1	chr11q13.4	1565908_at	NM_018161
3.60	3.50	0.10	6.30E-01	8.66E-01	FAM124A	family with sequence similarity 124A	chr13q14.3	230519_at	NM_145019
4.82	4.73	0.09	6.30E-01	8.66E-01	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	chr14q21	203101_s_at	NM_002408
2.40	2.31	0.09	6.30E-01	8.66E-01	N4BP2	NEDD4 binding protein 2	chr4p14	231996_at	NM_018177
4.31	4.18	0.13	6.30E-01	8.66E-01	ADAM23	ADAM metallopeptidase domain 23	chr2q33	206046_at	NM_003812
2.47	2.39	0.08	6.30E-01	8.66E-01	C8G	complement component 8, gamma polypeptide	chr9q34.3	210324_at	NM_000606
1.95	1.89	0.06	6.30E-01	8.67E-01	---	---	---	1560973_a_at	---
2.33	2.27	0.07	6.30E-01	8.67E-01	---	---	---	237749_at	---
3.30	3.21	0.08	6.30E-01	8.67E-01	LOC283914	hypothetical protein LOC283914	chr16p11.1	1561518_at	XM_378589 /// XM_934768 /// XM_942882 /// XM_942884
2.06	2.00	0.06	6.30E-01	8.67E-01	DCDC2	doublecortin domain containing 2	chr6p22.1	222926_at	NM_016356
2.53	2.47	0.06	6.30E-01	8.67E-01	---	---	---	1557060_at	---
4.49	4.38	0.11	6.30E-01	8.67E-01	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	chr22q11.21	206064_s_at	NM_014337 /// NM_148175 /// NM_148176
2.25	2.19	0.06	6.30E-01	8.67E-01	---	---	---	238752_at	---
2.65	2.57	0.08	6.30E-01	8.67E-01	---	---	---	240497_at	---
2.55	2.48	0.07	6.30E-01	8.67E-01	---	---	---	241407_at	---
6.85	6.73	0.12	6.30E-01	8.67E-01	PUM1	pumilio homolog 1 (Drosophila)	chr1p35.2	201165_s_at	NM_001020658 /// NM_014676
5.33	5.23	0.10	6.31E-01	8.67E-01	SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	chr6p23	219185_at	NM_012241 /// NM_031244
3.77	3.69	0.08	6.31E-01	8.67E-01	SFTPC	surfactant protein C	chr8p21	211735_x_at	NM_003018
2.15	2.10	0.05	6.31E-01	8.67E-01	---	---	---	1557280_s_at	---
2.49	2.41	0.08	6.31E-01	8.67E-01	C9orf68	chromosome 9 open reading frame 68	chr9p24.2-p24.1	1554707_at	NM_001039395
5.68	5.59	0.09	6.31E-01	8.67E-01	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	chr19p13.3	209416_s_at	NM_016263
4.46	4.36	0.10	6.31E-01	8.67E-01	GRK5	G protein-coupled receptor kinase 5	chr10q24-qter	1569949_at	NM_005308
6.25	6.08	0.18	6.31E-01	8.67E-01	FGL2	fibrinogen-like 2	chr7q11.23	227265_at	NM_006682
2.04	1.98	0.06	6.31E-01	8.67E-01	SRPX2	sushi-repeat-containing protein, X-linked 2	chrXq21.33-q23	216639_at	NM_014467
9.02	8.89	0.12	6.31E-01	8.67E-01	ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	chr5q35.1-q35.2	224576_at	NM_001031711 /// NM_020462
3.89	3.78	0.11	6.31E-01	8.67E-01	PLSCR1	phospholipid scramblase 1	chr3q23	202430_s_at	NM_021105
2.87	2.78	0.08	6.31E-01	8.67E-01	LOC100130979	hypothetical protein LOC100130979	chr13q12.11	243429_at	XM_001716739 /// XM_001722101 /// XM_001723317
3.00	2.92	0.08	6.31E-01	8.67E-01	STMN3	stathmin-like 3	chr20q13.3	218207_s_at	NM_015894
4.91	4.79	0.11	6.31E-01	8.67E-01	LIMK2	LIM domain kinase 2	chr22q12.2	210582_s_at	NM_001031801 /// NM_005569 /// NM_016733
2.19	2.12	0.07	6.31E-01	8.67E-01	FAM47B	family with sequence similarity 47, member B	chrXp21.1	240426_at	NM_152631
5.21	5.14	0.08	6.31E-01	8.67E-01	TRAPPC10	trafficking protein particle complex 10	chr21q22.3	209412_at	NM_001001723 /// NM_003274
3.46	3.38	0.08	6.31E-01	8.67E-01	WIPF3	WAS/WASL interacting protein family, member 3	chr7p15.1	232389_at	NM_001080529
2.15	2.10	0.05	6.32E-01	8.68E-01	ZNF471	zinc finger protein 471	chr19q13.43	211923_s_at	NM_020813
8.03	7.94	0.09	6.32E-01	8.68E-01	AIF1	allograft inflammatory factor 1	chr6p21.3	213095_x_at	NM_001623 /// NM_032955

2.62	2.56	0.07	6.32E-01	8.68E-01	LOC284219	hypothetical protein LOC284219	chr18p11.22	1556425_a_at	---
7.45	7.35	0.10	6.32E-01	8.68E-01	RAB1B	RAB1B, member RAS oncogene family	chr11q12	220964_s_at	NM_030981
2.37	2.31	0.05	6.32E-01	8.68E-01	NUP133	nucleoporin 133kDa	chr1q42.13	233420_at	NM_018230
2.53	2.48	0.05	6.32E-01	8.68E-01	---	---	---	240675_at	---
2.06	1.99	0.07	6.32E-01	8.68E-01	---	---	---	215619_at	---
3.80	3.68	0.12	6.32E-01	8.68E-01	FBXO5	F-box protein 5	chr6q25-q26	234863_x_at	NM_012177
5.00	4.85	0.15	6.32E-01	8.68E-01	JUP	junction plakoglobin	chr17q21	201015_s_at	NM_002230 /// NM_021991
2.30	2.25	0.05	6.32E-01	8.68E-01	IL1F8	interleukin 1 family, member 8 (eta)	chr2q12-q14.1	231755_at	NM_014438 /// NM_173178
2.73	2.64	0.08	6.32E-01	8.68E-01	---	---	---	228679_at	---
2.15	2.09	0.06	6.32E-01	8.68E-01	FLJ22763	hypothetical gene supported by AK026416	chr3q13.13	233604_at	XM_001128163 /// XM_001128720 /// XM_001715826
2.13	2.05	0.07	6.33E-01	8.68E-01	ZNF29	zinc finger protein 29 pseudogene	chr17p13-p12	1567855_at	---
3.33	3.22	0.11	6.33E-01	8.68E-01	LOC729986	hypothetical LOC729986	chr7q36.1	1566168_at	XM_001131545 /// XM_001132240 /// XM_001717334
3.36	3.28	0.08	6.33E-01	8.68E-01	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	chr2q31	206669_at	NM_000817 /// NM_013445
4.27	4.17	0.10	6.33E-01	8.68E-01	ARNT	Aryl hydrocarbon receptor nuclear translocator	chr1q21	231016_s_at	NM_001668 /// NM_178426 /// NM_178427
2.65	2.59	0.06	6.33E-01	8.68E-01	GON4L	gon-4-like (C. elegans)	chr1q22	219846_at	NM_001037533 /// NM_032292
2.06	2.00	0.07	6.33E-01	8.68E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	208181_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054
3.00	2.92	0.08	6.33E-01	8.68E-01	---	---	---	216475_at	---
2.08	2.02	0.06	6.33E-01	8.68E-01	---	---	---	242153_at	---
3.02	2.95	0.07	6.33E-01	8.69E-01	---	---	---	1569235_a_at	---
2.44	2.38	0.06	6.33E-01	8.69E-01	---	---	---	237207_at	---
6.67	6.48	0.19	6.33E-01	8.69E-01	ZBTB7C	zinc finger and BTB domain containing 7C	chr18q21.1	227782_at	NM_001039360
7.75	7.61	0.13	6.33E-01	8.69E-01	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	chr9p13	201883_s_at	NM_001497
2.99	2.92	0.07	6.33E-01	8.69E-01	F12	coagulation factor XII (Hageman factor)	chr5q33-qter	215961_at	NM_000505
2.36	2.29	0.08	6.33E-01	8.69E-01	FLJ33360	FLJ33360 protein	chr5p15.31	1563969_at	NM_001001702
2.03	1.98	0.05	6.34E-01	8.69E-01	---	---	---	1561432_at	---

2.04	1.98	0.06	6.34E-01	8.69E-01	---	---	---	1556289_at	---
2.34	2.28	0.06	6.34E-01	8.69E-01	TGM4	transglutaminase 4 (prostate)	chr3p22-p21.33	217566_s_at	NM_003241
2.11	2.06	0.05	6.34E-01	8.69E-01	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	---	1553151_at	NM_152565
3.11	3.03	0.08	6.34E-01	8.69E-01	KRT33A	keratin 33A	chr17q12-q21	208483_x_at	NM_004138
6.60	6.46	0.14	6.34E-01	8.69E-01	IVNS1ABP	influenza virus NS1A binding protein	chr1q25.1-q31.1	201363_s_at	NM_006469
2.23	2.16	0.07	6.34E-01	8.69E-01	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	chr6q22.31	231120_x_at	NM_032471 /// NM_181794 /// NM_181795
2.83	2.75	0.08	6.34E-01	8.69E-01	PNO1	partner of NOB1 homolog (S. cerevisiae)	chr2p14	242905_at	NM_020143
2.27	2.21	0.07	6.34E-01	8.69E-01	---	---	---	243299_at	---
2.49	2.41	0.08	6.34E-01	8.69E-01	---	---	---	1563469_at	---
4.28	4.10	0.17	6.34E-01	8.69E-01	HEL308	DNA helicase HEL308	chr4q21.23	228736_at	NM_133636
3.45	3.36	0.09	6.34E-01	8.69E-01	---	---	---	236216_at	---
2.29	2.24	0.06	6.34E-01	8.69E-01	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	chr19q13.1-q13.2	201884_at	NM_004363
2.31	2.26	0.05	6.34E-01	8.69E-01	KIAA1715	KIAA1715	chr2q31	225717_at	NM_030650
5.93	5.80	0.13	6.34E-01	8.69E-01	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	chr13q14.3	204759_at	NM_001268
2.58	2.50	0.08	6.34E-01	8.69E-01	RASL11A	RAS-like, family 11, member A	---	238353_at	NM_206827
2.75	2.69	0.06	6.35E-01	8.69E-01	RGAG1	retrotransposon gag domain containing 1	chrXq22.3	232785_at	NM_020769
2.26	2.20	0.06	6.35E-01	8.69E-01	MGEA5	Meningioma expressed antigen 5 (hyaluronidase)	chr10q24.1-q24.3	235868_at	NM_012215
3.27	3.18	0.08	6.35E-01	8.69E-01	CARD8	caspase recruitment domain family, member 8	chr19q13.32	228641_at	NM_014959
7.11	6.92	0.19	6.35E-01	8.69E-01	TARDBP	TAR DNA binding protein	chr1p36.22	200020_at	NM_007375
2.27	2.20	0.07	6.35E-01	8.69E-01	---	---	---	216447_at	---
2.43	2.36	0.07	6.35E-01	8.69E-01	PSEN1	presenilin 1	chr14q24.3	1567443_x_at	NM_000021 /// NM_007318
2.86	2.77	0.09	6.35E-01	8.69E-01	LOC100134317	hypothetical protein LOC100134317	---	230552_at	XM_001722661
2.67	2.55	0.12	6.35E-01	8.70E-01	C9orf102	chromosome 9 open reading frame 102	chr9q22.32	232013_at	NM_001010895 /// NM_001034155 /// NM_020207
2.02	1.97	0.05	6.35E-01	8.70E-01	---	---	---	235888_at	---
4.46	4.36	0.10	6.35E-01	8.70E-01	PTCD3	Pentatricopeptide repeat domain 3	chr2p11.2	228020_at	NM_017952
2.82	2.73	0.09	6.35E-01	8.70E-01	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	chr19q13.4	211242_x_at	NM_001080770 /// NM_001080772 /// NM_002255
7.78	7.68	0.10	6.35E-01	8.70E-01	MRPS35	mitochondrial ribosomal protein S35	chr12p11	217942_at	NM_021821
2.90	2.80	0.10	6.35E-01	8.70E-01	CLEC7A	C-type lectin domain family 7, member A	chr12p13.2	1555213_a_at	NM_022570 /// NM_197947 /// NM_197948 /// NM_197949 /// NM_197950 /// NM_197954
2.76	2.61	0.15	6.35E-01	8.70E-01	---	---	---	238951_at	---
2.20	2.15	0.05	6.35E-01	8.70E-01	---	---	---	1563376_at	---
2.48	2.42	0.06	6.35E-01	8.70E-01	TFIP11	tuftelin interacting protein 11	chr22q12.1	202751_at	NM_001008697 /// NM_012143
2.31	2.24	0.07	6.36E-01	8.70E-01	LOC400960	hypothetical gene supported by BC040598	chr2p14	1557727_at	XM_934552 /// XM_945536
2.09	2.03	0.06	6.36E-01	8.70E-01	ATP11C	ATPase, class VI, type 11C	chrXq27.1	242690_at	NM_001010986 /// NM_173694
6.86	6.77	0.09	6.36E-01	8.70E-01	PBRM1	polybromo 1	chr3p21	223238_s_at	NM_018165 /// NM_018313 /// NM_181042
2.87	2.77	0.10	6.36E-01	8.70E-01	FOXN3	forkhead box N3	chr14q31.3	229652_s_at	NM_001085471 /// NM_005197
1.95	1.89	0.06	6.36E-01	8.70E-01	IRF4	interferon regulatory factor 4	chr6p25-p23	216987_at	NM_002460
2.04	1.99	0.05	6.36E-01	8.70E-01	TOP1P2	topoisomerase (DNA) I pseudogene 2	chr22q11.2-q13.1|22q11.23	1566832_at	NR_001283

6.10	6.02	0.08	6.36E-01	8.70E-01	UNK	unkempt homolog (Drosophila)	chr17q25.1	226376_at	NM_001080419																			
8.15	8.05	0.09	6.36E-01	8.70E-01	TMBIM1	transmembrane BAX inhibitor motif containing 1	chr2p24.3-p24.1	217730_at	NM_022152																			
3.17	3.07	0.09	6.36E-01	8.70E-01	CABP7	calcium binding protein 7	chr22q12.2	234796_at	NM_182527																			
2.88	2.77	0.11	6.36E-01	8.70E-01	CLEC4M	C-type lectin domain family 4, member M	chr19p13	210481_s_at	NM_014257 /// NM_214675 /// NM_214676 /// NM_214677 /// NM_214678 /// NM_214679																			
2.59	2.51	0.08	6.36E-01	8.70E-01	CENPN	centromere protein N	chr16q23.2	222118_at	NM_001100624 /// NM_001100625 /// NM_018455																			
3.64	3.58	0.07	6.36E-01	8.70E-01	ZNF250	zinc finger protein 250	chr8q24.3	213858_at	NM_001109689 /// NM_021061																			
3.48	3.41	0.08	6.36E-01	8.70E-01	XIAP	X-linked inhibitor of apoptosis	chrXq25	206537_at	NM_001167																			
2.57	2.50	0.07	6.36E-01	8.70E-01	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	chr10q21.3	1568815_a_at	NM_024045																			
2.05	1.99	0.06	6.36E-01	8.70E-01	---	---	---	1569983_at	---																			
2.39	2.32	0.06	6.36E-01	8.70E-01	CCDC132	coiled-coil domain containing 132	chr7q21.3	207045_at	NM_017667 /// NM_024553																			
11.13	11.05	0.07	6.36E-01	8.70E-01	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	chr8q24.3	214394_x_at	NM_001130053 /// NM_001130054 /// NM_001130055 /// NM_001130056 /// NM_001130057 /// NM_001960 /// NM_032378																			
7.42	7.33	0.10	6.36E-01	8.70E-01	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19p13.3	213944_x_at	NM_002067																			
2.22	2.17	0.05	6.36E-01	8.70E-01	PAQR3	progestin and adipoQ receptor family member III	chr4q21.21	1557576_at	NM_001040202																			
3.00	2.94	0.06	6.36E-01	8.70E-01	MAP3K9	mitogen-activated protein kinase kinase kinase 9	chr14q24.3-q31	213927_at	NM_033141																			
3.43	3.14	0.29	6.36E-01	8.70E-01	DPP4	dipeptidyl-peptidase 4	chr2q24.3	203717_at	NM_001935																			
2.41	2.32	0.09	6.36E-01	8.70E-01	MGC12982	hypothetical protein MGC12982	---	224456_s_at	---																			
2.18	2.12	0.06	6.36E-01	8.70E-01	---	---	---	237034_at	---																			
2.38	2.29	0.09	6.36E-01	8.70E-01	---	---	---	231501_at	---																			
3.39	3.29	0.10	6.37E-01	8.70E-01	---	---	---	243020_at	---																			
3.93	3.85	0.07	6.37E-01	8.70E-01	---	---	---	238690_at	---																			
2.06	1.99	0.07	6.37E-01	8.70E-01	---	---	---	231536_at	---																			
4.06	3.94	0.12	6.37E-01	8.70E-01	---	---	---	239348_at	---																			
6.98	6.84	0.14	6.37E-01	8.70E-01	MRPS2	mitochondrial ribosomal protein S2	chr9q34	218001_at	NM_016034																			
3.17	3.09	0.08	6.37E-01	8.70E-01	TRIM69	Tripartite motif-containing 69	chr15q21.1	229037_at	NM_080745 /// NM_182985																			
4.92	4.68	0.24	6.37E-01	8.70E-01	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	chr11q14.3	218566_s_at	NM_012124																			
3.86	3.70	0.16	6.37E-01	8.70E-01	TRIM52	tripartite motif-containing 52	chr5q35.3	1568594_s_at	NM_032765																			
6.28	6.15	0.13	6.37E-01	8.70E-01	SHMT1	serine hydroxymethyltransferase 1 (soluble)	chr17p11.2	224954_at	NM_004169 /// NM_148918																			
3.77	3.68	0.09	6.37E-01	8.70E-01	TNFRSF13C	tumor necrosis factor receptor superfamily, member 13C	chr22q13.1-q13.31	1552892_at	NM_052945																			
5.47	5.36	0.10	6.37E-01	8.70E-01	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	chr1q21-q22	32625_at	NM_000906																			
3.29	3.20	0.09	6.37E-01	8.70E-01	---	---	---	1564773_x_at	---																			
2.02	1.95	0.07	6.37E-01	8.71E-01	C11orf87	chromosome 11 open reading frame 87	chr11q22.3	1557180_at	NM_207645																			
3.56	3.39	0.17	6.37E-01	8.71E-01	CCL8	chemokine (C-C motif) ligand 8	chr17q11.2	214038_at	NM_005623																			
2.77	2.70	0.07	6.37E-01	8.71E-01	C19orf41	chromosome 19 open reading frame 41	chr19q13.33	240559_at	NM_152358																			
5.37	5.26	0.11	6.37E-01	8.71E-01	ETV1	ets variant gene 1	chr7p21.3	217061_s_at	NM_004956																			
5.39	5.24	0.14	6.38E-01	8.71E-01	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	chr10q23-q25	226757_at	NM_001547																			

7.19	7.08	0.12	6.38E-01	8.71E-01	GTF2A1	General transcription factor IIA, 1, 19/37kDa	chr14q31.1	225433_at	NM_015859 /// NM_201595																				
4.60	4.52	0.08	6.38E-01	8.71E-01	DCAKD	dephospho-CoA kinase domain containing	chr17q21.31	221224_s_at	NM_001128631 /// NM_024819																				
2.46	2.39	0.07	6.38E-01	8.71E-01	---	---	---	239551_at	---																				
4.15	3.96	0.19	6.38E-01	8.71E-01	MAG	myelin associated glycoprotein	chr19q13.1	216617_s_at	NM_002361 /// NM_080600																				
2.95	2.86	0.09	6.38E-01	8.71E-01	ZNF662	zinc finger protein 662	chr3p22.1	228538_at	NM_001134656 /// NM_207404																				
2.26	2.18	0.08	6.38E-01	8.71E-01	LOC100128414 /// RAD54B	similar to fibrinogen silencer binding protein /// RAD54 homolog B (S. cerevisiae)	chr8q21.3-q22 /// chr8q22.1	220549_at	NM_012415 /// XM_001722831 /// XM_001722851 /// XM_001722896																				
3.61	3.51	0.10	6.38E-01	8.71E-01	C12orf72	chromosome 12 open reading frame 72	chr12p11.21	1554582_a_at	NM_173802																				
4.10	3.98	0.11	6.38E-01	8.71E-01	---	---	---	228799_at	---																				
5.13	5.01	0.11	6.38E-01	8.71E-01	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	chr7p22	204766_s_at	NM_002452 /// NM_198948 /// NM_198949 /// NM_198950 /// NM_198952 /// NM_198953 /// NM_198954																				
6.22	6.11	0.12	6.38E-01	8.71E-01	RNF111	ring finger protein 111	chr15q21	218761_at	NM_017610																				
2.41	2.33	0.08	6.38E-01	8.71E-01	FLJ40176	hypothetical LOC121951	chr13q33.1	1566664_at	XM_926977 /// XM_937542																				
7.36	7.23	0.13	6.38E-01	8.71E-01	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	chr8p23.1	218096_at	NM_018361																				
2.12	2.05	0.07	6.38E-01	8.71E-01	LOC285889	hypothetical protein LOC285889	chr7q36.3	1562424_at	---																				
2.40	2.33	0.07	6.38E-01	8.71E-01	LOC401074	hypothetical LOC401074	chr3p12.3	1559826_a_at	XM_001714392																				
1.87	1.82	0.05	6.38E-01	8.71E-01	---	---	---	1563561_at	---																				
2.13	2.07	0.06	6.38E-01	8.71E-01	LOC100133233 /// TRAF3IP3	hypothetical protein LOC100133233 /// TRAF3 interacting protein 3	chr1q32.2 /// chr1q32.3-q41	240265_at	NM_025228 /// XM_001718033 /// XM_001718553 /// XM_001720826																				
3.14	3.07	0.07	6.38E-01	8.71E-01	PSMA3	Proteasome (prosome, macropain) subunit, alpha type, 3	chr14q23	237300_at	NM_002788 /// NM_152132																				
3.80	3.60	0.20	6.38E-01	8.71E-01	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	chr4q31.21	205376_at	NM_001101669 /// NM_003866																				
7.19	7.02	0.18	6.39E-01	8.71E-01	NAPRT1	nicotinate phosphoribosyltransferase domain containing 1	chr8q24.3	226707_at	NM_145201																				
3.29	3.20	0.09	6.39E-01	8.71E-01	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	chr19q13.3-q13.4	207600_at	NM_004977																				
2.22	2.14	0.08	6.39E-01	8.71E-01	EHBP1L1	EH domain binding protein 1-like 1	chr11q13.1	1557749_at	NM_001099409																				
2.15	2.09	0.07	6.39E-01	8.71E-01	MSH4	mutS homolog 4 (E. coli)	chr1p31	210533_at	NM_002440																				
4.11	4.02	0.10	6.39E-01	8.71E-01	FLJ22374	hypothetical protein FLJ22374	chr7p15.1	1557141_at	NM_032222																				
3.88	3.82	0.06	6.39E-01	8.71E-01	---	---	---	216822_x_at	---																				
2.53	2.47	0.06	6.39E-01	8.71E-01	WFDC11	WAP four-disulfide core domain 11	chr20q13.12	1552608_at	NM_147197																				
2.40	2.32	0.08	6.39E-01	8.71E-01	TTLL5	tubulin tyrosine ligase-like family, member 5	chr14q24.3	210806_at	NM_015072																				
7.32	7.17	0.15	6.39E-01	8.71E-01	DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	chr12p13.1	220890_s_at	NM_016355 /// NM_201224																				
7.75	7.60	0.16	6.39E-01	8.71E-01	EGLN1	egl nine homolog 1 (C. elegans)	chr1q42.1	223046_at	NM_022051																				
2.28	2.24	0.05	6.39E-01	8.71E-01	KRT35	keratin 35	chr17q12-q21	216921_s_at	NM_002280																				

4.72	4.64	0.08	6.39E-01	8.71E-01	JMJD7 /// LOC100137047-PLA2G4B /// PLA2G4B	jumonji domain containing 7 /// hypothetical protein LOC8681 /// phospholipase A2, group IVB (cytosolic)	chr15q11.2-q21.3 /// chr15q15.1	219095_at	NM_001114632 /// NM_001114633 /// NM_005090 /// NR_015346 /// XM_001720570 /// XM_001723659 /// XM_001725545																				
3.28	3.19	0.09	6.39E-01	8.71E-01	SH3PXD2B	SH3 and PX domains 2B	chr5q35.1	1562910_at	NM_001017995																				
5.52	5.31	0.21	6.39E-01	8.71E-01	BAALC	brain and acute leukemia, cytoplasmic	chr8q22.3	218899_s_at	NM_001024372 /// NM_024812																				
2.13	2.06	0.07	6.39E-01	8.71E-01	---	---	---	242840_at	---																				
2.18	2.13	0.05	6.39E-01	8.71E-01	---	---	---	216802_at	---																				
6.58	6.38	0.20	6.39E-01	8.71E-01	ARL5A	ADP-ribosylation factor-like 5A	chr2q23.3	226617_at	NM_001037174 /// NM_012097 /// NM_177985																				
2.89	2.82	0.07	6.39E-01	8.71E-01	RANBP10	RAN binding protein 10	chr16q22.1	1558773_s_at	NM_020850																				
2.29	2.19	0.09	6.39E-01	8.72E-01	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	chr18q22-q23	1552736_a_at	NM_138966 /// NM_138999 /// NM_153181																				
2.17	2.11	0.06	6.39E-01	8.72E-01	C9	complement component 9	chr5p14-p12	206727_at	NM_001737																				
3.89	3.79	0.10	6.39E-01	8.72E-01	COL5A3	collagen, type V, alpha 3	chr19p13.2	52255_s_at	NM_015719																				
7.64	7.55	0.09	6.39E-01	8.72E-01	ANO6	anoctamin 6	chr12q12	224906_at	NM_001025356																				
5.44	5.31	0.13	6.39E-01	8.72E-01	RAVER1	ribonucleoprotein, PTB-binding 1	chr19p13.2	223425_at	NM_133452																				
2.08	2.02	0.06	6.40E-01	8.72E-01	GRIK2	glutamate receptor, ionotropic, kainate 2	chr6q16.3-q21	1560142_at	NM_021956 /// NM_175768																				
2.89	2.79	0.10	6.40E-01	8.72E-01	LOC100128821 /// ZEB2	hypothetical protein LOC100128821 /// zinc finger E-box binding homeobox 2	chr2q22 /// chr2q22.3	233031_at	NM_014795 /// XM_001723541 /// XM_001723999 /// XM_001724917																				
3.97	3.90	0.07	6.40E-01	8.72E-01	LOC728361	hypothetical LOC728361	chr19q13.12	216311_at	XM_001715091 /// XM_001716321 /// XM_001717165																				
6.56	6.39	0.17	6.40E-01	8.72E-01	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	chrXp22.12	201018_at	NM_001412																				
2.84	2.72	0.12	6.40E-01	8.72E-01	---	---	---	240045_at	---																				
7.12	6.98	0.13	6.40E-01	8.72E-01	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	chr5q13.3	205295_at	NM_001099735 /// NM_001099736 /// NM_001825																				
5.94	5.69	0.25	6.40E-01	8.72E-01	---	---	---	236251_at	---																				
2.22	2.15	0.07	6.40E-01	8.72E-01	OLAH	oleoyl-ACP hydrolase	chr10p13	219975_x_at	NM_001039702 /// NM_018324																				
2.27	2.20	0.08	6.40E-01	8.72E-01	WAC	WW domain containing adaptor with coiled-coil	---	242427_at	NM_016628 /// NM_100264 /// NM_100486																				
2.34	2.22	0.12	6.40E-01	8.72E-01	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	chr2q32.3-q33	208047_s_at	NM_005966																				
2.56	2.51	0.05	6.40E-01	8.72E-01	TMEM132B	transmembrane protein 132B	chr12q24.31-q24.32	1563488_at	NM_052907																				
2.28	2.22	0.06	6.40E-01	8.72E-01	ZNF709	zinc finger protein 709	chr19p13.2	1562267_s_at	NM_152601																				

3.09	2.97	0.13	6.40E-01	8.72E-01	CALN1	calneuron 1	chr7q11	230698_at	NM_001017440 /// NM_031468
2.77	2.67	0.11	6.40E-01	8.72E-01	LOC729970	Hypothetical LOC729970	chr1p21.3	235691_at	XM_001129522 /// XM_001134179 /// XM_001720397
2.24	2.19	0.05	6.40E-01	8.72E-01	KRT12	keratin 12	chr17q12	207811_at	NM_000223
2.21	2.15	0.06	6.40E-01	8.72E-01	VSTM1	V-set and transmembrane domain containing 1	chr19q13.42	235818_at	NM_198481
2.37	2.30	0.07	6.40E-01	8.72E-01	---	---	---	237083_at	---
3.17	3.08	0.09	6.40E-01	8.72E-01	LRSAM1	leucine rich repeat and sterile alpha motif containing 1	chr9q33.3-q34.11	235449_at	NM_001005373 /// NM_001005374 /// NM_138361
3.30	3.22	0.08	6.40E-01	8.72E-01	MYOM3	myomesin family, member 3	chr1p36.11	238124_at	NM_152372
1.82	1.77	0.05	6.40E-01	8.72E-01	SIM1	single-minded homolog 1 (Drosophila)	chr6q16.3-q21	1556300_s_at	NM_005068
2.36	2.28	0.08	6.40E-01	8.72E-01	---	---	---	1559523_at	---
3.18	3.12	0.07	6.40E-01	8.72E-01	---	---	---	1565735_at	---
3.10	3.04	0.06	6.40E-01	8.72E-01	---	---	---	238694_at	---
2.50	2.43	0.07	6.40E-01	8.72E-01	CBY1	chibby homolog 1 (Drosophila)	chr22q12	1560220_a_at	NM_001002880 /// NM_015373
3.59	3.47	0.12	6.40E-01	8.72E-01	LOC100130456 /// LOC100134611	hypothetical LOC100130456 /// hypothetical protein LOC100134611	chr7p22.3	1564021_at	XM_001715837 /// XM_001720710 /// XM_001720880 /// XM_001722400
4.15	4.03	0.12	6.40E-01	8.72E-01	RUNX3	runt-related transcription factor 3	chr1p36	204197_s_at	NM_001031680 /// NM_004350
2.22	2.16	0.06	6.40E-01	8.72E-01	HNRNPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	239052_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370
6.83	6.64	0.19	6.41E-01	8.72E-01	TUG1	taurine upregulated gene 1	chr22q12.2	212725_s_at	NR_002323
3.03	2.94	0.09	6.41E-01	8.72E-01	CD300LF	CD300 molecule-like family member f	chr17q25.1	1553043_a_at	NM_139018
3.17	3.07	0.10	6.41E-01	8.72E-01	---	---	---	1557505_a_at	---
2.82	2.74	0.09	6.41E-01	8.72E-01	---	---	---	1561917_at	---
3.35	3.29	0.05	6.41E-01	8.72E-01	CDCA5	cell division cycle associated 5	chr11q12.1	224753_at	NM_080668
3.49	3.40	0.09	6.41E-01	8.72E-01	LOC100130506	hypothetical protein LOC100130506	---	236657_at	XM_001720083 /// XM_001724500
4.48	4.38	0.10	6.41E-01	8.72E-01	---	---	---	229267_at	---
2.54	2.46	0.07	6.41E-01	8.72E-01	CALHM3	calcium homeostasis modulator 3	chr10q24.33	1554711_at	NM_001129742 /// XM_001723060 /// XM_001725622 /// XM_001725818
3.99	3.89	0.09	6.41E-01	8.72E-01	MGC5370	Hypothetical protein MGC5370	chr12q14.3	217542_at	---
3.02	2.94	0.08	6.41E-01	8.72E-01	---	---	---	241329_s_at	---
3.84	3.75	0.08	6.41E-01	8.72E-01	ZFP30	zinc finger protein 30 homolog (mouse)	chr19q13.12	207090_x_at	NM_014898
4.74	4.64	0.10	6.41E-01	8.73E-01	RPL15	Ribosomal protein L15	chr3p24.2	240806_at	NM_002948
2.74	2.65	0.09	6.41E-01	8.73E-01	RHBDL2	rhomboid, veinlet-like 2 (Drosophila)	chr1p34.3	1554897_s_at	NM_017821
6.71	6.56	0.15	6.41E-01	8.73E-01	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	chr9q34.11	225212_at	NM_001006641 /// NM_001006642 /// NM_001006643 /// NM_052901
2.61	2.54	0.07	6.42E-01	8.73E-01	SLC22A9	solute carrier family 22 (organic anion transporter), member 9	chr11q13.1	231625_at	NM_080866
6.23	6.04	0.19	6.42E-01	8.73E-01	---	---	---	222288_at	---
2.18	2.05	0.12	6.42E-01	8.73E-01	---	---	---	1566337_x_at	---

2.60	2.50	0.10	6.42E-01	8.73E-01	---	---	---	240798_at	---
2.23	2.18	0.06	6.42E-01	8.73E-01	MDS2	myelodysplastic syndrome 2 translocation associated	chr1p36	1553508_at	---
8.04	7.90	0.14	6.42E-01	8.73E-01	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	chr9q21.33	209274_s_at	NM_030940
3.81	3.71	0.10	6.42E-01	8.73E-01	SLURP1	secreted LY6/PLAUR domain containing 1	chr8q24.3	214536_at	NM_020427
2.41	2.33	0.07	6.42E-01	8.73E-01	---	---	---	242723_at	---
5.57	5.43	0.14	6.42E-01	8.73E-01	GOPC	golgi associated PDZ and coiled-coil motif containing	chr6q21	225022_at	NM_001017408 /// NM_020399
2.58	2.45	0.13	6.42E-01	8.73E-01	ELA2A	elastase 2A	chr1p36.21	206447_at	NM_033440
2.14	2.09	0.05	6.42E-01	8.73E-01	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	chr4q25	216720_at	NM_183075
4.08	4.01	0.07	6.42E-01	8.73E-01	---	---	---	232495_x_at	---
2.28	2.20	0.08	6.42E-01	8.73E-01	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	chr19q13.3	1554810_at	NM_003706
1.92	1.87	0.06	6.42E-01	8.73E-01	C1orf125	chromosome 1 open reading frame 125	chr1q25.2	1552870_s_at	NM_144696 /// NM_182766
3.49	3.42	0.07	6.42E-01	8.73E-01	---	---	---	1562674_at	---
1.92	1.87	0.05	6.42E-01	8.73E-01	---	---	---	239680_at	---
5.15	5.04	0.11	6.42E-01	8.73E-01	RNF26	ring finger protein 26	chr11q23	224338_s_at	NM_032015
4.48	4.41	0.07	6.42E-01	8.73E-01	C19orf59	chromosome 19 open reading frame 59	chr19p13.2	235568_at	NM_174918
2.95	2.89	0.06	6.42E-01	8.73E-01	ZBTB10	zinc finger and BTB domain containing 10	chr8q13-q21.1	235726_at	NM_001105539 /// NM_023929
2.95	2.86	0.09	6.42E-01	8.73E-01	---	---	---	239085_at	---
4.49	4.40	0.09	6.42E-01	8.73E-01	LOC283481	hypothetical protein LOC283481	chr13q33.1	230351_at	XM_001128325 /// XM_001133584 /// XM_001719299
2.69	2.60	0.10	6.42E-01	8.73E-01	TRAFD1	TRAF-type zinc finger domain containing 1	chr12q	242497_at	NM_006700
2.94	2.85	0.09	6.43E-01	8.73E-01	---	---	---	240248_at	---
2.36	2.29	0.07	6.43E-01	8.73E-01	ZBTB24	zinc finger and BTB domain containing 24	chr6q21	1554037_a_at	NM_014797
2.88	2.82	0.06	6.43E-01	8.73E-01	---	---	---	240656_at	---
2.19	2.13	0.06	6.43E-01	8.73E-01	ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	chr1q32	206919_at	NM_001973 /// NM_021795
1.98	1.92	0.06	6.43E-01	8.73E-01	LIN7A	lin-7 homolog A (C. elegans)	chr12q21	240027_at	NM_004664
2.85	2.79	0.06	6.43E-01	8.73E-01	SLIT3	slit homolog 3 (Drosophila)	chr5q35	216216_at	NM_003062
7.42	7.27	0.15	6.43E-01	8.73E-01	USP34	ubiquitin specific peptidase 34	chr2p15	212066_s_at	NM_014709
2.73	2.67	0.06	6.43E-01	8.73E-01	---	---	---	241100_at	---
2.49	2.43	0.06	6.43E-01	8.73E-01	LOC100130332	similar to PRO2474	chr7q33	223925_s_at	XM_001723315 /// XM_001723951 /// XM_001726675
4.83	4.76	0.06	6.43E-01	8.73E-01	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	chr1q41	232103_at	NM_006085
2.13	2.06	0.07	6.43E-01	8.73E-01	---	---	---	242899_at	---
3.54	3.36	0.18	6.43E-01	8.73E-01	TWIST2	twist homolog 2 (Drosophila)	chr2q37.3	229404_at	NM_057179
4.33	4.23	0.10	6.43E-01	8.73E-01	TRABD	TraB domain containing	chr22q13.33	221807_s_at	NM_025204
3.18	3.06	0.12	6.43E-01	8.73E-01	ZDHHC21	zinc finger, DHHC-type containing 21	chr9p22.3	235068_at	NM_178566
6.86	6.70	0.17	6.43E-01	8.73E-01	LOC729580	hypothetical LOC729580	chr20q11.22	225860_at	XM_001126751 /// XM_001130700 /// XM_001714754
4.89	4.79	0.10	6.44E-01	8.73E-01	ICA1	islet cell autoantigen 1, 69kDa	chr7p22	207949_s_at	NM_004968 /// NM_022307
2.72	2.65	0.07	6.44E-01	8.73E-01	---	---	---	234199_at	---
3.32	3.23	0.10	6.44E-01	8.73E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	208227_x_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723
2.66	2.59	0.06	6.44E-01	8.73E-01	---	---	---	1560347_at	---
2.88	2.81	0.07	6.44E-01	8.73E-01	TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	chr2q24.1-q24.2	234870_at	NM_033394
7.62	7.45	0.18	6.44E-01	8.73E-01	BBS2	Bardet-Biedl syndrome 2	chr16q21	223227_at	NM_031885
7.11	6.83	0.28	6.44E-01	8.73E-01	FLJ12993	Hypothetical LOC441027	chr4q21.22	229623_at	NM_001080506

2.41	2.34	0.07	6.44E-01	8.74E-01	LOC93444	hypothetical protein LOC93444	chr15q22.32	1564168_a_at	---																			
2.10	2.05	0.05	6.44E-01	8.74E-01	---	---	---	233491_at	---																			
6.22	6.08	0.14	6.44E-01	8.74E-01	SNRPN	small nuclear ribonucleoprotein polypeptide N	chr15q11.2	1560741_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																				
4.39	4.24	0.14	6.44E-01	8.74E-01	PCGF6	polycomb group ring finger 6	chr10q24.33	224326_s_at	NM_001011663 /// NM_032154																			
1.95	1.89	0.06	6.44E-01	8.74E-01	PCNA	proliferating cell nuclear antigen	chr20pter-p12	217400_at	NM_002592 /// NM_182649																			
5.86	5.79	0.08	6.44E-01	8.74E-01	C6orf223	chromosome 6 open reading frame 223	chr6p21.1	239137_x_at	NM_153246																			
2.79	2.73	0.06	6.44E-01	8.74E-01	SSTR1	somatostatin receptor 1	chr14q13	208482_at	NM_001049																			
2.42	2.37	0.05	6.44E-01	8.74E-01	---	---	---	237359_at	---																			
5.02	4.86	0.16	6.44E-01	8.74E-01	RAB8B	RAB8B, member RAS oncogene family	chr15q22.2	219210_s_at	NM_016530																			
8.77	8.70	0.08	6.44E-01	8.74E-01	STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	chr20q13.1	213037_x_at	NM_001037328 /// NM_004602 /// NM_017452 /// NM_017453 /// NM_017454																			
4.78	4.72	0.07	6.44E-01	8.74E-01	C2CD3	C2 calcium-dependent domain containing 3	chr11q13.4	213199_at	NM_015531																			

8.75	8.66	0.09	6.44E-01	8.74E-01	OCIAD1	OCIA domain containing 1	chr4p11	223011_s_at	NM_001079839 /// NM_001079840 /// NM_001079841 /// NM_001079842 /// NM_017830																			
3.68	3.53	0.14	6.44E-01	8.74E-01	PPP3R1 /// WDR92	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform /// WD repeat domain 92	chr2p14 /// chr2p15	204507_s_at	NM_000945 /// NM_138458																			
6.32	6.19	0.13	6.44E-01	8.74E-01	HOXB4	homeobox B4	chr17q21-q22	231767_at	NM_024015																			
3.47	3.35	0.12	6.45E-01	8.74E-01	KIAA1648	KIAA1648 protein	chr22q12.1	244189_at	XM_001720903 /// XM_001723353 /// XM_001726321																			
6.42	6.27	0.15	6.45E-01	8.74E-01	LOC645139 /// LOC651789 /// PAIP1	hypothetical LOC645139 /// similar to poly(A) binding protein interacting protein 1 isoform 1 /// poly(A) binding protein interacting protein 1	chr17p11.2 /// chr5p12	210283_x_at	NM_006451 /// NM_182789 /// NM_183323 /// XM_001718191 /// XM_001719017 /// XM_928169																			
6.12	5.97	0.15	6.45E-01	8.74E-01	---	---	---	230099_at	---																			
3.07	2.95	0.12	6.45E-01	8.74E-01	---	---	---	211444_at	---																			
2.01	1.95	0.06	6.45E-01	8.74E-01	---	---	---	240712_s_at	---																			
2.06	2.01	0.05	6.45E-01	8.74E-01	WDHD1	WD repeat and HMG-box DNA binding protein 1	chr14q22.3	204727_at	NM_001008396 /// NM_007086																			
2.14	2.09	0.06	6.45E-01	8.74E-01	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	chr8q24.2	230249_at	NM_006558																			
2.04	1.97	0.07	6.45E-01	8.74E-01	---	---	---	233170_at	---																			
2.61	2.54	0.06	6.45E-01	8.74E-01	MYH6	myosin, heavy chain 6, cardiac muscle, alpha	chr14q12	214468_at	NM_002471																			
3.43	3.34	0.08	6.45E-01	8.74E-01	GATA2	GATA binding protein 2	chr3q21.3	207954_at	NM_032638																			
3.22	3.12	0.10	6.45E-01	8.74E-01	HS1BP3	HCLS1 binding protein 3	chr2p24.1	1568734_a_at	NM_022460																			
2.94	2.80	0.14	6.45E-01	8.74E-01	USP28	ubiquitin specific peptidase 28	chr11q23	1552678_a_at	NM_020886																			
3.43	3.36	0.07	6.45E-01	8.74E-01	---	---	---	1561868_at	---																			
8.15	8.04	0.11	6.45E-01	8.74E-01	C11orf67	chromosome 11 open reading frame 67	chr11q14.1	221600_s_at	NM_024684																			
2.62	2.55	0.06	6.45E-01	8.74E-01	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	chr1p31	238489_at	NM_006252																			
2.16	2.10	0.06	6.45E-01	8.74E-01	---	---	---	242547_at	---																			
5.16	5.00	0.16	6.45E-01	8.74E-01	---	---	---	231513_at	---																			
2.29	2.23	0.06	6.45E-01	8.74E-01	---	---	---	244262_x_at	---																			
3.75	3.60	0.15	6.46E-01	8.74E-01	FMO3	flavin containing monooxygenase 3	chr1q23-q25	40665_at	NM_001002294 /// NM_006894																			
2.51	2.44	0.06	6.46E-01	8.74E-01	---	---	---	237200_at	---																			
2.50	2.43	0.06	6.46E-01	8.74E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	216540_at	---																			
6.91	6.81	0.10	6.46E-01	8.74E-01	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	209330_s_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370																			
3.56	3.41	0.14	6.46E-01	8.74E-01	---	---	---	224082_at	---																			
2.06	2.00	0.06	6.46E-01	8.75E-01	FLJ38379	hypothetical protein FLJ38379	chr2q37.3	1556474_a_at	XR_015732 /// XR_017906 /// XR_040034																			
4.40	4.29	0.11	6.46E-01	8.75E-01	ZNF227	zinc finger protein 227	---	227689_at	NM_182490																			
5.81	5.72	0.09	6.46E-01	8.75E-01	TBC1D22A	TBC1 domain family, member 22A	chr22q13.3	209650_s_at	NM_014346																			
8.43	8.32	0.11	6.46E-01	8.75E-01	TGFBI	transforming growth factor, beta-induced, 68kDa	chr5q31	201506_at	NM_000358																			
2.80	2.70	0.10	6.46E-01	8.75E-01	---	---	---	244362_at	---																			
3.49	3.44	0.05	6.46E-01	8.75E-01	ZNF77	zinc finger protein 77	chr19p13.3	1558673_s_at	NM_021217																			
3.71	3.64	0.07	6.46E-01	8.75E-01	LOC400573	hypothetical gene supported by BC015790; BC041634	chr17p13.1	236001_at	---																			
6.82	6.56	0.26	6.46E-01	8.75E-01	CPEB4	cytoplasmic polyadenylation element binding protein 4	chr5q21	224831_at	NM_030627																			
7.25	7.10	0.15	6.46E-01	8.75E-01	SLC16A2	solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	chrXq13.2	204462_s_at	NM_006517																			

4.46	4.34	0.12	6.46E-01	8.75E-01	TNRC6B	Trinucleotide repeat containing 6B	chr22q13.1	240044_x_at	NM_001024843 /// NM_015088																				
2.28	2.23	0.05	6.46E-01	8.75E-01	HIST1H2AD /// HIST1H2BN /// HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	histone cluster 1, H2ad /// histone cluster 1, H2bn /// histone cluster 1, H3a /// histone cluster 1, H3b /// histone cluster 1, H3c /// histone cluster 1, H3d /// histone cluster 1, H3e /// histone cluster 1, H3f /// histone cluster 1, H3g /// histone cluster 1, H3h /// histone cluster 1, H3i /// histone cluster 1, H3j	chr6p21.3 /// chr6p22-p21.3 /// chr6p22.1	208575_at	NM_003520 /// NM_003529 /// NM_003530 /// NM_003531 /// NM_003532 /// NM_003533 /// NM_003534 /// NM_003535 /// NM_003536 /// NM_003537 /// NM_021018 /// NM_021065																			
4.01	3.88	0.13	6.46E-01	8.75E-01	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	chr17q24.2	229414_at	NM_012417 /// NM_181671																				
3.07	2.98	0.09	6.47E-01	8.75E-01	NLRP5	NLR family, pyrin domain containing 5	chr19q13.42	1552405_at	NM_153447																				
2.35	2.28	0.07	6.47E-01	8.75E-01	---	---	---	1560941_a_at	---																				
6.59	6.44	0.15	6.47E-01	8.75E-01	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	chr6q22.31	213624_at	NM_006714																				
3.58	3.49	0.10	6.47E-01	8.75E-01	PARVG	Parvin, gamma	chr22q13.2-q13	244229_at	NM_022141																				
2.03	1.98	0.05	6.47E-01	8.75E-01	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	chr7p15.3	240717_at	NM_178559																				
3.26	3.11	0.15	6.47E-01	8.75E-01	ADCY7	adenylate cyclase 7	chr16q12-q13	203741_s_at	NM_001114																				
5.78	5.71	0.08	6.47E-01	8.75E-01	REXO4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	chr9q34.2	218767_at	NM_020385																				
6.24	5.96	0.28	6.47E-01	8.75E-01	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	chr5q35.3	213470_s_at	NM_005520																				
7.05	6.93	0.12	6.47E-01	8.75E-01	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	chr17q21	212383_at	NM_001130020 /// NM_001130021 /// NM_005177																				
6.75	6.61	0.14	6.47E-01	8.75E-01	FRG1	FSHD region gene 1	chr4q35	204145_at	NM_004477																				
2.37	2.33	0.04	6.47E-01	8.75E-01	---	---	---	1556008_a_at	---																				
3.88	3.76	0.12	6.47E-01	8.75E-01	DMXL2	Dmx-like 2	chr15q21.2	212820_at	NM_015263																				
8.64	8.53	0.11	6.47E-01	8.75E-01	IFI30	interferon, gamma-inducible protein 30	chr19p13.1	201422_at	NM_006332																				
2.14	2.08	0.06	6.48E-01	8.75E-01	---	---	---	1558497_a_at	---																				
6.62	6.49	0.13	6.48E-01	8.75E-01	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	chr9q31-q33	209162_s_at	NM_004697																				
3.23	3.12	0.11	6.48E-01	8.75E-01	PRMT2	protein arginine methyltransferase 2	chr21q22.3	228722_at	NM_001535 /// NM_206962																				
3.55	3.33	0.22	6.48E-01	8.75E-01	KIAA1377	KIAA1377	chr11q22.1	232166_at	NM_020802																				
2.64	2.54	0.09	6.48E-01	8.75E-01	LOC441461	hypothetical gene supported by BC030123	chr9q31.1	1558689_a_at	XR_041357 /// XR_041358 /// XR_041359																				
3.46	3.39	0.07	6.48E-01	8.75E-01	PCDHB6	protocadherin beta 6	chr5q31	221317_x_at	NM_018939																				
5.10	4.98	0.12	6.48E-01	8.75E-01	SECTM1	secreted and transmembrane 1	chr17q25	213716_s_at	NM_003004																				
2.21	2.16	0.05	6.48E-01	8.75E-01	---	---	---	242811_x_at	---																				
2.53	2.46	0.07	6.48E-01	8.75E-01	XDH	xanthine dehydrogenase	chr2p23.1	241994_at	NM_000379																				
5.25	5.11	0.14	6.48E-01	8.75E-01	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	chrXq25	221514_at	NM_006649																				
3.06	2.99	0.07	6.48E-01	8.75E-01	C3orf46	chromosome 3 open reading frame 46	chr3q21.3	244681_at	XR_040325 /// XR_040326 /// XR_040327																				
4.69	4.62	0.07	6.48E-01	8.75E-01	---	---	---	227504_s_at	---																				
3.50	3.44	0.06	6.48E-01	8.75E-01	TTC15	tetratricopeptide repeat domain 15	chr2p25.3	229556_at	NM_016030																				
5.10	4.97	0.12	6.48E-01	8.75E-01	EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	chr15q24.1	226042_at	NM_025083																				
4.72	4.57	0.15	6.48E-01	8.75E-01	SF3A2	splicing factor 3a, subunit 2, 66kDa	chr19p13.3|19p13.3-p13.2	209381_x_at	NM_007165																				
9.03	8.86	0.17	6.48E-01	8.75E-01	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	chr1q24	201242_s_at	NM_001001787 /// NM_001677																				

2.58	2.51	0.07	6.48E-01	8.75E-01	---	---	---	233834_at	---
5.14	4.87	0.26	6.48E-01	8.75E-01	IL7R	interleukin 7 receptor	chr5p13	226218_at	NM_002185
3.67	3.57	0.10	6.48E-01	8.75E-01	LOC730432 /// STYX	similar to serine/threonine/tyrosine interacting protein /// serine/threonine/tyrosine interacting protein	---	228853_at	NM_001130701 /// NM_145251 /// XM_001125680
3.14	3.02	0.11	6.48E-01	8.75E-01	MGC16291	hypothetical protein MGC16291	chr10q11.21	233562_at	XR_017865 /// XR_017966 /// XR_040081
2.61	2.52	0.09	6.48E-01	8.75E-01	---	---	---	1563621_at	---
2.28	2.20	0.08	6.48E-01	8.75E-01	---	---	---	230545_at	---
2.77	2.71	0.07	6.49E-01	8.76E-01	SYN2	synapsin II	chr3p25	210315_at	NM_003178 /// NM_133625
2.58	2.52	0.06	6.49E-01	8.76E-01	DNAH10	dynein, axonemal, heavy chain 10	chr12q24.31	1565339_at	NM_001083900 /// NM_207437
7.28	7.16	0.12	6.49E-01	8.76E-01	NPEPPS	aminopeptidase puromycin sensitive	chr17q21	201455_s_at	NM_006310
3.45	3.34	0.11	6.49E-01	8.76E-01	LOC100134226	hypothetical protein LOC100134226	---	238097_at	XM_001721602
2.35	2.30	0.05	6.49E-01	8.76E-01	COPA	coatomer protein complex, subunit alpha	chr1q23-q25	214337_at	NM_001098398 /// NM_004371
2.52	2.44	0.07	6.49E-01	8.76E-01	---	---	---	1563319_at	---
2.29	2.24	0.06	6.49E-01	8.76E-01	DKFZP434L187	Hypothetical LOC26082	chr15q13.2	1569476_at	XM_496054
3.17	3.09	0.08	6.49E-01	8.76E-01	---	---	---	1561320_at	---
2.36	2.29	0.07	6.49E-01	8.76E-01	TLR10	toll-like receptor 10	chr4p14	223751_x_at	NM_001017388 /// NM_030956
6.21	6.13	0.08	6.49E-01	8.76E-01	---	---	---	235659_at	---
2.47	2.39	0.08	6.49E-01	8.76E-01	---	---	---	1565929_s_at	---
6.75	6.55	0.20	6.49E-01	8.76E-01	IREB2	iron-responsive element binding protein 2	chr15q25.1	225892_at	NM_004136
3.40	3.27	0.13	6.49E-01	8.76E-01	---	---	---	230294_at	---
5.32	5.22	0.10	6.49E-01	8.76E-01	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	chr2p13	211121_s_at	NM_001381
7.15	6.97	0.18	6.49E-01	8.76E-01	LOC54492	hypothetical LOC54492	chr5q35.1	225355_at	NR_015355 /// XM_001715114 /// XM_001715867 /// XM_001718086
2.81	2.72	0.09	6.50E-01	8.76E-01	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	chr3p14	238339_x_at	NM_015541
2.30	2.18	0.12	6.50E-01	8.76E-01	CASZ1	castor zinc finger 1	chr1p36.22	243386_at	NM_001079843 /// NM_017766
2.91	2.82	0.09	6.50E-01	8.76E-01	YWHAH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	chr22q12.3	242325_at	NM_003405
1.98	1.92	0.07	6.50E-01	8.76E-01	AGBL3	ATP/GTP binding protein-like 3	chr7q33	232395_x_at	XM_001723112 /// XM_001723784 /// XM_001726535 /// XM_001726650
2.34	2.28	0.06	6.50E-01	8.76E-01	PTPN2	protein tyrosine phosphatase, non-receptor type 2	chr18p11.3-p11.2	241623_at	NM_002828 /// NM_080422 /// NM_080423
2.80	2.74	0.05	6.50E-01	8.76E-01	---	---	---	230978_at	---
5.05	4.96	0.09	6.50E-01	8.76E-01	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	chr17q22-q23	227489_at	NM_022739
2.04	1.98	0.05	6.50E-01	8.76E-01	SLC25A36	solute carrier family 25, member 36	chr3q23	223698_at	NM_001104647 /// NM_018155
2.60	2.52	0.08	6.50E-01	8.76E-01	---	---	---	241410_at	---
4.69	4.61	0.08	6.50E-01	8.76E-01	---	---	---	241223_x_at	---
5.15	5.02	0.12	6.50E-01	8.76E-01	---	---	---	1555846_a_at	---
2.18	2.11	0.08	6.50E-01	8.76E-01	LOC285878 /// VSTM2A	hypothetical protein LOC285878 /// V-set and transmembrane domain containing 2A	chr7p11.2	1560692_at	NM_182546

2.88	2.79	0.09	6.50E-01	8.76E-01	TMEM107	transmembrane protein 107	chr17p13.1	224495_at	NM_032354 /// NM_183065																				
2.14	2.07	0.07	6.50E-01	8.76E-01	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	chr5q11-q14	210801_at	NM_014473																				
1.89	1.84	0.05	6.50E-01	8.76E-01	---	---	---	1567182_at	---																				
5.92	5.80	0.11	6.50E-01	8.76E-01	---	---	---	236515_at	---																				
2.32	2.26	0.06	6.50E-01	8.76E-01	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	chr19q13.2	203757_s_at	NM_002483																				
2.28	2.21	0.07	6.51E-01	8.76E-01	SKIL	SKI-like oncogene	chr3q26	232379_at	NM_005414																				
2.75	2.69	0.06	6.51E-01	8.76E-01	PHACTR1	phosphatase and actin regulator 1	chr6p24.1	213638_at	NM_030948																				
2.08	2.02	0.06	6.51E-01	8.76E-01	---	---	---	234389_x_at	---																				
2.74	2.66	0.08	6.51E-01	8.76E-01	TOR1AIP1	torsin A interacting protein 1	chr1q24.2	240310_at	NM_015602																				
6.68	6.59	0.08	6.51E-01	8.76E-01	LMF1	lipase maturation factor 1	chr16p13.3	219135_s_at	NM_022773																				
2.10	2.05	0.05	6.51E-01	8.76E-01	FBXO3	F-box protein 3	chr11p13	242791_at	NM_012175 /// NM_033406																				
2.38	2.31	0.07	6.51E-01	8.76E-01	---	---	---	239829_at	---																				
5.91	5.76	0.15	6.51E-01	8.76E-01	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	chr2q32.3-q33	209272_at	NM_005966																				
4.43	4.36	0.07	6.51E-01	8.76E-01	DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	chr1p35.3	212490_at	NM_014280																				
4.61	4.45	0.15	6.51E-01	8.76E-01	DOCK8	dedicator of cytokinesis 8	chr9p24.3	232843_s_at	NM_203447																				
3.75	3.67	0.08	6.51E-01	8.76E-01	ZNF544	zinc finger protein 544	chr19q13.43	244466_at	NM_014480																				
2.56	2.48	0.07	6.51E-01	8.76E-01	---	---	---	240018_at	---																				
2.99	2.89	0.10	6.51E-01	8.76E-01	SRCAP	Snf2-related CREBBP activator protein	chr16p11.2	1569138_a_at	NM_006662																				
2.77	2.69	0.09	6.51E-01	8.76E-01	---	---	---	236591_at	---																				
2.21	2.14	0.07	6.51E-01	8.76E-01	---	---	---	215893_x_at	---																				
3.44	3.35	0.08	6.51E-01	8.76E-01	---	---	---	220969_s_at	---																				
5.63	5.41	0.22	6.51E-01	8.76E-01	P2RY8	purinergic receptor P2Y, G-protein coupled, 8	chrXp22.33; Yp11.3	229686_at	NM_178129																				
2.48	2.42	0.07	6.51E-01	8.76E-01	LOC280665	putative anti-CNG alpha 1 cation channel translation product	---	1554840_at	---																				
2.51	2.46	0.05	6.51E-01	8.76E-01	FLJ14327	hypothetical protein FLJ14327	chr16q23.2	220809_at	XR_040939 /// XR_040940 /// XR_040941																				
1.97	1.92	0.05	6.52E-01	8.76E-01	BDNFOS	BDNF opposite strand (non-protein coding)	chr11p14.1	1567359_at	NR_002832																				
10.41	10.33	0.08	6.52E-01	8.76E-01	CLTA	clathrin, light chain (Lca)	chr9p13	200960_x_at	NM_001076677 /// NM_001833 /// NM_007096																				
2.38	2.31	0.07	6.52E-01	8.76E-01	ZRANB3	zinc finger, RAN-binding domain containing 3	chr2q21.3	224124_at	NM_032143																				
2.96	2.86	0.09	6.52E-01	8.76E-01	FLJ42351 /// LOC100131455	hypothetical gene supported by AK124342 /// hypothetical protein LOC100131455	chr2q13	230452_at	XM_001715661 /// XM_001716367 /// XM_001716534																				
3.26	3.17	0.10	6.52E-01	8.76E-01	---	---	---	234468_at	---																				
4.94	4.72	0.22	6.52E-01	8.76E-01	ADAMTSL1	ADAMTS-like 1	chr9p22.2-p22.1	229585_at	NM_001040272 /// NM_052866																				
2.57	2.48	0.09	6.52E-01	8.76E-01	---	---	---	215811_at	---																				
6.32	6.19	0.13	6.52E-01	8.76E-01	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase	chr16q24.3	206335_at	NM_000512																				
3.98	3.88	0.11	6.52E-01	8.76E-01	GZF1	GDNF-inducible zinc finger protein 1	chr20p12.3-p11.21	234055_s_at	NM_022482																				
2.10	2.04	0.06	6.52E-01	8.76E-01	---	---	---	1560565_at	---																				
2.07	2.02	0.05	6.52E-01	8.76E-01	HERC6	Hect domain and RLD 6	chr4q22.1	244760_at	NM_017912																				
7.63	7.42	0.21	6.52E-01	8.76E-01	SCN1B	sodium channel, voltage-gated, type I, beta	chr19q13.1	205508_at	NM_001037 /// NM_199037																				
5.66	5.58	0.07	6.52E-01	8.76E-01	PRDX2	peroxiredoxin 2	chr19p13.2	215067_x_at	NM_005809 /// NM_181738																				
3.93	3.79	0.14	6.52E-01	8.76E-01	DOC2A	double C2-like domains, alpha	chr16p11.2	205744_at	NM_003586																				

3.21	3.12	0.09	6.52E-01	8.76E-01	EMR2	egf-like module containing, mucin-like, hormone receptor-like 2	chr19p13.1	207610_s_at	NM_013447 /// NM_152916 /// NM_152917 /// NM_152918 /// NM_152919 /// NM_152920 /// NM_152921																				
8.42	8.33	0.10	6.52E-01	8.76E-01	HLA-C	major histocompatibility complex, class I, C	chr6p21.3	211799_x_at	NM_002117 /// XM_001715881 /// XM_001717045 /// XM_001719879																				
2.69	2.63	0.06	6.52E-01	8.77E-01	GLT8D1	Glycosyltransferase 8 domain containing 1	chr3p21.1	228395_at	NM_001010983 /// NM_018446 /// NM_152932																				
2.04	1.97	0.07	6.52E-01	8.77E-01	---	---	---	1569491_at	---																				
2.14	2.07	0.06	6.52E-01	8.77E-01	LOC283713	hypothetical protein LOC283713	chr15q13.1	230783_at	---																				
4.12	4.00	0.12	6.52E-01	8.77E-01	C10orf119	chromosome 10 open reading frame 119	chr10q26.11	217905_at	NM_024834																				
2.32	2.23	0.09	6.52E-01	8.77E-01	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	chr14q12-q13	1554242_a_at	NM_004086																				
3.77	3.66	0.11	6.53E-01	8.77E-01	---	---	---	1565692_at	---																				
7.51	7.46	0.05	6.53E-01	8.77E-01	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	chr10q11.21-q11.23	218118_s_at	NM_006327																				
3.15	3.08	0.08	6.53E-01	8.77E-01	RPL10	ribosomal protein L10	chrXq28	200724_at	NM_006013																				
2.01	1.94	0.06	6.53E-01	8.77E-01	LOC646168	hypothetical protein LOC646168	chr3q26.1	1560168_at	XM_934868 /// XM_934869 /// XM_934871																				
6.20	6.12	0.08	6.53E-01	8.77E-01	ZNF469	zinc finger protein 469	chr16q24	230440_at	NM_001127464 /// XR_040936 /// XR_040937 /// XR_040938																				
7.54	7.43	0.10	6.53E-01	8.77E-01	PRKCSH	protein kinase C substrate 80K-H	chr19p13.2	200707_at	NM_001001329 /// NM_002743																				
6.52	6.43	0.09	6.53E-01	8.77E-01	CHMP4B	chromatin modifying protein 4B	chr20q11.22	225119_at	NM_176812																				
5.82	5.63	0.19	6.53E-01	8.77E-01	SS18	synovial sarcoma translocation, chromosome 18	chr18q11.2	209954_x_at	NM_001007559 /// NM_005637																				
2.37	2.31	0.06	6.53E-01	8.77E-01	DKFZp667E0512	hypothetical protein DKFZp667E0512	chr4p16.1	236079_at	---																				
2.12	2.06	0.06	6.53E-01	8.77E-01	MAGEB1	melanoma antigen family B, 1	chrXp21.3	207534_at	NM_002363 /// NM_177404 /// NM_177415																				
3.55	3.46	0.09	6.53E-01	8.77E-01	---	---	---	230655_at	---																				
2.01	1.95	0.06	6.54E-01	8.77E-01	---	---	---	1560325_at	---																				
7.41	7.31	0.09	6.54E-01	8.77E-01	GNA12	guanine nucleotide binding protein (G protein) alpha 12	chr7p22.2	224681_at	NM_007353																				
5.93	5.78	0.15	6.54E-01	8.77E-01	ND6	NADH dehydrogenase, subunit 6 (complex I)	---	1553575_at	---																				
4.07	4.00	0.07	6.54E-01	8.77E-01	ADARB2	adenosine deaminase, RNA-specific, B2 (RED2 homolog rat)	chr10p15.3	237437_s_at	NM_018702																				
2.04	1.97	0.07	6.54E-01	8.77E-01	FLJ12078	hypothetical protein FLJ12078	chr5q15	220900_at	XR_040970 /// XR_040971 /// XR_040972																				
5.36	5.23	0.13	6.54E-01	8.77E-01	PRPF38A	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	chr1p33-p32.1	223230_at	NM_032864																				
2.35	2.26	0.08	6.54E-01	8.77E-01	---	---	---	234892_at	---																				

8.38	8.22	0.16	6.54E-01	8.77E-01	CSNK1A1	casein kinase 1, alpha 1	chr5q32	213860_x_at	NM_001025105 /// NM_001892
1.91	1.87	0.04	6.54E-01	8.77E-01	CNTNAP3	contactin associated protein-like 3	chr9p13.1	233202_at	NM_033655
6.30	6.10	0.21	6.54E-01	8.77E-01	SS18	synovial sarcoma translocation, chromosome 18	chr18q11.2	202816_s_at	NM_001007559 /// NM_005637
2.21	2.15	0.06	6.54E-01	8.77E-01	---	---	---	1562604_at	---
5.03	4.89	0.14	6.54E-01	8.77E-01	ETV1	ets variant gene 1	chr7p21.3	217053_x_at	NM_004956
6.72	6.55	0.17	6.54E-01	8.77E-01	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	chr8q21.13-q21.3	203011_at	NM_005536
5.18	5.00	0.19	6.54E-01	8.77E-01	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	chr11q12.1	230550_at	NM_022349 /// NM_152851 /// NM_152852
2.44	2.36	0.08	6.54E-01	8.78E-01	FBXW2	F-box and WD repeat domain containing 2	chr9q34	241736_at	NM_012164
2.78	2.70	0.08	6.54E-01	8.78E-01	---	---	---	1570108_at	---
3.75	3.65	0.09	6.54E-01	8.78E-01	ACTR8	ARP8 actin-related protein 8 homolog (yeast)	---	218658_s_at	NM_022899
2.11	2.06	0.05	6.54E-01	8.78E-01	ZSCAN4	zinc finger and SCAN domain containing 4	chr19q13.43	1552852_a_at	NM_152677
5.03	4.93	0.10	6.55E-01	8.78E-01	CC2D1B	coiled-coil and C2 domain containing 1B	chr1p32.3	225323_at	NM_032449
5.01	4.94	0.07	6.55E-01	8.78E-01	APOC4	apolipoprotein C-IV	chr19q13.2	206738_at	NM_001646
2.47	2.40	0.06	6.55E-01	8.78E-01	ACAN	aggrecan	chr15q26.1	1554950_at	NM_001135 /// NM_013227
1.91	1.86	0.05	6.55E-01	8.78E-01	KIAA0241	KIAA0241	chr7p14.3	1555055_at	NM_015060
2.65	2.59	0.06	6.55E-01	8.78E-01	---	---	---	229223_at	---
5.24	5.08	0.16	6.55E-01	8.78E-01	FLJ20323	hypothetical protein FLJ20323	chr7p22-p21	206860_s_at	NM_019005
5.01	4.93	0.08	6.55E-01	8.78E-01	TOMM22	Translocase of outer mitochondrial membrane 22 homolog (yeast)	chr22q12-q13	229076_s_at	NM_020243
4.15	4.08	0.07	6.55E-01	8.78E-01	CDYL	chromodomain protein, Y-like	chr6p25.1	203100_s_at	NM_004824 /// NM_170751 /// NM_170752
6.09	5.87	0.22	6.55E-01	8.78E-01	IMPAD1	inositol monophosphatase domain containing 1	chr8q12.1	224744_at	NM_017813
6.96	6.88	0.08	6.55E-01	8.78E-01	HDAC7	histone deacetylase 7	chr12q13.1	217937_s_at	NM_001098415 /// NM_001098416 /// NM_015401 /// NM_016596
4.11	4.04	0.06	6.55E-01	8.78E-01	CREBZF	CREB/ATF bZIP transcription factor	chr11q14	202977_s_at	NM_001039618
4.70	4.56	0.14	6.55E-01	8.78E-01	ASPHD1	aspartate beta-hydroxylase domain containing 1	chr16p11.2	1553997_a_at	NM_181718
5.39	5.22	0.17	6.55E-01	8.78E-01	NUP50	nucleoporin 50kDa	chr22q13.31	218295_s_at	NM_007172 /// NM_153645
3.27	3.15	0.12	6.55E-01	8.78E-01	CGNL1	Cingulin-like 1	chr15q21.3	1569847_at	NM_032866
1.84	1.79	0.05	6.55E-01	8.78E-01	GPR22	G protein-coupled receptor 22	chr7q22-q31.1	244493_at	NM_005295
2.48	2.42	0.06	6.55E-01	8.78E-01	TMEM71	transmembrane protein 71	chr8q24.22	238429_at	NM_144649
2.86	2.80	0.06	6.55E-01	8.78E-01	KIF1A	kinesin family member 1A	chr2q37.3	203849_s_at	NM_004321
2.83	2.78	0.05	6.55E-01	8.78E-01	---	---	---	244737_at	---
2.27	2.20	0.07	6.56E-01	8.78E-01	KRT14	keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)	chr17q12-q21	209351_at	NM_000526
2.02	1.96	0.07	6.56E-01	8.78E-01	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	chr6p22.3-p22.1	224101_x_at	NM_020662
8.42	8.25	0.17	6.56E-01	8.78E-01	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	chr1q44	200593_s_at	NM_004501 /// NM_031844
2.28	2.18	0.10	6.56E-01	8.78E-01	---	---	---	240330_at	---
2.91	2.81	0.10	6.56E-01	8.78E-01	---	---	---	244868_at	---
2.13	2.08	0.06	6.56E-01	8.78E-01	RLBP1L2	retinaldehyde binding protein 1-like 2	chr6q22.31	1562443_at	NM_001010852
6.12	5.98	0.14	6.56E-01	8.78E-01	HDGFRP3	hepatoma-derived growth factor, related protein 3	chr15q25.2	216693_x_at	NM_016073
3.24	3.11	0.13	6.56E-01	8.78E-01	---	---	---	242769_at	---
3.45	3.29	0.16	6.56E-01	8.78E-01	RSRC1	arginine/serine-rich coiled-coil 1	chr3q25.32	1555501_s_at	NM_016625
3.36	3.31	0.05	6.56E-01	8.78E-01	DEFT1P	defensin, theta 1 pseudogene	chr8p23.1	1553518_at	---
5.85	5.71	0.14	6.56E-01	8.78E-01	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	chr8p23	223912_s_at	NM_018941
4.68	4.62	0.06	6.56E-01	8.78E-01	C20orf117	chromosome 20 open reading frame 117	chr20q11.23	207711_at	NM_199181
9.57	9.52	0.05	6.56E-01	8.78E-01	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	chr5q35.2	214150_x_at	NM_003945
2.93	2.85	0.09	6.56E-01	8.78E-01	FBXO27	F-box protein 27	chr19q13.2	235169_at	NM_178820
3.97	3.83	0.14	6.56E-01	8.78E-01	LOC493754	Hypothetical LOC441245	chr7q11.21	1569296_a_at	NR_002933

2.75	2.68	0.06	6.56E-01	8.78E-01	PTPRA	Protein tyrosine phosphatase, receptor type, A	chr20p13	240618_at	NM_002836 /// NM_080840 /// NM_080841																				
2.87	2.80	0.07	6.56E-01	8.78E-01	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	chr6p22.3-p22.2	217405_x_at	NM_001503 /// NM_177483																				
3.12	3.02	0.09	6.56E-01	8.78E-01	TNK2	tyrosine kinase, non-receptor, 2	chr3q29	203838_s_at	NM_001010938 /// NM_005781																				
4.72	4.53	0.19	6.56E-01	8.78E-01	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	chr4q24	202541_at	NM_004757																				
3.97	3.82	0.14	6.56E-01	8.78E-01	NOTCH4	Notch homolog 4 (Drosophila)	chr6p21.3	205247_at	NM_004557																				
2.03	1.97	0.06	6.56E-01	8.78E-01	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	chr2q21.3	239527_at	NM_012233																				
4.29	4.16	0.13	6.57E-01	8.78E-01	MLH3	mutL homolog 3 (E. coli)	chr14q24.3	217216_x_at	NM_001040108 /// NM_014381																				
3.55	3.32	0.22	6.57E-01	8.78E-01	DPP4	dipeptidyl-peptidase 4	chr2q24.3	211478_s_at	NM_001935																				
5.10	4.88	0.22	6.57E-01	8.79E-01	FAM133B /// LOC728153	family with sequence similarity 133, member B /// similar to FAM133B protein	chr5q12.1 /// chr7q21.2	226332_at	NM_001040057 /// NM_152789 /// XM_001128002 /// XM_001722995																				
2.30	2.23	0.07	6.57E-01	8.79E-01	C10orf63	chromosome 10 open reading frame 63	chr10p12.1	237314_at	NM_145010																				
3.64	3.55	0.09	6.57E-01	8.79E-01	NFRKB	nuclear factor related to kappaB binding protein	chr11q24-q25	237209_s_at	NM_006165																				
7.70	7.61	0.09	6.57E-01	8.79E-01	PPP6C	protein phosphatase 6, catalytic subunit	chr9q33.3	206174_s_at	NM_001123355 /// NM_001123369 /// NM_002721																				
5.96	5.78	0.18	6.57E-01	8.79E-01	GPR125	G protein-coupled receptor 125	chr4p15.31	210473_s_at	NM_145290																				
9.73	9.62	0.11	6.57E-01	8.79E-01	EIF4B	eukaryotic translation initiation factor 4B	chr12q13.13	211938_at	NM_001417																				
2.10	2.04	0.06	6.57E-01	8.79E-01	---	---	---	1567664_at	---																				
2.32	2.25	0.07	6.57E-01	8.79E-01	DPPA4	developmental pluripotency associated 4	chr3q13.13	232985_s_at	NM_018189																				
2.03	1.97	0.06	6.57E-01	8.79E-01	LOC283682	Hypothetical protein LOC283682	chr15q26.1-q26.2	1561247_at	XM_378544 /// XM_944000																				
3.20	3.03	0.17	6.57E-01	8.79E-01	LOC728264	hypothetical protein LOC728264	chr5q33.1	227183_at	XR_041006 /// XR_041007 /// XR_041008																				
5.71	5.52	0.19	6.57E-01	8.79E-01	IGSF11	immunoglobulin superfamily, member 11	chr3q13.32	228375_at	NM_001015887 /// NM_152538																				
4.76	4.65	0.10	6.57E-01	8.79E-01	GLYCTK	glycerate kinase	chr3p21.1	238518_x_at	NM_145262																				
4.42	4.32	0.10	6.57E-01	8.79E-01	TBX2	T-box 2	chr17q23	40560_at	NM_005994																				
2.65	2.61	0.04	6.57E-01	8.79E-01	KCNQ3	potassium voltage-gated channel, KQT-like subfamily, member 3	chr8q24	206573_at	NM_004519																				
6.10	6.00	0.10	6.58E-01	8.79E-01	ANGPTL4	angiopoietin-like 4	chr19p13.3	221009_s_at	NM_001039667 /// NM_139314																				
2.88	2.83	0.04	6.58E-01	8.79E-01	CGN	cingulin	chr1q21	223232_s_at	NM_020770																				
3.74	3.66	0.07	6.58E-01	8.79E-01	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	chr17p11.2	1552484_at	NM_144775																				
4.49	4.33	0.16	6.58E-01	8.79E-01	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	chr16q22	223786_at	NM_021615																				
3.08	2.93	0.15	6.58E-01	8.79E-01	ERO1LB	ERO1-like beta (S. cerevisiae)	chr1q42.2-q43	220012_at	NM_019891																				
1.80	1.76	0.05	6.58E-01	8.79E-01	KRT40	keratin 40	chr17q21.2	1562628_at	NM_182497																				
2.05	1.99	0.06	6.58E-01	8.79E-01	TAPT1	Transmembrane anterior posterior transformation 1	chr4p15.32	242318_at	NM_153365																				
2.12	2.07	0.05	6.58E-01	8.79E-01	LOC285500	hypothetical protein LOC285500	chr4q34.3	1558451_at	XM_496726 /// XM_939876																				
2.54	2.47	0.07	6.58E-01	8.79E-01	---	---	---	1566457_at	---																				
4.83	4.74	0.09	6.58E-01	8.79E-01	VANGL1	vang-like 1 (van gogh, Drosophila)	chr1p11-p13.1	219330_at	NM_138959																				
2.78	2.70	0.08	6.58E-01	8.79E-01	---	---	---	1563235_at	---																				
3.13	3.05	0.09	6.58E-01	8.79E-01	LOC338588	hypothetical LOC338588	chr10p15.1	1560472_at	XR_040266 /// XR_040267 /// XR_040268																				
5.25	5.09	0.16	6.59E-01	8.79E-01	LRRC40	leucine rich repeat containing 40	chr1p31.1	218577_at	NM_017768																				
2.95	2.89	0.06	6.59E-01	8.79E-01	---	---	---	234731_at	---																				
4.44	4.33	0.10	6.59E-01	8.79E-01	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	chr10q26.3	1554757_a_at	NM_005539																				

2.52	2.45	0.07	6.59E-01	8.79E-01	---	---	---	1559144_x_at	---
2.79	2.64	0.15	6.59E-01	8.80E-01	CLEC5A	C-type lectin domain family 5, member A	chr7q33	219890_at	NM_013252
7.81	7.69	0.11	6.59E-01	8.80E-01	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19p13.3	564_at	NM_002067
1.90	1.86	0.05	6.59E-01	8.80E-01	---	---	---	240179_at	---
2.83	2.75	0.07	6.59E-01	8.80E-01	TCF25	transcription factor 25 (basic helix-loop-helix)	chr16q24.3	214704_at	NM_014972
8.43	8.31	0.12	6.59E-01	8.80E-01	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	chr10q26	201457_x_at	NM_001007793 /// NM_004725
5.78	5.69	0.09	6.59E-01	8.80E-01	ADRBK1	adrenergic, beta, receptor kinase 1	chr11q13.1	38447_at	NM_001619
9.53	9.45	0.09	6.59E-01	8.80E-01	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	chr3q26.33	203621_at	NM_002492
4.44	4.35	0.10	6.59E-01	8.80E-01	C16orf75	chromosome 16 open reading frame 75	chr16p13.13	226456_at	NM_152308
3.84	3.75	0.09	6.59E-01	8.80E-01	AKAP8L	A kinase (PRKA) anchor protein 8-like	chr19p13.12	240554_at	NM_014371
2.42	2.36	0.07	6.59E-01	8.80E-01	TSGA14	Testis specific, 14	chr7q32	1563997_at	NM_018718
2.95	2.88	0.07	6.59E-01	8.80E-01	---	---	---	1566041_at	---
3.41	3.28	0.13	6.59E-01	8.80E-01	MAPK14	mitogen-activated protein kinase 14	chr6p21.3-p21.2	211087_x_at	NM_001315 /// NM_139012 /// NM_139013 /// NM_139014
7.49	7.41	0.09	6.59E-01	8.80E-01	PAAF1	proteasomal ATPase-associated factor 1	chr11q13.4	218957_s_at	NM_025155
2.72	2.66	0.06	6.59E-01	8.80E-01	MDM4	Mdm4 p53 binding protein homolog (mouse)	chr1q32	241876_at	NM_002393
2.22	2.15	0.07	6.60E-01	8.80E-01	WDR20	WD repeat domain 20	chr14q32.31	1554549_a_at	NM_144574 /// NM_181291 /// NM_181302 /// NM_181308
2.46	2.40	0.06	6.60E-01	8.80E-01	---	---	---	243890_at	---
2.05	2.00	0.05	6.60E-01	8.80E-01	---	---	---	1562750_at	---
5.11	4.99	0.12	6.60E-01	8.80E-01	SPATA2	spermatogenesis associated 2	chr20q13.1-q13.2	204434_at	NM_006038
2.39	2.33	0.07	6.60E-01	8.80E-01	---	---	---	244405_s_at	---
5.14	5.04	0.10	6.60E-01	8.80E-01	---	---	---	238002_at	---
7.72	7.66	0.07	6.60E-01	8.80E-01	LOC100131861 /// SAMM50	hypothetical protein LOC100131861 /// sorting and assembly machinery component 50 homolog (S. cerevisiae)	chr22q13.31	201569_s_at	NM_015380 /// XM_001716418 /// XM_001724537 /// XM_001725780
2.11	2.05	0.06	6.60E-01	8.80E-01	LOC284952	hypothetical protein LOC284952	chr2p24.2	1557267_s_at	XM_001126137 /// XM_001722633
8.34	8.23	0.11	6.60E-01	8.80E-01	GSTP1	glutathione S-transferase pi 1	chr11q13	200824_at	NM_000852
2.83	2.74	0.08	6.60E-01	8.80E-01	---	---	---	216774_at	---
4.87	4.76	0.11	6.60E-01	8.80E-01	LIMD1	LIM domains containing 1	chr3p21.3	222762_x_at	NM_014240
2.08	2.03	0.05	6.60E-01	8.80E-01	RBM20	RNA binding motif protein 20	chr10q25.2	238763_at	NM_001134363 /// XM_001716119 /// XM_291671 /// XM_939337
2.19	2.14	0.06	6.60E-01	8.80E-01	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	chr13q13.3	1570153_at	NM_017826
7.69	7.57	0.12	6.60E-01	8.80E-01	MBNL1	muscleblind-like (Drosophila)	chr3q25	201153_s_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297
4.23	4.13	0.10	6.60E-01	8.80E-01	---	---	---	228207_at	---
2.43	2.37	0.06	6.60E-01	8.80E-01	---	---	---	241625_at	---

2.05	1.99	0.05	6.61E-01	8.81E-01	---	---	---	1560328_s_at	---
1.94	1.89	0.05	6.61E-01	8.81E-01	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	chr18q23	232132_at	NM_032510
2.57	2.51	0.06	6.61E-01	8.81E-01	---	---	---	1560659_at	---
2.91	2.84	0.07	6.61E-01	8.81E-01	FAM149A	family with sequence similarity 149, member A	chr4q35.2	222291_at	NM_001006655 /// NM_015398
2.65	2.58	0.07	6.61E-01	8.81E-01	---	---	---	1554219_at	---
2.03	1.98	0.04	6.61E-01	8.81E-01	LOC283079	hypothetical protein LOC283079	chr10p12.1	215929_at	---
2.85	2.79	0.06	6.61E-01	8.81E-01	41343	membrane-associated ring finger (C3HC4) 10	chr17q23.2	230824_at	NM_001100875 /// NM_152598
2.62	2.54	0.08	6.61E-01	8.81E-01	---	---	---	240855_at	---
2.96	2.90	0.06	6.61E-01	8.81E-01	---	---	---	230979_at	---
6.54	6.43	0.11	6.61E-01	8.81E-01	PAPD5	PAP associated domain containing 5	chr16q12.1	229043_at	NM_001040284 /// NM_001040285
5.21	5.13	0.09	6.61E-01	8.81E-01	C2orf27	chromosome 2 open reading frame 27	chr2q21.1-q21.2	206611_at	NM_013310
5.64	5.58	0.06	6.61E-01	8.81E-01	NFX1	nuclear transcription factor, X-box binding 1	chr9p13.3	202584_at	NM_002504 /// NM_147133 /// NM_147134
9.40	9.06	0.35	6.61E-01	8.81E-01	LDLR	low density lipoprotein receptor	chr19p13.3	202068_s_at	NM_000527
3.60	3.48	0.13	6.61E-01	8.81E-01	USP25	ubiquitin specific peptidase 25	chr21q11.2	223167_s_at	NM_013396
3.01	2.91	0.09	6.62E-01	8.81E-01	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	chr7p15.3	204680_s_at	NM_012294
2.16	2.09	0.07	6.62E-01	8.81E-01	---	---	---	238174_at	---
2.39	2.31	0.08	6.62E-01	8.81E-01	---	---	---	238934_at	---
2.74	2.66	0.09	6.62E-01	8.81E-01	SIGLEC6	sialic acid binding Ig-like lectin 6	chr19q13.3	210796_x_at	NM_001245 /// NM_198845 /// NM_198846
8.27	8.09	0.17	6.62E-01	8.81E-01	BDH2	3-hydroxybutyrate dehydrogenase, type 2	chr4q24	218285_s_at	NM_020139
2.40	2.34	0.06	6.62E-01	8.81E-01	FAM161A	family with sequence similarity 161, member A	chr2p15	1564467_at	NM_032180
5.29	4.93	0.35	6.62E-01	8.81E-01	---	---	---	1554007_at	---
5.10	4.86	0.24	6.62E-01	8.81E-01	DPP4	dipeptidyl-peptidase 4	chr2q24.3	203716_s_at	NM_001935
2.50	2.39	0.11	6.62E-01	8.81E-01	XIAP	X-linked inhibitor of apoptosis	chrXq25	206536_s_at	NM_001167
2.18	2.13	0.05	6.62E-01	8.81E-01	---	---	---	238358_x_at	---
4.10	3.97	0.13	6.62E-01	8.81E-01	MAMLD1	mastermind-like domain containing 1	chrXq28	205088_at	NM_005491
3.34	3.28	0.06	6.62E-01	8.81E-01	RPRD2	regulation of nuclear pre-mRNA domain containing 2	chr1q21.2	235415_at	NM_015203
3.15	3.09	0.06	6.62E-01	8.81E-01	DHRS12	Dehydrogenase/reductase (SDR family) member 12	chr13q14.3	231345_s_at	NM_001031719 /// NM_024705
3.85	3.70	0.15	6.62E-01	8.81E-01	MGC39821	hypothetical protein MGC39821	chr19p13.11	1555363_s_at	XR_041448 /// XR_041449 /// XR_041450
3.55	3.49	0.06	6.62E-01	8.81E-01	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	chr20q13.33	228230_at	NM_001037335 /// NM_033405
6.39	6.23	0.15	6.62E-01	8.81E-01	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	chr6q15	217823_s_at	NM_016021
2.65	2.60	0.05	6.62E-01	8.81E-01	LIPF	lipase, gastric	chr10q23.31	206334_at	NM_004190
3.06	2.99	0.07	6.62E-01	8.81E-01	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2	chr5q34	207352_s_at	NM_000813 /// NM_021911
6.08	5.84	0.24	6.62E-01	8.81E-01	---	---	---	239033_at	---
2.52	2.46	0.06	6.62E-01	8.81E-01	---	---	---	1562765_at	---
4.36	4.27	0.09	6.62E-01	8.81E-01	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	chr14q11.2	205897_at	NM_004554
6.11	5.97	0.14	6.62E-01	8.81E-01	DKC1	dyskeratosis congenita 1, dyskerin	chrXq28	201478_s_at	NM_001363
4.22	4.14	0.08	6.62E-01	8.81E-01	---	---	---	232749_at	---
5.62	5.52	0.10	6.63E-01	8.81E-01	TMEM88	transmembrane protein 88	chr17p13.1	229452_at	NM_203411
2.28	2.22	0.06	6.63E-01	8.81E-01	TRO	trophinin	chrXp11.22-p11.21	210882_s_at	NM_001039705 /// NM_016157 /// NM_177556
2.48	2.39	0.09	6.63E-01	8.81E-01	---	---	---	217108_at	---
2.55	2.48	0.07	6.63E-01	8.81E-01	---	---	---	1562463_at	---

2.44	2.34	0.09	6.63E-01	8.81E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	215025_at	NM_001007156 /// NM_001012338 /// NM_002530																				
4.29	4.20	0.09	6.63E-01	8.81E-01	TNK1	tyrosine kinase, non-receptor, 1	chr17p13.1	217149_x_at	NM_003985																				
2.51	2.45	0.06	6.63E-01	8.81E-01	---	---	---	241219_at	---																				
1.96	1.91	0.05	6.63E-01	8.81E-01	LOC100134769 /// LOC643955 /// ZNF479 /// ZNF733 /// ZNF734	similar to Zinc finger protein 679 /// zinc finger protein 479 pseudogene /// zinc finger protein 479 /// zinc finger protein 733 /// zinc finger protein 734	chr7p11.2 /// chr7q11.21	1554996_at	NM_033273 /// NR_003952 /// XM_001714591 /// XM_001715089 /// XM_001719979																				
4.70	4.60	0.10	6.63E-01	8.81E-01	CENTB2	centaurin, beta 2	chr3q29	212476_at	NM_012287																				
2.21	2.15	0.06	6.63E-01	8.81E-01	---	---	---	AFFX-r2-Bs-thr-M_s_at	---																				
2.73	2.68	0.05	6.63E-01	8.82E-01	---	---	---	242507_at	---																				
4.35	4.28	0.07	6.63E-01	8.82E-01	RFFL	Ring finger and FYVE-like domain containing 1	chr17q12	237919_at	NM_001017368 /// NM_057178																				
1.97	1.93	0.05	6.63E-01	8.82E-01	---	---	---	1568449_at	---																				
2.36	2.30	0.06	6.63E-01	8.82E-01	COL13A1	collagen, type XIII, alpha 1	chr10q22	211343_s_at	NM_001130103 /// NM_005203 /// NM_080798 /// NM_080799 /// NM_080800 /// NM_080801 /// NM_080802 /// NM_080803 /// NM_080804 /// NM_080805 /// NM_080806 /// NM_080807 /// NM_080808 /// NM_080809 /// NM_080810 /// NM_080811 /// NM_080812 /// NM_080813 /// NM_080814 /// NM_080815																				
5.38	5.24	0.14	6.63E-01	8.82E-01	MSL2L1	male-specific lethal 2-like 1 (Drosophila)	chr3q22.2	218733_at	NM_018133																				
3.52	3.43	0.09	6.63E-01	8.82E-01	---	---	---	237078_at	---																				
2.24	2.19	0.06	6.63E-01	8.82E-01	C9orf93	Chromosome 9 open reading frame 93	chr9p22.3	1556516_at	NM_173550																				
4.26	4.08	0.18	6.63E-01	8.82E-01	---	---	---	1556194_a_at	---																				
4.40	4.32	0.09	6.63E-01	8.82E-01	---	---	---	241351_at	---																				
4.28	4.20	0.08	6.63E-01	8.82E-01	---	---	---	238672_at	---																				
6.48	6.37	0.11	6.63E-01	8.82E-01	UCK1	uridine-cytidine kinase 1	chr9q34.13	223141_at	NM_031432																				
2.11	2.02	0.10	6.64E-01	8.82E-01	---	---	---	234581_at	---																				

7.05	6.95	0.11	6.64E-01	8.82E-01	LOC648245	hypothetical LOC648245	chr9q34.3	227739_at	XM_001715437 /// XM_001720502 /// XM_001723031																			
7.05	6.97	0.08	6.64E-01	8.82E-01	JARID1B	jumonji, AT rich interactive domain 1B	chr1q32.1	211202_s_at	NM_006618																			
3.25	3.17	0.08	6.64E-01	8.82E-01	MSLN	mesothelin	chr16p13.3	204885_s_at	NM_005823 /// NM_013404																			
3.08	2.94	0.14	6.64E-01	8.82E-01	SFRS11	splicing factor, arginine/serine-rich 11	chr1p31	200685_at	NM_004768																			
3.30	3.21	0.09	6.64E-01	8.82E-01	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	chr12q24.2	210787_s_at	NM_006549 /// NM_153499 /// NM_153500 /// NM_172214 /// NM_172215 /// NM_172216 /// NM_172226																			
8.18	8.10	0.07	6.64E-01	8.82E-01	SCPEP1	serine carboxypeptidase 1	chr17q22	218217_at	NM_021626																			
2.32	2.26	0.06	6.64E-01	8.82E-01	FLJ38773	hypothetical protein FLJ38773	chr20q11.22	1559614_at	XR_001008 /// XR_001422																			
2.20	2.15	0.05	6.64E-01	8.82E-01	FOXP2	forkhead box P2	chr7q31	1562139_a_at	NM_014491 /// NM_148898 /// NM_148899																			
5.06	4.67	0.40	6.64E-01	8.82E-01	---	---	---	233401_at	---																			
8.98	8.89	0.09	6.64E-01	8.82E-01	C11orf59	chromosome 11 open reading frame 59	chr11q13.4	223009_at	NM_017907																			
1.93	1.88	0.05	6.64E-01	8.82E-01	KCNH5	potassium voltage-gated channel, subfamily H (eag-related), member 5	chr14q23.1	242502_at	NM_139318 /// NM_172375 /// NM_172376																			
3.25	3.19	0.06	6.64E-01	8.82E-01	---	---	---	215180_at	---																			
7.04	6.94	0.10	6.64E-01	8.82E-01	RAD23A	RAD23 homolog A (S. cerevisiae)	chr19p13.2	201039_s_at	NM_005053																			
3.53	3.46	0.07	6.64E-01	8.82E-01	IGHE	immunoglobulin heavy constant epsilon	chr14q32.33	234373_x_at	---																			
2.93	2.87	0.06	6.64E-01	8.82E-01	---	---	---	243921_at	---																			
4.43	4.33	0.10	6.64E-01	8.82E-01	C1orf96	chromosome 1 open reading frame 96	chr1q42.13	225904_at	NM_145257																			
5.64	5.54	0.10	6.65E-01	8.82E-01	LOC441642	similar to hCG27427	chr12q21.2	234254_at	XM_001714198 /// XM_001724644 /// XM_001726036																			
2.41	2.36	0.05	6.65E-01	8.82E-01	---	---	---	1562112_at	---																			
3.27	3.20	0.07	6.65E-01	8.82E-01	ACPP	acid phosphatase, prostate	chr3q21-q23	237030_at	NM_001099 /// NM_001134194																			
2.03	1.96	0.06	6.65E-01	8.82E-01	GABRA2	gamma-aminobutyric acid (GABA) A receptor, alpha 2	chr4p12	1554308_s_at	NM_000807 /// NM_001114175																			
7.50	7.43	0.07	6.65E-01	8.82E-01	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	chr4q35	202825_at	NM_001151																			
3.53	3.44	0.09	6.65E-01	8.82E-01	---	---	---	242994_at	---																			
6.23	6.12	0.11	6.65E-01	8.82E-01	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	chr12q21.33-q23.1	209833_at	NM_003805																			
12.11	12.04	0.07	6.65E-01	8.82E-01	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	chr12p13	212581_x_at	NM_002046																			

3.53	3.41	0.12	6.65E-01	8.82E-01	GABPB1 /// RP11-68I18.1	GA binding protein transcription factor, beta subunit 2 /// hypothetical protein MGC29891	chr15q21.2 /// chr1q21.2	206173_x_at	NM_002041 /// NM_005254 /// NM_016654 /// NM_016655 /// NM_144618 /// NM_181427																				
5.42	5.30	0.12	6.65E-01	8.82E-01	NSUN3	NOL1/NOP2/Sun domain family, member 3	chr3q11.2	219458_s_at	NM_022072																				
3.83	3.73	0.10	6.65E-01	8.82E-01	NEURL2	neuralized homolog 2 (Drosophila)	chr20q13.12	230283_at	NM_080749																				
3.69	3.56	0.13	6.65E-01	8.82E-01	---	---	---	230734_x_at	---																				
3.92	3.81	0.11	6.65E-01	8.83E-01	POLN	polymerase (DNA directed) nu	chr4p16.3	242804_at	NM_181808																				
5.84	5.69	0.14	6.65E-01	8.83E-01	CIAPIN1	cytokine induced apoptosis inhibitor 1	chr16q13-q21	208424_s_at	NM_020313																				
3.05	2.96	0.10	6.65E-01	8.83E-01	NPHP1	nephronophthisis 1 (juvenile)	chr2q13	238844_s_at	NM_000272 /// NM_001128178 /// NM_001128179 /// NM_207181																				
2.27	2.21	0.06	6.65E-01	8.83E-01	---	---	---	216414_at	---																				
5.08	4.96	0.12	6.65E-01	8.83E-01	MARCKS	myristoylated alanine-rich protein kinase C substrate	chr6q22.2	213002_at	NM_002356																				
2.75	2.70	0.05	6.66E-01	8.83E-01	---	---	---	234497_s_at	---																				
3.79	3.69	0.10	6.66E-01	8.83E-01	NCOA3	nuclear receptor coactivator 3	chr20q12	209062_x_at	NM_006534 /// NM_181659																				
5.24	5.05	0.19	6.66E-01	8.83E-01	PRKCH	protein kinase C, eta	chr14q22-q23	218764_at	NM_006255																				
2.38	2.28	0.10	6.66E-01	8.83E-01	---	---	---	1562610_at	---																				
3.57	3.48	0.09	6.66E-01	8.83E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	213375_s_at	NM_001079691 /// NM_052818																				
3.38	3.26	0.12	6.66E-01	8.83E-01	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	chr1p22.3	203017_s_at	NM_014021																				
6.68	6.60	0.08	6.66E-01	8.83E-01	KIF9	kinesin family member 9	chr3p21.31	231319_x_at	NM_022342 /// NM_182902 /// NM_182903																				
2.80	2.68	0.12	6.66E-01	8.83E-01	BMS1P5	BMS1 pseudogene 5	chr10q11.22	238924_at	NR_003611																				
5.45	5.30	0.15	6.66E-01	8.83E-01	TSEN15	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	chr1q25	225399_at	NM_001127394 /// NM_052965 /// NR_023349																				
5.58	5.46	0.13	6.66E-01	8.83E-01	TRIM34 /// TRIM6 /// TRIM6-TRIM34	tripartite motif-containing 34 /// tripartite motif-containing 6 /// TRIM6-TRIM34	chr11p15 /// chr11p15.4	221044_s_at	NM_001003818 /// NM_001003819 /// NM_001003827 /// NM_021616 /// NM_058166 /// NM_130389 /// NM_130390																				
5.47	5.34	0.13	6.66E-01	8.83E-01	LOC147343	hypothetical protein LOC147343	chr18q21.1	236110_at	---																				
6.53	6.35	0.17	6.66E-01	8.83E-01	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	chr11q22	202169_s_at	NM_015423																				
6.20	6.13	0.07	6.66E-01	8.83E-01	HERPUD2	HERPUD family member 2	chr7p14.2	1552628_a_at	NM_022373 /// XM_001716505 /// XM_001717741 /// XM_001717961 /// XM_001718593																				
2.42	2.34	0.09	6.66E-01	8.83E-01	AGR2	anterior gradient homolog 2 (Xenopus laevis)	chr7p21.3	209173_at	NM_006408																				
3.67	3.60	0.08	6.66E-01	8.83E-01	BCL6B	B-cell CLL/lymphoma 6, member B (zinc finger protein)	chr17p13.1	1554625_at	NM_181844																				
2.06	2.02	0.05	6.66E-01	8.83E-01	CCL28	chemokine (C-C motif) ligand 28	chr5p12	224027_at	NM_148672																				
2.21	2.16	0.05	6.66E-01	8.83E-01	---	---	---	217423_at	---																				

4.60	4.51	0.09	6.66E-01	8.83E-01	SGPL1	sphingosine-1-phosphate lyase 1	chr10q21	212321_at	NM_003901
4.65	4.57	0.07	6.66E-01	8.83E-01	---	---	---	244149_at	---
4.16	3.92	0.23	6.66E-01	8.83E-01	---	---	---	242751_at	---
2.52	2.38	0.13	6.66E-01	8.83E-01	RBM39	RNA binding motif protein 39	chr20q11.22	226404_at	NM_004902 /// NM_184234
2.60	2.52	0.08	6.67E-01	8.83E-01	TET1	tet oncogene 1	chr10q21	228906_at	NM_030625
4.96	4.85	0.11	6.67E-01	8.83E-01	---	---	---	232681_at	---
3.33	3.13	0.20	6.67E-01	8.83E-01	JAM3	junctional adhesion molecule 3	chr11q25	231721_at	NM_032801
2.09	2.04	0.05	6.67E-01	8.83E-01	ORC5L	origin recognition complex, subunit 5-like (yeast)	chr7q22.1	211213_at	NM_002553 /// NM_181747
2.38	2.31	0.07	6.67E-01	8.83E-01	C15orf51	chromosome 15 open reading frame 51	chr15q26.3	231318_at	NR_003260
3.17	3.11	0.06	6.67E-01	8.83E-01	ASAH3	N-acylsphingosine amidohydrolase (alkaline ceramidase) 3	chr19p13.3	1553929_at	NM_133492
4.04	3.92	0.12	6.67E-01	8.83E-01	---	---	---	230461_s_at	---
2.37	2.30	0.08	6.67E-01	8.83E-01	GRIA3	glutamate receptor, ionotrophic, AMPA 3	chrXq25-q26	206730_at	NM_000828 /// NM_007325
2.30	2.23	0.06	6.67E-01	8.83E-01	CDR1	cerebellar degeneration-related protein 1, 34kDa	chrXq27.1-q27.2	207276_at	NM_004065
3.17	3.09	0.08	6.67E-01	8.83E-01	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	chr3q22.3	219149_x_at	NM_016216
5.90	5.76	0.13	6.67E-01	8.83E-01	MARVELD1	MARVEL domain containing 1	chr10q24.2	223095_at	XR_041875 /// XR_041876 /// XR_041877
6.74	6.62	0.12	6.67E-01	8.83E-01	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	chr4q32.1	203097_s_at	NM_014247
4.61	4.54	0.07	6.67E-01	8.83E-01	LOC146325	similar to hypothetical protein FLJ13841	chr16p13.3	1553826_a_at	NM_145270
3.18	3.11	0.08	6.67E-01	8.83E-01	---	---	---	242368_at	---
3.62	3.47	0.15	6.67E-01	8.83E-01	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	chr15q24	202986_at	NM_014862
2.52	2.44	0.08	6.67E-01	8.83E-01	LOC284837	hypothetical protein LOC284837	chr21q22.3	1563088_a_at	XR_041150 /// XR_041151 /// XR_041152
2.13	2.08	0.05	6.67E-01	8.83E-01	EMX2	empty spiracles homeobox 2	chr10q26.1	221950_at	NM_004098
4.71	4.58	0.13	6.67E-01	8.83E-01	LRRC33	leucine rich repeat containing 33	chr3q29	235359_at	NM_198565
2.45	2.40	0.06	6.67E-01	8.84E-01	LOC100131316	Hypothetical protein LOC100131316	chr2q21.3	243355_at	XM_001717835 /// XM_001717991 /// XM_001718000
2.45	2.39	0.06	6.67E-01	8.84E-01	---	---	---	234252_at	---
2.35	2.29	0.05	6.67E-01	8.84E-01	MEI1	meiosis inhibitor 1	chr22q13.2	1564621_a_at	NM_152513
2.77	2.69	0.07	6.67E-01	8.84E-01	CABP5	calcium binding protein 5	chr19q13.33	221160_s_at	NM_019855
2.41	2.33	0.08	6.67E-01	8.84E-01	C1orf100	chromosome 1 open reading frame 100	chr1q44	237603_at	NM_001012970
9.85	9.77	0.09	6.67E-01	8.84E-01	GAS5	growth arrest-specific 5 (non-protein coding)	chr1q25.1	224741_x_at	NR_002578
2.14	2.08	0.06	6.68E-01	8.84E-01	LOC641365	hypothetical protein LOC641365	chr4q28-q31	1561098_at	XR_001033 /// XR_001034 /// XR_001258 /// XR_001259
3.17	3.05	0.12	6.68E-01	8.84E-01	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	1556820_a_at	NR_002612
3.16	3.10	0.07	6.68E-01	8.84E-01	---	---	---	1558877_at	---
2.60	2.52	0.08	6.68E-01	8.84E-01	TOR1A	torsin family 1, member A (torsin A)	chr9q34	1554849_at	NM_000113
2.75	2.68	0.07	6.68E-01	8.84E-01	BTN2A1	butyrophilin, subfamily 2, member A1	chr6p22.1	244063_at	NM_007049 /// NM_078476
2.82	2.75	0.07	6.68E-01	8.84E-01	---	---	---	1560966_at	---
2.07	2.01	0.06	6.68E-01	8.84E-01	---	---	---	224127_at	---
1.90	1.85	0.05	6.68E-01	8.84E-01	LOC100131637	hypothetical protein LOC100131637	chr8q21.2	222051_s_at	XM_001716033 /// XM_001716143 /// XM_001716209
3.79	3.64	0.14	6.68E-01	8.84E-01	CRLS1	Cardiolipin synthase 1	chr20p13-p12.3	237502_at	NM_001127458 /// NM_019095
3.88	3.73	0.15	6.68E-01	8.84E-01	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	chr8q12.3	203560_at	NM_003878
3.44	3.40	0.05	6.68E-01	8.84E-01	EDAR	ectodysplasin A receptor	chr2q11-q13	220048_at	NM_022336
7.29	7.16	0.12	6.68E-01	8.84E-01	MPHOSPH6	M-phase phosphoprotein 6	chr16q23.3	203740_at	NM_005792
2.68	2.59	0.09	6.68E-01	8.84E-01	---	---	---	1569201_a_at	---

9.63	9.42	0.21	6.68E-01	8.84E-01	CXCR4	chemokine (C-X-C motif) receptor 4	chr2q21	209201_x_at	NM_001008540 /// NM_003467																					
3.80	3.71	0.09	6.69E-01	8.84E-01	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	chr2q11.2	204553_x_at	NM_001134224 /// NM_001134225 /// NM_001566 /// NM_004027																					
2.24	2.17	0.07	6.69E-01	8.84E-01	PGM5P1	phosphoglucomutase 5 pseudogene 1	chr9q12	1560431_at	---																					
2.56	2.48	0.08	6.69E-01	8.84E-01	IPO11	importin 11	chr5q12.1	234304_s_at	NM_016338																					
6.30	6.24	0.06	6.69E-01	8.84E-01	ZNF622	zinc finger protein 622	chr5p15.1	225152_at	NM_033414																					
4.44	4.36	0.07	6.69E-01	8.84E-01	C6orf106	chromosome 6 open reading frame 106	chr6p21.31	217924_at	NM_022758 /// NM_024294																					
1.89	1.82	0.07	6.69E-01	8.84E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	1555435_at	NM_014423																					
8.58	8.36	0.22	6.69E-01	8.84E-01	AS3MT	arsenic (+3 oxidation state) methyltransferase	chr10q24.32	223652_at	NM_020682																					
1.96	1.90	0.05	6.69E-01	8.84E-01	CENPI	centromere protein I	chrXq22.1	1563223_a_at	NM_006733																					
5.70	5.54	0.16	6.69E-01	8.84E-01	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	chr6q22.31	203427_at	NM_014034																					
2.60	2.55	0.05	6.69E-01	8.84E-01	JMJD5	Jumonji domain containing 5	chr16p12.1	237229_at	NM_024773																					
5.35	5.19	0.16	6.69E-01	8.84E-01	INSR	insulin receptor	chr19p13.3-p13.2	226212_s_at	NM_000208 /// NM_001079817																					
4.01	3.95	0.06	6.69E-01	8.84E-01	KIAA0664	KIAA0664	chr17p13.3	243258_at	NM_015229																					
1.99	1.94	0.04	6.69E-01	8.84E-01	---	---	---	1562677_at	---																					
2.17	2.12	0.05	6.69E-01	8.84E-01	ZNF208	zinc finger protein 208	chr19p12	1568646_x_at	NM_007153																					
6.15	5.97	0.18	6.69E-01	8.84E-01	CCDC50	coiled-coil domain containing 50	chr3q28	226713_at	NM_174908 /// NM_178335																					
2.02	1.96	0.06	6.69E-01	8.84E-01	FLJ41747	hypothetical gene supported by AK123741	chr12q13.13	239153_at	---																					
5.68	5.49	0.19	6.69E-01	8.84E-01	TMEM161B	transmembrane protein 161B	chr5q14.3	227861_at	NM_153354																					
7.92	7.74	0.19	6.69E-01	8.84E-01	SF3B1	splicing factor 3b, subunit 1, 155kDa	chr2q33.1	211185_s_at	NM_001005526 /// NM_012433																					
5.78	5.57	0.21	6.69E-01	8.84E-01	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	chr3p12-q12	223217_s_at	NM_001005474 /// NM_031419																					
5.19	5.03	0.16	6.69E-01	8.84E-01	WDR5	WD repeat domain 5	chr9q34	225170_at	NM_017588 /// NM_052821																					
3.88	3.76	0.12	6.69E-01	8.84E-01	FAM78A	family with sequence similarity 78, member A	chr9q34	227002_at	NM_033387																					
7.58	7.48	0.10	6.69E-01	8.84E-01	NDFIP1	Nedd4 family interacting protein 1	chr5q31.3	217800_s_at	NM_030571																					
6.73	6.57	0.16	6.69E-01	8.84E-01	HECTD3	HECT domain containing 3	chr1p34.1	218632_at	NM_024602																					
2.65	2.58	0.07	6.69E-01	8.84E-01	---	---	---	244388_at	---																					
7.95	7.84	0.11	6.69E-01	8.84E-01	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	chr3q13.2	221492_s_at	NM_022488																					
2.81	2.74	0.07	6.69E-01	8.84E-01	---	---	---	1556620_at	---																					
3.58	3.48	0.10	6.69E-01	8.84E-01	GPR157	G protein-coupled receptor 157	chr1p36.23	220901_at	NM_024980																					
6.05	5.95	0.10	6.70E-01	8.84E-01	DAGLB	diacylglycerol lipase, beta	chr7p22.1	226640_at	NM_139179																					
2.34	2.28	0.07	6.70E-01	8.84E-01	---	---	---	241057_x_at	---																					
2.16	2.12	0.05	6.70E-01	8.84E-01	LOC286123	hypothetical protein LOC286123	chr8q24.3	1564601_at	---																					
2.66	2.59	0.06	6.70E-01	8.84E-01	---	---	---	233788_at	---																					
1.88	1.83	0.04	6.70E-01	8.85E-01	KCTD4	potassium channel tetramerisation domain containing 4	chr13q14.12	240512_x_at	NM_198404																					
6.52	6.43	0.09	6.70E-01	8.85E-01	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	chr19p13.3	228278_at	NM_002501																					
2.66	2.59	0.07	6.70E-01	8.85E-01	NKX3-2	NK3 homeobox 2	chr4p16.1	207031_at	NM_001189																					
4.62	4.45	0.18	6.70E-01	8.85E-01	KREMEN1	kringle containing transmembrane protein 1	chr22q12.1	227250_at	NM_001039570 /// NM_001039571																					
5.20	4.99	0.21	6.70E-01	8.85E-01	ACSS3	acyl-CoA synthetase short-chain family member 3	chr12q21.31	229222_at	NM_024560																					
3.44	3.34	0.10	6.70E-01	8.85E-01	---	---	---	230234_at	---																					
4.22	3.98	0.24	6.70E-01	8.85E-01	---	---	---	1569208_a_at	---																					
3.52	3.44	0.08	6.70E-01	8.85E-01	---	---	---	1563404_at	---																					
6.68	6.58	0.10	6.70E-01	8.85E-01	SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	chr16q22.1	209402_s_at	NM_005072																					
2.13	2.08	0.05	6.70E-01	8.85E-01	FANCD2	Fanconi anemia, complementation group D2	chr3p26	1568889_at	NM_001018115 /// NM_033084																					
7.49	7.26	0.23	6.70E-01	8.85E-01	IER3	immediate early response 3	chr6p21.3	201631_s_at	NM_003897																					
3.10	3.00	0.10	6.70E-01	8.85E-01	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	chr20p12	211925_s_at	NM_015192 /// NM_182734																					

3.03	2.96	0.06	6.70E-01	8.85E-01	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	chr11p15.5	219533_at	NM_000076 /// NM_001122630 /// NM_001122631
2.60	2.50	0.10	6.70E-01	8.85E-01	---	---	---	242267_x_at	---
3.34	3.22	0.12	6.70E-01	8.85E-01	HBB /// HBD	hemoglobin, beta /// hemoglobin, delta	chr11p15.5	206834_at	NM_000518 /// NM_000519
4.94	4.79	0.14	6.70E-01	8.85E-01	TATDN3	TatD DNase domain containing 3	chr1q32.3	228867_at	NM_001042552 /// NM_001042553
1.91	1.87	0.04	6.71E-01	8.85E-01	RNF6	ring finger protein (C3H2C3 type) 6	chr13q12.2	210931_at	NM_005977 /// NM_183043 /// NM_183044
5.21	4.94	0.28	6.71E-01	8.85E-01	HSPA6	heat shock 70kDa protein 6 (HSP70B')	chr1q23	213418_at	NM_002155
4.49	4.39	0.10	6.71E-01	8.85E-01	MOCS3	molybdenum cofactor synthesis 3	chr20q13.13	206141_at	NM_014484
7.31	7.16	0.15	6.71E-01	8.85E-01	COPZ2	coatomer protein complex, subunit zeta 2	chr17q21.32	219561_at	NM_016429
6.16	6.07	0.09	6.71E-01	8.85E-01	TOM1	target of myb1 (chicken)	chr22q13.1	202807_s_at	NM_005488
2.44	2.37	0.06	6.71E-01	8.85E-01	DBF4B	DBF4 homolog B (S. cerevisiae)	chr17q21.31|17q21	238757_at	NM_025104 /// NM_145663
4.10	4.05	0.05	6.71E-01	8.85E-01	TBC1D2B	TBC1 domain family, member 2B	chr15q24.3-q25.1	215640_at	NM_015079 /// NM_144572
2.49	2.43	0.06	6.71E-01	8.85E-01	CCDC150	coiled-coil domain containing 150	chr2q33.1	1553459_at	NM_001080539
5.88	5.69	0.19	6.71E-01	8.85E-01	ARL1	ADP-ribosylation factor-like 1	chr12q23.2	201657_at	NM_001177
4.92	4.81	0.12	6.71E-01	8.85E-01	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	chr1q42.13	203723_at	NM_002221
3.21	3.13	0.08	6.71E-01	8.85E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	215115_x_at	NM_001007156 /// NM_001012338 /// NM_002530
2.26	2.21	0.06	6.71E-01	8.85E-01	---	---	---	1562162_at	---
2.97	2.92	0.05	6.71E-01	8.85E-01	LOC400604	hypothetical gene supported by BC039664	chr17q21.33	241405_at	---
5.81	5.69	0.12	6.71E-01	8.85E-01	NENF	neuron derived neurotrophic factor	chr1q32.3	214075_at	NM_013349
2.16	2.10	0.05	6.71E-01	8.85E-01	---	---	---	1556617_a_at	---
2.13	2.07	0.06	6.71E-01	8.85E-01	---	---	---	244306_at	---
4.39	4.33	0.06	6.71E-01	8.85E-01	C1orf20	chromosome 1 open reading frame 20	chr1q25	216186_at	---
7.86	7.61	0.25	6.71E-01	8.85E-01	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	chr5q31	202363_at	NM_004598
2.50	2.40	0.11	6.71E-01	8.85E-01	ZDHHC21	Zinc finger, DHHC-type containing 21	chr9p22.3	243835_at	NM_178566
2.42	2.37	0.05	6.71E-01	8.85E-01	---	---	---	1559777_at	---
2.24	2.18	0.06	6.71E-01	8.85E-01	KIN	KIN, antigenic determinant of recA protein homolog (mouse)	chr10p15-p14	236887_at	NM_012311
2.10	2.04	0.06	6.71E-01	8.85E-01	NEK2	NIMA (never in mitosis gene a)-related kinase 2	chr1q32.2-q41	204641_at	NM_002497
4.44	4.34	0.10	6.71E-01	8.85E-01	LOXL4	lysyl oxidase-like 4	chr10q24	227145_at	NM_032211
3.08	3.02	0.06	6.72E-01	8.85E-01	C20orf120	chromosome 20 open reading frame 120	---	233962_at	---
5.80	5.42	0.38	6.72E-01	8.85E-01	ANGPTL1	angiopoietin-like 1	chr1q25.2	224339_s_at	NM_004673
4.37	4.25	0.13	6.72E-01	8.85E-01	ZNF498	zinc finger protein 498	chr7q22.1	242621_at	NM_145115
9.01	8.95	0.06	6.72E-01	8.85E-01	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	chr12q22	201524_x_at	NM_003348
2.63	2.55	0.08	6.72E-01	8.85E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	240913_at	NM_000141 /// NM_022970
3.06	2.99	0.07	6.72E-01	8.85E-01	PSG1 /// PSG3	pregnancy specific beta-1-glycoprotein 1 /// pregnancy specific beta-1-glycoprotein 3	chr19q13.2	215821_x_at	NM_006905 /// NM_021016
6.55	6.46	0.10	6.72E-01	8.85E-01	DGCR6 /// DGCR6L	DiGeorge syndrome critical region gene 6 /// DiGeorge syndrome critical region gene 6-like	chr22q11 /// chr22q11.21|22q11	208024_s_at	NM_005675 /// NM_033257
3.79	3.69	0.10	6.72E-01	8.85E-01	METTL6	methyltransferase like 6	chr3p24.3	1553689_s_at	NM_152396
5.31	5.25	0.06	6.72E-01	8.85E-01	NHEJ1	nonhomologous end-joining factor 1	chr2q35	219418_at	NM_024782
6.11	6.02	0.09	6.72E-01	8.85E-01	AEN	apoptosis enhancing nuclease	chr15q26.1	219361_s_at	NM_022767
7.05	6.95	0.10	6.72E-01	8.85E-01	ALG8	asparagine-linked glycosylation 8 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)	chr11q14.1	203545_at	NM_001007027 /// NM_024079
8.08	8.02	0.07	6.72E-01	8.85E-01	LMNA	lamin A/C	chr1q21.2-q21.3	1554600_s_at	NM_005572 /// NM_170707 /// NM_170708

4.31	4.15	0.16	6.72E-01	8.85E-01	---	---	---	237586_at	---
4.01	3.94	0.07	6.72E-01	8.85E-01	CXorf39	chromosome X open reading frame 39	chrXq22.2	242781_at	NM_207318
4.15	4.09	0.06	6.72E-01	8.85E-01	---	---	---	242327_x_at	---
1.90	1.85	0.05	6.72E-01	8.85E-01	---	---	---	1566202_at	---
2.59	2.52	0.07	6.72E-01	8.85E-01	PKD1L2	polycystic kidney disease 1-like 2	chr16q23.2	1561849_at	NM_001076780 /// NM_052892
2.86	2.81	0.05	6.72E-01	8.85E-01	NELL1	NEL-like 1 (chicken)	chr11p15.2-p15.1	206089_at	NM_006157
2.33	2.27	0.06	6.72E-01	8.85E-01	LOC401022	hypothetical LOC401022	chr2q31.2	242042_s_at	---
2.35	2.27	0.07	6.72E-01	8.85E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	215118_s_at	---
2.22	2.16	0.06	6.72E-01	8.85E-01	DNAH6 /// DNHL1 /// LOC200383	dynein, axonemal, heavy chain 6 /// dynein heavy chain-like 1 /// similar to Dynein heavy chain at 16F	chr2p11.2	234893_s_at	NM_001370 /// NM_173645
2.61	2.55	0.06	6.73E-01	8.86E-01	---	---	---	208039_at	---
2.67	2.62	0.05	6.73E-01	8.86E-01	C10orf75	Chromosome 10 open reading frame 75	chr10q24.31	232230_at	XR_041970 /// XR_041971 /// XR_041972
2.11	2.04	0.07	6.73E-01	8.86E-01	---	---	---	242703_at	---
4.43	4.36	0.08	6.73E-01	8.86E-01	JRKL	jerky homolog-like (mouse)	chr11q21	206734_at	NM_003772
5.09	4.79	0.30	6.73E-01	8.86E-01	FGFR1OP2	FGFR1 oncogene partner 2	chr12p11.23	223263_s_at	NM_015633
3.01	2.96	0.05	6.73E-01	8.86E-01	LOC440356	hypothetical LOC440356	chr16p11.2	240537_s_at	XR_040481 /// XR_040482 /// XR_040483
3.77	3.60	0.17	6.73E-01	8.86E-01	GPM6A	glycoprotein M6A	chr4q34	209469_at	NM_005277 /// NM_201591 /// NM_201592
4.16	4.08	0.08	6.73E-01	8.86E-01	WNK2	WNK lysine deficient protein kinase 2	chr9q22.3	229547_s_at	NM_006648
1.98	1.93	0.05	6.73E-01	8.86E-01	LOC203547	hypothetical protein LOC203547	chrXq28	242474_s_at	NM_001017980
3.61	3.56	0.05	6.73E-01	8.86E-01	CASP10	caspase 10, apoptosis-related cysteine peptidase	chr2q33-q34	210955_at	NM_001230 /// NM_032974 /// NM_032977
5.70	5.63	0.07	6.73E-01	8.86E-01	CAMK1D	calcium/calmodulin-dependent protein kinase ID	chr10p13	235626_at	NM_020397 /// NM_153498
2.46	2.40	0.06	6.73E-01	8.86E-01	CRISP1	cysteine-rich secretory protein 1	chr6p21.3	207032_s_at	NM_001131 /// NM_170609
2.74	2.66	0.07	6.73E-01	8.86E-01	OR1C1	olfactory receptor, family 1, subfamily C, member 1	chr1q44	1567054_at	NM_012353
2.72	2.63	0.08	6.73E-01	8.86E-01	---	---	---	241216_at	---
2.13	2.08	0.05	6.73E-01	8.86E-01	TXNDC13	thioredoxin domain containing 13	chr20p12	216027_at	NM_021156
4.95	4.69	0.25	6.73E-01	8.86E-01	PLK2	polo-like kinase 2 (Drosophila)	chr5q12.1-q13.2	201939_at	NM_006622
2.31	2.25	0.06	6.73E-01	8.86E-01	---	---	---	242709_s_at	---
5.94	5.83	0.11	6.73E-01	8.86E-01	CRABP2	cellular retinoic acid binding protein 2	chr1q21.3	202575_at	NM_001878
3.17	3.11	0.06	6.73E-01	8.86E-01	ITGAD	integrin, alpha D	chr16p11.2	1560686_at	NM_005353
5.81	5.56	0.25	6.73E-01	8.86E-01	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	chr1q32.1	217196_s_at	NM_203459
3.08	3.01	0.07	6.73E-01	8.86E-01	FLJ41278	hypothetical gene supported by AK123272	chr12q14.3	215186_at	XM_001129851 /// XM_001133877 /// XM_001723805
4.07	3.98	0.08	6.73E-01	8.86E-01	---	---	---	1569579_at	---
7.14	6.97	0.17	6.73E-01	8.86E-01	MSI2	musashi homolog 2 (Drosophila)	chr17q22	225237_s_at	NM_138962 /// NM_170721
5.56	5.45	0.11	6.73E-01	8.86E-01	JMJD3	jumonji domain containing 3, histone lysine demethylase	chr17p13.1	1556066_at	NM_001080424
2.19	2.13	0.07	6.73E-01	8.86E-01	C18orf2	chromosome 18 open reading frame 2	---	224181_at	NM_031416 /// NR_023925 /// NR_023926 /// NR_023927 /// NR_023928
3.87	3.79	0.08	6.74E-01	8.86E-01	GSDMC	gasdermin C	chr8q24.1-q24.2	234305_s_at	NM_031415

3.51	3.38	0.13	6.74E-01	8.86E-01	GPC6	Glypican 6	chr13q32	227059_at	NM_005708
2.58	2.53	0.05	6.74E-01	8.86E-01	---	---	---	217569_x_at	---
6.80	6.70	0.10	6.74E-01	8.86E-01	RPS15A	Ribosomal protein S15a	chr16p	235309_at	NM_001019 /// NM_001030009
4.59	4.51	0.08	6.74E-01	8.86E-01	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	chr2p24.1	209756_s_at	NM_005378
7.73	7.57	0.16	6.74E-01	8.86E-01	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	chr9p13-p12	200880_at	NM_001539
2.04	1.98	0.05	6.74E-01	8.86E-01	---	---	---	211187_at	---
2.69	2.62	0.07	6.74E-01	8.86E-01	LOC254028	hypothetical protein LOC254028	chr14q11.2	1562581_at	XR_040777 /// XR_040778 /// XR_040779
2.61	2.56	0.05	6.74E-01	8.86E-01	CRHR1	corticotropin releasing hormone receptor 1	chr17q12-q22	211897_s_at	NM_004382
4.58	4.48	0.10	6.74E-01	8.86E-01	SCYL3	SCY1-like 3 (S. cerevisiae)	chr1q24.2	205607_s_at	NM_020423 /// NM_181093
3.00	2.90	0.10	6.74E-01	8.86E-01	OSTM1	osteopetrosis associated transmembrane protein 1	chr6q21	243287_s_at	NM_014028
8.91	8.78	0.13	6.74E-01	8.86E-01	HIBADH	3-hydroxyisobutyrate dehydrogenase	chr7p15.2	224812_at	NM_152740
6.61	6.55	0.06	6.74E-01	8.86E-01	PLXNA1	plexin A1	chr3q21.3	221537_at	NM_032242
7.79	7.74	0.05	6.74E-01	8.86E-01	UBE2NL	ubiquitin-conjugating enzyme E2N-like	chrXq27.3	217393_x_at	NM_001012989
2.24	2.18	0.06	6.74E-01	8.86E-01	PLCB4	phospholipase C, beta 4	chr20p12	203896_s_at	NM_000933 /// NM_182797
2.09	2.03	0.06	6.74E-01	8.86E-01	LOC286297	Hypothetical protein LOC286297	chr9q12	1564280_x_at	XM_372109 /// XM_933054 /// XM_933058
2.30	2.23	0.07	6.74E-01	8.86E-01	LOC729143	similar to Myosin phosphatase Rho-interacting protein (Rho-interacting protein 3) (M-RIP) (RIP3) (p116Rip)	chr3p21.32	241714_at	XR_015907 /// XR_015979 /// XR_037739
3.50	3.44	0.06	6.74E-01	8.86E-01	LSDP5	Lipid storage droplet protein 5	chr19p13.3	1560457_x_at	NM_001013706
2.92	2.79	0.14	6.74E-01	8.86E-01	CEP76	centrosomal protein 76kDa	chr18p11.21	52285_f_at	NM_024899
2.13	2.07	0.05	6.74E-01	8.86E-01	TKTL2	transketolase-like 2	chr4q32.3	223829_at	NM_032136
6.36	6.24	0.12	6.74E-01	8.86E-01	NT5C2	5'-nucleotidase, cytosolic II	chr10q24.32-q24.33	209155_s_at	NM_001134373 /// NM_012229
2.65	2.58	0.07	6.75E-01	8.86E-01	C2orf67	chromosome 2 open reading frame 67	chr2q34	230561_s_at	NM_152519
3.29	3.21	0.08	6.75E-01	8.86E-01	NAP1L2	nucleosome assembly protein 1-like 2	chrXq13	219368_at	NM_021963
8.08	7.95	0.13	6.75E-01	8.86E-01	NADK	NAD kinase	chr1p36.33-p36.21	208919_s_at	NM_023018
5.50	5.35	0.16	6.75E-01	8.86E-01	ABLIM3	actin binding LIM protein family, member 3	chr5q33.1	205730_s_at	NM_014945
2.22	2.15	0.07	6.75E-01	8.86E-01	---	---	---	1569846_at	---
3.43	3.35	0.08	6.75E-01	8.86E-01	---	---	---	243449_at	---
2.30	2.23	0.07	6.75E-01	8.86E-01	---	---	---	1557190_at	---
2.12	2.06	0.06	6.75E-01	8.86E-01	GBP6	guanylate binding protein family, member 6	chr1p22.2	1559607_s_at	NM_198460
3.10	3.03	0.07	6.75E-01	8.86E-01	---	---	---	239242_at	---
6.09	5.98	0.11	6.75E-01	8.86E-01	CTTN	cortactin	chr11q13	214074_s_at	NM_005231 /// NM_138565
2.25	2.19	0.06	6.75E-01	8.86E-01	AZGP1	alpha-2-glycoprotein 1, zinc-binding	chr7q22.1	209309_at	NM_001185
2.54	2.47	0.07	6.75E-01	8.86E-01	FAM13A1	family with sequence similarity 13, member A1	chr4q22.1	1569024_at	NM_001015045 /// NM_014883
2.24	2.17	0.06	6.75E-01	8.86E-01	TMEM161B	transmembrane protein 161B	chr5q14.3	244513_at	NM_153354
8.68	8.59	0.09	6.75E-01	8.86E-01	PPIF	peptidylprolyl isomerase F (cyclophilin F)	chr10q22-q23	201490_s_at	NM_005729
4.24	4.10	0.14	6.75E-01	8.87E-01	DENND2A	DENN/MADD domain containing 2A	chr7q34	53991_at	NM_015689
4.86	4.71	0.15	6.75E-01	8.87E-01	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	chr1p36	203722_at	NM_003748 /// NM_170726
6.67	6.52	0.15	6.75E-01	8.87E-01	KIAA0195	KIAA0195	chr17q25.1	202650_s_at	NM_014738
5.63	5.54	0.09	6.76E-01	8.87E-01	LOC100134427 /// PIAS4	similar to PIAS4 protein /// protein inhibitor of activated STAT, 4	chr19p13.3	212879_x_at	NM_015897 /// XM_001719136
2.95	2.89	0.07	6.76E-01	8.87E-01	---	---	---	230325_at	---
3.93	3.84	0.09	6.76E-01	8.87E-01	---	---	---	227772_at	---
3.65	3.58	0.07	6.76E-01	8.87E-01	LOC153364	similar to metallo-beta-lactamase superfamily protein	chr5q14.3	230298_at	NM_203406

6.55	6.24	0.31	6.76E-01	8.87E-01	FRMD6	FERM domain containing 6	chr14q22.1	225464_at	NM_001042481 /// NM_152330
2.99	2.91	0.08	6.76E-01	8.87E-01	ZBTB12	zinc finger and BTB domain containing 12	chr6p21.32	233843_at	NM_181842
2.47	2.41	0.06	6.76E-01	8.87E-01	---	---	---	216369_at	---
2.18	2.13	0.05	6.76E-01	8.87E-01	---	---	---	216764_at	---
2.77	2.70	0.07	6.76E-01	8.87E-01	TRAF3IP3	TRAF3 interacting protein 3	chr1q32.3-q41	205804_s_at	NM_025228
4.05	4.00	0.05	6.76E-01	8.87E-01	MIAT	myocardial infarction associated transcript (non-protein coding)	chr22q12.1	227168_at	NR_003491
2.58	2.51	0.07	6.76E-01	8.87E-01	RP11-251J8.3	hypothetical LOC646871	chr13q13.3	230775_s_at	XM_001132009 /// XM_001714513 /// XM_929830
3.36	3.28	0.08	6.76E-01	8.87E-01	---	---	---	240164_at	---
2.35	2.27	0.08	6.76E-01	8.87E-01	RNF32	ring finger protein 32	chr7q36	1554642_at	NM_030936
3.87	3.79	0.09	6.76E-01	8.87E-01	LOC387790	hypothetical LOC387790	chr11q13.5	1558844_at	NM_001013634
2.11	2.06	0.05	6.76E-01	8.87E-01	FAM3C	family with sequence similarity 3, member C	chr7q31	240062_at	NM_001040020 /// NM_014888
4.55	4.46	0.08	6.76E-01	8.87E-01	BCL6B	B-cell CLL/lymphoma 6, member B (zinc finger protein)	chr17p13.1	243825_at	NM_181844
2.07	2.01	0.06	6.76E-01	8.87E-01	LOC285370	hypothetical protein LOC285370	chr3p25.3	1556447_at	---
3.33	3.26	0.06	6.76E-01	8.87E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	229718_at	NM_001079691 /// NM_052818
4.46	4.34	0.11	6.76E-01	8.87E-01	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	chr17q25	210400_at	NM_000835
2.29	2.23	0.06	6.76E-01	8.87E-01	---	---	---	1560164_at	---
10.10	10.03	0.06	6.77E-01	8.87E-01	C20orf30	chromosome 20 open reading frame 30	chr20p12.3	224584_at	NM_001009923 /// NM_001009924 /// NM_001009925 /// NM_014145
5.73	5.52	0.20	6.77E-01	8.87E-01	IL13RA1	interleukin 13 receptor, alpha 1	chrXq24	210904_s_at	NM_001560
3.39	3.30	0.08	6.77E-01	8.87E-01	JMJD4	jumonji domain containing 4	chr1q42.13	230810_at	NM_023007
7.55	7.49	0.06	6.77E-01	8.87E-01	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	chr1p32	201488_x_at	NM_006559
6.08	5.92	0.16	6.77E-01	8.87E-01	UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)	chr17q11.2	218715_at	NM_018428
2.68	2.61	0.07	6.77E-01	8.87E-01	BC036928	hypothetical protein BC036928	chr19q13.43	231260_at	---
2.21	2.14	0.07	6.77E-01	8.87E-01	C1QTNF3	C1q and tumor necrosis factor related protein 3	chr5p13	1561263_at	NM_030945 /// NM_181435
2.86	2.78	0.09	6.77E-01	8.87E-01	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	chr2q11.2	221592_at	NM_001102426
2.13	2.07	0.06	6.77E-01	8.87E-01	---	---	---	228767_at	---
7.21	7.02	0.19	6.77E-01	8.87E-01	NR1H4	nuclear receptor subfamily 1, group H, member 4	chr12q23.1	206340_at	NM_005123
2.73	2.65	0.09	6.77E-01	8.87E-01	FAM27A /// LOC100132948	family with sequence similarity 27, member A /// similar to Protein FAM27A/B/C	chr9p11.2 /// chr9q12	223791_at	NR_024060 /// XM_001719272 /// XM_001719274
4.20	4.14	0.06	6.77E-01	8.87E-01	NGB	neuroglobin	chr14q24.3	220337_at	NM_021257
2.81	2.74	0.07	6.77E-01	8.87E-01	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	chr20p13	57588_at	NM_020689
3.96	3.88	0.08	6.77E-01	8.87E-01	SSTR3	somatostatin receptor 3	chr22q13.1	1553178_a_at	NM_001051
2.14	2.08	0.06	6.77E-01	8.87E-01	---	---	---	228780_at	---
4.36	4.23	0.13	6.77E-01	8.87E-01	USP24	ubiquitin specific peptidase 24	chr1p32.3	230004_at	NM_015306
5.84	5.75	0.09	6.77E-01	8.87E-01	CLASP1	cytoplasmic linker associated protein 1	chr2q14.2-q14.3	212752_at	NM_015282
2.03	1.98	0.05	6.77E-01	8.87E-01	COP1	caspase-1 dominant-negative inhibitor pseudo-ICE	---	1554744_at	NM_001017534 /// NM_052889
4.04	3.93	0.11	6.77E-01	8.87E-01	LOC100131062 /// PTP4A3	similar to protein tyrosine phosphatase type IVA, member 3 /// protein tyrosine phosphatase type IVA, member 3	chr8q24.3	206574_s_at	NM_007079 /// NM_032611 /// XM_001717048
2.08	2.02	0.05	6.78E-01	8.87E-01	---	---	---	240711_at	---
2.25	2.18	0.06	6.78E-01	8.87E-01	CYCS /// CYCSP52	cytochrome c, somatic /// cytochrome c, somatic pseudogene 52	chr1q22 /// chr7p15.2	217206_at	NM_018947 /// NR_001560
4.72	4.56	0.16	6.78E-01	8.87E-01	---	---	---	237400_at	---

7.04	6.87	0.17	6.78E-01	8.88E-01	LOC100128155 /// VAV2	hypothetical protein LOC100128155 /// vav 2 guanine nucleotide exchange factor	chr9q34.1 /// chr9q34.2	226063_at	NM_001134398 /// NM_003371 /// XM_001719399 /// XM_001722275 /// XM_001722967																				
1.99	1.95	0.05	6.78E-01	8.88E-01	---	---	---	1564144_at	---																				
4.21	4.02	0.19	6.78E-01	8.88E-01	---	---	---	244779_at	---																				
2.00	1.95	0.04	6.78E-01	8.88E-01	UMODL1	uromodulin-like 1	chr21q22.3	1553183_at	NM_001004416 /// NM_173568																				
7.23	7.11	0.12	6.78E-01	8.88E-01	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	chrXp22.2-p22.1	224935_at	NM_001415																				
2.13	2.07	0.06	6.78E-01	8.88E-01	---	---	---	1561129_at	---																				
4.10	4.03	0.07	6.78E-01	8.88E-01	SPATS1 /// TMEM151B	spermatogenesis associated, serine-rich 1 /// transmembrane protein 151B	chr6p21.1	1564067_x_at	NM_145026 /// XM_001723534 /// XM_001723740 /// XM_001725716																				
8.59	8.49	0.10	6.78E-01	8.88E-01	PEA15	phosphoprotein enriched in astrocytes 15	chr1q21.1	200788_s_at	NM_003768																				
5.38	5.26	0.12	6.78E-01	8.88E-01	COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)	chr6q16.3	223515_s_at	NM_017421																				
2.04	1.99	0.05	6.78E-01	8.88E-01	C12orf37	chromosome 12 open reading frame 37	chr12q21.33	1553497_at	XR_041585 /// XR_041586 /// XR_041587																				
2.02	1.97	0.05	6.78E-01	8.88E-01	C3orf48	chromosome 3 open reading frame 48	chr3p24.3	1552747_a_at	XM_001716709 /// XM_001717727 /// XM_001718092																				
1.91	1.87	0.04	6.78E-01	8.88E-01	---	---	---	1563203_at	---																				
2.61	2.56	0.05	6.79E-01	8.88E-01	---	---	---	232657_at	---																				
7.00	6.91	0.09	6.79E-01	8.88E-01	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	chr1q42|17p13.2	209141_at	NM_003342																				
2.25	2.20	0.06	6.79E-01	8.88E-01	---	---	---	232088_x_at	---																				
2.95	2.86	0.09	6.79E-01	8.88E-01	---	---	---	235080_at	---																				
5.48	5.37	0.11	6.79E-01	8.88E-01	ZC3H3	zinc finger CCCH-type containing 3	chr8q24.3	213445_at	NM_015117																				
2.27	2.22	0.05	6.79E-01	8.88E-01	---	---	---	241648_at	---																				
5.15	5.05	0.10	6.79E-01	8.88E-01	MED8	mediator complex subunit 8	chr1p34.2	213126_at	NM_052877 /// NM_201542																				
4.14	4.07	0.08	6.79E-01	8.88E-01	HES4	hairy and enhancer of split 4 (Drosophila)	chr1p36.33	227347_x_at	NM_021170																				
3.04	2.95	0.09	6.79E-01	8.88E-01	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	chr22q12|7p14.3-p14.1	210404_x_at	NM_001220 /// NM_172078 /// NM_172079 /// NM_172080 /// NM_172081 /// NM_172082 /// NM_172083 /// NM_172084																				
2.58	2.52	0.06	6.79E-01	8.88E-01	WWC1	WW and C2 domain containing 1	chr5q35.1	1554511_at	NM_015238																				
2.41	2.34	0.07	6.79E-01	8.88E-01	---	---	---	233142_at	---																				
2.77	2.69	0.08	6.79E-01	8.88E-01	REXO1L1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 1	chr8q21.2	1553009_s_at	NM_172239																				
5.53	5.45	0.08	6.79E-01	8.88E-01	HIF1AN	hypoxia-inducible factor 1, alpha subunit inhibitor	chr10q24	59999_at	NM_017902																				
6.50	6.39	0.11	6.79E-01	8.88E-01	DHRSX	dehydrogenase/reductase (SDR family) X-linked	chrXp22.33; Yp11.2	225503_at	NM_145177																				
2.46	2.40	0.06	6.79E-01	8.88E-01	---	---	---	236897_at	---																				
2.31	2.24	0.06	6.79E-01	8.88E-01	ANKRD45	ankyrin repeat domain 45	chr1q25.1	236421_at	NM_198493																				

4.25	4.15	0.10	6.79E-01	8.88E-01	ABLIM2	actin binding LIM protein family, member 2	chr4p16-p15	242624_at	NM_001130083 /// NM_001130084 /// NM_001130085 /// NM_001130086 /// NM_001130087 /// NM_001130088 /// NM_032432																				
3.79	3.56	0.23	6.79E-01	8.88E-01	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	chr7q33	206561_s_at	NM_020299																				
3.74	3.69	0.06	6.79E-01	8.88E-01	TMEM65	transmembrane protein 65	chr8q24.13	238045_at	NM_194291																				
7.83	7.74	0.09	6.79E-01	8.88E-01	FLNB	filamin B, beta (actin binding protein 278)	chr3p14.3	208614_s_at	NM_001457																				
2.10	2.04	0.06	6.79E-01	8.88E-01	---	---	---	230149_at	---																				
2.82	2.76	0.06	6.79E-01	8.88E-01	EP400NL	EP400 N-terminal like	chr12q24.33	1562845_at	NR_003290																				
2.92	2.84	0.08	6.79E-01	8.88E-01	---	---	---	1559161_at	---																				
4.45	4.38	0.07	6.80E-01	8.88E-01	---	---	---	241667_x_at	---																				
2.47	2.40	0.07	6.80E-01	8.88E-01	C8orf46	chromosome 8 open reading frame 46	chr8q13.1	228701_at	NM_152765																				
2.90	2.84	0.06	6.80E-01	8.88E-01	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	chrXp11.23	1559909_a_at	NM_005834																				
5.65	5.58	0.07	6.80E-01	8.88E-01	SGPP1	sphingosine-1-phosphate phosphatase 1	chr14q23.2	223391_at	NM_030791																				
2.63	2.57	0.06	6.80E-01	8.88E-01	---	---	---	242612_at	---																				
3.49	3.42	0.07	6.80E-01	8.88E-01	---	---	---	231637_at	---																				
3.90	3.85	0.05	6.80E-01	8.89E-01	LOC286121	hypothetical protein LOC286121	chr8q24.3	1561671_at	---																				
3.98	3.92	0.06	6.80E-01	8.89E-01	DPYSL5	dihydropyrimidinase-like 5	chr2p23.3	224100_s_at	NM_020134																				
2.23	2.17	0.07	6.80E-01	8.89E-01	---	---	---	1560971_a_at	---																				
2.29	2.24	0.06	6.80E-01	8.89E-01	FAM120AOS	Family with sequence similarity 120A opposite strand	chr9q22.31	1563112_at	NM_198841																				
6.67	6.38	0.29	6.80E-01	8.89E-01	NXN	nucleoredoxin	chr17p13.3	219489_s_at	NM_022463																				
4.90	4.81	0.09	6.80E-01	8.89E-01	SPRR4	small proline-rich protein 4	chr1q21.3	1552620_at	NM_173080																				
3.19	3.02	0.17	6.80E-01	8.89E-01	HIPK3	homeodomain interacting protein kinase 3	chr11p13	207764_s_at	NM_001048200 /// NM_005734																				
2.92	2.85	0.07	6.80E-01	8.89E-01	CSHL1	chorionic somatomammotropin hormone-like 1	chr17q24.2	208293_x_at	NM_001318 /// NM_022579 /// NM_022580 /// NM_022581																				
2.28	2.21	0.06	6.80E-01	8.89E-01	---	---	---	232319_at	---																				
2.29	2.24	0.05	6.80E-01	8.89E-01	PDE1A	phosphodiesterase 1A, calmodulin-dependent	chr2q32.1	236234_at	NM_001003683 /// NM_005019																				
2.92	2.83	0.09	6.80E-01	8.89E-01	AP3B2	adaptor-related protein complex 3, beta 2 subunit	chr15q	205678_at	NM_004644																				
2.39	2.33	0.05	6.80E-01	8.89E-01	---	---	---	1561192_at	---																				
2.88	2.81	0.07	6.81E-01	8.89E-01	KIAA1731	KIAA1731	chr11q21	1569302_at	NM_033395																				
3.59	3.54	0.06	6.81E-01	8.89E-01	PAX8	paired box 8	chr2q12-q14	213917_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992																				
2.84	2.79	0.05	6.81E-01	8.89E-01	MPO	myeloperoxidase	chr17q23.1	203948_s_at	NM_000250																				
2.72	2.66	0.06	6.81E-01	8.89E-01	RBM35A	RNA binding motif protein 35A	chr8q22.1	219121_s_at	NM_001034915 /// NM_001122825 /// NM_001122826 /// NM_001122827 /// NM_017697																				
2.81	2.72	0.08	6.81E-01	8.89E-01	---	---	---	227458_at	---																				
5.63	5.53	0.10	6.81E-01	8.89E-01	RNF169	ring finger protein 169	chr11q13.4	226739_at	NM_001098638																				

4.94	4.78	0.16	6.81E-01	8.89E-01	LOC100132990	PRO0633	chr4q23	227562_at	XM_001723301 /// XM_001723365 /// XM_001724550																			
5.79	5.73	0.06	6.81E-01	8.89E-01	ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	chr16q22.1	217650_x_at	NM_006927																			
1.82	1.77	0.05	6.81E-01	8.89E-01	LOC284260	hypothetical gene supported by BC011527; BC021928; BC011527; BC021928	chr18q12.3	1570208_at	XM_001720683 /// XM_001721958 /// XM_001723622																			
2.75	2.70	0.05	6.81E-01	8.89E-01	HOOK1	hook homolog 1 (Drosophila)	chr1p32.1	219976_at	NM_015888																			
8.64	8.57	0.07	6.81E-01	8.89E-01	TXNL4A	thioredoxin-like 4A	chr18q23	202836_s_at	NM_006701																			
2.08	2.03	0.05	6.81E-01	8.89E-01	IL26	interleukin 26	chr12q15	221111_at	NM_018402																			
6.17	6.02	0.15	6.81E-01	8.89E-01	IL13RA1	interleukin 13 receptor, alpha 1	chrXq24	201888_s_at	NM_001560																			
5.86	5.78	0.08	6.81E-01	8.89E-01	EBNA1BP2	EBNA1 binding protein 2	chr1p35-p33	201323_at	NM_006824																			
5.10	5.02	0.08	6.82E-01	8.89E-01	NLRX1	NLR family member X1	chr11q23.3	1553695_a_at	NM_024618 /// NM_170722																			
2.04	2.00	0.04	6.82E-01	8.89E-01	C9orf93	chromosome 9 open reading frame 93	chr9p22.3	1558082_at	NM_173550																			
2.82	2.75	0.06	6.82E-01	8.89E-01	---	---	---	236345_at	---																			
3.82	3.73	0.09	6.82E-01	8.89E-01	WBSCR27	Williams Beuren syndrome chromosome region 27	chr7q11.23	1553778_at	NM_152559																			
6.28	6.19	0.09	6.82E-01	8.89E-01	RNF8	ring finger protein 8	chr6p21.3	203160_s_at	NM_003958 /// NM_183078																			
2.32	2.27	0.05	6.82E-01	8.89E-01	---	---	---	1562766_at	---																			
6.81	6.75	0.06	6.82E-01	8.89E-01	ECSIT	ECSIT homolog (Drosophila)	chr19p13.2	218225_at	NM_016581																			
2.01	1.96	0.05	6.82E-01	8.89E-01	---	---	---	237213_at	---																			
2.46	2.39	0.07	6.82E-01	8.89E-01	---	---	---	1559696_at	---																			
2.80	2.72	0.08	6.82E-01	8.89E-01	TAS1R1	taste receptor, type 1, member 1	chr1p36.23	1564883_a_at	NM_138697 /// NM_177539 /// NM_177540 /// NM_177541																			
3.12	2.99	0.13	6.82E-01	8.89E-01	EHD4	EH-domain containing 4	chr15q11.1	233660_at	NM_139265																			
3.55	3.49	0.05	6.82E-01	8.89E-01	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	chr17q22	214979_at	NM_003786																			
5.93	5.82	0.12	6.82E-01	8.89E-01	DMPK	dystrophia myotonica-protein kinase	chr19q13.3	37996_s_at	NM_001081560 /// NM_001081562 /// NM_001081563 /// NM_004409																			
8.70	8.60	0.10	6.82E-01	8.89E-01	C20orf24	chromosome 20 open reading frame 24	chr20q11.23	224376_s_at	NM_018840 /// NM_199483																			
3.37	3.31	0.06	6.82E-01	8.89E-01	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	chr16p11.2	210184_at	NM_000887																			
2.10	2.03	0.07	6.82E-01	8.89E-01	RP4-662A9.2	hypothetical protein MGC34034	chr6q23.2	1552900_a_at	---																			
2.53	2.48	0.05	6.82E-01	8.90E-01	VSX1	visual system homeobox 1	chr20p11.23-p11.22	224074_at	NM_014588 /// NM_199425																			
3.78	3.70	0.08	6.82E-01	8.90E-01	GON4L	gon-4-like (C. elegans)	chr1q22	223555_at	NM_001037533 /// NM_032292																			
2.41	2.34	0.06	6.82E-01	8.90E-01	KITLG	KIT ligand	chr12q22	207029_at	NM_000899 /// NM_003994																			
2.31	2.26	0.05	6.83E-01	8.90E-01	---	---	---	232738_at	---																			

6.82	6.66	0.16	6.83E-01	8.90E-01	ZNF655	zinc finger protein 655	chr7q22.1	225945_at	NM_001009958 /// NM_001009960 /// NM_001083956 /// NM_001085366 /// NM_001085367 /// NM_001085368 /// NM_024061 /// NM_138494
5.30	5.23	0.07	6.83E-01	8.90E-01	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	chr10q24	207535_s_at	NM_001077493 /// NM_001077494 /// NM_002502
2.27	2.21	0.06	6.83E-01	8.90E-01	---	---	---	217651_at	---
4.73	4.53	0.20	6.83E-01	8.90E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	223577_x_at	NR_002819
9.49	9.42	0.07	6.83E-01	8.90E-01	DYNLRB1	dynein, light chain, roadblock-type 1	chr20q11.21	217918_at	NM_014183
2.86	2.80	0.06	6.83E-01	8.90E-01	GRLF1	Glucocorticoid receptor DNA binding factor 1	chr19q13.3	229397_s_at	NM_004491
3.71	3.58	0.13	6.83E-01	8.90E-01	GPR65	G protein-coupled receptor 65	chr14q31-q32.1	214467_at	NM_003608
3.41	3.30	0.11	6.83E-01	8.90E-01	FAM71E1	family with sequence similarity 71, member E1	chr19q13.33	229289_at	NM_138411
7.99	7.89	0.10	6.83E-01	8.90E-01	NR2F2	nuclear receptor subfamily 2, group F, member 2	chr15q26	209120_at	NM_021005
4.45	4.38	0.07	6.83E-01	8.90E-01	---	---	---	232579_at	---
2.68	2.63	0.05	6.83E-01	8.90E-01	LOC100133945 /// UCA1	similar to pol protein /// urothelial cancer associated 1	chr19p13	227919_at	NR_015379 /// XM_001714463 /// XR_042077 /// XR_042078
2.66	2.59	0.07	6.83E-01	8.90E-01	SAP30	Sin3A-associated protein, 30kDa	chr4q34.1	204898_at	NM_003864
6.34	6.22	0.12	6.83E-01	8.90E-01	C1GALT1C1	C1GALT1-specific chaperone 1	chrXq24	219283_at	NM_001011551 /// NM_152692
2.20	2.15	0.05	6.83E-01	8.90E-01	---	---	---	244107_at	---
2.46	2.40	0.06	6.83E-01	8.90E-01	---	---	---	238976_at	---
4.16	4.08	0.08	6.83E-01	8.90E-01	CHD6	chromodomain helicase DNA binding protein 6	chr20q12	225026_at	NM_032221
2.52	2.46	0.06	6.83E-01	8.90E-01	---	---	---	234516_at	---
4.41	4.34	0.07	6.83E-01	8.90E-01	SAPS2	SAPS domain family, member 2	chr22q13.33	1570210_x_at	NM_014678
1.93	1.88	0.04	6.84E-01	8.90E-01	IQCH	IQ motif containing H	chr15q23	1569610_at	NM_001031715 /// NM_022784
2.12	2.08	0.05	6.84E-01	8.90E-01	---	---	---	1564744_at	---
4.56	4.50	0.06	6.84E-01	8.90E-01	C19orf6	Chromosome 19 open reading frame 6	chr19p13.3	213985_s_at	NM_001033026 /// NM_033420
7.76	7.67	0.09	6.84E-01	8.90E-01	TMEM109	transmembrane protein 109	chr11q12.2	201361_at	NM_024092
6.19	6.10	0.09	6.84E-01	8.90E-01	FLJ14154	hypothetical protein FLJ14154	chr16p13.3	218661_at	NM_001083600 /// NM_001083601 /// NM_024845
2.32	2.26	0.06	6.84E-01	8.90E-01	GPR109B	G protein-coupled receptor 109B	chr12q24.31	205220_at	NM_006018
2.22	2.17	0.05	6.84E-01	8.90E-01	COX11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	chr17q22	214277_at	NM_004375
6.62	6.51	0.10	6.84E-01	8.90E-01	WIPF2	WAS/WASL interacting protein family, member 2	chr17q21.2	212050_at	NM_133264
3.29	3.23	0.06	6.84E-01	8.90E-01	---	---	---	1556734_at	---
2.88	2.78	0.10	6.84E-01	8.90E-01	OR2H1	olfactory receptor, family 2, subfamily H, member 1	chr6p21.3	1556987_s_at	NM_030883
2.17	2.11	0.06	6.84E-01	8.90E-01	---	---	---	233397_at	---
5.68	5.50	0.19	6.84E-01	8.90E-01	IL13RA1	interleukin 13 receptor, alpha 1	chrXq24	211612_s_at	NM_001560
3.47	3.37	0.10	6.84E-01	8.91E-01	LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	chr19q13.4	210152_at	NM_001081438 /// NM_006847
2.06	2.00	0.05	6.84E-01	8.91E-01	OR2C3	olfactory receptor, family 2, subfamily C, member 3	chr1q44	1555018_at	NM_198074
2.52	2.45	0.07	6.84E-01	8.91E-01	PER2	period homolog 2 (Drosophila)	chr2q37.3	208518_s_at	NM_022817
2.68	2.62	0.06	6.84E-01	8.91E-01	LOC254559	hypothetical LOC254559	chr15q26.1	235936_at	XM_943723
3.04	2.95	0.09	6.84E-01	8.91E-01	PRKCQ	protein kinase C, theta	chr10p15	210039_s_at	NM_006257

4.22	4.15	0.06	6.85E-01	8.91E-01	EXOC3L /// LOC100130525 /// LOC100134333	exocyst complex component 3-like /// hypothetical protein LOC100130525 /// hypothetical protein LOC100134333	chr16q22.1	1559272_at	NM_178516 /// XM_001713762 /// XM_001713763																				
2.23	2.14	0.09	6.85E-01	8.91E-01	---	---	---	235949_at	---																				
5.47	5.40	0.08	6.85E-01	8.91E-01	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	chr1p22.1	207654_x_at	NM_001938																				
2.52	2.46	0.06	6.85E-01	8.91E-01	OR4D2	olfactory receptor, family 4, subfamily D, member 2	chr17q22	1555377_at	NM_001004707																				
4.34	4.25	0.09	6.85E-01	8.91E-01	C10orf67	chromosome 10 open reading frame 67	chr10p12.2	1553845_x_at	NM_153714																				
4.11	4.04	0.07	6.85E-01	8.91E-01	ASCL2	achaete-scute complex homolog 2 (Drosophila)	chr11p15.5	229215_at	NM_005170																				
5.40	5.21	0.19	6.85E-01	8.91E-01	GTF2I	general transcription factor II, i	chr7q11.23	210892_s_at	NM_001518 /// NM_032999 /// NM_033000 /// NM_033001																				
6.40	6.31	0.09	6.85E-01	8.91E-01	PHRF1	PHD and ring finger domains 1	chr11p15.5	234952_s_at	NM_020901																				
3.35	3.26	0.09	6.85E-01	8.91E-01	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	chr16p13.1	208480_s_at	NM_001079528 /// NM_001171																				
2.17	2.12	0.05	6.85E-01	8.91E-01	---	---	---	1569790_at	---																				
4.02	3.96	0.07	6.85E-01	8.91E-01	C8orf42	chromosome 8 open reading frame 42	chr8p23.3	226778_at	NM_175075																				
2.38	2.32	0.06	6.85E-01	8.91E-01	---	---	---	1554266_at	---																				
4.99	4.87	0.12	6.86E-01	8.92E-01	SNX12	sorting nexin 12	chrXq13.1	231723_at	NM_013346																				
1.89	1.84	0.05	6.86E-01	8.92E-01	BTRC	beta-transducin repeat containing	chr10q24.32	1563620_at	NM_003939 /// NM_033637																				
2.39	2.31	0.08	6.86E-01	8.92E-01	CST9L	cystatin 9-like	chr20p11.21	230829_at	NM_080610																				
2.16	2.10	0.06	6.86E-01	8.92E-01	---	---	---	1561112_at	---																				
9.34	9.24	0.10	6.86E-01	8.92E-01	H3F3A /// H3F3B	H3 histone, family 3A /// H3 histone, family 3B (H3.3B)	chr17q25 /// chr1q41	211999_at	NM_002107 /// NM_005324																				
3.49	3.39	0.10	6.86E-01	8.92E-01	SIGLEC7	sialic acid binding Ig-like lectin 7	chr19q13.3	207224_s_at	NM_014385 /// NM_016543																				
7.10	7.01	0.09	6.86E-01	8.92E-01	SLC39A7	solute carrier family 39 (zinc transporter), member 7	chr6p21.3	202667_s_at	NM_001077516 /// NM_006979																				
5.25	5.19	0.07	6.86E-01	8.92E-01	OSBPL2	oxysterol binding protein-like 2	chr20q13.3	209221_s_at	NM_014835 /// NM_144498																				
3.75	3.61	0.14	6.86E-01	8.92E-01	STARD5	StAR-related lipid transfer (START) domain containing 5	chr15q26	213820_s_at	NM_181900																				
5.70	5.61	0.09	6.86E-01	8.92E-01	---	---	---	241865_at	---																				
3.83	3.71	0.12	6.86E-01	8.92E-01	DTNBP1	dystrobrevin binding protein 1	chr6p22.3	223763_at	NM_032122 /// NM_183040 /// NM_183041																				
2.30	2.24	0.06	6.86E-01	8.92E-01	LOC401324	acyloxyacyl hydrolase (neutrophil)	chr7p14.2	1563586_at	---																				
2.51	2.43	0.07	6.86E-01	8.92E-01	F2RL2	coagulation factor II (thrombin) receptor-like 2	chr5q13	230147_at	NM_004101																				
9.62	9.53	0.09	6.86E-01	8.92E-01	TRAPPC2L	trafficking protein particle complex 2-like	chr16q24.3	218354_at	NM_016209																				
6.87	6.79	0.08	6.86E-01	8.92E-01	UBXN2A	UBX domain protein 2A	chr2p23.3	235327_x_at	NM_181713																				
2.58	2.51	0.07	6.86E-01	8.92E-01	---	---	---	243069_at	---																				
3.02	2.92	0.10	6.86E-01	8.92E-01	---	---	---	239808_at	---																				
3.60	3.52	0.08	6.87E-01	8.92E-01	LOC116349	hypothetical protein BC014011	chr5p15.33	235219_at	NM_138464																				
2.38	2.33	0.05	6.87E-01	8.92E-01	CAT	Catalase	chr11p13	238363_at	NM_001752																				
3.77	3.59	0.18	6.87E-01	8.92E-01	AGPS	alkylglycerone phosphate synthase	chr2q31.2	225114_at	NM_003659																				
3.35	3.26	0.09	6.87E-01	8.92E-01	---	---	---	237383_at	---																				
2.34	2.29	0.06	6.87E-01	8.92E-01	---	---	---	238075_at	---																				
8.44	8.36	0.08	6.87E-01	8.92E-01	AIF1	allograft inflammatory factor 1	chr6p21.3	215051_x_at	NM_001623 /// NM_032955																				
2.26	2.20	0.06	6.87E-01	8.92E-01	C14orf135 /// LOC100130173	chromosome 14 open reading frame 135 /// hypothetical protein LOC100130173	chr14q23.1	1568971_at	NM_022495 /// XM_001719623 /// XM_001723734																				
3.00	2.92	0.08	6.87E-01	8.92E-01	---	---	---	1569518_at	---																				
2.73	2.65	0.07	6.87E-01	8.92E-01	GSX1	GS homeobox 1	chr13q12.2	234791_at	NM_145657																				
2.45	2.39	0.06	6.87E-01	8.92E-01	BTN2A2	butyrophilin, subfamily 2, member A2	chr6p22.1	1564684_at	NM_006995 /// NM_181531																				

8.12	7.97	0.16	6.87E-01	8.92E-01	---	---	---	238780_s_at	---
3.60	3.53	0.07	6.87E-01	8.92E-01	IL25	interleukin 25	chr14q11.2	220971_at	NM_022789 /// NM_172314
2.35	2.29	0.06	6.87E-01	8.92E-01	B4GALNT4	Beta-1,4-N-acetyl-galactosaminyl transferase 4	chr11p15.5	238060_s_at	NM_178537
4.38	4.24	0.14	6.87E-01	8.92E-01	TMEM185B	transmembrane protein 185B (pseudogene)	chr2q14.2	219253_at	NR_000034
5.52	5.45	0.07	6.87E-01	8.92E-01	SHQ1	SHQ1 homolog (S. cerevisiae)	chr3p13	63009_at	NM_018130
4.88	4.78	0.10	6.87E-01	8.92E-01	GK	glycerol kinase	chrXp21.3	215977_x_at	NM_000167 /// NM_001128127 /// NM_203391
6.32	6.26	0.06	6.87E-01	8.92E-01	MYST2	MYST histone acetyltransferase 2	chr17q21.32	200049_at	NM_007067
5.62	5.52	0.09	6.87E-01	8.92E-01	FLJ32065	hypothetical protein FLJ32065	chr17q24.1	223443_s_at	XR_040666 /// XR_040667 /// XR_040668
2.43	2.38	0.05	6.87E-01	8.92E-01	---	---	---	244036_at	---
6.32	6.22	0.10	6.88E-01	8.92E-01	KIAA1539	KIAA1539	chr9p13.3	211433_x_at	NM_025182
1.87	1.82	0.05	6.88E-01	8.92E-01	---	---	---	1557746_at	---
2.62	2.56	0.07	6.88E-01	8.92E-01	SLC5A9	solute carrier family 5 (sodium/glucose cotransporter), member 9	chr1p33	1569337_at	NM_001011547
3.75	3.70	0.05	6.88E-01	8.92E-01	MFAP3L	Microfibrillar-associated protein 3-like	chr4q32.3	1569300_at	NM_001009554 /// NM_021647
7.40	7.29	0.10	6.88E-01	8.92E-01	BTF3L4	basic transcription factor 3-like 4	chr1p32.3	225976_at	NM_152265
5.75	5.59	0.16	6.88E-01	8.92E-01	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	chr17p13	219184_x_at	NM_013337
1.90	1.86	0.05	6.88E-01	8.93E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	215879_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376
2.26	2.19	0.07	6.88E-01	8.93E-01	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	chr4q21	206336_at	NM_002993

									NM_001011724 /// NM_001011725 /// NM_002136 /// NM_031157 /// NR_002944 /// NR_003277 /// XM_001718684 /// XM_062025 /// XM_937967 /// XR_015330 /// XR_015514 /// XR_015658 /// XR_015746 /// XR_015895 /// XR_015958 /// XR_015974 /// XR_016080 /// XR_016093 /// XR_016314 /// XR_016373 /// XR_016388 /// XR_017084 /// XR_017337 /// XR_017501 /// XR_018564 /// XR_019025 /// XR_019262 /// XR_019573 /// XR_037462 /// XR_037720 /// XR_037797 /// XR_038280 /// XR_038288 /// XR_038331 /// XR_038689 /// XR_038697 /// XR_038725 /// XR_038755 /// XR_038765 /// XR_038785 /// XR_038911 /// XR_039047 /// XR_039155 /// XR_039380 /// XR_039402 /// XR_039425 /// XR_039446 /// XR_039541
2.35	2.30	0.05	6.88E-01	8.93E-01	HNRNPA1 /// HNRPA1L-2 /// HNRPA1P5 /// LOC100128701 /// LOC100128836 /// LOC120364 /// LOC391670 /// LOC402112 /// LOC440125 /// LOC642817 /// LOC643033 /// LOC644037 /// LOC645001 /// LOC728170 /// LOC728643 /// LOC728732 /// LOC729102 /// LOC729366 /// LOC730246 /// RP11-78J21.1	heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1 pseudogene /// heterogeneous nuclear ribonucleoprotein A1 pseudogene 5 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC642817 /// similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed) /// hypothetical LOC644037 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1 pseudogene /// hypothetical LOC728732 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC7	chr10q11.22 /// chr11p15.4 /// chr11q23.1 /// chr12q13.1 /// chr12q22 /// chr13q12.11 /// chr13q14.3 /// chr19p13.2 /// chr19q13.2 /// chr1q32.1 /// chr2q31.1 /// chr2q33.3 /// chr3p22.1 /// chr4q21.1 /// chr5q14.1 /// chr6p25.1 /// chr8q21.13 /// chr9p24.1 /// chrXq22 /// chrXq24	216497_at	
2.39	2.34	0.05	6.89E-01	8.93E-01	TSSK4	testis-specific serine kinase 4	chr14q12	242595_at	NM_174944
2.73	2.65	0.07	6.89E-01	8.93E-01	---	---	---	236174_at	---
5.63	5.51	0.12	6.89E-01	8.93E-01	TRIM38	tripartite motif-containing 38	chr6p21.3	203568_s_at	NM_006355
3.27	3.17	0.11	6.89E-01	8.93E-01	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	chr16p13.3	222711_s_at	NM_022450
4.65	4.60	0.06	6.89E-01	8.93E-01	C2orf72	chromosome 2 open reading frame 72	chr2q37.1	213143_at	XM_001129456 /// XM_001132119 /// XM_001715135
3.72	3.56	0.15	6.89E-01	8.93E-01	SR140	U2-associated SR140 protein	chr3q23	212061_at	NM_001080415
2.06	2.02	0.05	6.89E-01	8.93E-01	---	---	---	234282_at	---
3.11	3.02	0.09	6.89E-01	8.93E-01	RBM33	RNA binding motif protein 33	chr7q36.3	231833_at	NM_001008408 /// NM_053043
2.22	2.17	0.05	6.89E-01	8.93E-01	---	---	---	236639_at	---
2.58	2.53	0.05	6.89E-01	8.93E-01	DOCK5 /// PPP2R2A	dedicator of cytokinesis 5 /// protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	chr8p21.2	237636_at	NM_002717 /// NM_024940
6.93	6.68	0.25	6.89E-01	8.93E-01	SCRN1	secernin 1	chr7p14.3-p14.1	201462_at	NM_014766
2.27	2.22	0.05	6.89E-01	8.93E-01	GPR22	G protein-coupled receptor 22	chr7q22-q31.1	221288_at	NM_005295
4.56	4.49	0.07	6.89E-01	8.93E-01	---	---	---	215697_at	---
2.50	2.44	0.06	6.89E-01	8.93E-01	---	---	---	230614_at	---
2.44	2.39	0.04	6.89E-01	8.93E-01	IQSEC3	IQ motif and Sec7 domain 3	chr12p13.33	1553949_at	NM_015232
2.70	2.65	0.05	6.89E-01	8.93E-01	PASK	PAS domain containing serine/threonine kinase	chr2q37.3	206594_at	NM_015148
6.90	6.82	0.08	6.89E-01	8.93E-01	ZNF830	zinc finger protein 830	chr17q12	226323_at	NM_052857

2.13	2.08	0.05	6.90E-01	8.93E-01	---	---	---	1564820_at	---
2.87	2.81	0.06	6.90E-01	8.93E-01	CSPP1	centrosome and spindle pole associated protein 1	chr8q13.2	242041_at	NM_001077204 /// NM_024790
6.24	6.15	0.08	6.90E-01	8.93E-01	CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	chr10q11	212901_s_at	NM_015235
3.37	3.30	0.07	6.90E-01	8.93E-01	---	---	---	220708_at	---
5.37	5.19	0.19	6.90E-01	8.93E-01	NUDCD1	NudC domain containing 1	chr8q23	225439_at	NM_001128211 /// NM_032869
1.91	1.86	0.05	6.90E-01	8.93E-01	---	---	---	210703_at	---
3.06	2.98	0.08	6.90E-01	8.93E-01	---	---	---	1559119_at	---
3.38	3.30	0.08	6.90E-01	8.93E-01	CTNNA1	Catenin (cadherin-associated protein), alpha 1, 102kDa	chr5q31	215883_at	NM_001903
6.59	6.41	0.19	6.90E-01	8.93E-01	MED21	mediator complex subunit 21	chr12p11.23	209362_at	NM_004264
2.81	2.73	0.08	6.90E-01	8.94E-01	PARP11	poly (ADP-ribose) polymerase family, member 11	chr12p13.3	220315_at	NM_020367
5.15	5.02	0.13	6.90E-01	8.94E-01	LOC221710	Hypothetical protein LOC221710	chr6p24.1	227124_at	XM_001720414 /// XM_001724989 /// XM_001725361
2.56	2.50	0.07	6.90E-01	8.94E-01	AIPL1	aryl hydrocarbon receptor interacting protein-like 1	chr17p13.1	219977_at	NM_001033054 /// NM_001033055 /// NM_014336
2.22	2.17	0.05	6.90E-01	8.94E-01	RP11-291L22.2	similar to cell division cycle 10	chr10p11.21	1556222_at	---
6.61	6.48	0.13	6.90E-01	8.94E-01	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	chr16q13	224830_at	NM_007006
2.12	2.08	0.05	6.90E-01	8.94E-01	---	---	---	1569287_at	---
1.85	1.81	0.04	6.91E-01	8.94E-01	---	---	---	1561240_at	---
5.32	5.26	0.07	6.91E-01	8.94E-01	MASP2	mannan-binding lectin serine peptidase 2	chr1p36.3-p36.2	210798_x_at	NM_006610 /// NM_139208
2.03	1.98	0.05	6.91E-01	8.94E-01	---	---	---	234374_at	---
13.04	13.00	0.04	6.91E-01	8.94E-01	hCG_16001 /// RPL23A	similar to ribosomal protein L23A /// ribosomal protein L23a	chr17q11 /// chr3q26.1	208825_x_at	NM_000984 /// NM_001093758
2.81	2.74	0.07	6.91E-01	8.94E-01	---	---	---	1556451_at	---
4.12	4.06	0.06	6.91E-01	8.94E-01	GLP1R	glucagon-like peptide 1 receptor	chr6p21	208401_s_at	NM_002062
2.84	2.77	0.06	6.91E-01	8.94E-01	MLF1IP	MLF1 interacting protein	chr4q35.1	229304_s_at	NM_024629
4.87	4.74	0.13	6.91E-01	8.94E-01	CENPC1	centromere protein C 1	chr4q12-q13.3	204739_at	NM_001812
5.35	5.27	0.08	6.91E-01	8.94E-01	HMOX2	heme oxygenase (decycling) 2	chr16p13.3	218121_at	NM_001127204 /// NM_001127205 /// NM_001127206 /// NM_002134
3.01	2.95	0.07	6.91E-01	8.94E-01	---	---	---	230654_at	---
5.03	4.95	0.08	6.91E-01	8.94E-01	SBNO2	strawberry notch homolog 2 (Drosophila)	chr19p13.3	215760_s_at	NM_001100122 /// NM_014963
2.14	2.08	0.05	6.91E-01	8.94E-01	---	---	---	232679_at	---
5.77	5.69	0.08	6.91E-01	8.94E-01	CUL5	cullin 5	chr11q22-q23	230393_at	NM_003478
4.39	4.31	0.08	6.91E-01	8.94E-01	SHMT1	serine hydroxymethyltransferase 1 (soluble)	chr17p11.2	209980_s_at	NM_004169 /// NM_148918
3.20	3.14	0.07	6.91E-01	8.94E-01	P53AIP1	p53-regulated apoptosis-inducing protein 1	chr11q24	223919_at	NM_022112
3.34	3.27	0.06	6.91E-01	8.94E-01	TIPIN	TIMELESS interacting protein	chr15q22.31	219258_at	NM_017858
2.33	2.27	0.06	6.91E-01	8.94E-01	---	---	---	1557658_at	---
6.22	6.03	0.19	6.91E-01	8.94E-01	---	---	---	213549_at	---
2.71	2.64	0.08	6.91E-01	8.94E-01	NLRP1	NLR family, pyrin domain containing 1	chr17p13.2	211824_x_at	NM_001033053 /// NM_014922 /// NM_033004 /// NM_033006 /// NM_033007
2.31	2.26	0.05	6.92E-01	8.94E-01	---	---	---	1561255_at	---
3.02	2.94	0.08	6.92E-01	8.94E-01	PMS2L5	Postmeiotic segregation increased 2-like 5	chr7q11-q22	242201_at	NM_174930 /// XM_001713820

6.16	6.06	0.10	6.92E-01	8.94E-01	SSRP1	structure specific recognition protein 1	chr11q12	200956_s_at	NM_003146
6.97	6.91	0.07	6.92E-01	8.94E-01	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	chr9q34	216105_x_at	NM_021131 /// NM_178000 /// NM_178001 /// NM_178003
2.86	2.79	0.08	6.92E-01	8.94E-01	---	---	---	1556494_at	---
3.98	3.91	0.06	6.92E-01	8.94E-01	STX6	syntaxin 6	chr1q25.3	214441_at	NM_005819
1.98	1.93	0.04	6.92E-01	8.94E-01	---	---	---	234579_at	---
10.70	10.60	0.10	6.92E-01	8.94E-01	HMGB1	high-mobility group box 1	chr13q12	214938_x_at	NM_002128
2.13	2.07	0.06	6.92E-01	8.94E-01	---	---	---	1564337_at	---
2.04	1.98	0.07	6.92E-01	8.94E-01	CDH8	cadherin 8, type 2	chr16q22.1	217574_at	NM_001796
2.00	1.94	0.06	6.92E-01	8.94E-01	COL25A1	collagen, type XXV, alpha 1	chr4q25	1555253_at	NM_032518 /// NM_198721
2.36	2.29	0.07	6.92E-01	8.94E-01	---	---	---	240074_at	---
3.04	2.96	0.08	6.92E-01	8.94E-01	---	---	---	239534_at	---
2.40	2.34	0.05	6.92E-01	8.94E-01	---	---	---	1569685_at	---
2.04	2.00	0.05	6.92E-01	8.94E-01	LOC284801	hypothetical protein LOC284801	chr20p11.1	237670_at	XM_001714287 /// XM_378973 /// XM_944897
3.13	3.07	0.07	6.92E-01	8.94E-01	OR51J1	olfactory receptor, family 51, subfamily J, member 1 (gene/pseudogene)	chr11p15.4	233736_at	---
2.56	2.49	0.07	6.93E-01	8.94E-01	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	chr13q32	1555039_a_at	NM_001105515 /// NM_005845
3.09	3.02	0.08	6.93E-01	8.94E-01	---	---	---	235439_at	---
5.46	5.26	0.20	6.93E-01	8.94E-01	ERAP1	endoplasmic reticulum aminopeptidase 1	chr5q15	209788_s_at	NM_001040458 /// NM_016442
2.66	2.59	0.07	6.93E-01	8.94E-01	---	---	---	1560604_at	---
7.71	7.63	0.08	6.93E-01	8.94E-01	TRAPPC4	trafficking protein particle complex 4	chr11q23.3	217959_s_at	NM_016146
1.97	1.93	0.04	6.93E-01	8.94E-01	KIAA1833	hypothetical protein KIAA1833	chr8q24.3	1565653_at	NM_001099280 /// NM_001099281 /// NM_032450
3.47	3.40	0.07	6.93E-01	8.94E-01	---	---	---	233689_at	---
6.86	6.73	0.13	6.93E-01	8.95E-01	RAP2C	RAP2C, member of RAS oncogene family	chrXq25	218669_at	NM_021183
2.17	2.12	0.05	6.93E-01	8.95E-01	---	---	---	234378_at	---
4.18	4.10	0.08	6.93E-01	8.95E-01	SQSTM1	Sequestosome 1	chr5q35	239004_at	NM_003900
2.64	2.56	0.08	6.93E-01	8.95E-01	---	---	---	1556122_at	---
2.80	2.73	0.07	6.93E-01	8.95E-01	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	chr5q14.3	206654_s_at	NM_006467
5.68	5.62	0.06	6.93E-01	8.95E-01	ARID1B /// LOC729446	AT rich interactive domain 1B (SWI1-like) /// hypothetical LOC729446	chr6q25.1	225184_at	NM_017519 /// NM_020732 /// NM_175863 /// XM_001133842
2.35	2.29	0.06	6.93E-01	8.95E-01	C9orf93	chromosome 9 open reading frame 93	chr9p22.3	1558160_at	NM_173550
2.81	2.73	0.08	6.93E-01	8.95E-01	MLANA	melan-A	chr9p24.1	206427_s_at	NM_005511
3.10	3.00	0.10	6.93E-01	8.95E-01	LOC550643	hypothetical LOC550643	chrXp11.1	225028_at	NR_015367 /// XM_001718993 /// XM_001720195 /// XM_001721066
2.26	2.21	0.05	6.93E-01	8.95E-01	BEAN	brain expressed, associated with Nedd4	chr16q21	214068_at	XM_001717857 /// XM_001719451 /// XM_001723219
4.26	4.14	0.12	6.93E-01	8.95E-01	---	---	---	232150_at	---
3.98	3.93	0.06	6.93E-01	8.95E-01	CTRC	chymotrypsin C (caldecrin)	chr1p36.21	206297_at	NM_007272
7.70	7.62	0.08	6.93E-01	8.95E-01	ERGIC1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	chr5q35.1-q35.2	224577_at	NM_001031711 /// NM_020462

5.65	5.54	0.11	6.93E-01	8.95E-01	KLHL26	kelch-like 26 (Drosophila)	chr19p13.11	219354_at	NM_018316
2.08	2.04	0.05	6.93E-01	8.95E-01	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	chr18q11-q12	229151_at	NM_001128588 /// NM_015865
3.66	3.57	0.09	6.94E-01	8.95E-01	LRRC43	leucine rich repeat containing 43	chr12q24.31	1553730_x_at	NM_001098519 /// NM_152759
2.11	2.06	0.05	6.94E-01	8.95E-01	---	---	---	1569768_at	---
2.13	2.06	0.07	6.94E-01	8.95E-01	FILIP1	filamin A interacting protein 1	chr6q14.1	1570515_a_at	NM_015687
7.67	7.57	0.09	6.94E-01	8.95E-01	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	chr16q13	225110_at	NM_018233
2.08	2.03	0.06	6.94E-01	8.95E-01	COL28A1	collagen, type XXVIII, alpha 1	chr7p21.3	239921_at	NM_001037763
3.21	3.08	0.12	6.94E-01	8.95E-01	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	chr12p11.23-p11.22	203736_s_at	NM_003622 /// NM_177444
3.16	3.10	0.07	6.94E-01	8.95E-01	COL6A1	collagen, type VI, alpha 1	chr21q22.3	212939_at	NM_001848
2.37	2.31	0.06	6.94E-01	8.95E-01	---	---	---	235655_at	---
7.13	7.06	0.07	6.94E-01	8.95E-01	KCTD10	potassium channel tetramerisation domain containing 10	chr12q24.11	223208_at	NM_031954
2.67	2.61	0.06	6.94E-01	8.95E-01	---	---	---	234255_at	---
2.12	2.06	0.06	6.94E-01	8.95E-01	STT3B	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	chr3p23	231294_at	NM_178862
2.26	2.22	0.04	6.94E-01	8.95E-01	PNLIPRP3	pancreatic lipase-related protein 3	chr10q25.3	1558846_at	NM_001011709
2.58	2.53	0.05	6.94E-01	8.95E-01	LOC400655	hypothetical gene supported by BC013370; BC034583	chr18q22.3	1569264_at	XM_378753 /// XM_932193 /// XM_944987 /// XM_944989
2.29	2.23	0.06	6.94E-01	8.95E-01	LOC415056	hypothetical gene LOC415056	chr9p13	1561590_a_at	---
2.23	2.16	0.07	6.94E-01	8.95E-01	C4orf16	chromosome 4 open reading frame 16	chr4q25	242753_x_at	NM_001128426 /// NM_018569
2.35	2.29	0.06	6.95E-01	8.95E-01	---	---	---	1562384_at	---
5.15	4.96	0.19	6.95E-01	8.95E-01	RAI2	retinoic acid induced 2	chrXp22	219440_at	NM_021785
2.37	2.32	0.06	6.95E-01	8.95E-01	---	---	---	241182_at	---
2.61	2.55	0.06	6.95E-01	8.95E-01	ERLIN2	ER lipid raft associated 2	chr8p11.2	238615_at	NM_001003790 /// NM_001003791 /// NM_007175
4.28	4.19	0.08	6.95E-01	8.95E-01	---	---	---	242959_at	---
2.57	2.52	0.05	6.95E-01	8.95E-01	MED25	mediator complex subunit 25	chr19q13.3	215897_at	NM_030973
6.78	6.68	0.10	6.95E-01	8.95E-01	PTRH2	peptidyl-tRNA hydrolase 2	chr17q23.1	218732_at	NM_016077
4.29	4.19	0.10	6.95E-01	8.96E-01	PLXNB1	plexin B1	chr3p21.31	215807_s_at	NM_001130082 /// NM_002673
2.97	2.91	0.06	6.95E-01	8.96E-01	ZNF491	zinc finger protein 491	chr19p13.2	1562211_a_at	NM_152356
3.44	3.39	0.05	6.95E-01	8.96E-01	SCIN	scinderin	chr7p21.3	222272_x_at	NM_001112706 /// NM_033128
2.13	2.07	0.06	6.95E-01	8.96E-01	HEATR1	HEAT repeat containing 1	chr1q43	232414_at	NM_018072
3.38	3.21	0.17	6.95E-01	8.96E-01	ATRNL1	attractin-like 1	chr10q26	213745_at	NM_207303
3.04	2.96	0.09	6.95E-01	8.96E-01	---	---	---	241282_at	---
2.28	2.21	0.07	6.95E-01	8.96E-01	---	---	---	1560954_at	---
2.89	2.77	0.12	6.95E-01	8.96E-01	FLJ30851 /// LOC375190	hypothetical LOC653140 /// hypothetical LOC375190	chr2p23.3	231386_at	NM_001040710 /// XR_040244 /// XR_040245 /// XR_040246
2.72	2.67	0.05	6.95E-01	8.96E-01	---	---	---	243148_at	---
2.71	2.64	0.07	6.95E-01	8.96E-01	CALML3	calmodulin-like 3	chr10pter-p13	210020_x_at	NM_005185
3.11	3.05	0.07	6.95E-01	8.96E-01	---	---	---	230948_at	---
2.99	2.92	0.07	6.95E-01	8.96E-01	NUP88	Nucleoporin 88kDa	chr17p13.2	214192_at	NM_002532
2.70	2.63	0.08	6.95E-01	8.96E-01	DNAJC5B	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	chr8q13.1	1554258_a_at	NM_033105
2.90	2.66	0.24	6.96E-01	8.96E-01	---	---	---	1561657_at	---
2.14	2.10	0.04	6.96E-01	8.96E-01	---	---	---	216463_at	---
3.02	2.93	0.09	6.96E-01	8.96E-01	ZNF174	zinc finger protein 174	chr16p13.3	210290_at	NM_001032292 /// NM_003450
3.58	3.53	0.05	6.96E-01	8.96E-01	HERC3	hect domain and RLD 3	chr4q21	206183_s_at	NM_014606
4.26	4.11	0.16	6.96E-01	8.96E-01	---	---	---	237483_at	---
2.45	2.38	0.07	6.96E-01	8.96E-01	---	---	---	240109_at	---

3.72	3.61	0.11	6.96E-01	8.96E-01	C21orf91	chromosome 21 open reading frame 91	chr21q21.1	220941_s_at	NM_001100420 /// NM_001100421 /// NM_017447																			
2.00	1.95	0.05	6.96E-01	8.96E-01	CYP4Z1	cytochrome P450, family 4, subfamily Z, polypeptide 1	chr1p33	237395_at	NM_178134																			
2.77	2.71	0.06	6.96E-01	8.96E-01	TTN	titin	chr2q31	208195_at	NM_003319 /// NM_133378 /// NM_133379 /// NM_133432 /// NM_133437																			
8.05	7.97	0.09	6.96E-01	8.96E-01	TSPAN3	tetraspanin 3	chr15q24.3	200973_s_at	NM_005724 /// NM_198902																			
2.01	1.96	0.05	6.96E-01	8.96E-01	FAM9B	family with sequence similarity 9, member B	chrXp22.32	1555538_s_at	NM_205849																			
6.71	6.65	0.06	6.96E-01	8.96E-01	MRPS15	mitochondrial ribosomal protein S15	chr1p35-p34.1	221437_s_at	NM_031280																			
1.95	1.91	0.04	6.96E-01	8.96E-01	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	chr1p13.3-p13.1	236539_at	NM_012411 /// NM_015967																			
8.22	8.12	0.10	6.96E-01	8.96E-01	IRAK1	interleukin-1 receptor-associated kinase 1	chrXq28	201587_s_at	NM_001025242 /// NM_001025243 /// NM_001569																			
5.58	5.43	0.15	6.96E-01	8.96E-01	TYMS	thymidylate synthetase	chr18p11.32	202589_at	NM_001071																			
1.95	1.91	0.04	6.96E-01	8.96E-01	SEC16B	SEC16 homolog B (S. cerevisiae)	chr1q25.2	239618_at	NM_033127																			
2.97	2.91	0.06	6.96E-01	8.96E-01	FLJ40330	hypothetical LOC645784	chr2p11.2	1556183_at	XR_015919																			
2.82	2.72	0.11	6.96E-01	8.96E-01	BAHCC1	BAH domain and coiled-coil containing 1	chr17q25.3	1559049_a_at	NM_001080519																			
2.95	2.88	0.06	6.96E-01	8.96E-01	C5orf47	chromosome 5 open reading frame 47	chr5q35.2	1557056_at	XM_001715744 /// XM_376444 /// XM_941190																			
2.64	2.59	0.05	6.96E-01	8.96E-01	---	---	---	1558758_s_at	---																			
2.23	2.17	0.06	6.96E-01	8.96E-01	SPHKAP	SPHK1 interactor, AKAP domain containing	chr2q36	228509_at	NM_030623																			
8.46	8.40	0.06	6.96E-01	8.96E-01	TSPAN3	tetraspanin 3	chr15q24.3	200972_at	NM_005724 /// NM_198902																			
2.05	2.00	0.05	6.96E-01	8.96E-01	SLC25A30	solute carrier family 25, member 30	chr13q14.12	216712_at	NM_001010875																			
2.64	2.59	0.05	6.97E-01	8.96E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	1561429_a_at	NM_033364																			
3.49	3.39	0.10	6.97E-01	8.96E-01	SLC26A6	solute carrier family 26, member 6	chr3p21.3	221572_s_at	NM_001040454 /// NM_022911 /// NM_134263 /// NM_134426																			
10.04	9.91	0.13	6.97E-01	8.96E-01	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	chr2q14.1	213101_s_at	NM_005721																			
2.69	2.61	0.08	6.97E-01	8.96E-01	EPHB1	EPH receptor B1	chr3q21-q23	211898_s_at	NM_004441																			
2.15	2.09	0.06	6.97E-01	8.96E-01	---	---	---	1561682_at	---																			
6.26	6.15	0.11	6.97E-01	8.96E-01	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	chr5p15.3-p15.2	203200_s_at	NM_002454 /// NM_024010																			
3.28	3.15	0.12	6.97E-01	8.96E-01	FLJ32255	hypothetical protein LOC643977	chr5p12	235291_s_at	XM_001720829 /// XM_001722479 /// XM_001723787																			
2.20	2.14	0.06	6.97E-01	8.96E-01	KIAA0430	KIAA0430	chr16p13.11	1558697_a_at	NM_014647																			
2.31	2.26	0.06	6.97E-01	8.96E-01	---	---	---	242798_at	---																			
2.73	2.68	0.05	6.97E-01	8.96E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	217263_x_at	NM_001001890 /// NM_001122607 /// NM_001754																			
2.17	2.12	0.05	6.97E-01	8.96E-01	KIAA1310	KIAA1310	chr2p12-p11.2	1558652_at	NM_001115016 /// NM_017991																			
2.32	2.25	0.07	6.97E-01	8.96E-01	---	---	---	241872_at	---																			

2.14	2.09	0.05	6.97E-01	8.96E-01	---	---	---	1566715_at	---																				
2.91	2.85	0.06	6.97E-01	8.97E-01	---	---	---	1558475_at	---																				
2.57	2.50	0.08	6.97E-01	8.97E-01	---	---	---	241785_at	---																				
2.20	2.15	0.05	6.97E-01	8.97E-01	LOC285423	hypothetical gene supported by BC031092	chr4q31.23	1569781_at	XR_041267 /// XR_041268 /// XR_041269																				
3.18	3.12	0.06	6.97E-01	8.97E-01	FAM105B	family with sequence similarity 105, member B	chr5p15.2	240834_at	NM_138348																				
5.82	5.70	0.12	6.97E-01	8.97E-01	GPATCH4	G patch domain containing 4	chr1q22	224634_at	NM_015590 /// NM_182679																				
2.85	2.79	0.06	6.97E-01	8.97E-01	---	---	---	234906_at	---																				
3.47	3.41	0.06	6.97E-01	8.97E-01	LOC256273 /// TRIM66	hypothetical protein LOC256273 /// tripartite motif-containing 66	chr11p15.3 /// chr11p15.4	229466_at	XM_001716253 /// XM_001716830 /// XM_001717903																				
1.82	1.78	0.04	6.97E-01	8.97E-01	---	---	---	243040_at	---																				
2.97	2.90	0.07	6.97E-01	8.97E-01	FLJ38028	hypothetical gene supported by AK095347	chr18p11.31	242683_at	XR_040234 /// XR_040235 /// XR_040236																				
2.64	2.55	0.09	6.97E-01	8.97E-01	CCDC66	coiled-coil domain containing 66	chr3p14.3	228122_at	NM_001012506 /// NM_001130911																				
7.11	7.02	0.09	6.98E-01	8.97E-01	MAP4	microtubule-associated protein 4	chr3p21	212566_at	NM_001134364 /// NM_001134365 /// NM_002375 /// NM_030884 /// NM_030885																				
4.98	4.89	0.09	6.98E-01	8.97E-01	ANP32A	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	chr15q22.3-q23	201038_s_at	NM_006305																				
3.53	3.46	0.07	6.98E-01	8.97E-01	---	---	---	238729_x_at	---																				
3.35	3.29	0.06	6.98E-01	8.97E-01	---	---	---	215476_at	---																				
5.53	5.45	0.08	6.98E-01	8.97E-01	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	chr11q14.1	222521_x_at	NM_004549																				
3.25	3.19	0.06	6.98E-01	8.97E-01	CD84	CD84 molecule	chr1q24	211189_x_at	NM_003874																				
3.53	3.46	0.07	6.98E-01	8.97E-01	FLJ42562	similar to echinoderm microtubule associated protein like 5	chr2p16.1	242785_at	XM_001725001 /// XM_001725002 /// XM_001725718 /// XM_001725719 /// XM_001726920 /// XM_001726921																				
3.42	3.33	0.09	6.98E-01	8.97E-01	RICH2	Rho-type GTPase-activating protein RICH2	chr17p12	205414_s_at	NM_014859																				
2.26	2.21	0.05	6.98E-01	8.97E-01	---	---	---	1560038_at	---																				
3.02	2.95	0.07	6.98E-01	8.97E-01	ZNF324B	Zinc finger protein 324B	chr19q13.43	236406_at	NM_207395																				
2.20	2.15	0.05	6.98E-01	8.97E-01	---	---	---	235743_at	---																				
2.90	2.85	0.05	6.98E-01	8.97E-01	---	---	---	233218_at	---																				
2.28	2.23	0.05	6.98E-01	8.97E-01	LOC645431	hypothetical LOC645431	chr14q23.3	236835_at	XR_015289 /// XR_015673 /// XR_040487																				
5.38	5.24	0.13	6.98E-01	8.97E-01	PARVB	parvin, beta	chr22q13.2-q13.33	204629_at	NM_001003828 /// NM_013327																				
2.61	2.55	0.06	6.98E-01	8.97E-01	---	---	---	234434_at	---																				
2.81	2.75	0.06	6.98E-01	8.97E-01	SHANK2	SH3 and multiple ankyrin repeat domains 2	chr11q13.3	215829_at	NM_012309 /// NM_133266																				
2.18	2.12	0.06	6.98E-01	8.97E-01	---	---	---	207479_at	---																				
1.84	1.79	0.04	6.98E-01	8.97E-01	---	---	---	1559842_at	---																				
2.29	2.24	0.06	6.98E-01	8.97E-01	WDR49	WD repeat domain 49	chr3q26.1	1564238_a_at	NM_178824																				

2.50	2.46	0.05	6.99E-01	8.97E-01	TRPM3	transient receptor potential cation channel, subfamily M, member 3	chr9q21.11-q21.12	220463_at	NM_001007470 /// NM_001007471 /// NM_020952 /// NM_024971 /// NM_206944 /// NM_206945 /// NM_206946 /// NM_206947 /// NM_206948																				
3.99	3.92	0.07	6.99E-01	8.97E-01	---	---	---	1566690_at	---																				
2.28	2.20	0.08	6.99E-01	8.97E-01	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	chr4q31.3	223700_at	NM_032117																				
5.26	5.20	0.06	6.99E-01	8.97E-01	HN1L	hematological and neurological expressed 1-like	chr16p13.3	212109_at	NM_144570																				
5.79	5.70	0.09	6.99E-01	8.97E-01	MKL1	megakaryoblastic leukemia (translocation) 1	chr22q13	212748_at	NM_020831																				
10.13	10.07	0.05	6.99E-01	8.97E-01	PGK1	phosphoglycerate kinase 1	chrXq13	200738_s_at	NM_000291																				
2.10	2.06	0.04	6.99E-01	8.97E-01	GLULD1	glutamate-ammonia ligase (glutamine synthetase) domain containing 1	chr6pter-q22.33	220393_at	NM_016571																				
2.95	2.88	0.07	6.99E-01	8.97E-01	---	---	---	237166_at	---																				
1.94	1.90	0.04	6.99E-01	8.97E-01	---	---	---	1566716_at	---																				
1.89	1.85	0.04	6.99E-01	8.97E-01	---	---	---	1552972_at	---																				
6.39	6.27	0.12	6.99E-01	8.97E-01	CTTN	cortactin	chr11q13	214073_at	NM_005231 /// NM_138565																				
2.25	2.20	0.04	6.99E-01	8.97E-01	FBXL14	F-box and leucine-rich repeat protein 14	chr12p13.33	1553682_at	NM_152441																				
5.05	4.85	0.19	6.99E-01	8.97E-01	CD86	CD86 molecule	chr3q21	210895_s_at	NM_006889 /// NM_175862																				
2.53	2.48	0.05	6.99E-01	8.97E-01	---	---	---	239407_at	---																				
2.35	2.31	0.04	6.99E-01	8.97E-01	---	---	---	1566524_a_at	---																				
3.22	3.14	0.09	6.99E-01	8.97E-01	IL1RAP	interleukin 1 receptor accessory protein	chr3q28	205227_at	NM_002182 /// NM_134470																				
3.44	3.33	0.10	7.00E-01	8.97E-01	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	chr8p11.23	238013_at	NM_021623																				
6.50	6.40	0.10	7.00E-01	8.97E-01	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	chr10p14-p13	203544_s_at	NM_003473																				
2.48	2.40	0.08	7.00E-01	8.97E-01	LOC647309	hypothetical LOC647309	chr3q28	1569616_at	XM_001716035 /// XM_930379 /// XM_942007																				
2.86	2.81	0.05	7.00E-01	8.98E-01	LOC285205	hypothetical LOC285205	chr3q13.12	1560514_at	XR_040986 /// XR_040987 /// XR_040988																				
7.35	7.22	0.13	7.00E-01	8.98E-01	ZFP91	zinc finger protein 91 homolog (mouse)	chr11q12	224636_at	NM_053023																				
4.94	4.81	0.13	7.00E-01	8.98E-01	SARS2	seryl-tRNA synthetase 2, mitochondrial	chr19q13.2	218702_at	NM_017827																				
3.43	3.37	0.05	7.00E-01	8.98E-01	WDR31	WD repeat domain 31	chr9q32	229516_at	NM_001006615 /// NM_001012361 /// NM_145241																				
2.32	2.27	0.05	7.00E-01	8.98E-01	CD300LG	CD300 molecule-like family member g	chr17q21.31	1555636_at	NM_145273																				
3.30	3.22	0.08	7.00E-01	8.98E-01	IL22RA1	interleukin 22 receptor, alpha 1	chr1p36.11	220056_at	NM_021258																				
2.03	1.99	0.05	7.00E-01	8.98E-01	---	---	---	233346_at	---																				
3.99	3.90	0.09	7.00E-01	8.98E-01	TMEM102	transmembrane protein 102	chr17p13.1	230633_at	NM_178518																				
2.31	2.27	0.04	7.00E-01	8.98E-01	RND2	Rho family GTPase 2	chr17q21	214393_at	NM_005440																				
2.05	2.00	0.05	7.00E-01	8.98E-01	---	---	---	1566585_at	---																				
8.90	8.71	0.18	7.00E-01	8.98E-01	GLIPR1	GLI pathogenesis-related 1	chr12q21.2	214085_x_at	NM_006851																				
8.89	8.79	0.10	7.00E-01	8.98E-01	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	chr1q42	212773_s_at	NM_014765																				
3.36	3.28	0.08	7.00E-01	8.98E-01	MESP2	mesoderm posterior 2 homolog (mouse)	chr15q26.1	1556015_a_at	NM_001039958																				
2.23	2.18	0.06	7.00E-01	8.98E-01	FAM111B	family with sequence similarity 111, member B	chr11q12.1	1557129_a_at	NM_198947																				
2.65	2.60	0.05	7.00E-01	8.98E-01	---	---	---	1557196_a_at	---																				
2.34	2.29	0.06	7.00E-01	8.98E-01	STXBP5L	syntaxin binding protein 5-like	chr3q13.33	240236_at	NM_014980																				
4.58	4.50	0.08	7.01E-01	8.98E-01	ZNF609	zinc finger protein 609	chr15q22.31	212618_at	NM_015042																				

2.16	2.10	0.06	7.01E-01	8.98E-01	LOC727933	hypothetical LOC727933	chr1p21.1	244540_at	XM_001128972 /// XM_001130924 /// XM_001722270																			
2.69	2.61	0.08	7.01E-01	8.98E-01	C14orf162	chromosome 14 open reading frame 162	chr14q24.1	220887_at	XR_040527 /// XR_040528 /// XR_040529																			
2.70	2.64	0.06	7.01E-01	8.98E-01	---	---	---	1561732_at	---																			
2.81	2.76	0.06	7.01E-01	8.98E-01	SNORA71A	small nucleolar RNA, H/ACA box 71A	chr20q11.23	1565858_at	NR_002911																			
3.10	3.02	0.08	7.01E-01	8.98E-01	---	---	---	233063_s_at	---																			
4.57	4.46	0.11	7.01E-01	8.98E-01	CABLES1	Cdk5 and Abl enzyme substrate 1	chr18q11.2	225531_at	NM_001100619 /// NM_138375 /// NR_023359																			
3.40	3.30	0.09	7.01E-01	8.98E-01	---	---	---	237744_at	---																			
2.70	2.65	0.05	7.01E-01	8.98E-01	---	---	---	217355_at	---																			
5.85	5.77	0.09	7.01E-01	8.98E-01	RANBP3	RAN binding protein 3	chr19p13.3	210120_s_at	NM_003624 /// NM_007320 /// NM_007322																			
3.51	3.44	0.08	7.01E-01	8.98E-01	C1orf86	chromosome 1 open reading frame 86	chr1p36.33	1556309_s_at	NM_182533 /// XM_001718861																			
4.85	4.77	0.08	7.01E-01	8.98E-01	N4BP1	NEDD4 binding protein 1	chr16q12.1	221867_at	NM_153029																			
2.77	2.71	0.05	7.01E-01	8.98E-01	LOC286135	hypothetical LOC286135	chr8p12	1569887_a_at	---																			
2.05	2.01	0.04	7.01E-01	8.98E-01	---	---	---	1561606_at	---																			
2.27	2.22	0.04	7.01E-01	8.98E-01	RP11-35N6.1	plasticity related gene 3	chr9q31.1	219732_at	NM_017753 /// NM_207299																			
4.72	4.63	0.09	7.01E-01	8.98E-01	USP24	ubiquitin specific peptidase 24	chr1p32.3	212381_at	NM_015306																			
8.75	8.69	0.06	7.02E-01	8.98E-01	GTF3A	general transcription factor IIIA	chr13q12.3-q13.1	201338_x_at	NM_002097 /// XM_001715623 /// XM_001716951 /// XM_001717641																			
2.30	2.25	0.05	7.02E-01	8.98E-01	---	---	---	244846_at	---																			
2.97	2.91	0.06	7.02E-01	8.98E-01	NKX6-1	NK6 homeobox 1	chr4q21.2-q22	221366_at	NM_006168																			
7.45	7.37	0.08	7.02E-01	8.99E-01	TMEM222	transmembrane protein 222	chr1p36.11	52078_at	NM_032125																			
3.50	3.44	0.06	7.02E-01	8.99E-01	PROCA1	proline-rich cyclin A1-interacting protein	chr17q11.2	232647_at	NM_152465																			
5.10	5.03	0.07	7.02E-01	8.99E-01	TTC23	tetratricopeptide repeat domain 23	chr15q26.3	219838_at	NM_001040655 /// NM_001040656 /// NM_001040657 /// NM_001040658 /// NM_001040659 /// NM_001040660 /// NM_022905																			
2.94	2.89	0.05	7.02E-01	8.99E-01	OR51E2	olfactory receptor, family 51, subfamily E, member 2	chr11p15	221424_s_at	NM_030774																			
2.57	2.52	0.06	7.02E-01	8.99E-01	VTCN1	V-set domain containing T cell activation inhibitor 1	chr1p13.1	219768_at	NM_024626																			
3.30	3.24	0.06	7.02E-01	8.99E-01	RASGEF1C	RasGEF domain family, member 1C	chr5q35.3	236748_at	NM_175062																			
2.58	2.52	0.06	7.02E-01	8.99E-01	MYL4	myosin, light chain 4, alkali; atrial, embryonic	chr17q21-qter	216054_x_at	NM_001002841 /// NM_002476																			
4.05	3.98	0.08	7.02E-01	8.99E-01	ORAI2	ORAI calcium release-activated calcium modulator 2	chr7q22.1	218811_at	NM_001126340 /// NM_032831																			
1.81	1.77	0.04	7.02E-01	8.99E-01	C14orf39	chromosome 14 open reading frame 39	chr14q23.1	1561985_at	NM_174978																			
3.24	3.11	0.13	7.03E-01	8.99E-01	GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa	chr5q12.2-q13.3	223758_s_at	NM_001515																			
2.13	2.07	0.06	7.03E-01	8.99E-01	---	---	---	217126_at	---																			
3.29	3.24	0.05	7.03E-01	8.99E-01	---	---	---	239256_at	---																			
2.02	1.98	0.04	7.03E-01	8.99E-01	---	---	---	1556486_at	---																			

2.41	2.36	0.05	7.03E-01	8.99E-01	---	---	---	236005_at	---
2.39	2.33	0.06	7.03E-01	8.99E-01	OR5AK4P	olfactory receptor, family 5, subfamily AK, member 4 pseudogene	chr11q12.1	1567022_at	---
2.16	2.11	0.05	7.03E-01	8.99E-01	---	---	---	237798_at	---
3.93	3.85	0.08	7.03E-01	8.99E-01	---	---	---	221242_at	---
4.20	4.13	0.07	7.03E-01	8.99E-01	HOXB9	homeobox B9	chr17q21.3	226461_at	NM_024017
4.46	4.37	0.09	7.03E-01	8.99E-01	---	---	---	1558801_at	---
3.08	3.01	0.07	7.03E-01	8.99E-01	---	---	---	237371_at	---
2.50	2.44	0.05	7.03E-01	8.99E-01	---	---	---	1557721_at	---
4.48	4.34	0.13	7.03E-01	8.99E-01	JARID1A	jumonji, AT rich interactive domain 1A	chr12p11	226371_at	NM_001042603 /// NM_005056
4.10	4.04	0.05	7.03E-01	8.99E-01	CYTH3	Cytohesin 3	chr7p22.1	236136_at	NM_004227
2.77	2.66	0.11	7.03E-01	8.99E-01	SEH1L	SEH1-like (S. cerevisiae)	chr18p11.21	223225_s_at	NM_001013437 /// NM_031216
12.19	12.12	0.06	7.04E-01	8.99E-01	RPS20	ribosomal protein S20	chr8q12	200949_x_at	NM_001023
9.19	9.07	0.12	7.04E-01	8.99E-01	NFIC	Nuclear factor I/C (CCAAT-binding transcription factor)	chr19p13.3	226895_at	NM_005597 /// NM_205843
2.88	2.80	0.08	7.04E-01	8.99E-01	---	---	---	241948_at	---
2.69	2.64	0.05	7.04E-01	8.99E-01	CCDC78	coiled-coil domain containing 78	chr16p13.3	236745_at	NM_001031737 /// NM_173476
2.58	2.48	0.10	7.04E-01	8.99E-01	INTU	inturned planar cell polarity effector homolog (Drosophila)	chr4q28.1	228946_at	NM_015693
4.34	4.28	0.06	7.04E-01	8.99E-01	---	---	---	1559821_at	---
7.31	7.20	0.11	7.04E-01	8.99E-01	ZDHHC3	zinc finger, DHHC-type containing 3	chr3p21.31	218078_s_at	NM_016598
4.11	4.02	0.09	7.04E-01	8.99E-01	HSPA1L	heat shock 70kDa protein 1-like	chr6p21.3	210189_at	NM_005527
3.73	3.46	0.26	7.04E-01	8.99E-01	---	---	---	244026_at	---
3.03	2.95	0.08	7.04E-01	8.99E-01	IL1RAPL2	interleukin 1 receptor accessory protein-like 2	chrXq22.2-q22.3	221112_at	NM_017416
3.00	2.92	0.08	7.04E-01	8.99E-01	FBXW7	F-box and WD repeat domain containing 7	chr4q31.3	229419_at	NM_001013415 /// NM_018315 /// NM_033632
2.67	2.61	0.06	7.04E-01	8.99E-01	MED12L	mediator complex subunit 12-like	chr3q25.1	1555300_a_at	NM_053002
5.18	5.09	0.09	7.04E-01	9.00E-01	FZD8	frizzled homolog 8 (Drosophila)	chr10p11.21	227405_s_at	NM_031866
4.97	4.80	0.17	7.04E-01	9.00E-01	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	chr2p22.1	218311_at	NM_003618
3.88	3.79	0.08	7.04E-01	9.00E-01	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	chr10q11.21	239077_at	NM_018590
2.20	2.15	0.05	7.04E-01	9.00E-01	---	---	---	1566981_at	---
3.94	3.86	0.08	7.04E-01	9.00E-01	C5orf15	Chromosome 5 open reading frame 15	chr5q31.1	229260_at	NM_020199
4.78	4.66	0.13	7.04E-01	9.00E-01	B4GALNT3	beta-1,4-N-acetyl-galactosaminyl transferase 3	chr12p13.33	229909_at	NM_173593
4.51	4.44	0.07	7.04E-01	9.00E-01	SLC22A18AS	solute carrier family 22 (organic cation transporter), member 18 antisense	chr11p15.5	206097_at	XR_041457 /// XR_041458 /// XR_041459
2.07	2.02	0.04	7.04E-01	9.00E-01	---	---	---	235337_at	---
6.38	6.24	0.13	7.04E-01	9.00E-01	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	chr1p36.1	212908_at	NM_015291
2.85	2.79	0.06	7.04E-01	9.00E-01	MAPRE3	microtubule-associated protein, RP/EB family, member 3	chr2p23.3-p23.1	214270_s_at	NM_012326
5.51	5.44	0.08	7.05E-01	9.00E-01	CSTF2	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	chrXq22.1	204459_at	NM_001325
2.46	2.39	0.07	7.05E-01	9.00E-01	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	chr5q33.1	244396_at	NM_005754 /// NM_198395
3.17	3.09	0.08	7.05E-01	9.00E-01	ALS2CL	ALS2 C-terminal like	chr3p21.31	229887_at	NM_147129 /// NM_182775
3.96	3.90	0.06	7.05E-01	9.00E-01	---	---	---	1570607_at	---
2.51	2.44	0.07	7.05E-01	9.00E-01	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	chr11q13	207497_s_at	NM_000139
3.94	3.86	0.09	7.05E-01	9.00E-01	LPHN1	latrophilin 1	chr19p13.2	219145_at	NM_001008701 /// NM_014921
5.41	5.32	0.09	7.05E-01	9.00E-01	BPHL	biphenyl hydrolase-like (serine hydrolase)	chr6p25	205750_at	NM_004332
6.75	6.67	0.08	7.05E-01	9.00E-01	PMS2L11	postmeiotic segregation increased 2-like 11 pseudogene	chr7q11.23	179_at	NR_023383 /// XM_001715908 /// XM_001717503
4.14	3.93	0.21	7.05E-01	9.00E-01	GMFB	glia maturation factor, beta	chr14q22.2	202543_s_at	NM_004124
4.51	4.35	0.17	7.05E-01	9.00E-01	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	chr1q32-q41	205404_at	NM_005525 /// NM_181755

8.25	8.11	0.15	7.05E-01	9.00E-01	FBXO21	F-box protein 21	chr12q24.22	212229_s_at	NM_015002 /// NM_033624																				
4.34	4.26	0.07	7.05E-01	9.00E-01	LOC100128071	similar to hCG41624	chr1p35.1	1556560_a_at	XM_001724365 /// XM_001724643 /// XM_001724939																				
3.97	3.90	0.07	7.05E-01	9.00E-01	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	chr19p13.3	211865_s_at	NM_016263																				
4.74	4.69	0.05	7.05E-01	9.00E-01	MGC5370	Hypothetical protein MGC5370	chr12q14.3	244616_x_at	---																				
2.64	2.58	0.06	7.05E-01	9.00E-01	---	---	---	1559026_at	---																				
3.27	3.20	0.07	7.05E-01	9.00E-01	EIF4E	eukaryotic translation initiation factor 4E	chr4q21-q25	237718_at	NM_001130678 /// NM_001130679 /// NM_001968																				
6.82	6.73	0.09	7.06E-01	9.01E-01	STAT1	signal transducer and activator of transcription 1, 91kDa	chr2q32.2	AFFX-HUMISGF3A/M97935_3_at	NM_007315 /// NM_139266																				
2.55	2.46	0.08	7.06E-01	9.01E-01	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	chr11q23.1-q23.2	239616_at	NM_015523																				
2.80	2.75	0.05	7.06E-01	9.01E-01	SNX19	sorting nexin 19	chr11q25	1561710_at	NM_014758																				
3.91	3.86	0.05	7.06E-01	9.01E-01	PRDM12	PR domain containing 12	chr9q33-q34	220894_x_at	NM_021619																				
2.21	2.17	0.04	7.06E-01	9.01E-01	FLJ12331	ribosomal protein S2 pseudogene	chr16q22.1	207489_at	---																				
2.28	2.23	0.05	7.06E-01	9.01E-01	---	---	---	1569573_at	---																				
2.97	2.87	0.10	7.06E-01	9.01E-01	GLIS3	GLIS family zinc finger 3	chr9p24.2	229435_at	NM_001042413 /// NM_152629																				
2.65	2.58	0.07	7.06E-01	9.01E-01	MANEA	mannosidase, endo-alpha	chr6q16.1	1554193_s_at	NM_024641																				
6.44	6.35	0.09	7.06E-01	9.01E-01	ZYX	zyxin	chr7q32	215706_x_at	NM_001010972 /// NM_003461																				
3.40	3.29	0.11	7.06E-01	9.01E-01	---	---	---	235000_at	---																				
2.26	2.20	0.06	7.06E-01	9.01E-01	---	---	---	1570005_at	---																				
2.08	2.04	0.05	7.06E-01	9.01E-01	OR2W1	olfactory receptor, family 2, subfamily W, member 1	chr6p21.33-p21.31	221451_s_at	NM_030903																				
2.83	2.76	0.07	7.06E-01	9.01E-01	---	---	---	1560817_at	---																				
6.40	6.30	0.10	7.06E-01	9.01E-01	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	chr6q23-q24	212642_s_at	NM_006734																				
5.84	5.74	0.09	7.06E-01	9.01E-01	---	---	---	227087_at	---																				
2.04	2.00	0.04	7.06E-01	9.01E-01	ITGB6	integrin, beta 6	chr2q24.2	226535_at	NM_000888																				
2.74	2.66	0.07	7.06E-01	9.01E-01	---	---	---	237562_at	---																				
11.74	11.70	0.05	7.06E-01	9.01E-01	PEBP1	phosphatidylethanolamine binding protein 1	chr12q24.23	205353_s_at	NM_002567																				
3.17	3.12	0.06	7.07E-01	9.01E-01	BCCIP	BRCA2 and CDKN1A interacting protein	chr10q26.1	227896_at	NM_016567 /// NM_078468 /// NM_078469																				
2.79	2.72	0.06	7.07E-01	9.01E-01	TDH	L-threonine dehydrogenase	chr8p23.1	1553493_a_at	NR_001578																				
2.23	2.18	0.05	7.07E-01	9.01E-01	---	---	---	237633_at	---																				
4.72	4.66	0.06	7.07E-01	9.01E-01	---	---	---	244087_at	---																				
2.71	2.66	0.05	7.07E-01	9.01E-01	CARS	Cysteinyl-tRNA synthetase	chr11p15.5	1562436_at	NM_001014437 /// NM_001014438 /// NM_001751 /// NM_139273																				
1.90	1.86	0.04	7.07E-01	9.01E-01	---	---	---	1564909_at	---																				
2.42	2.36	0.06	7.07E-01	9.01E-01	SAP30L	SAP30-like	chr5q33.2	226772_s_at	NM_001131062 /// NM_001131063 /// NM_024632 /// NR_024084																				
2.41	2.36	0.06	7.07E-01	9.01E-01	FANCA	Fanconi anemia, complementation group A	chr16q24.3	236976_at	NM_000135 /// NM_001018112																				
2.64	2.59	0.05	7.07E-01	9.01E-01	FLJ10404	hypothetical protein FLJ10404	chr5q35.3	243047_at	NM_019057 /// NR_024019																				

4.09	3.99	0.10	7.07E-01	9.01E-01	PGAM5	phosphoglycerate mutase family member 5	chr12q24.33	1555943_at	NM_138575 /// XM_001713960																				
1.91	1.86	0.05	7.07E-01	9.01E-01	KIAA1430	KIAA1430	chr4q35.1	1554550_at	NM_020827																				
3.66	3.61	0.05	7.07E-01	9.01E-01	---	---	---	238467_at	---																				
2.14	2.09	0.04	7.07E-01	9.01E-01	FAM55C	family with sequence similarity 55, member C	chr3q12.3	235030_at	NM_001134456 /// NM_145037																				
2.52	2.46	0.06	7.07E-01	9.02E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	241208_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257																				
3.16	3.10	0.05	7.07E-01	9.02E-01	AXIN2	axin 2	chr17q23-q24	222695_s_at	NM_004655																				
2.27	2.22	0.05	7.08E-01	9.02E-01	ROS1	c-ros oncogene 1 , receptor tyrosine kinase	chr6q22	244363_at	NM_002944																				
1.95	1.90	0.05	7.08E-01	9.02E-01	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	1569021_at	NM_002645																				
5.95	5.81	0.14	7.08E-01	9.02E-01	---	---	---	226932_at	---																				
2.19	2.12	0.07	7.08E-01	9.02E-01	BTG3	BTG family, member 3	chr21q21.1-q21.2	215425_at	NM_001130914 /// NM_006806																				
2.91	2.83	0.08	7.08E-01	9.02E-01	C12orf30	chromosome 12 open reading frame 30	chr12q24.13	236816_at	NM_024953																				
2.79	2.73	0.06	7.08E-01	9.02E-01	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	chr13q32	205338_s_at	NM_001129889 /// NM_001922																				
2.81	2.76	0.06	7.08E-01	9.02E-01	RXFP1	relaxin/insulin-like family peptide receptor 1	chr4q32.1	238206_at	NM_021634																				
7.90	7.83	0.07	7.08E-01	9.02E-01	RNF12	Ring finger protein 12	chrXq13-q21	242121_at	NM_016120 /// NM_183353																				
2.20	2.15	0.04	7.08E-01	9.02E-01	ZSCAN12	zinc finger and SCAN domain containing 12	chr6p22.2-p21.3	217098_s_at	XR_041200 /// XR_041201 /// XR_041202																				
5.07	4.92	0.15	7.08E-01	9.02E-01	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	215434_x_at	NM_001037675 /// NM_001039703 /// NM_001101663 /// NM_001102663 /// NM_015383 /// NM_017940 /// NM_173638 /// NM_183372 /// XM_001717398 /// XM_001717802 /// XM_001721345 /// XM_001721349 /// XM_001722184 /// XM_001723523 /// XM_001726946																				
1.85	1.81	0.04	7.08E-01	9.02E-01	PCDHB13	protocadherin beta 13	chr5q31	232415_at	NM_018933																				
3.21	3.15	0.06	7.08E-01	9.02E-01	---	---	---	237025_at	---																				
6.97	6.88	0.09	7.08E-01	9.02E-01	NAGLU	N-acetylglucosaminidase, alpha-	chr17q21	204360_s_at	NM_000263																				
2.34	2.29	0.05	7.08E-01	9.02E-01	---	---	---	1569859_at	---																				
2.08	2.04	0.04	7.08E-01	9.02E-01	TLL1	tolloid-like 1	chr4q32-q33	1555071_at	NM_012464																				
2.44	2.36	0.08	7.09E-01	9.02E-01	---	---	---	242763_at	---																				
8.27	8.19	0.08	7.09E-01	9.02E-01	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr19p13.11	202737_s_at	NM_012321																				

2.12	2.06	0.05	7.09E-01	9.02E-01	---	---	---	215627_at	---
7.18	7.10	0.08	7.09E-01	9.02E-01	AP1B1	adaptor-related protein complex 1, beta 1 subunit	chr22q12|22q12.2	205423_at	NM_001127 /// NM_145730
5.92	5.84	0.08	7.09E-01	9.02E-01	---	---	---	216421_at	---
2.07	2.02	0.06	7.09E-01	9.02E-01	PTPRC	protein tyrosine phosphatase, receptor type, C	chr1q31-q32	1552480_s_at	NM_002838 /// NM_080921 /// NM_080922 /// NM_080923
2.52	2.47	0.05	7.09E-01	9.02E-01	LOC100129895	Hypothetical protein LOC100129895	chr16p13.2	1560290_at	XM_001722541 /// XM_001722704 /// XM_001725097
8.40	8.33	0.07	7.09E-01	9.02E-01	---	---	---	226282_at	---
2.24	2.19	0.05	7.09E-01	9.02E-01	FKBP4	FK506 binding protein 4, 59kDa	chr12p13.33	1560305_x_at	NM_002014
2.34	2.29	0.05	7.09E-01	9.02E-01	STON2	Stonin 2	chr14q31.1	242583_at	NM_033104
2.49	2.43	0.06	7.09E-01	9.02E-01	IKIP	IKK interacting protein	chr12q23.1	235202_x_at	NM_153687 /// NM_201612 /// NM_201613
2.38	2.33	0.05	7.09E-01	9.02E-01	---	---	---	1565787_at	---
4.74	4.70	0.04	7.09E-01	9.02E-01	---	---	---	241520_x_at	---
2.89	2.81	0.08	7.09E-01	9.02E-01	PCMTD1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	chr8q11.23	238114_at	NM_052937
2.03	1.97	0.05	7.09E-01	9.02E-01	---	---	---	241072_s_at	---
4.60	4.55	0.05	7.09E-01	9.02E-01	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	chr1p36.2	216042_at	NM_001039664 /// NM_003790 /// NM_148965 /// NM_148966 /// NM_148967 /// NM_148970
8.67	8.52	0.15	7.09E-01	9.02E-01	CD163	CD163 molecule	chr12p13.3	215049_x_at	NM_004244 /// NM_203416
6.68	6.55	0.13	7.09E-01	9.02E-01	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	chr22q13.1	213603_s_at	NM_002872
2.36	2.30	0.06	7.10E-01	9.02E-01	---	---	---	1558371_a_at	---
4.78	4.72	0.07	7.10E-01	9.02E-01	C12orf49	chromosome 12 open reading frame 49	chr12q24.22	218867_s_at	NM_024738
1.82	1.78	0.04	7.10E-01	9.02E-01	---	---	---	216737_at	---
2.41	2.37	0.04	7.10E-01	9.02E-01	---	---	---	237845_at	---
3.52	3.45	0.07	7.10E-01	9.02E-01	LOC645722	hypothetical LOC645722	chr17q23.2	228978_at	XM_944447
5.63	5.57	0.06	7.10E-01	9.02E-01	TGIF2	TGFB-induced factor homeobox 2	chr20q11.2-q12	216262_s_at	NM_021809
2.74	2.68	0.06	7.10E-01	9.02E-01	SH3GL3	SH3-domain GRB2-like 3	chr15q24	205636_at	NM_003027
6.98	6.92	0.07	7.10E-01	9.03E-01	NDFIP1	Nedd4 family interacting protein 1	chr5q31.3	222422_s_at	NM_030571
2.20	2.14	0.06	7.10E-01	9.03E-01	HELLS	helicase, lymphoid-specific	chr10q24.2	227349_at	NM_018063
1.87	1.83	0.04	7.10E-01	9.03E-01	---	---	---	1561564_at	---
3.56	3.49	0.07	7.10E-01	9.03E-01	---	---	---	235769_at	---
2.18	2.13	0.05	7.10E-01	9.03E-01	---	---	---	1562732_at	---
2.86	2.81	0.06	7.10E-01	9.03E-01	---	---	---	240217_s_at	---
3.25	3.09	0.16	7.10E-01	9.03E-01	TACSTD2	tumor-associated calcium signal transducer 2	chr1p32-p31	202286_s_at	NM_002353
3.52	3.43	0.09	7.10E-01	9.03E-01	---	---	---	1563222_at	---
2.24	2.19	0.05	7.10E-01	9.03E-01	LOC100130458	Hypothetical protein LOC100130458	chr9p13.2	239214_at	XM_001716901 /// XM_001724442 /// XM_001725999
3.79	3.68	0.11	7.10E-01	9.03E-01	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	chr9p13-p12	205407_at	NM_021111
2.11	2.06	0.05	7.10E-01	9.03E-01	IFNA16	interferon, alpha 16	chr9p22	208448_x_at	NM_002173
6.63	6.49	0.14	7.11E-01	9.03E-01	EPC2	enhancer of polycomb homolog 2 (Drosophila)	chr2q23.1	225838_at	NM_015630
2.94	2.88	0.06	7.11E-01	9.03E-01	MUC20	mucin 20, cell surface associated	chr3q29	230043_at	NM_001098516 /// NM_152673 /// XM_001726694

5.80	5.61	0.19	7.11E-01	9.03E-01	---	---	---	242108_at	---
2.68	2.60	0.08	7.11E-01	9.03E-01	---	---	---	238407_at	---
6.35	6.25	0.10	7.11E-01	9.03E-01	CYLD	cylindromatosis (turban tumor syndrome)	chr16q12.1	213295_at	NM_001042355 /// NM_001042412 /// NM_015247
3.26	3.19	0.08	7.11E-01	9.03E-01	---	---	---	1561942_x_at	---
6.81	6.68	0.12	7.11E-01	9.03E-01	PPP4R2	protein phosphatase 4, regulatory subunit 2	chr3p13	225519_at	NM_174907
2.83	2.72	0.11	7.11E-01	9.03E-01	NSD1	nuclear receptor binding SET domain protein 1	chr5q35.2-q35.3	243612_at	NM_022455 /// NM_172349
4.93	4.85	0.08	7.11E-01	9.03E-01	HABP4	hyaluronan binding protein 4	chr9q22.3-q31	233919_s_at	NM_014282
2.54	2.49	0.05	7.11E-01	9.03E-01	ST7L	suppression of tumorigenicity 7 like	chr1p13.2	1552738_a_at	NM_017744 /// NM_138727 /// NM_138728 /// NM_138729
2.68	2.63	0.04	7.11E-01	9.03E-01	RS1	retinoschisin 1	chrXp22.2-p22.1	216937_s_at	NM_000330
2.05	2.00	0.05	7.11E-01	9.03E-01	---	---	---	240864_at	---
5.90	5.72	0.17	7.11E-01	9.04E-01	KCTD20	potassium channel tetramerisation domain containing 20	chr6p21.31	223176_at	NM_173562
2.22	2.16	0.06	7.11E-01	9.04E-01	NUDCD1	NudC domain containing 1	chr8q23	225438_at	NM_001128211 /// NM_032869
3.01	2.96	0.05	7.11E-01	9.04E-01	ZNF540	zinc finger protein 540	chr19q13.12	242697_at	NM_152606
2.14	2.09	0.05	7.11E-01	9.04E-01	BXDC5	brix domain containing 5	chr1p22.3	234244_at	NM_025065
6.28	6.21	0.06	7.11E-01	9.04E-01	SPECC1L	SPECC1-like	chr22q11.23	212480_at	NM_015330
2.68	2.63	0.06	7.12E-01	9.04E-01	CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	chr15q22	206227_at	NM_003613
2.34	2.30	0.05	7.12E-01	9.04E-01	PCSK6	proprotein convertase subtilisin/kexin type 6	chr15q26.3	211262_at	NM_002570 /// NM_138319 /// NM_138320 /// NM_138321 /// NM_138322 /// NM_138323 /// NM_138324 /// NM_138325
3.52	3.47	0.05	7.12E-01	9.04E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1564590_a_at	NM_153003
2.46	2.39	0.07	7.12E-01	9.04E-01	LOC339975	hypothetical protein LOC339975	chr4q35.2	1561323_at	---
3.07	2.98	0.09	7.12E-01	9.04E-01	STK32B	serine/threonine kinase 32B	chr4p16.2-p16.1	219686_at	NM_018401
6.01	5.91	0.10	7.12E-01	9.04E-01	PCGF1	polycomb group ring finger 1	chr2p13.1	210023_s_at	NM_032673
2.59	2.55	0.04	7.12E-01	9.04E-01	VNN3	vanin 3	chr6q23-q24	220528_at	NM_001024460 /// NM_018399 /// NM_078625
8.34	8.26	0.09	7.12E-01	9.04E-01	APRT	adenine phosphoribosyltransferase	chr16q24	213892_s_at	NM_000485 /// NM_001030018
10.14	10.06	0.08	7.12E-01	9.04E-01	GPI /// LOC100133951	glucose phosphate isomerase /// similar to Glucose phosphate isomerase	chr19q13.1	208308_s_at	NM_000175 /// XM_001716177
1.95	1.91	0.04	7.12E-01	9.04E-01	WNT16	wingless-type MMTV integration site family, member 16	chr7q31	224022_x_at	NM_016087 /// NM_057168
7.10	7.00	0.10	7.12E-01	9.04E-01	CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4	chr3p25.1	229595_at	NM_001098502 /// NM_144636
2.50	2.44	0.06	7.12E-01	9.04E-01	---	---	---	236334_at	---
2.58	2.55	0.04	7.12E-01	9.04E-01	---	---	---	1561806_at	---
5.90	5.83	0.07	7.12E-01	9.04E-01	KIAA0141	KIAA0141	chr5q31.3	227056_at	NM_014773
1.88	1.84	0.04	7.12E-01	9.04E-01	---	---	---	234779_at	---
2.62	2.55	0.07	7.12E-01	9.04E-01	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2	chr1p13	208564_at	NM_004974

2.23	2.19	0.04	7.12E-01	9.04E-01	TMEM132D	transmembrane protein 132D	chr12q24.32-q24.33	236377_at	NM_133448
6.70	6.61	0.09	7.12E-01	9.04E-01	GIYD1 /// GIYD2	GIY-YIG domain containing 1 /// GIY-YIG domain containing 2	chr16p11.2	218317_x_at	NM_001014999 /// NM_001015000 /// NM_024044 /// NM_178044
7.41	7.26	0.16	7.12E-01	9.04E-01	CTSC	cathepsin C	chr11q14.1-q14.3	225646_at	NM_001114173 /// NM_001814 /// NM_148170
2.20	2.14	0.06	7.12E-01	9.04E-01	---	---	---	1560185_at	---
2.71	2.65	0.07	7.12E-01	9.04E-01	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	chr21q22.11	234938_at	NM_001011545 /// NM_001186 /// NM_206866
2.82	2.76	0.06	7.12E-01	9.04E-01	PADI4	peptidyl arginine deiminase, type IV	chr1p36.13	220001_at	NM_012387
1.96	1.92	0.04	7.12E-01	9.04E-01	---	---	---	235118_at	---
3.05	2.99	0.06	7.13E-01	9.04E-01	MAP3K15	Mitogen-activated protein kinase kinase kinase 15	chrXp22.12	242581_at	NM_001001671
6.09	6.00	0.09	7.13E-01	9.04E-01	CABIN1	calcineurin binding protein 1	chr22q11.23	37652_at	NM_012295
2.70	2.64	0.06	7.13E-01	9.04E-01	FAM13A1OS	FAM13A1 opposite strand (non-protein coding)	chr4q22.1	1558711_at	NR_002806
6.30	6.11	0.19	7.13E-01	9.04E-01	---	---	---	243514_at	---
2.95	2.88	0.07	7.13E-01	9.04E-01	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	chr10p15.3	1565680_at	NM_014974
7.39	7.33	0.06	7.13E-01	9.04E-01	LMNA	lamin A/C	chr1q21.2-q21.3	212089_at	NM_005572 /// NM_170707 /// NM_170708
2.41	2.37	0.04	7.13E-01	9.04E-01	LOC390933	Hypothetical LOC390933	chr19q13.2	244818_at	XR_019076 /// XR_037749 /// XR_037783
2.47	2.42	0.05	7.13E-01	9.04E-01	SKIL	SKI-like oncogene	chr3q26	215889_at	NM_005414
3.56	3.49	0.07	7.13E-01	9.04E-01	---	---	---	1570065_at	---
3.28	3.21	0.06	7.13E-01	9.04E-01	C21orf58	chromosome 21 open reading frame 58	chr21q22.3	1555198_x_at	NM_058180
6.15	5.95	0.20	7.13E-01	9.04E-01	SR140	U2-associated SR140 protein	chr3q23	212058_at	NM_001080415
4.92	4.85	0.06	7.13E-01	9.04E-01	C1orf69	chromosome 1 open reading frame 69	chr1q42.13	236629_at	NM_001010867
2.52	2.47	0.05	7.13E-01	9.04E-01	USP44	ubiquitin specific peptidase 44	chr12q22	224048_at	NM_001042403 /// NM_032147
5.73	5.64	0.09	7.13E-01	9.04E-01	SH3RF3	SH3 domain containing ring finger 3	chr2q13	228461_at	NM_001099289
2.67	2.61	0.06	7.13E-01	9.04E-01	---	---	---	242425_at	---
4.07	4.00	0.07	7.14E-01	9.04E-01	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	chr20p11.23	205218_at	NM_006466
2.09	2.05	0.04	7.14E-01	9.04E-01	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	chr1p33	1554931_at	NM_000778
2.19	2.13	0.06	7.14E-01	9.04E-01	RHPN2	rhophilin, Rho GTPase binding protein 2	chr19q13.11	227196_at	NM_033103
2.78	2.71	0.07	7.14E-01	9.04E-01	---	---	---	244702_at	---
2.58	2.54	0.04	7.14E-01	9.04E-01	---	---	---	220822_at	---
2.68	2.62	0.05	7.14E-01	9.04E-01	---	---	---	216431_at	---
6.94	6.83	0.11	7.14E-01	9.04E-01	PLEKHM2	pleckstrin homology domain containing, family M (with RUN domain) member 2	chr1p36.21	212146_at	NM_015164
4.64	4.49	0.15	7.14E-01	9.04E-01	MGC4172	short-chain dehydrogenase/reductase	chr17q12	218756_s_at	NM_024308
11.02	10.95	0.07	7.14E-01	9.04E-01	RPL5	ribosomal protein L5	chr1p22.1	200937_s_at	NM_000969
5.34	5.18	0.16	7.14E-01	9.05E-01	BAHCC1	BAH domain and coiled-coil containing 1	chr17q25.3	219218_at	NM_001080519
3.61	3.54	0.07	7.14E-01	9.05E-01	MTMR12	myotubularin related protein 12	chr5p13.3	220953_s_at	NM_001040446
3.73	3.62	0.11	7.14E-01	9.05E-01	FAM164C	family with sequence similarity 164, member C	chr14q24.3	220107_s_at	NM_001042430 /// NM_024643
2.49	2.44	0.06	7.14E-01	9.05E-01	THNSL1	threonine synthase-like 1 (S. cerevisiae)	chr10p12.1	219800_s_at	NM_024838
1.93	1.88	0.04	7.14E-01	9.05E-01	---	---	---	1555365_x_at	---
7.97	7.87	0.09	7.14E-01	9.05E-01	USF2	upstream transcription factor 2, c-fos interacting	chr19q13	202152_x_at	NM_003367 /// NM_207291
2.56	2.50	0.06	7.14E-01	9.05E-01	---	---	---	1562468_at	---
2.06	2.01	0.04	7.14E-01	9.05E-01	---	---	---	243162_at	---
2.29	2.25	0.04	7.15E-01	9.05E-01	---	---	---	1566768_at	---

5.60	5.50	0.11	7.15E-01	9.05E-01	ZNF131	Zinc finger protein 131	chr5p12-p11	1557384_at	NM_003432																				
5.98	5.83	0.14	7.15E-01	9.05E-01	GAS7	growth arrest-specific 7	chr17p13.1	202191_s_at	NM_001130831 /// NM_003644 /// NM_201432 /// NM_201433																				
2.70	2.62	0.09	7.15E-01	9.05E-01	CTLA4	cytotoxic T-lymphocyte-associated protein 4	chr2q33	221331_x_at	NM_001037631 /// NM_005214																				
3.55	3.48	0.07	7.15E-01	9.05E-01	C2orf53	chromosome 2 open reading frame 53	chr2p23.3	237319_at	NM_178553																				
2.99	2.94	0.05	7.15E-01	9.05E-01	---	---	---	243455_at	---																				
7.08	7.00	0.08	7.15E-01	9.05E-01	OSBP	oxysterol binding protein	chr11q12-q13	201799_s_at	NM_002556																				
6.79	6.69	0.09	7.15E-01	9.05E-01	GAPVD1	GTPase activating protein and VPS9 domains 1	chr9q33.3	212802_s_at	NM_015635																				
3.26	3.20	0.06	7.15E-01	9.05E-01	TAC4	tachykinin 4 (hemokinin)	chr17q21.33	1553094_at	NM_001077503 /// NM_001077504 /// NM_001077505 /// NM_001077506 /// NM_170685																				
4.70	4.56	0.14	7.15E-01	9.05E-01	PMEPA1	prostate transmembrane protein, androgen induced 1	chr20q13.31|20q13 .31-q13.33	222450_at	NM_020182 /// NM_199169 /// NM_199170 /// NM_199171																				
1.97	1.92	0.04	7.15E-01	9.05E-01	SH3BP2	SH3-domain binding protein 2	chr4p16.3	217257_at	NM_001122681 /// NM_003023																				
2.29	2.25	0.04	7.15E-01	9.05E-01	---	---	---	216812_at	---																				
4.71	4.64	0.07	7.15E-01	9.05E-01	---	---	---	239873_at	---																				
2.09	2.02	0.07	7.15E-01	9.05E-01	ARL11	ADP-ribosylation factor-like 11	chr13q14.3	1552691_at	NM_138450																				
2.33	2.27	0.06	7.15E-01	9.05E-01	MEX3C	mex-3 homolog C (C. elegans)	chr18q21.2	1556874_a_at	NM_016626																				
2.97	2.88	0.09	7.15E-01	9.05E-01	---	---	---	242431_at	---																				
6.97	6.77	0.20	7.15E-01	9.05E-01	PNMAL2	PNMA-like 2	chr19q13.32	232003_at	NM_020709																				
3.66	3.60	0.05	7.15E-01	9.05E-01	ZFX	zinc finger protein, X-linked	chrXp21.3	214678_x_at	NM_003410																				
2.14	2.09	0.05	7.15E-01	9.05E-01	---	---	---	1557812_a_at	---																				
2.39	2.33	0.06	7.15E-01	9.05E-01	DAPK1	death-associated protein kinase 1	chr9q34.1	211214_s_at	NM_004938																				
2.40	2.35	0.05	7.16E-01	9.05E-01	---	---	---	1562006_at	---																				
1.98	1.94	0.04	7.16E-01	9.05E-01	MYOZ2	myozenin 2	chr4q26-q27	211476_at	NM_016599																				
2.38	2.32	0.06	7.16E-01	9.05E-01	---	---	---	1564070_s_at	---																				
3.35	3.28	0.06	7.16E-01	9.05E-01	LOC494150	prohibitin pseudogene	chr12q13	238788_at	---																				
9.77	9.65	0.12	7.16E-01	9.05E-01	SLC47A1	solute carrier family 47, member 1	chr17p11.2	219525_at	NM_018242																				
7.29	7.24	0.04	7.16E-01	9.05E-01	PHB	prohibitin	chr17q21	200659_s_at	NM_002634																				
5.02	4.88	0.14	7.16E-01	9.05E-01	CNOT3	CCR4-NOT transcription complex, subunit 3	chr19q13.4	203239_s_at	NM_014516																				
1.88	1.84	0.04	7.16E-01	9.05E-01	---	---	---	1559341_at	---																				
4.31	4.24	0.08	7.16E-01	9.05E-01	YEATS2	YEATS domain containing 2	chr3q27.1	1557047_at	NM_018023																				
4.73	4.59	0.14	7.16E-01	9.05E-01	UBR5	ubiquitin protein ligase E3 component n-recognin 5	chr8q22	208882_s_at	NM_015902																				
2.38	2.31	0.07	7.16E-01	9.05E-01	EDARADD /// ENO1P	EDAR-associated death domain /// enolase 1, (alpha) pseudogene	chr1q43	1553430_a_at	NM_080738 /// NM_145861																				
3.39	3.33	0.07	7.16E-01	9.05E-01	USP22	ubiquitin specific peptidase 22	chr17p11.2	220862_s_at	NM_015276																				
3.26	3.19	0.07	7.16E-01	9.05E-01	CHST13	carbohydrate (chondroitin 4) sulfotransferase 13	chr3q21.3	239647_at	NM_152889																				
2.93	2.87	0.06	7.16E-01	9.05E-01	RP5-1000E10.4	suppressor of IKK epsilon	chr1p13.2	221705_s_at	NM_001102396 /// NM_025073																				
5.04	4.98	0.06	7.16E-01	9.05E-01	---	---	---	240780_at	---																				
2.92	2.86	0.06	7.16E-01	9.05E-01	DNAH7	dynein, axonemal, heavy chain 7	chr2q32.3	214222_at	NM_018897																				
6.97	6.85	0.12	7.16E-01	9.05E-01	HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	chr19q13.33	224494_x_at	NM_016246																				
3.94	3.85	0.09	7.16E-01	9.05E-01	EXOSC2	exosome component 2	chr9q34	209527_at	NM_014285																				
2.24	2.18	0.06	7.16E-01	9.05E-01	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	chr7p14-p13	203106_s_at	NM_014396 /// NM_080631																				
2.27	2.23	0.05	7.16E-01	9.05E-01	PALLD	Palladin, cytoskeletal associated protein	chr4q32.3	1557535_at	NM_016081																				
5.90	5.82	0.08	7.16E-01	9.05E-01	NRARP	Notch-regulated ankyrin repeat protein	chr9q34.3	226499_at	NM_001004354																				
6.98	6.87	0.10	7.16E-01	9.05E-01	---	---	---	226146_at	---																				
3.24	3.15	0.08	7.16E-01	9.05E-01	KRTAP4-2	keratin associated protein 4-2	chr17q12-q21	234671_at	NM_033062																				

3.28	3.22	0.07	7.17E-01	9.05E-01	OTUD1	OTU domain containing 1	chr10p12.2	238998_x_at	XR_040063 /// XR_040064 /// XR_040065																				
8.53	8.44	0.09	7.17E-01	9.05E-01	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	chr5q23.1	223449_at	NM_020796																				
2.78	2.72	0.05	7.17E-01	9.05E-01	EFCAB6	EF-hand calcium binding domain 6	chr22q13.1-q13.33	234732_s_at	NM_022785 /// NM_198856																				
6.23	6.13	0.10	7.17E-01	9.05E-01	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	chr6p21.3	1566303_s_at	NM_021959																				
4.22	4.14	0.07	7.17E-01	9.05E-01	---	---	---	1556033_at	---																				
3.23	3.16	0.07	7.17E-01	9.05E-01	---	---	---	243420_at	---																				
4.40	4.33	0.08	7.17E-01	9.05E-01	DOK4	docking protein 4	chr16q13	209690_s_at	NM_018110																				
2.22	2.16	0.06	7.17E-01	9.05E-01	DUSP19	dual specificity phosphatase 19	chr2q32.1	1552708_a_at	NM_080876																				
3.05	2.96	0.09	7.17E-01	9.05E-01	---	---	---	229490_s_at	---																				
3.19	3.12	0.08	7.17E-01	9.05E-01	---	---	---	216847_at	---																				
2.13	2.06	0.06	7.17E-01	9.05E-01	---	---	---	1556159_at	---																				
4.26	4.19	0.08	7.17E-01	9.05E-01	UNC5C	unc-5 homolog C (C. elegans)	chr4q21-q23	206189_at	NM_003728																				
5.93	5.82	0.11	7.17E-01	9.05E-01	FLOT1	flotillin 1	chr6p21.3	208748_s_at	NM_005803																				
5.72	5.63	0.09	7.17E-01	9.05E-01	PIGM	phosphatidylinositol glycan anchor biosynthesis, class M	chr1q23.2	223470_at	NM_145167																				
2.85	2.78	0.07	7.17E-01	9.05E-01	HEY2	hairy/enhancer-of-split related with YRPW motif 2	chr6q21	222921_s_at	NM_012259																				
3.39	3.29	0.10	7.18E-01	9.06E-01	---	---	---	1566249_at	---																				
2.65	2.48	0.18	7.18E-01	9.06E-01	---	---	---	241616_at	---																				
2.61	2.56	0.05	7.18E-01	9.06E-01	---	---	---	1564237_at	---																				
2.79	2.73	0.06	7.18E-01	9.06E-01	KIAA1975	KIAA1975 protein similar to MRIP2	chr10q23.2	1557382_x_at	NM_133447																				
1.98	1.94	0.04	7.18E-01	9.06E-01	---	---	---	217402_at	---																				
3.06	2.99	0.07	7.18E-01	9.06E-01	LOC100133885	hypothetical protein LOC100133885	---	1569386_at	XM_001714113																				
2.15	2.10	0.05	7.18E-01	9.06E-01	ZNF440	Zinc finger protein 440	chr19p13.2	216291_at	NM_152357																				
2.61	2.55	0.06	7.18E-01	9.06E-01	LOC441528	hypothetical protein LOC441528	chrXp22.33	1564232_at	XR_041386																				
2.00	1.96	0.04	7.18E-01	9.06E-01	IVNS1ABP	influenza virus NS1A binding protein	chr1q25.1-q31.1	244235_at	NM_006469																				
1.87	1.83	0.04	7.18E-01	9.06E-01	CCDC7	coiled-coil domain containing 7	chr10p11.22	1553214_a_at	NM_001026383 /// NM_145023																				
2.64	2.59	0.05	7.18E-01	9.06E-01	---	---	---	1569615_at	---																				
6.21	6.12	0.09	7.18E-01	9.06E-01	HRB	HIV-1 Rev binding protein	chr2q36.3	218091_at	NM_004504																				
2.32	2.24	0.08	7.18E-01	9.06E-01	MUM1L1	melanoma associated antigen (mutated) 1-like 1	chrXq22.3	229160_at	NM_152423																				
3.96	3.85	0.10	7.18E-01	9.06E-01	LMF1	lipase maturation factor 1	chr16p13.3	219136_s_at	NM_022773																				
4.32	4.26	0.06	7.18E-01	9.06E-01	---	---	---	238352_s_at	---																				
2.09	2.03	0.06	7.18E-01	9.06E-01	ZNF717	zinc finger protein 717	chr3p12.3	221370_at	NM_001128223 /// XM_001714275 /// XM_001719548 /// XM_001719561																				
3.03	2.95	0.08	7.18E-01	9.06E-01	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	chr1q42-q44	211138_s_at	NM_003679																				
3.76	3.69	0.07	7.18E-01	9.06E-01	HN1L	hematological and neurological expressed 1-like	chr16p13.3	216031_x_at	NM_144570																				
2.11	2.07	0.04	7.19E-01	9.06E-01	GPR98	G protein-coupled receptor 98	chr5q13	234871_at	NM_032119 /// NR_003149																				
2.12	2.08	0.04	7.19E-01	9.06E-01	LOC285045	hypothetical LOC285045	chr2p22.3	1563082_at	---																				
7.84	7.75	0.09	7.19E-01	9.06E-01	PCNP	PEST proteolytic signal containing nuclear protein	chr3q12.3	217816_s_at	NM_020357																				
3.33	3.27	0.06	7.19E-01	9.06E-01	SIPA1L3	Signal-induced proliferation-associated 1 like 3	chr19q13.13	230564_at	NM_015073																				
3.26	3.15	0.11	7.19E-01	9.06E-01	PIBF1	progesterone immunomodulatory binding factor 1	chr13q22.1	213239_at	NM_006346																				
5.63	5.56	0.07	7.19E-01	9.06E-01	PCTP	phosphatidylcholine transfer protein	chr17q21-q24	218676_s_at	NM_001102402 /// NM_021213																				
2.13	2.08	0.05	7.19E-01	9.06E-01	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	chr2q11.1-q11.2	205342_s_at	NM_001056 /// NM_176825																				
5.32	5.21	0.11	7.19E-01	9.06E-01	STAT5B	signal transducer and activator of transcription 5B	chr17q11.2	212550_at	NM_012448																				
5.10	4.96	0.14	7.19E-01	9.06E-01	TMEM53	transmembrane protein 53	chr1p34.1	1554077_a_at	NM_024587																				
2.14	2.09	0.05	7.19E-01	9.06E-01	---	---	---	237738_at	---																				
5.11	5.05	0.06	7.19E-01	9.06E-01	---	---	---	217205_at	---																				
3.13	3.09	0.04	7.19E-01	9.06E-01	IQCE	IQ motif containing E	chr7p22.2	217124_at	NM_001100390 /// NM_152558																				
3.27	3.04	0.23	7.19E-01	9.06E-01	---	---	---	241740_at	---																				
2.46	2.40	0.06	7.19E-01	9.06E-01	VCL	vinculin	chr10q22.2	200930_s_at	NM_003373 /// NM_014000																				

6.11	6.04	0.07	7.19E-01	9.06E-01	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	chrXq28	36004_at	NM_001099856 /// NM_001099857 /// NM_003639																			
5.39	5.30	0.09	7.19E-01	9.06E-01	EPS8L2	EPS8-like 2	chr11p15.5	218180_s_at	NM_022772																			
3.71	3.64	0.08	7.19E-01	9.06E-01	NSUN6	NOL1/NOP2/Sun domain family, member 6	chr10p12.33	222128_at	NM_182543																			
3.52	3.46	0.05	7.19E-01	9.06E-01	SH2D3A	SH2 domain containing 3A	chr19p13.3	222169_x_at	NM_005490																			
2.63	2.58	0.05	7.19E-01	9.06E-01	C3orf20	chromosome 3 open reading frame 20	chr3p25.1-p24.3	224273_at	NM_032137																			
3.04	2.98	0.06	7.19E-01	9.06E-01	ACVR1B	activin A receptor, type IB	chr12q13	208219_at	NM_004302 /// NM_020327 /// NM_020328																			
4.67	4.60	0.07	7.19E-01	9.06E-01	WDR55	WD repeat domain 55	chr5q31.3	222114_x_at	NM_017706																			
2.94	2.89	0.05	7.19E-01	9.06E-01	RHEB	Ras homolog enriched in brain	chr7q36	201451_x_at	NM_005614																			
2.96	2.89	0.07	7.20E-01	9.06E-01	AGMAT	agmatine ureohydrolase (agmatinase)	chr1p36.21	222930_s_at	NM_024758																			
9.26	9.18	0.08	7.20E-01	9.06E-01	FLOT1	flotillin 1	chr6p21.3	210142_x_at	NM_005803																			
3.31	3.25	0.07	7.20E-01	9.06E-01	PRMT1	protein arginine methyltransferase 1	chr19q13.3	1565016_at	NM_001536 /// NM_198318 /// NM_198319																			
5.42	5.26	0.15	7.20E-01	9.06E-01	RNF213	ring finger protein 213	chr17q25.3	230000_at	NM_020914																			
3.09	3.02	0.07	7.20E-01	9.06E-01	IGFL2	IGF-like family member 2	chr19q13.32	231148_at	NM_001002915																			
2.89	2.82	0.07	7.20E-01	9.06E-01	---	---	---	1556728_at	---																			
2.57	2.51	0.06	7.20E-01	9.06E-01	NBR1	Neighbor of BRCA1 gene 2	chr17q21.31	1568856_at	NM_005899 /// NM_031858 /// NM_031862																			
4.02	3.95	0.07	7.20E-01	9.06E-01	---	---	---	208769_at	---																			
4.80	4.73	0.07	7.20E-01	9.06E-01	KBTBD4	kelch repeat and BTB (POZ) domain containing 4	chr11p11.2	223765_s_at	NM_016506 /// NM_018095																			
5.13	5.04	0.09	7.20E-01	9.06E-01	GLTP	glycolipid transfer protein	chr12q24.11	219267_at	NM_016433																			
2.01	1.97	0.04	7.20E-01	9.06E-01	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	chr1pter-q31.3	204721_s_at	NM_014787																			
2.90	2.84	0.06	7.20E-01	9.07E-01	---	---	---	228714_at	---																			
2.26	2.21	0.05	7.20E-01	9.07E-01	SARDH	sarcosine dehydrogenase	chr9q33-q34	207889_at	NM_001134707 /// NM_007101																			
6.81	6.71	0.10	7.20E-01	9.07E-01	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	chr1q21-q22	209435_s_at	NM_004723																			
6.29	6.23	0.06	7.20E-01	9.07E-01	PTDSS2	phosphatidylserine synthase 2	chr11p15	221005_s_at	NM_030783																			
3.93	3.88	0.05	7.20E-01	9.07E-01	---	---	---	239388_at	---																			
7.33	7.20	0.14	7.20E-01	9.07E-01	MMP24	Matrix metallopeptidase 24 (membrane-inserted)	chr20q11.2	221953_s_at	NM_006690																			
2.61	2.55	0.06	7.20E-01	9.07E-01	---	---	---	1562827_at	---																			
6.03	5.80	0.24	7.21E-01	9.07E-01	KRT18	keratin 18	chr12q13	201596_x_at	NM_000224 /// NM_199187																			
6.75	6.55	0.20	7.21E-01	9.07E-01	DUSP16	dual specificity phosphatase 16	chr12p13	224336_s_at	NM_030640																			
5.45	5.37	0.07	7.21E-01	9.07E-01	BCAR3	breast cancer anti-estrogen resistance 3	chr1p22.1	204032_at	NM_003567																			
2.65	2.58	0.06	7.21E-01	9.07E-01	---	---	---	1561392_at	---																			
2.54	2.47	0.07	7.21E-01	9.07E-01	---	---	---	237883_at	---																			
2.26	2.22	0.04	7.21E-01	9.07E-01	LOC729124	hypothetical LOC729124	chr1p36.23	237028_at	XM_001127818 /// XM_001129378 /// XM_001719835																			
4.93	4.83	0.11	7.21E-01	9.07E-01	SCARA3	scavenger receptor class A, member 3	chr8p21	219416_at	NM_016240 /// NM_182826																			
2.63	2.58	0.05	7.21E-01	9.07E-01	PPHLN1	periphilin 1	chr12q12	1555350_at	NM_016488 /// NM_201438 /// NM_201439 /// NM_201440 /// NM_201515																			
3.07	3.01	0.06	7.21E-01	9.07E-01	DEFB4	defensin, beta 4	chr8p23.1-p22	207356_at	NM_004942																			
5.95	5.87	0.08	7.21E-01	9.07E-01	SAP30BP	SAP30 binding protein	chr17q25.1	222475_at	NM_013260																			

4.16	4.09	0.07	7.22E-01	9.07E-01	DISC1	disrupted in schizophrenia 1	chr1q42.1	206090_s_at	NM_001012957 /// NM_001012958 /// NM_001012959 /// NM_018662																			
3.09	3.03	0.05	7.22E-01	9.07E-01	---	---	---	236101_at	---																			
4.81	4.71	0.09	7.22E-01	9.07E-01	---	---	---	1559467_at	---																			
2.18	2.14	0.05	7.22E-01	9.07E-01	ARMETL1	arginine-rich, mutated in early stage tumors-like 1	chr10p13	1568696_at	NM_001029954																			
4.96	4.86	0.10	7.22E-01	9.08E-01	PLAU	plasminogen activator, urokinase	chr10q24	205479_s_at	NM_002658																			
2.59	2.54	0.06	7.22E-01	9.08E-01	---	---	---	229950_s_at	---																			
3.75	3.65	0.10	7.22E-01	9.08E-01	TCF21	transcription factor 21	chr6pter-qter	204931_at	NM_003206 /// NM_198392																			
3.25	3.20	0.05	7.22E-01	9.08E-01	---	---	---	239121_at	---																			
2.84	2.80	0.04	7.22E-01	9.08E-01	---	---	---	240156_at	---																			
4.89	4.77	0.12	7.22E-01	9.08E-01	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	chr6q23.2	244353_s_at	NM_145176																			
7.47	7.35	0.12	7.22E-01	9.08E-01	ARHGAP21	Rho GTPase activating protein 21	chr10p12.1|10p12.3	224764_at	NM_020824																			
2.09	2.04	0.05	7.22E-01	9.08E-01	MGC3196	hypothetical protein MGC3196	chr11q12.3	238981_at	NM_001080501																			
2.55	2.49	0.06	7.22E-01	9.08E-01	---	---	---	236750_at	---																			
6.72	6.59	0.13	7.22E-01	9.08E-01	C11orf54	chromosome 11 open reading frame 54	chr11q21	223268_at	NM_014039																			
2.29	2.25	0.05	7.22E-01	9.08E-01	LOC283392	hypothetical protein LOC283392	chr12q21.1	1560697_at	XR_039893 /// XR_039894 /// XR_039895																			
2.33	2.28	0.05	7.22E-01	9.08E-01	TMC5	transmembrane channel-like 5	chr16p12.3	240304_s_at	NM_001105248 /// NM_001105249 /// NM_024780																			
2.49	2.45	0.04	7.23E-01	9.08E-01	---	---	---	231365_at	---																			
2.44	2.38	0.06	7.23E-01	9.08E-01	---	---	---	243105_at	---																			
2.82	2.76	0.06	7.23E-01	9.08E-01	ATM	ataxia telangiectasia mutated	chr11q22-q23	1554631_at	NM_000051 /// NM_138292																			
5.74	5.62	0.12	7.23E-01	9.08E-01	TBC1D13	TBC1 domain family, member 13	chr9q34.11	218596_at	NM_018201																			
2.92	2.85	0.07	7.23E-01	9.08E-01	---	---	---	216805_at	---																			
6.69	6.59	0.10	7.23E-01	9.08E-01	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	chr7q36.3	208811_s_at	NM_005494 /// NM_058246																			
2.62	2.56	0.06	7.23E-01	9.08E-01	SEL1L2	sel-1 suppressor of lin-12-like 2 (C. elegans)	chr20p12.1	234018_s_at	NM_025229																			
8.08	8.03	0.05	7.23E-01	9.08E-01	DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	chr1p35.3	205545_x_at	NM_014280																			
4.45	4.32	0.13	7.23E-01	9.08E-01	---	---	---	1559654_s_at	---																			
5.88	5.79	0.09	7.23E-01	9.08E-01	UBE2J2	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	chr1p36.33	224347_x_at	NM_058167 /// NM_194315 /// NM_194457 /// NM_194458																			
3.41	3.31	0.10	7.23E-01	9.08E-01	NBR1	Neighbor of BRCA1 gene 2	chr17q21.31	1568857_a_at	NM_005899 /// NM_031858 /// NM_031862																			
3.35	3.29	0.06	7.24E-01	9.08E-01	---	---	---	240115_at	---																			
3.38	3.30	0.08	7.24E-01	9.08E-01	---	---	---	239882_at	---																			
3.67	3.62	0.05	7.24E-01	9.08E-01	PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta	chr4p16.3	1557777_at	NM_000283																			
6.72	6.66	0.06	7.24E-01	9.08E-01	BFAR	bifunctional apoptosis regulator	chr16p13.12	218056_at	NM_016561																			
3.40	3.36	0.04	7.24E-01	9.08E-01	---	---	---	229571_at	---																			
9.83	9.71	0.12	7.24E-01	9.08E-01	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	chr10q23-q24	203058_s_at	NM_001015880 /// NM_004670																			
3.33	3.24	0.09	7.24E-01	9.08E-01	CCNB1	cyclin B1	chr5q12	214710_s_at	NM_031966																			
9.29	9.23	0.06	7.24E-01	9.08E-01	ERH	enhancer of rudimentary homolog (Drosophila)	chr14q24.1|7q34	200043_at	NM_004450																			
5.64	5.51	0.13	7.24E-01	9.08E-01	SMAD4	SMAD family member 4	chr18q21.1	202527_s_at	NM_005359																			
7.84	7.77	0.07	7.24E-01	9.08E-01	---	---	---	225494_at	---																			
2.23	2.19	0.05	7.24E-01	9.08E-01	ARHGAP26	Rho GTPase activating protein 26	chr5q31	226576_at	NM_015071																			
2.62	2.57	0.05	7.24E-01	9.09E-01	COG1	component of oligomeric golgi complex 1	chr17q25.1	231813_s_at	NM_018714																			

2.33	2.28	0.05	7.24E-01	9.09E-01	LOC644215	Hypothetical LOC644215	chr10q24.1	1566084_at	XM_927403 /// XM_938015
6.35	6.15	0.21	7.24E-01	9.09E-01	---	---	---	244726_at	---
3.04	3.00	0.05	7.24E-01	9.09E-01	WDR59	WD repeat domain 59	chr16q23.1	219586_at	NM_030581
2.91	2.85	0.06	7.24E-01	9.09E-01	ZCCHC4	zinc finger, CCHC domain containing 4	chr4p15.2	219917_at	NM_024936
5.36	5.27	0.09	7.25E-01	9.09E-01	SHKBP1	SH3KBP1 binding protein 1	chr19q13.2	224846_at	NM_138392
2.36	2.31	0.05	7.25E-01	9.09E-01	OPALIN	oligodendrocytic myelin paranodal and inner loop protein	chr10q23-q24	239575_at	NM_001040102 /// NM_001040103 /// NM_033207
1.81	1.77	0.04	7.25E-01	9.09E-01	C4orf33	chromosome 4 open reading frame 33	chr4q28.2	1552372_at	NM_001099783 /// NM_173487
3.33	3.27	0.07	7.25E-01	9.09E-01	---	---	---	232658_at	---
2.00	1.96	0.04	7.25E-01	9.09E-01	KIF1A	kinesin family member 1A	chr2q37.3	203850_s_at	NM_004321
3.62	3.56	0.05	7.25E-01	9.09E-01	LPAR2	lysophosphatidic acid receptor 2	chr19p12	206722_s_at	NM_004720
5.86	5.72	0.14	7.25E-01	9.09E-01	N4BP2L2	NEDD4 binding protein 2-like 2	chr13q13.1	221899_at	NM_014887 /// NM_033111
2.85	2.78	0.07	7.25E-01	9.09E-01	TBRG4	transforming growth factor beta regulator 4	chr7p14-p13	220961_s_at	NM_004749 /// NM_030900 /// NM_199122
8.44	8.37	0.07	7.25E-01	9.09E-01	MVP	major vault protein	chr16p13.1-p11.2	202180_s_at	NM_005115 /// NM_017458
2.18	2.14	0.04	7.25E-01	9.09E-01	---	---	---	243015_at	---
2.54	2.50	0.04	7.25E-01	9.09E-01	PHKG2	phosphorylase kinase, gamma 2 (testis)	chr16p12.1-p11.2	1556369_a_at	NM_000294
2.13	2.08	0.06	7.25E-01	9.09E-01	GRIA1	glutamate receptor, ionotropic, AMPA 1	chr5q33|5q31.1	211520_s_at	NM_000827 /// NM_001114183
2.67	2.62	0.05	7.25E-01	9.09E-01	PDX1	pancreatic and duodenal homeobox 1	chr13q12.1	210937_s_at	NM_000209
3.87	3.77	0.10	7.26E-01	9.09E-01	GPR155	G protein-coupled receptor 155	chr2q31.1	231166_at	NM_001033045 /// NM_152529
2.60	2.54	0.05	7.26E-01	9.09E-01	C4orf41	chromosome 4 open reading frame 41	chr4q35.1	234747_at	NM_021942 /// NM_199053
2.80	2.76	0.04	7.26E-01	9.09E-01	---	---	---	236445_at	---
5.00	4.80	0.20	7.26E-01	9.09E-01	---	---	---	1562794_at	---
2.37	2.31	0.07	7.26E-01	9.09E-01	---	---	---	209353_s_at	---
4.99	4.86	0.14	7.26E-01	9.09E-01	DOCK9	dedicator of cytokinesis 9	chr13q32.3	212538_at	NM_001130048 /// NM_001130049 /// NM_001130050 /// NM_015296
4.10	4.03	0.07	7.26E-01	9.09E-01	TDG	thymine-DNA glycosylase	chr12q24.1	203742_s_at	NM_003211
11.75	11.70	0.05	7.26E-01	9.09E-01	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	chr12p13	AFFX-HUMGAPDH/M33197_M_at	NM_002046
2.33	2.29	0.05	7.26E-01	9.09E-01	TMEM126B	transmembrane protein 126B	chr11q14.1	1554537_at	NM_018480
4.64	4.57	0.07	7.26E-01	9.09E-01	NXPH3	neurexophilin 3	chr17q21.33	228210_at	NM_007225
5.26	5.12	0.13	7.26E-01	9.10E-01	SASH3	SAM and SH3 domain containing 3	chrXq26	204923_at	NM_018990
5.41	5.30	0.11	7.26E-01	9.10E-01	VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)	chr2p13-p14	218423_x_at	NM_001005739 /// NM_016516
4.76	4.70	0.06	7.26E-01	9.10E-01	GLYCTK	glycerate kinase	chr3p21.1	242341_x_at	NM_145262
3.05	2.99	0.07	7.26E-01	9.10E-01	CNOT3	CCR4-NOT transcription complex, subunit 3	chr19q13.4	211141_s_at	NM_014516
5.88	5.80	0.08	7.26E-01	9.10E-01	ZCCHC6	zinc finger, CCHC domain containing 6	chr9q21	220933_s_at	NM_024617
4.59	4.51	0.08	7.26E-01	9.10E-01	ETAA1	Ewing tumor-associated antigen 1	chr2p13-p15	219216_at	NM_019002
4.16	4.06	0.09	7.26E-01	9.10E-01	RICS	Rho GTPase-activating protein	chr11q24-q25	203431_s_at	NM_014715
3.81	3.71	0.10	7.26E-01	9.10E-01	TACSTD1	tumor-associated calcium signal transducer 1	chr2p21	201839_s_at	NM_002354
2.08	2.05	0.04	7.27E-01	9.10E-01	---	---	---	1557443_s_at	---
1.96	1.91	0.05	7.27E-01	9.10E-01	NUP54	nucleoporin 54kDa	chr4q21.1	231301_at	NM_017426
4.65	4.58	0.07	7.27E-01	9.10E-01	ISYNA1	myo-inositol 1-phosphate synthase A1	chr19p13.11	228552_s_at	NM_016368
3.92	3.81	0.12	7.27E-01	9.10E-01	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	chr1q21.2	208103_s_at	NM_030920
2.34	2.30	0.04	7.27E-01	9.10E-01	CNOT7	CCR4-NOT transcription complex, subunit 7	chr8p22-p21.3	233019_at	NM_013354 /// NM_054026
1.99	1.94	0.04	7.27E-01	9.10E-01	---	---	---	243479_at	---

5.75	5.64	0.10	7.27E-01	9.10E-01	TAPBPL	TAP binding protein-like	chr12p13.31	218747_s_at	NM_018009
4.09	4.04	0.06	7.27E-01	9.10E-01	SPRR2G	small proline-rich protein 2G	chr1q21-q22	236119_s_at	NM_001014291
2.08	2.04	0.03	7.27E-01	9.10E-01	ANK1	ankyrin 1, erythrocytic	chr8p11.1	205389_s_at	NM_000037 /// NM_020475 /// NM_020476 /// NM_020477 /// NM_020478 /// NM_020480
2.46	2.41	0.05	7.27E-01	9.10E-01	TTLL5	tubulin tyrosine ligase-like family, member 5	chr14q24.3	1566102_at	NM_015072
1.93	1.89	0.04	7.27E-01	9.10E-01	---	---	---	232049_at	---
8.33	8.24	0.09	7.27E-01	9.10E-01	ARF3	ADP-ribosylation factor 3	chr12q13	200011_s_at	NM_001659
2.46	2.41	0.05	7.27E-01	9.10E-01	---	---	---	243089_at	---
1.91	1.87	0.04	7.27E-01	9.10E-01	SSX1	synovial sarcoma, X breakpoint 1	chrXp11.23-p11.22	206627_s_at	NM_005635
7.36	7.25	0.11	7.27E-01	9.10E-01	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	chr1q25	202420_s_at	NM_001357
3.93	3.81	0.11	7.27E-01	9.10E-01	KLC2	kinesin light chain 2	chr11q13.1	218906_x_at	NM_022822
2.07	2.03	0.04	7.27E-01	9.10E-01	---	---	---	231677_at	---
8.65	8.54	0.11	7.27E-01	9.10E-01	LOC729082	Hypothetical protein LOC729082	chr15q15.1	225225_at	XR_040992 /// XR_040993 /// XR_040994
4.03	3.90	0.12	7.27E-01	9.10E-01	PNMA6A	paraneoplastic antigen like 6A	chrXq28	235758_at	NM_032882
2.46	2.42	0.04	7.27E-01	9.10E-01	C5orf34	chromosome 5 open reading frame 34	chr5p12	229886_at	NM_198566
9.73	9.63	0.10	7.28E-01	9.10E-01	CAPN2	calpain 2, (m/II) large subunit	chr1q41-q42	208683_at	NM_001748
2.64	2.60	0.04	7.28E-01	9.10E-01	DGCR12	DiGeorge syndrome critical region gene 12	chr22q11.21	1566235_at	---
2.74	2.70	0.04	7.28E-01	9.10E-01	---	---	---	217665_at	---
2.16	2.11	0.05	7.28E-01	9.10E-01	---	---	---	1561427_at	---
6.20	6.08	0.12	7.28E-01	9.10E-01	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	chr10q24.1-q24.3	200899_s_at	NM_012215
2.28	2.23	0.05	7.28E-01	9.10E-01	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	chr5q21	230261_at	NM_005668 /// NM_175052
7.11	6.96	0.15	7.28E-01	9.10E-01	C10orf10	chromosome 10 open reading frame 10	chr10q11.21	209183_s_at	NM_007021
2.24	2.20	0.04	7.28E-01	9.10E-01	LILRP2	leukocyte immunoglobulin-like receptor pseudogene 2	chr19q13.4	214561_at	NR_003061
4.46	4.35	0.10	7.28E-01	9.10E-01	BBS4	Bardet-Biedl syndrome 4	chr15q22.3-q23	212745_s_at	NM_033028
11.32	11.27	0.06	7.28E-01	9.10E-01	RPL23	ribosomal protein L23	chr17q	200888_s_at	NM_000978
1.95	1.91	0.04	7.28E-01	9.10E-01	---	---	---	1561208_at	---
3.18	3.09	0.09	7.28E-01	9.10E-01	---	---	---	232375_at	---
6.56	6.44	0.12	7.28E-01	9.10E-01	DST	dystonin	chr6p12.1	212253_x_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380
3.86	3.80	0.06	7.28E-01	9.10E-01	HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	chr1p34	232581_x_at	NM_001127714 /// NM_024503
2.33	2.28	0.05	7.28E-01	9.10E-01	LHX9	LIM homeobox 9	chr1q31-q32	1560253_at	NM_001014434 /// NM_020204
5.95	5.88	0.07	7.28E-01	9.10E-01	GNA12	guanine nucleotide binding protein (G protein) alpha 12	chr7p22.2	221737_at	NM_007353
2.33	2.28	0.05	7.28E-01	9.10E-01	---	---	---	239840_at	---
2.29	2.25	0.04	7.28E-01	9.10E-01	---	---	---	1559109_a_at	---
4.54	4.50	0.04	7.28E-01	9.10E-01	---	---	---	242742_at	---
7.17	7.06	0.10	7.28E-01	9.11E-01	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	chr17q23.3	201788_at	NM_007372 /// NM_203499
4.90	4.83	0.07	7.29E-01	9.11E-01	SLC35D2	solute carrier family 35, member D2	chr9q22.32	213082_s_at	NM_007001
2.48	2.43	0.05	7.29E-01	9.11E-01	C3orf62	chromosome 3 open reading frame 62	chr3p21.31	1569374_at	NM_198562
5.55	5.47	0.08	7.29E-01	9.11E-01	---	---	---	206936_x_at	---
8.18	8.06	0.12	7.29E-01	9.11E-01	VTN	vitronectin	chr17q11	204534_at	NM_000638
4.91	4.83	0.08	7.29E-01	9.11E-01	---	---	---	238896_at	---
1.80	1.76	0.03	7.29E-01	9.11E-01	LOC283788	hypothetical protein LOC283788	---	1558107_at	XM_001721615 /// XM_001723582 /// XM_001723589
3.02	2.95	0.07	7.29E-01	9.11E-01	PTN	pleiotrophin	chr7q33-q34	208408_at	NM_002825

3.05	2.99	0.06	7.29E-01	9.11E-01	VIL1	villin 1	chr2q35-q36	205506_at	NM_007127																			
2.89	2.84	0.05	7.29E-01	9.11E-01	CALML6	calmodulin-like 6	chr1p36.33	1552402_at	NM_138705																			
1.96	1.91	0.04	7.29E-01	9.11E-01	PDE5A	Phosphodiesterase 5A, cGMP-specific	chr4q25-q27	1556786_at	NM_001083 /// NM_033430 /// NM_033437																			
2.63	2.57	0.06	7.29E-01	9.11E-01	PPP3CC	Protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	chr8p21.3	32540_at	NM_005605																			
2.39	2.35	0.04	7.29E-01	9.11E-01	LRRC8B	leucine rich repeat containing 8 family, member B	chr1p22.2	242038_at	NM_001134476 /// NM_015350																			
3.67	3.61	0.06	7.29E-01	9.11E-01	OBP2B	odorant binding protein 2B	chr9q34	234722_x_at	NM_014581																			
5.89	5.75	0.14	7.29E-01	9.11E-01	MTERFD3	MTERF domain containing 3	chr12q24.1	225346_at	NM_001033050 /// NM_025198																			
6.28	6.21	0.08	7.29E-01	9.11E-01	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	chr22q11.23|22q11	212167_s_at	NM_001007468 /// NM_003073																			
2.99	2.94	0.06	7.29E-01	9.11E-01	P2RY10	purinergic receptor P2Y, G-protein coupled, 10	chrXq21.1	1553856_s_at	NM_014499 /// NM_198333																			
2.32	2.25	0.07	7.29E-01	9.11E-01	C5orf44	chromosome 5 open reading frame 44	chr5q12.3	218674_at	NM_001093755 /// NM_001093756 /// NM_024941 /// NR_003545																			
2.51	2.46	0.05	7.29E-01	9.11E-01	ZNF41	zinc finger protein 41	chrXp11.23	1553217_s_at	NM_007130 /// NM_153380																			
3.07	3.02	0.05	7.29E-01	9.11E-01	C22orf27	Chromosome 22 open reading frame 27	chr22q12.2	228449_at	XR_041215 /// XR_041216 /// XR_041217																			
2.63	2.54	0.09	7.29E-01	9.11E-01	BHMT	betaine-homocysteine methyltransferase	chr5q13.1-q15	206119_at	NM_001713																			
5.15	5.06	0.09	7.29E-01	9.11E-01	FBXW9	F-box and WD repeat domain containing 9	chr19p13.13	223419_at	NM_032301																			
7.12	7.04	0.07	7.29E-01	9.11E-01	STRA13	stimulated by retinoic acid 13 homolog (mouse)	chr17q25.3	209478_at	NM_144998																			
5.24	5.09	0.15	7.30E-01	9.11E-01	SASH1	SAM and SH3 domain containing 1	chr6q24.3	226022_at	NM_015278																			
2.16	2.12	0.04	7.30E-01	9.11E-01	---	---	---	231174_s_at	---																			
3.55	3.49	0.06	7.30E-01	9.11E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1565027_at	NM_153003																			
2.48	2.43	0.06	7.30E-01	9.11E-01	LOC440888	ARP3 actin-related protein 3 homolog B pseudogene	chr2p11.1	224425_x_at	---																			
2.29	2.23	0.06	7.30E-01	9.11E-01	---	---	---	1555059_at	---																			
2.39	2.32	0.07	7.30E-01	9.11E-01	---	---	---	234785_at	---																			
4.44	4.38	0.06	7.30E-01	9.11E-01	AP2A1	Adaptor-related protein complex 2, alpha 1 subunit	chr19q13.33	1558792_x_at	NM_014203 /// NM_130787																			
7.87	7.78	0.08	7.30E-01	9.11E-01	C10orf11	chromosome 10 open reading frame 11	chr10q22.2-q22.3	223703_at	NM_032024																			
2.56	2.51	0.05	7.30E-01	9.11E-01	---	---	---	217060_at	---																			
2.05	2.01	0.05	7.30E-01	9.11E-01	---	---	---	240153_at	---																			
2.31	2.26	0.05	7.30E-01	9.11E-01	EXOSC6	exosome component 6	chr16q22.1	231916_at	NM_058219																			
6.18	6.13	0.06	7.30E-01	9.11E-01	ATAD3A	ATPase family, AAA domain containing 3A	chr1p36.33	227700_x_at	NM_018188																			
5.65	5.58	0.08	7.30E-01	9.11E-01	OSBP2	oxysterol binding protein 2	chr22q12.2	223432_at	NM_030758																			
4.71	4.56	0.15	7.31E-01	9.11E-01	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	chr3q24-q25	229759_s_at	NM_024621																			
7.45	7.29	0.16	7.31E-01	9.11E-01	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	chr7p11.2	201327_s_at	NM_001009186 /// NM_001762																			
5.32	5.25	0.07	7.31E-01	9.11E-01	---	---	---	228341_at	---																			
8.24	8.16	0.08	7.31E-01	9.11E-01	PRDX2	peroxiredoxin 2	chr19p13.2	211658_at	NM_005809 /// NM_181738																			
2.92	2.85	0.07	7.31E-01	9.11E-01	FAM184A	family with sequence similarity 184, member A	chr6q22.31	220150_s_at	NM_001100411 /// NM_024581																			
6.40	6.29	0.11	7.31E-01	9.11E-01	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	chr16q22-q23	206363_at	NM_001031804 /// NM_005360																			
7.05	6.94	0.11	7.31E-01	9.11E-01	SLC25A36	solute carrier family 25, member 36	chr3q23	201919_at	NM_001104647 /// NM_018155																			
4.00	3.92	0.08	7.31E-01	9.11E-01	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	chr19p13.3	242168_at	NM_024407																			

2.97	2.92	0.05	7.31E-01	9.11E-01	LOC387826	Similar to hCG2001114	chr12p13.32	1563300_at	XM_001720063 /// XM_001720064 /// XM_001720652 /// XM_001720653 /// XM_001721909 /// XM_001721912																			
4.69	4.53	0.16	7.31E-01	9.11E-01	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	chr15q22.2-q22.3	204809_at	NM_006660																			
1.85	1.81	0.04	7.31E-01	9.11E-01	---	---	---	1569192_at	---																			
4.60	4.46	0.14	7.31E-01	9.11E-01	LMAN1	lectin, mannose-binding, 1	chr18q21.3-q22	203294_s_at	NM_005570																			
7.43	7.34	0.10	7.31E-01	9.11E-01	SCAMP1	secretory carrier membrane protein 1	chr5q13.3-q14.1	212416_at	NM_004866																			
2.60	2.55	0.05	7.31E-01	9.12E-01	ZNF3	zinc finger protein 3	chr7q22.1	219604_s_at	NM_017715 /// NM_032924																			
2.10	2.05	0.05	7.31E-01	9.12E-01	---	---	---	1557845_at	---																			
1.97	1.93	0.04	7.31E-01	9.12E-01	---	---	---	1569740_at	---																			
8.50	8.42	0.09	7.31E-01	9.12E-01	CSDA	cold shock domain protein A	chr12p13.1	201161_s_at	NM_003651																			
4.81	4.73	0.09	7.31E-01	9.12E-01	KLHL25	kelch-like 25 (Drosophila)	chr15q25.3	210307_s_at	NM_022480 /// XM_001719329 /// XM_001721147 /// XM_001721166																			
5.59	5.53	0.06	7.31E-01	9.12E-01	SPDEF	SAM pointed domain containing ets transcription factor	chr6p21.3	213441_x_at	NM_012391																			
2.21	2.17	0.05	7.31E-01	9.12E-01	---	---	---	207672_at	---																			
2.16	2.12	0.05	7.32E-01	9.12E-01	LOC283484	hypothetical protein LOC283484	chr13q33.3	1556941_a_at	---																			
1.90	1.86	0.04	7.32E-01	9.12E-01	GPATCH2	G patch domain containing 2	chr1q41	1556125_at	NM_018040																			
2.82	2.64	0.19	7.32E-01	9.12E-01	LOC728198 /// TAF9B	similar to transcription associated factor TAFII31L /// TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	chrXq13.1-q21.1	221618_s_at	NM_015975 /// XM_001126120																			
3.13	3.04	0.09	7.32E-01	9.12E-01	CLEC4M	C-type lectin domain family 4, member M	chr19p13	207995_s_at	NM_014257 /// NM_214675 /// NM_214676 /// NM_214677 /// NM_214678 /// NM_214679																			
2.52	2.46	0.05	7.32E-01	9.12E-01	---	---	---	1567913_at	---																			
5.43	5.37	0.06	7.32E-01	9.12E-01	CADM4	cell adhesion molecule 4	chr19q13.31	215258_at	NM_145296																			
6.74	6.61	0.12	7.32E-01	9.12E-01	TAPT1	transmembrane anterior posterior transformation 1	chr4p15.32	227407_at	NM_153365																			
3.94	3.87	0.06	7.32E-01	9.12E-01	---	---	---	230662_at	---																			
1.90	1.87	0.03	7.32E-01	9.12E-01	IL1RN	interleukin 1 receptor antagonist	chr2q14.2	216244_at	NM_000577 /// NM_173841 /// NM_173842 /// NM_173843																			
4.16	3.93	0.23	7.32E-01	9.12E-01	XIST	X (inactive)-specific transcript (non-protein coding)	chrXq13.2	224590_at	NR_001564																			
2.78	2.73	0.05	7.32E-01	9.12E-01	LOC284417	hCG1651476	chr19q13.42	1570225_at	NM_001085488																			
2.12	2.07	0.05	7.32E-01	9.12E-01	SERPINB11	serpin peptidase inhibitor, clade B (ovalbumin), member 11	---	1552463_at	NM_080475																			
2.05	2.01	0.04	7.32E-01	9.12E-01	RG9MTD2	RNA (guanine-9-) methyltransferase domain containing 2	chr4q23	242442_x_at	NM_001134665 /// NM_001134666 /// NM_152292																			
2.76	2.72	0.04	7.32E-01	9.12E-01	---	---	---	1560071_a_at	---																			
2.14	2.10	0.04	7.32E-01	9.12E-01	LOC202459	similar to RIKEN cDNA 2310008M10	chr6q25.3	1553931_at	NM_145303																			
6.31	6.20	0.11	7.32E-01	9.12E-01	GPRC5C	G protein-coupled receptor, family C, group 5, member C	chr17q25	219327_s_at	NM_018653 /// NM_022036																			
3.31	3.26	0.06	7.32E-01	9.12E-01	---	---	---	236069_at	---																			
3.50	3.45	0.05	7.32E-01	9.12E-01	LOC440602	hypothetical gene supported by BC042100	chr1p13.3	1561335_at	---																			

3.80	3.72	0.08	7.32E-01	9.12E-01	DENND1C	DENN/MADD domain containing 1C	chr19p13.3	221080_s_at	NM_024898																				
2.85	2.80	0.05	7.32E-01	9.12E-01	WSB1	WD repeat and SOCS box-containing 1	chr17q11.1	213406_at	NM_015626 /// NM_134265																				
2.91	2.84	0.07	7.33E-01	9.12E-01	TRIM2	tripartite motif-containing 2	chr4q31.3	214248_s_at	NM_001130067 /// NM_015271																				
2.16	2.12	0.04	7.33E-01	9.12E-01	---	---	---	1559686_a_at	---																				
2.36	2.30	0.06	7.33E-01	9.12E-01	LOC360030	homeobox C14	chr12p13.31	1570021_at	XR_040558 /// XR_040559 /// XR_040560																				
2.18	2.13	0.05	7.33E-01	9.12E-01	RNASE7	ribonuclease, RNase A family, 7	chr14q11.2	234699_at	NM_032572																				
2.93	2.86	0.07	7.33E-01	9.12E-01	C14orf145	chromosome 14 open reading frame 145	chr14q31.1	233859_at	NM_152446																				
2.71	2.65	0.05	7.33E-01	9.12E-01	NEK6	NIMA (never in mitosis gene a)-related kinase 6	chr9q33.3-q34.11	223561_at	NM_014397																				
2.48	2.43	0.05	7.33E-01	9.12E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	235524_at	NM_014990 /// NM_194301																				
2.00	1.94	0.06	7.33E-01	9.12E-01	---	---	---	1555816_at	---																				
6.67	6.64	0.03	7.33E-01	9.12E-01	ARPC5L	actin related protein 2/3 complex, subunit 5-like	chr9q33.3	223101_s_at	NM_030978																				
6.39	6.33	0.06	7.33E-01	9.12E-01	---	---	---	217586_x_at	---																				
4.47	4.40	0.07	7.33E-01	9.12E-01	SH3BP2	SH3-domain binding protein 2	chr4p16.3	211250_s_at	NM_001122681 /// NM_003023																				
3.01	2.95	0.06	7.33E-01	9.12E-01	LOC153328	similar to CG4995 gene product	chr5q31.1	1554542_at	NM_145282																				
9.72	9.67	0.05	7.33E-01	9.12E-01	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	chr4p16.3	209492_x_at	NM_007100																				
2.65	2.59	0.06	7.33E-01	9.12E-01	MYO18B	myosin XVIIIB	chr22q11.2-q12.1	1554579_a_at	NM_032608																				
2.34	2.30	0.04	7.33E-01	9.12E-01	KIAA0232	KIAA0232	chr4p16.1	232366_at	NM_001100590 /// NM_014743																				
2.39	2.35	0.04	7.33E-01	9.13E-01	---	---	---	234613_at	---																				
1.86	1.82	0.04	7.33E-01	9.13E-01	TIGD4	tigger transposable element derived 4	chr4q31.3	1552522_at	NM_145720																				
2.54	2.49	0.05	7.34E-01	9.13E-01	LOC338620	hypothetical protein LOC338620	chr10p11.23	230930_at	---																				
2.34	2.29	0.05	7.34E-01	9.13E-01	---	---	---	243701_at	---																				
4.15	4.00	0.15	7.34E-01	9.13E-01	C21orf57	Chromosome 21 open reading frame 57	chr21q22.3	239208_s_at	NM_001006114 /// NM_058181																				
1.92	1.89	0.03	7.34E-01	9.13E-01	---	---	---	244169_x_at	---																				
2.11	2.06	0.05	7.34E-01	9.13E-01	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	chr5p12	1555177_at	NM_006251 /// NM_206907																				
2.04	2.00	0.04	7.34E-01	9.13E-01	IL4	interleukin 4	chr5q31.1	207538_at	NM_000589 /// NM_172348																				
2.45	2.41	0.04	7.34E-01	9.13E-01	ABCC12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	chr16q12.1	1553410_a_at	NM_033226																				
7.52	7.46	0.06	7.34E-01	9.13E-01	PFKL	phosphofructokinase, liver	chr21q22.3	201102_s_at	NM_001002021 /// NM_002626 /// NR_024108																				
5.09	4.99	0.10	7.34E-01	9.13E-01	TBC1D25	TBC1 domain family, member 25	chrXp11.3-p11.23	226173_at	NM_002536																				
2.27	2.22	0.05	7.34E-01	9.13E-01	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif, 17	chr15q24	1552727_s_at	NM_139057																				
4.31	4.25	0.06	7.34E-01	9.13E-01	SDK2	sidekick homolog 2 (chicken)	chr17q25.1	233585_at	NM_019064																				
2.23	2.18	0.04	7.34E-01	9.13E-01	---	---	---	1562193_at	---																				
1.92	1.88	0.04	7.34E-01	9.13E-01	RGS13	regulator of G-protein signaling 13	chr1q31.2	210258_at	NM_002927 /// NM_144766																				
2.12	2.08	0.05	7.34E-01	9.13E-01	DCUN1D3 /// EXOD1	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) /// exonuclease domain containing 1	chr16p12.2	240603_s_at	NM_080663 /// NM_173475																				
5.91	5.76	0.15	7.34E-01	9.13E-01	UBE3A	ubiquitin protein ligase E3A	chr15q11-q13	213291_s_at	NM_000462 /// NM_130838 /// NM_130839																				
2.94	2.88	0.07	7.34E-01	9.13E-01	GTPBP3	GTP binding protein 3 (mitochondrial)	chr19p13.11	1555062_s_at	NM_001128855 /// NM_032620 /// NM_133644																				

8.37	8.30	0.07	7.35E-01	9.13E-01	MAT2B	methionine adenosyltransferase II, beta	chr5q34-q35	217993_s_at	NM_013283 /// NM_182796
2.02	1.98	0.04	7.35E-01	9.13E-01	CD47	CD47 molecule	chr3q13.1-q13.2	242974_at	NM_001025079 /// NM_001777 /// NM_198793
6.04	5.87	0.17	7.35E-01	9.13E-01	SUB1	SUB1 homolog (S. cerevisiae)	chr5p13.3	221727_at	NM_006713
4.07	4.00	0.07	7.35E-01	9.13E-01	KIAA0922	KIAA0922	chr4q31.3	235674_at	NM_001131007 /// NM_015196
2.36	2.31	0.05	7.35E-01	9.13E-01	C9orf27	chromosome 9 open reading frame 27	chr9q31.3	220660_at	NM_021208 /// NR_024032
2.21	2.17	0.04	7.35E-01	9.13E-01	---	---	---	222350_at	---
5.74	5.63	0.10	7.35E-01	9.13E-01	GULP1	GULP, engulfment adaptor PTB domain containing 1	chr2q32.3-q33	204237_at	NM_016315
2.34	2.31	0.03	7.35E-01	9.14E-01	---	---	---	240895_at	---
2.15	2.10	0.05	7.35E-01	9.14E-01	---	---	---	237096_at	---
7.23	7.07	0.15	7.35E-01	9.14E-01	HIBADH	3-hydroxyisobutyrate dehydrogenase	chr7p15.2	231955_s_at	NM_152740
6.25	6.20	0.05	7.35E-01	9.14E-01	LOC100130886 /// TMEM164	hypothetical protein LOC100130886 /// transmembrane protein 164	chrXq22.3	223202_s_at	NM_032227 /// XM_001714477
3.44	3.34	0.10	7.35E-01	9.14E-01	C10orf114	chromosome 10 open reading frame 114	chr10p12.31	1555923_a_at	NM_001010911
2.30	2.24	0.05	7.35E-01	9.14E-01	JPH3	junctophilin 3	chr16q24.3	229294_at	NM_020655
2.24	2.20	0.04	7.35E-01	9.14E-01	PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	chr6q25.3	1564414_a_at	NM_173516
2.20	2.16	0.04	7.35E-01	9.14E-01	---	---	---	1555817_s_at	---
7.44	7.37	0.07	7.35E-01	9.14E-01	PLEKHJ1	pleckstrin homology domain containing, family J member 1	chr19p13.3	218290_at	NM_018049
2.12	2.09	0.03	7.35E-01	9.14E-01	CLEC12A	C-type lectin domain family 12, member A	chr12p13.2	243106_at	NM_138337 /// NM_201623
7.58	7.46	0.12	7.35E-01	9.14E-01	DST	dystonin	chr6p12.1	212254_s_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380
2.88	2.83	0.04	7.36E-01	9.14E-01	INPP5F	inositol polyphosphate-5-phosphatase F	chr10q26.11	230362_at	NM_014937 /// NR_003251 /// NR_003252
4.01	3.94	0.07	7.36E-01	9.14E-01	KRTAP1-3	keratin associated protein 1-3	chr17q12-q21	234880_x_at	NM_030966
6.29	6.18	0.11	7.36E-01	9.14E-01	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	chr8q13	210754_s_at	NM_001111097 /// NM_002350
3.31	3.25	0.06	7.36E-01	9.14E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	236283_x_at	NM_002577
2.13	2.09	0.04	7.36E-01	9.14E-01	ALB	albumin	chr4q11-q13	214842_s_at	NM_000477
2.67	2.60	0.06	7.36E-01	9.14E-01	---	---	---	1564391_at	---
3.07	2.99	0.08	7.36E-01	9.14E-01	TRIO	Triple functional domain (PTPRF interacting)	chr5p15.2	216700_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929
4.53	4.39	0.14	7.36E-01	9.14E-01	ITIH4	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	chr3p21-p14	206287_s_at	NM_002218
2.18	2.13	0.05	7.36E-01	9.14E-01	THAP6	THAP domain containing 6	chr4q21.1	235653_s_at	NM_144721
2.18	2.14	0.04	7.36E-01	9.14E-01	CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	chr2q35	217564_s_at	NM_001122633 /// NM_001122634 /// NM_001875
8.08	7.99	0.09	7.36E-01	9.14E-01	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	chr5q23-q31	202333_s_at	NM_003337
3.53	3.43	0.10	7.36E-01	9.14E-01	TMC4	transmembrane channel-like 4	chr19q13.42	226403_at	NM_144686
2.42	2.38	0.04	7.36E-01	9.14E-01	RNFT1	ring finger protein, transmembrane 1	chr17q23.1	221195_at	NM_016125
2.71	2.66	0.05	7.36E-01	9.14E-01	PSG6	pregnancy specific beta-1-glycoprotein 6	chr19q13.2	209738_x_at	NM_001031850 /// NM_002782
2.85	2.81	0.05	7.36E-01	9.14E-01	---	---	---	233582_at	---
3.32	3.25	0.06	7.36E-01	9.14E-01	---	---	---	1559444_at	---

5.35	5.20	0.14	7.36E-01	9.14E-01	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	chr2q32.1	225174_at	NM_018981
2.12	2.08	0.04	7.36E-01	9.14E-01	SRrp35	serine-arginine repressor protein (35 kDa)	chr6q15	1552381_at	NM_080743
2.62	2.58	0.04	7.37E-01	9.14E-01	---	---	---	1560827_at	---
2.11	2.07	0.04	7.37E-01	9.14E-01	---	---	---	1569230_at	---
3.48	3.42	0.06	7.37E-01	9.14E-01	C4orf38	chromosome 4 open reading frame 38	chr4q35.1	230572_at	NM_153008 /// NR_024008
1.84	1.80	0.04	7.37E-01	9.14E-01	ADSS	Adenylosuccinate synthase	chr1cen-q12	227310_at	NM_001126
8.04	7.87	0.17	7.37E-01	9.15E-01	HSPB6	heat shock protein, alpha-crystallin-related, B6	chr19q13.12	226304_at	NM_144617
4.62	4.56	0.06	7.37E-01	9.15E-01	TTLL4	Tubulin tyrosine ligase-like family, member 4	chr2p24.3-p24.1	1557611_at	NM_014640
5.68	5.58	0.10	7.37E-01	9.15E-01	SLC25A13	solute carrier family 25, member 13 (citrin)	chr7q21.3	203775_at	NM_014251
2.36	2.31	0.05	7.37E-01	9.15E-01	DEFB104A /// DEFB104B	defensin, beta 104A /// defensin, beta 104B	chr8p23.1	1553521_at	NM_001040702 /// NM_080389
3.86	3.72	0.14	7.37E-01	9.15E-01	PTPRC	protein tyrosine phosphatase, receptor type, C	chr1q31-q32	212588_at	NM_002838 /// NM_080921 /// NM_080922 /// NM_080923
2.37	2.32	0.05	7.37E-01	9.15E-01	ELMOD2	ELMO/CED-12 domain containing 2	chr4q31.1	1557836_at	NM_153702
6.15	6.01	0.14	7.37E-01	9.15E-01	ANAPC4	anaphase promoting complex subunit 4	chr4p15.2	226917_s_at	NM_013367
1.93	1.90	0.03	7.37E-01	9.15E-01	---	---	---	244318_at	---
2.87	2.82	0.05	7.37E-01	9.15E-01	GANC	glucosidase, alpha; neutral C	chr15q15.2	235340_at	NM_198141
7.15	7.04	0.10	7.37E-01	9.15E-01	DBP	D site of albumin promoter (albumin D-box) binding protein	chr19q13.3	209782_s_at	NM_001352
1.97	1.93	0.04	7.37E-01	9.15E-01	ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif, 19	chr5q31	1553180_at	NM_133638
2.18	2.12	0.06	7.37E-01	9.15E-01	---	---	---	1561084_at	---
2.44	2.40	0.04	7.37E-01	9.15E-01	---	---	---	1562941_at	---
4.55	4.49	0.06	7.37E-01	9.15E-01	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	chrXp11.22	222109_at	NM_019067
4.45	4.36	0.09	7.38E-01	9.15E-01	FAM178A	family with sequence similarity 178, member A	chr10q24.31	1553909_x_at	NM_018121
1.91	1.87	0.04	7.38E-01	9.15E-01	---	---	---	1566952_at	---
5.63	5.44	0.18	7.38E-01	9.15E-01	---	---	---	238967_at	---
4.57	4.51	0.06	7.38E-01	9.15E-01	SLC26A1	solute carrier family 26 (sulfate transporter), member 1	chr4p16.3	205058_at	NM_022042 /// NM_134425 /// NM_213613
2.79	2.75	0.04	7.38E-01	9.15E-01	---	---	---	236509_at	---
9.21	9.11	0.10	7.38E-01	9.15E-01	LTA4H	leukotriene A4 hydrolase	chr12q22	208771_s_at	NM_000895
2.23	2.17	0.05	7.38E-01	9.15E-01	FAM148A	family with sequence similarity 148, member A	chr15q22.2	241031_at	NM_207322
3.13	3.06	0.07	7.38E-01	9.15E-01	WDR37	WD repeat domain 37	chr10p15.3	1554869_at	NM_014023
2.86	2.78	0.08	7.38E-01	9.15E-01	LOC653188 /// SMA4 /// SMA5	similar to Beta-glucuronidase-like protein SMA3 /// glucuronidase, beta pseudogene /// glucuronidase, beta pseudogene	chr5q13 /// chr5q13.2	215043_s_at	XM_001721330 /// XM_001721429
2.40	2.34	0.06	7.38E-01	9.15E-01	ZNF223	zinc finger protein 223	chr19q13.2	207128_s_at	NM_013361
7.46	7.40	0.06	7.38E-01	9.15E-01	MTHFS	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	chr15q25.1	203433_at	NM_006441
5.83	5.75	0.07	7.38E-01	9.15E-01	NOL6	nucleolar protein family 6 (RNA-associated)	chr9p13.3	218199_s_at	NM_022917 /// NM_139235
2.11	2.07	0.04	7.38E-01	9.15E-01	---	---	---	235764_at	---
2.05	2.01	0.04	7.38E-01	9.15E-01	HSF5	heat shock transcription factor family member 5	chr17q22	230718_at	NM_001080439
6.37	6.28	0.09	7.38E-01	9.15E-01	PBLD	phenazine biosynthesis-like protein domain containing	chr10pter-q25.3	219543_at	NM_001033083 /// NM_022129
3.00	2.93	0.07	7.38E-01	9.15E-01	PHF6	PHD finger protein 6	chrXq26.3	224442_at	NM_001015877 /// NM_032335 /// NM_032458
4.40	4.33	0.07	7.38E-01	9.15E-01	FLOT2	flotillin 2	chr17q11-q12	211299_s_at	NM_004475
7.15	7.06	0.09	7.38E-01	9.15E-01	PPIL3	peptidylprolyl isomerase (cyclophilin)-like 3	chr2q33.1	224364_s_at	NM_032472 /// NM_130906 /// NM_131916
9.38	9.32	0.06	7.38E-01	9.15E-01	UFC1	ubiquitin-fold modifier conjugating enzyme 1	chr1q23.3	217797_at	NM_016406
2.22	2.17	0.05	7.38E-01	9.15E-01	---	---	---	1563103_at	---
2.71	2.66	0.05	7.38E-01	9.15E-01	ARID5B	AT rich interactive domain 5B (MRF1-like)	chr10q21.2	1558001_s_at	NM_032199

2.04	2.00	0.04	7.38E-01	9.15E-01	C3orf53	chromosome 3 open reading frame 53	chr3p24.1	1564250_at	XR_041222 /// XR_041223 /// XR_041224																				
6.93	6.84	0.09	7.39E-01	9.15E-01	PSMD5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	chr9q33.2	203447_at	NM_005047																				
3.72	3.62	0.09	7.39E-01	9.15E-01	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	chr17q21	200988_s_at	NM_005789 /// NM_176863																				
2.12	2.05	0.07	7.39E-01	9.15E-01	C3orf30	chromosome 3 open reading frame 30	chr3q13.32	1553146_at	NM_152539																				
4.07	4.01	0.06	7.39E-01	9.15E-01	RAB4A /// SPHAR	RAB4A, member RAS oncogene family /// S-phase response (cyclin-related)	chr1q42-q43 /// chr1q42.11-q42.3	206272_at	NM_004578 /// NM_006542																				
2.34	2.30	0.04	7.39E-01	9.15E-01	SOX30	SRY (sex determining region Y)-box 30	chr5q33	1559235_a_at	NM_007017 /// NM_178424																				
4.36	4.30	0.06	7.39E-01	9.15E-01	ARID1B	AT rich interactive domain 1B (SWI1-like)	chr6q25.1	233339_s_at	NM_017519 /// NM_020732 /// NM_175863																				
4.25	4.13	0.12	7.39E-01	9.15E-01	HIC1	hypermethylated in cancer 1	chr17p13.3	230218_at	NM_001098202 /// NM_006497																				
2.85	2.77	0.08	7.39E-01	9.15E-01	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	chr8q21.11	202823_at	NM_005648																				
4.25	4.20	0.05	7.39E-01	9.15E-01	LOC219347	hypothetical protein LOC219347	chr10q23.1	232294_at	XM_001723637																				
4.64	4.57	0.07	7.39E-01	9.15E-01	---	---	---	228951_at	---																				
2.62	2.56	0.06	7.39E-01	9.15E-01	LOC728723	hypothetical LOC728723	chr5q14.1	1564475_s_at	XR_042120 /// XR_042121 /// XR_042122																				
4.07	4.02	0.05	7.39E-01	9.15E-01	---	---	---	228842_at	---																				
3.27	3.13	0.13	7.39E-01	9.15E-01	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	chr9p22	1569652_at	NM_004529																				
2.27	2.22	0.04	7.39E-01	9.15E-01	TRPM6	transient receptor potential cation channel, subfamily M, member 6	chr9q21.13	221102_s_at	NM_017662																				
3.48	3.43	0.05	7.39E-01	9.15E-01	PRSS36	protease, serine, 36	chr16p11.2	1552555_at	NM_173502																				
2.66	2.59	0.07	7.39E-01	9.15E-01	---	---	---	235759_at	---																				
2.73	2.68	0.05	7.39E-01	9.15E-01	---	---	---	244207_at	---																				
5.02	4.97	0.05	7.39E-01	9.15E-01	CIAO1	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	chr2q11.2	239053_at	NM_004804																				
2.19	2.15	0.05	7.39E-01	9.15E-01	CRYBB2P1	Crystallin, beta B2 pseudogene 1	chr22q11.2-q12.1	1561274_at	---																				
6.35	6.27	0.08	7.39E-01	9.15E-01	YIPF2	Yip1 domain family, member 2	chr19p13.2	65086_at	NM_024029																				
6.70	6.58	0.12	7.39E-01	9.15E-01	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	chr18q11	235333_at	NM_004775																				
4.35	4.27	0.08	7.39E-01	9.15E-01	SLC26A6	solute carrier family 26, member 6	chr3p21.3	232551_at	NM_001040454 /// NM_022911 /// NM_134263 /// NM_134426																				
1.91	1.88	0.03	7.39E-01	9.15E-01	SH3GL2	SH3-domain GRB2-like 2	chr9p22	205751_at	NM_003026																				
7.39	7.27	0.12	7.39E-01	9.15E-01	ZBED5	zinc finger, BED-type containing 5	chr11p15.3	218263_s_at	XR_041298 /// XR_041299 /// XR_041300																				
2.81	2.76	0.06	7.39E-01	9.15E-01	C14orf82	chromosome 14 open reading frame 82	chr14q22.1	233106_at	XM_001716509 /// XM_498578 /// XM_944991																				
2.17	2.11	0.06	7.39E-01	9.15E-01	GPR18	G protein-coupled receptor 18	chr13q32	210279_at	NM_001098200 /// NM_005292																				
6.62	6.47	0.15	7.40E-01	9.15E-01	RPA1	replication protein A1, 70kDa	chr17p13.3	201529_s_at	NM_002945																				
6.57	6.50	0.07	7.40E-01	9.15E-01	DHPS	deoxyhypusine synthase	chr19p13.2-p13.1	202802_at	NM_001930 /// NM_013406 /// NM_013407																				
3.35	3.30	0.05	7.40E-01	9.15E-01	ZBTB25	zinc finger and BTB domain containing 25	chr14q23-q24	214482_at	NM_006977																				

3.67	3.58	0.09	7.40E-01	9.15E-01	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	chr16p13.3|16p13.3-p13.11	210158_at	NM_005236																				
2.66	2.61	0.05	7.40E-01	9.15E-01	PPHLN1	periphilin 1	chr12q12	234459_at	NM_016488 /// NM_201438 /// NM_201439 /// NM_201440 /// NM_201515																				
3.18	3.12	0.05	7.40E-01	9.15E-01	DNAH3	dynein, axonemal, heavy chain 3	chr16p12.2	1563290_at	NM_017539																				
2.84	2.77	0.07	7.40E-01	9.15E-01	VAX2	ventral anterior homeobox 2	chr2p13	220443_s_at	NM_012476																				
2.27	2.23	0.04	7.40E-01	9.15E-01	LOC285181	hypothetical protein LOC285181	chr2q36.1	1561334_at	---																				
3.35	3.31	0.04	7.40E-01	9.15E-01	KCNT1	potassium channel, subfamily T, member 1	chr9q34.3	1563608_a_at	NM_020822 /// XM_001719828 /// XM_001722509 /// XM_001723196																				
5.49	5.37	0.12	7.40E-01	9.15E-01	UTX	ubiquitously transcribed tetratricopeptide repeat, X chromosome	chrXp11.2	203992_s_at	NM_021140																				
5.61	5.50	0.11	7.40E-01	9.15E-01	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	chr21q22.3	223182_s_at	NM_001037553 /// NM_020132																				
3.20	3.09	0.11	7.40E-01	9.15E-01	MEGF6	multiple EGF-like-domains 6	chr1p36.3	226869_at	NM_001409																				
3.88	3.81	0.06	7.40E-01	9.15E-01	C9orf102	chromosome 9 open reading frame 102	chr9q22.32	228211_at	NM_001010895 /// NM_001034155 /// NM_020207																				
2.49	2.40	0.09	7.40E-01	9.15E-01	ZDHHC21	zinc finger, DHHC-type containing 21	chr9p22.3	241946_at	NM_178566																				
3.23	3.18	0.05	7.40E-01	9.15E-01	SMTN	Smoothelin	chr22q12.2	1556030_at	NM_006932 /// NM_134269 /// NM_134270																				
2.24	2.19	0.05	7.40E-01	9.15E-01	LOC51190	neutral sphingomyelinase	---	221405_at	---																				
1.96	1.90	0.06	7.40E-01	9.15E-01	RSRC1	arginine/serine-rich coiled-coil 1	chr3q25.32	235354_s_at	NM_016625																				
3.14	3.08	0.06	7.40E-01	9.15E-01	EXOC4	exocyst complex component 4	chr7q31	235974_at	NM_001037126 /// NM_021807																				
5.60	5.50	0.11	7.40E-01	9.15E-01	LIPT1	lipoyltransferase 1	chr2q11.2	205571_at	NM_015929 /// NM_145196 /// NM_145197 /// NM_145198 /// NM_145199																				
7.08	7.02	0.06	7.40E-01	9.15E-01	C19orf42	chromosome 19 open reading frame 42	chr19p13.11	229650_s_at	NM_024104																				
2.32	2.29	0.03	7.41E-01	9.15E-01	OR51B6	olfactory receptor, family 51, subfamily B, member 6	chr11p15.4	234526_at	NM_001004750																				
2.26	2.22	0.04	7.41E-01	9.15E-01	RNF216	Ring finger protein 216	chr7p22.1	1563361_at	NM_207111 /// NM_207116																				
12.42	12.39	0.04	7.41E-01	9.16E-01	RPS20	ribosomal protein S20	chr8q12	214003_x_at	NM_001023																				
2.49	2.44	0.05	7.41E-01	9.16E-01	LIN9	lin-9 homolog (C. elegans)	chr1q42.12	1552771_a_at	NM_173083																				
2.70	2.66	0.04	7.41E-01	9.16E-01	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	chr10q24	216025_x_at	NM_000771																				
3.10	3.04	0.06	7.41E-01	9.16E-01	KLK6	kallikrein-related peptidase 6	chr19q13.3	204733_at	NM_001012964 /// NM_001012965 /// NM_002774																				
4.18	4.12	0.06	7.41E-01	9.16E-01	ZBTB38	zinc finger and BTB domain containing 38	chr3q23	236557_at	NM_001080412																				
2.55	2.50	0.06	7.41E-01	9.16E-01	LOC100131354	Hypothetical protein LOC100131354	chr1q32.1	1557311_at	XM_001718006 /// XM_001719406																				
2.15	2.10	0.05	7.41E-01	9.16E-01	---	---	---	240596_at	---																				
2.99	2.95	0.04	7.41E-01	9.16E-01	---	---	---	1567270_at	---																				

2.90	2.84	0.06	7.41E-01	9.16E-01	MYH11	myosin, heavy chain 11, smooth muscle	chr16p13.11	228133_s_at	NM_001040113 /// NM_001040114 /// NM_002474 /// NM_022844																				
2.74	2.69	0.05	7.41E-01	9.16E-01	PAX1	paired box 1	chr20p11.2	214401_at	NM_006192																				
3.31	3.24	0.07	7.41E-01	9.16E-01	C9orf53	chromosome 9 open reading frame 53	chr9p21-p22	220505_at	XM_001723106 /// XM_001725384																				
4.58	4.51	0.07	7.41E-01	9.16E-01	LOC100133142	similar to hCG2008267	chr19q13.42	238665_at	XM_001718400																				
5.24	5.18	0.06	7.41E-01	9.16E-01	BCAN	brevican	chr1q31	91920_at	NM_021948 /// NM_198427																				
6.64	6.55	0.09	7.41E-01	9.16E-01	SEPN1	selenoprotein N, 1	chr1p36.13	224659_at	NM_020451 /// NM_206926																				
4.34	4.26	0.08	7.41E-01	9.16E-01	---	---	---	229572_at	---																				
2.42	2.36	0.07	7.41E-01	9.16E-01	---	---	---	1565628_at	---																				
2.39	2.35	0.04	7.41E-01	9.16E-01	---	---	---	233248_at	---																				
1.98	1.94	0.03	7.42E-01	9.16E-01	EFCAB3 /// LOC100133744	EF-hand calcium binding domain 3 /// similar to hypoxia-inducible protein 2	chr17q23.2	1553392_at	NM_173503 /// XM_001721922																				
3.23	3.14	0.09	7.42E-01	9.16E-01	LOC386597	hypothetical protein LOC386597	chr2p25.2	1559145_at	---																				
2.29	2.24	0.05	7.42E-01	9.16E-01	---	---	---	AFFX-r2-Bs-thr-5_s_at	---																				
2.78	2.73	0.05	7.42E-01	9.16E-01	MCTP1	multiple C2 domains, transmembrane 1	chr5q15	1554730_at	NM_001002796 /// NM_024717																				
3.18	3.13	0.05	7.42E-01	9.16E-01	CPA5	carboxypeptidase A5	chr7q32	240744_at	NM_001127441 /// NM_001127442 /// NM_080385																				
3.98	3.92	0.06	7.42E-01	9.16E-01	LOC348761	hypothetical protein LOC348761	chr2q37.1	240590_at	---																				
7.92	7.80	0.12	7.42E-01	9.16E-01	CSNK1A1	casein kinase 1, alpha 1	chr5q32	213086_s_at	NM_001025105 /// NM_001892																				
4.87	4.80	0.07	7.42E-01	9.16E-01	SH2B2	SH2B adaptor protein 2	chr7q22	205367_at	NM_020979																				
2.58	2.53	0.04	7.42E-01	9.16E-01	DKFZp761H2121	hypothetical protein DKFZp761H2121	chr10q26.13	1553865_a_at	---																				
2.76	2.69	0.07	7.42E-01	9.16E-01	MBTD1	mbt domain containing 1	chr17q21.33	243552_at	NM_017643																				
3.61	3.43	0.17	7.42E-01	9.16E-01	ADRB2	adrenergic, beta-2-, receptor, surface	chr5q31-q32	206170_at	NM_000024																				
3.38	3.30	0.08	7.42E-01	9.16E-01	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	chr10q24.32	236713_at	NM_005736																				
2.78	2.70	0.08	7.42E-01	9.16E-01	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	chr4q32.3	228152_s_at	NM_001012967																				
7.48	7.39	0.09	7.42E-01	9.16E-01	YTHDF3	YTH domain family, member 3	chr8q12.3	221749_at	NM_152758																				
2.09	2.04	0.04	7.42E-01	9.16E-01	LOC727924 /// OR4N4	hypothetical LOC727924 /// olfactory receptor, family 4, subfamily N, member 4	chr15q11.2	1560735_s_at	NM_001005241 /// XR_039952																				
6.18	6.07	0.11	7.42E-01	9.16E-01	LIMS1	LIM and senescent cell antigen-like domains 1	chr2q12.3-q13	207198_s_at	NM_004987																				
2.06	2.02	0.04	7.42E-01	9.16E-01	FOXG1	forkhead box G1	chr14q13	206018_at	NM_005249																				
6.52	6.48	0.04	7.42E-01	9.16E-01	HIGD2A	HIG1 domain family, member 2A	chr5q35.2	209328_x_at	NM_138820																				
2.84	2.77	0.06	7.42E-01	9.17E-01	---	---	---	1563472_at	---																				
3.47	3.43	0.05	7.43E-01	9.17E-01	SYNPO2L	synaptopodin 2-like	chr10q22.2	243313_at	NM_001114133 /// NM_024875																				
2.15	2.11	0.04	7.43E-01	9.17E-01	UNC45B	unc-45 homolog B (C. elegans)	chr17q12	235261_at	NM_001033576 /// NM_173167																				
2.35	2.31	0.04	7.43E-01	9.17E-01	MAGEC1	melanoma antigen family C, 1	chrXq26	206609_at	NM_005462																				
3.72	3.67	0.06	7.43E-01	9.17E-01	PROM2	prominin 2	chr2q11.1	239528_at	NM_144707																				
2.93	2.87	0.06	7.43E-01	9.17E-01	---	---	---	230376_at	---																				
7.35	7.23	0.12	7.43E-01	9.17E-01	ZBTB38	zinc finger and BTB domain containing 38	chr3q23	225512_at	NM_001080412																				
4.09	4.01	0.08	7.43E-01	9.17E-01	---	---	---	240060_at	---																				
3.99	3.89	0.10	7.43E-01	9.17E-01	---	---	---	226520_at	---																				
4.37	4.27	0.10	7.43E-01	9.17E-01	LOC100128718	Hypothetical protein LOC100128718	chr19p13.11	1556643_at	XM_001719043 /// XM_001719695																				

7.69	7.56	0.13	7.43E-01	9.17E-01	CLCN3	Chloride channel 3	chr4q33	201734_at	NM_001829 /// NM_173872																			
3.44	3.36	0.08	7.43E-01	9.17E-01	PPHLN1	periphilin 1	chr12q12	1555351_s_at	NM_016488 /// NM_201438 /// NM_201439 /// NM_201440 /// NM_201515																			
2.39	2.34	0.05	7.43E-01	9.17E-01	---	---	---	243340_at	---																			
2.65	2.61	0.04	7.43E-01	9.17E-01	---	---	---	236987_at	---																			
2.34	2.29	0.05	7.43E-01	9.17E-01	DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	chr5p15.2-p13.1	221630_s_at	NM_024415																			
2.94	2.90	0.04	7.43E-01	9.17E-01	MTRF1L	Mitochondrial translational release factor 1-like	chr6q25-q26	215560_x_at	NM_001114184 /// NM_019041																			
2.10	2.06	0.04	7.43E-01	9.17E-01	HSD3B1	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	chr1p13.1	241111_at	NM_000862																			
7.36	7.26	0.10	7.44E-01	9.17E-01	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	chr1p34.2	218028_at	NM_022821																			
2.54	2.49	0.05	7.44E-01	9.17E-01	C10orf49	chromosome 10 open reading frame 49	chr10p13	236800_at	NM_145314																			
7.41	7.34	0.06	7.44E-01	9.17E-01	CLCN7	chloride channel 7	chr16p13	38069_at	NM_001114331 /// NM_001287																			
2.22	2.18	0.04	7.44E-01	9.17E-01	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	chr15q15.1	205023_at	NM_002875 /// NM_133487																			
7.59	7.51	0.08	7.44E-01	9.17E-01	LOC100128443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	chr5q12.3	40016_g_at	NM_015183 /// NM_198828 /// XM_001720470 /// XM_001720479 /// XM_001722488																			
6.45	6.36	0.09	7.44E-01	9.17E-01	AKIRIN2	akirin 2	chr6q15	223144_s_at	NM_018064																			
3.07	3.00	0.07	7.44E-01	9.17E-01	NOD1	nucleotide-binding oligomerization domain containing 1	chr7p15-p14	224190_x_at	NM_006092																			
2.84	2.80	0.05	7.44E-01	9.17E-01	DUSP19	dual specificity phosphatase 19	chr2q32.1	1555598_a_at	NM_080876																			
1.97	1.92	0.04	7.44E-01	9.17E-01	ARMETL1 /// GPER /// NFRKB	arginine-rich, mutated in early stage tumors-like 1 /// G protein-coupled estrogen receptor 1 /// nuclear factor related to kappaB binding protein	chr10p13 /// chr11q24-q25 /// chr7p22.3	222227_at	NM_001029954 /// NM_001039966 /// NM_001098201 /// NM_001505 /// NM_006165																			
2.52	2.46	0.06	7.44E-01	9.17E-01	FUCA1	Fucosidase, alpha-L- 1, tissue	chr1p34	229137_at	NM_000147																			
2.60	2.55	0.06	7.44E-01	9.17E-01	KRIT1	KRIT1, ankyrin repeat containing	chr7q21-q22	229785_at	NM_001013406 /// NM_004912 /// NM_194454 /// NM_194455 /// NM_194456																			
2.60	2.55	0.05	7.44E-01	9.17E-01	ATP2A3	ATPase, Ca++ transporting, ubiquitous	chr17p13.3	207521_s_at	NM_005173 /// NM_174953 /// NM_174954 /// NM_174955 /// NM_174956 /// NM_174957 /// NM_174958																			
2.58	2.52	0.06	7.44E-01	9.17E-01	---	---	---	244186_at	---																			
2.29	2.25	0.05	7.44E-01	9.17E-01	---	---	---	237161_at	---																			

3.01	2.97	0.04	7.44E-01	9.17E-01	LOC170082	TFIIS central domain-containing protein 1	chrXp22.2	1563863_x_at	NM_152634																			
2.18	2.13	0.05	7.44E-01	9.17E-01	LOC157273	hypothetical protein LOC157273	chr8p23.1	1563610_at	---																			
2.45	2.41	0.04	7.44E-01	9.17E-01	CTNNA3	catenin (cadherin-associated protein), alpha 3	chr10q22.2	220815_at	NM_001127384 /// NM_013266																			
2.94	2.89	0.05	7.44E-01	9.17E-01	RPUSD3	RNA pseudouridylate synthase domain containing 3	chr3p25.3	1566602_at	NM_173659																			
5.32	5.22	0.11	7.44E-01	9.17E-01	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	chr6p25	239213_at	NM_030666																			
2.37	2.32	0.05	7.44E-01	9.17E-01	VWA3B	von Willebrand factor A domain containing 3B	chr2q11.2	1555298_a_at	NM_144992																			
2.64	2.59	0.05	7.44E-01	9.17E-01	---	---	---	1562499_at	---																			
2.93	2.89	0.05	7.44E-01	9.17E-01	---	---	---	240791_at	---																			
2.10	2.05	0.04	7.44E-01	9.17E-01	BCL2L15	BCL2-like 15	chr1p13.2	242013_at	NM_001010922																			
3.35	3.29	0.07	7.44E-01	9.17E-01	IPP	Intracisternal A particle-promoted polypeptide	chr1p34-p32	241393_at	NM_005897																			
2.82	2.77	0.04	7.44E-01	9.17E-01	ZNF333	Zinc finger protein 333	chr19p13	231369_at	NM_032433																			
5.88	5.73	0.15	7.45E-01	9.17E-01	JMJD1A	jumonji domain containing 1A	chr2p11.2	212689_s_at	NM_018433																			
4.63	4.59	0.04	7.45E-01	9.17E-01	CASP6	caspase 6, apoptosis-related cysteine peptidase	chr4q25	211464_x_at	NM_001226 /// NM_032992																			
4.15	3.94	0.21	7.45E-01	9.17E-01	CXorf15	chromosome X open reading frame 15	chrXp22.2	219969_at	NM_018360																			
2.72	2.61	0.11	7.45E-01	9.17E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	238900_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447																				
2.80	2.75	0.05	7.45E-01	9.17E-01	---	---	---	216943_at	---																			
2.67	2.62	0.05	7.45E-01	9.17E-01	---	---	---	239328_at	---																			
2.29	2.25	0.04	7.45E-01	9.17E-01	HERC2P7	hect domain and RLD 2 pseudogene 7	chr15q11-q13	233075_at	---																			
4.57	4.50	0.07	7.45E-01	9.17E-01	---	---	---	221379_at	---																			

6.27	6.21	0.06	7.45E-01	9.17E-01	MAX	MYC associated factor X	chr14q23	208403_x_at	NM_002382 /// NM_145112 /// NM_145113 /// NM_145114 /// NM_145116 /// NM_197957																				
1.91	1.88	0.04	7.45E-01	9.17E-01	FANCB	Fanconi anemia, complementation group B	chrXp22.2	1553244_at	NM_001018113 /// NM_152633																				
2.71	2.66	0.05	7.45E-01	9.17E-01	LOC730031 /// MLLT4	similar to Afadin (Protein AF-6) /// myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	chr6q27	208512_s_at	NM_001040000 /// NM_001040001 /// NM_005936 /// XM_001132155																				
2.72	2.67	0.05	7.45E-01	9.17E-01	FRMPD1	FERM and PDZ domain containing 1	chr9p13.2	206774_at	NM_014907																				
2.94	2.88	0.06	7.45E-01	9.17E-01	BTG3	BTG family, member 3	chr21q21.1-q21.2	1556213_a_at	NM_001130914 /// NM_006806																				
3.24	3.15	0.08	7.45E-01	9.17E-01	---	---	---	233921_s_at	---																				
2.23	2.18	0.05	7.45E-01	9.17E-01	---	---	---	237584_at	---																				
12.76	12.73	0.04	7.45E-01	9.17E-01	RPL23A	ribosomal protein L23a	chr17q11	203012_x_at	NM_000984																				
2.30	2.25	0.05	7.45E-01	9.17E-01	---	---	---	222355_at	---																				
4.08	3.99	0.09	7.45E-01	9.17E-01	---	---	---	240279_at	---																				
2.54	2.51	0.04	7.45E-01	9.18E-01	---	---	---	1569743_at	---																				
4.82	4.68	0.14	7.45E-01	9.18E-01	---	---	---	239327_at	---																				
3.23	3.18	0.06	7.45E-01	9.18E-01	LOC219688	hypothetical protein LOC219688	chr10p12.33	1564385_at	---																				
1.98	1.95	0.03	7.45E-01	9.18E-01	CXorf57	chromosome X open reading frame 57	chrXq22.3	215803_at	NM_018015																				
2.41	2.36	0.05	7.45E-01	9.18E-01	FOXN2	forkhead box N2	chr2p22-p16	206708_at	NM_002158																				
2.24	2.18	0.06	7.46E-01	9.18E-01	HHLA2	HERV-H LTR-associating 2	chr3q13.13	234673_at	NM_007072																				
2.49	2.44	0.05	7.46E-01	9.18E-01	CCL20	chemokine (C-C motif) ligand 20	chr2q33-q37	205476_at	NM_001130046 /// NM_004591																				
2.81	2.77	0.04	7.46E-01	9.18E-01	CDK5RAP2	CDK5 regulatory subunit associated protein 2	chr9q33.2	237418_at	NM_001011649 /// NM_018249																				
2.66	2.61	0.05	7.46E-01	9.18E-01	MAP2K2	Mitogen-activated protein kinase kinase 2	chr19p13.3	213487_at	NM_030662																				
2.71	2.66	0.05	7.46E-01	9.18E-01	TFCP2L1	transcription factor CP2-like 1	chr2q14	219735_s_at	NM_014553																				
6.18	6.12	0.06	7.46E-01	9.18E-01	NCOA3	nuclear receptor coactivator 3	chr20q12	209061_at	NM_006534 /// NM_181659																				
2.03	1.99	0.04	7.46E-01	9.18E-01	---	---	---	1561600_at	---																				
3.03	2.97	0.06	7.46E-01	9.18E-01	FAM174B	family with sequence similarity 174, member B	chr15q26.1	51158_at	NM_207446																				
5.52	5.44	0.07	7.46E-01	9.18E-01	LOC100128343	hypothetical protein LOC100128343	chr14q32.33	1568929_at	XM_001724408 /// XM_001726665																				
1.98	1.94	0.03	7.46E-01	9.18E-01	---	---	---	1559770_at	---																				
9.39	9.31	0.07	7.46E-01	9.18E-01	EIF3D	eukaryotic translation initiation factor 3, subunit D	chr22q13.1	200005_at	NM_003753																				
1.95	1.92	0.04	7.46E-01	9.18E-01	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	chr1p21	205288_at	NM_003672 /// NM_033312 /// NM_033313																				
2.07	2.02	0.05	7.46E-01	9.18E-01	CASD1	CAS1 domain containing 1	chr7q21.3	243500_at	NM_022900																				
2.71	2.67	0.04	7.46E-01	9.18E-01	---	---	---	216787_at	---																				
3.69	3.63	0.06	7.46E-01	9.18E-01	DOCK6	dedicator of cytokinesis 6	chr19p13.2	222003_s_at	NM_020812																				
3.10	3.04	0.06	7.46E-01	9.18E-01	---	---	---	1557330_at	---																				
3.07	2.98	0.09	7.47E-01	9.18E-01	---	---	---	239696_at	---																				
1.95	1.91	0.04	7.47E-01	9.18E-01	---	---	---	1569818_at	---																				
5.84	5.76	0.08	7.47E-01	9.18E-01	LIMS2	LIM and senescent cell antigen-like domains 2	chr2q14.3	220765_s_at	NM_017980																				
5.51	5.43	0.08	7.47E-01	9.18E-01	GPR175	G protein-coupled receptor 175	chr3q21.2	218855_at	NM_016372																				
2.75	2.70	0.06	7.47E-01	9.18E-01	PRAMEF1 /// PRAMEF13 /// PRAMEF2	PRAME family member 1 /// PRAME family member 13 /// PRAME family member 2	chr1p36.21	208312_s_at	NM_001024661 /// NM_023013 /// NM_023014 /// XM_001713933																				

5.97	5.87	0.09	7.47E-01	9.18E-01	---	---	---	1569202_x_at	---																				
4.42	4.30	0.12	7.47E-01	9.18E-01	---	---	---	242273_at	---																				
4.10	3.87	0.23	7.47E-01	9.18E-01	HNRNPU	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	chr1q44	236244_at	NM_004501 /// NM_031844																				
2.14	2.10	0.05	7.47E-01	9.18E-01	---	---	---	243418_at	---																				
3.31	3.24	0.07	7.47E-01	9.18E-01	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	chr1p22.3	203016_s_at	NM_014021																				
2.31	2.27	0.04	7.47E-01	9.18E-01	---	---	---	1561573_at	---																				
2.19	2.16	0.03	7.47E-01	9.19E-01	---	---	---	237546_at	---																				
1.98	1.94	0.04	7.47E-01	9.19E-01	LOC100132853	hypothetical LOC100132853	chr11q13.4	224094_at	XM_001723645 /// XM_001723747 /// XM_001724410																				
2.08	2.04	0.04	7.47E-01	9.19E-01	SYT15	Synaptotagmin XV	chr10q11.1	244308_at	NM_031912 /// NM_181519 /// XM_001720092																				
3.67	3.61	0.06	7.48E-01	9.19E-01	PRSS7	protease, serine, 7 (enterokinase)	chr21q21|21q21.1	217269_s_at	NM_002772																				
2.66	2.60	0.06	7.48E-01	9.19E-01	FLJ30594	hypothetical locus FLJ30594	chr2p25.2	239168_at	XR_041760 /// XR_041761 /// XR_041762																				
3.56	3.52	0.04	7.48E-01	9.19E-01	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	chr13q12.3	204742_s_at	NM_015032																				
2.94	2.84	0.10	7.48E-01	9.19E-01	---	---	---	239893_at	---																				
2.14	2.10	0.04	7.48E-01	9.19E-01	ZNF586	zinc finger protein 586	chr19q13.43	1554665_at	NM_001077426 /// NM_017652																				
2.23	2.18	0.05	7.48E-01	9.19E-01	---	---	---	1561543_at	---																				
3.69	3.62	0.07	7.48E-01	9.19E-01	KIAA0195	KIAA0195	chr17q25.1	222210_at	NM_014738																				
3.25	3.21	0.04	7.48E-01	9.19E-01	---	---	---	233108_at	---																				
3.02	2.96	0.06	7.48E-01	9.19E-01	LOC503519	hypothetical LOC503519	chr15q11.2	1562972_at	---																				
2.68	2.62	0.05	7.48E-01	9.19E-01	---	---	---	224119_at	---																				
2.50	2.46	0.04	7.48E-01	9.19E-01	---	---	---	1569826_at	---																				
2.60	2.53	0.07	7.49E-01	9.19E-01	SOX3	SRY (sex determining region Y)-box 3	chrXq27.1	214633_at	NM_005634																				
3.06	2.98	0.08	7.49E-01	9.19E-01	MFAP3	microfibrillar-associated protein 3	chr5q32-q33.2	1552312_a_at	NM_005927																				
2.21	2.18	0.03	7.49E-01	9.19E-01	ARPP-21	cyclic AMP-regulated phosphoprotein, 21 kD	chr3p22.3	220359_s_at	NM_001025068 /// NM_001025069 /// NM_016300 /// NM_198399																				
2.40	2.36	0.04	7.49E-01	9.19E-01	TMEM74	Transmembrane protein 74	chr8q23.1	1555159_at	NM_153015																				
4.88	4.80	0.08	7.49E-01	9.19E-01	PLEKHH3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	chr17q21.31	227248_at	NM_024927																				
2.48	2.44	0.04	7.49E-01	9.19E-01	---	---	---	243990_at	---																				
5.77	5.69	0.08	7.49E-01	9.19E-01	TBC1D17	TBC1 domain family, member 17	chr19q13.33	218466_at	NM_024682																				
1.89	1.86	0.03	7.49E-01	9.19E-01	RGS13	regulator of G-protein signaling 13	chr1q31.2	1568751_at	NM_002927 /// NM_144766																				
2.07	2.04	0.03	7.49E-01	9.20E-01	ZNF622	Zinc finger protein 622	chr5p15.1	1560075_at	NM_033414																				
7.72	7.68	0.04	7.49E-01	9.20E-01	C19orf42	chromosome 19 open reading frame 42	chr19p13.11	219097_x_at	NM_024104																				
2.11	2.07	0.04	7.49E-01	9.20E-01	---	---	---	231293_at	---																				
2.00	1.96	0.04	7.49E-01	9.20E-01	SP2	Sp2 transcription factor	chr17q21.32	211736_at	NM_003110																				
6.63	6.53	0.10	7.49E-01	9.20E-01	CHM	choroideremia (Rab escort protein 1)	chrXq21.2	227871_at	NM_000390																				
4.67	4.61	0.06	7.49E-01	9.20E-01	OTUD7B	OTU domain containing 7B	chr1q21.2	229488_at	NM_020205																				
3.99	3.94	0.05	7.49E-01	9.20E-01	P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1	chr17p13.3	210401_at	NM_002558																				
2.51	2.45	0.06	7.49E-01	9.20E-01	C9orf14	Chromosome 9 open reading frame 14	chr9p21	1559291_at	XM_376821 /// XM_938938																				
2.80	2.74	0.06	7.49E-01	9.20E-01	MGC15885	hypothetical protein MGC15885	chr15q22.2	1569393_at	XR_039858 /// XR_039859																				
3.09	2.95	0.13	7.49E-01	9.20E-01	GPM6A	glycoprotein M6A	chr4q34	209470_s_at	NM_005277 /// NM_201591 /// NM_201592																				

13.00	12.97	0.03	7.50E-01	9.20E-01	hCG_16001 /// RPL23A	similar to ribosomal protein L23A /// ribosomal protein L23a	chr17q11 /// chr3q26.1	208834_x_at	NM_000984 /// NM_001093758
1.99	1.95	0.04	7.50E-01	9.20E-01	VWA3B	von Willebrand factor A domain containing 3B	chr2q11.2	1561200_at	NM_144992
8.32	8.16	0.16	7.50E-01	9.20E-01	MAP3K5	mitogen-activated protein kinase kinase kinase 5	chr6q22.33	203837_at	NM_005923
2.58	2.52	0.06	7.50E-01	9.20E-01	---	---	---	233590_at	---
6.94	6.88	0.06	7.50E-01	9.20E-01	FXR2	fragile X mental retardation, autosomal homolog 2	chr17p13.1	35265_at	NM_004860
2.12	2.07	0.05	7.50E-01	9.20E-01	---	---	---	1560610_at	---
4.02	3.96	0.06	7.50E-01	9.20E-01	---	---	---	1559461_at	---
2.78	2.73	0.05	7.50E-01	9.20E-01	SLC25A42	Solute carrier family 25, member 42	chr19p13.11	214029_at	NM_178526
2.94	2.88	0.06	7.50E-01	9.20E-01	---	---	---	236587_at	---
3.85	3.74	0.10	7.50E-01	9.20E-01	FLJ31306	hypothetical protein FLJ31306	chr14q23.1	239432_at	XM_001715627 /// XM_001717968
6.00	5.92	0.08	7.50E-01	9.20E-01	SLC39A3	solute carrier family 39 (zinc transporter), member 3	chr19p13.3	223917_s_at	NM_144564 /// NM_213568
3.18	3.13	0.06	7.50E-01	9.20E-01	---	---	---	1561019_at	---
2.25	2.20	0.05	7.50E-01	9.20E-01	TMPRSS3	transmembrane protease, serine 3	chr21q22.3	223949_at	NM_024022 /// NM_032401 /// NM_032404 /// NM_032405
2.47	2.42	0.05	7.50E-01	9.20E-01	---	---	---	238217_at	---
3.53	3.45	0.07	7.50E-01	9.20E-01	PLEKHG6	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	chr12p13.31	220073_s_at	NM_018173
10.90	10.84	0.06	7.50E-01	9.20E-01	GABARAP	GABA(A) receptor-associated protein	chr17p13.1	200645_at	NM_007278
3.93	3.86	0.08	7.50E-01	9.20E-01	---	---	---	239774_at	---
5.10	5.04	0.06	7.50E-01	9.20E-01	TTL	tubulin tyrosine ligase	chr2q13	224896_s_at	NM_153712
3.79	3.74	0.06	7.50E-01	9.20E-01	SYN1	synapsin I	chrXp11.23	1553264_a_at	NM_006950 /// NM_133499
1.93	1.89	0.04	7.51E-01	9.20E-01	---	---	---	1562990_at	---
2.87	2.83	0.04	7.51E-01	9.20E-01	LOC340947	similar to eukaryotic translation initiation factor 3, subunit 6 interacting protein	chr10p11.21	234485_at	XM_001131609 /// XM_001717615 /// XM_001719114
3.35	3.29	0.05	7.51E-01	9.20E-01	PRKCA	protein kinase C, alpha	chr17q22-q23.2	1560074_at	NM_002737
2.13	2.08	0.04	7.51E-01	9.20E-01	C1orf67 /// DNAH14 /// RP11-328N1.1	chromosome 1 open reading frame 67 /// dynein, axonemal, heavy chain 14 /// similar to CG7092-PA	chr1q42.12	1567862_at	NM_144989 /// XM_001721899 /// XM_059166 /// XM_927520 /// XM_938194
2.52	2.47	0.05	7.51E-01	9.20E-01	RMST	rhabdomyosarcoma 2 associated transcript (non-protein coding)	chr12q23.1|12q21	1560834_a_at	NR_024037 /// XR_000219 /// XR_001330
2.07	2.03	0.03	7.51E-01	9.20E-01	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	chr2q24.1	237183_at	NM_014568
2.17	2.13	0.04	7.51E-01	9.20E-01	---	---	---	243399_at	---
2.72	2.67	0.05	7.51E-01	9.20E-01	CORIN	corin, serine peptidase	chr4p13-p12	239261_s_at	NM_006587
2.45	2.39	0.06	7.51E-01	9.20E-01	RFTN1	raftlin, lipid raft linker 1	chr3p24.3	1569787_at	NM_015150
3.04	2.99	0.04	7.51E-01	9.20E-01	TAGAP	T-cell activation RhoGTPase activating protein	chr6q25.3	234050_at	NM_054114 /// NM_138810 /// NM_152133

2.47	2.42	0.05	7.51E-01	9.20E-01	IL5RA	interleukin 5 receptor, alpha	chr3p26-p24	211517_s_at	NM_000564 /// NM_175724 /// NM_175725 /// NM_175726 /// NM_175727 /// NM_175728																				
4.63	4.55	0.08	7.51E-01	9.20E-01	C11orf80	chromosome 11 open reading frame 80	chr11q13.1	204922_at	NM_024650																				
9.26	9.18	0.08	7.51E-01	9.20E-01	C20orf24	chromosome 20 open reading frame 24	chr20q11.23	217835_x_at	NM_018840 /// NM_199483																				
3.39	3.32	0.07	7.51E-01	9.20E-01	---	---	---	1559533_at	---																				
4.77	4.70	0.06	7.51E-01	9.20E-01	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	chr12q24.3-qter	201355_s_at	NM_013449																				
6.69	6.62	0.07	7.51E-01	9.20E-01	WBP11	WW domain binding protein 11	chr12p12.3	217821_s_at	NM_016312																				
7.57	7.51	0.06	7.51E-01	9.20E-01	ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3	chr3q27.1	202394_s_at	NM_018358																				
2.55	2.50	0.05	7.52E-01	9.20E-01	---	---	---	231937_at	---																				
2.44	2.41	0.04	7.52E-01	9.20E-01	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	chr18q21.33	206421_s_at	NM_001040147 /// NM_003784																				
5.75	5.66	0.09	7.52E-01	9.20E-01	---	---	---	242646_at	---																				
2.64	2.60	0.04	7.52E-01	9.20E-01	---	---	---	216800_at	---																				
3.56	3.50	0.07	7.52E-01	9.20E-01	LOC730631	Hypothetical LOC730631	chr1q21.2	230738_at	XM_001715137 /// XM_001720519 /// XM_001723714																				
2.89	2.82	0.07	7.52E-01	9.20E-01	LOC645851	Hypothetical LOC645851	chr17q11.2	244547_at	XM_001726201 /// XM_928834 /// XM_940488																				
2.05	2.01	0.04	7.52E-01	9.20E-01	---	---	---	242967_at	---																				
6.30	6.21	0.09	7.52E-01	9.20E-01	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	chr20q13.33	224611_s_at	NM_025219																				
8.19	8.14	0.05	7.52E-01	9.20E-01	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	chr9q33-q34	208611_s_at	NM_001130438 /// NM_003127																				
2.33	2.27	0.06	7.52E-01	9.21E-01	ZNF829	zinc finger protein 829	chr19q13.12	237306_at	NM_001037232																				
3.15	3.07	0.09	7.52E-01	9.21E-01	PGBD3	piggyBac transposable element derived 3	chr10q11	232287_at	NM_170753																				
6.00	5.89	0.11	7.52E-01	9.21E-01	ARRB2	arrestin, beta 2	chr17p13	203388_at	NM_004313 /// NM_199004																				
4.30	4.22	0.08	7.52E-01	9.21E-01	TSGA14	testis specific, 14	chr7q32	225485_at	NM_018718																				
7.26	7.19	0.07	7.52E-01	9.21E-01	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19p13.3	204248_at	NM_002067																				
2.30	2.24	0.05	7.52E-01	9.21E-01	PBK	PDZ binding kinase	chr8p21.2	219148_at	NM_018492																				
4.57	4.50	0.07	7.52E-01	9.21E-01	---	---	---	215261_at	---																				
2.95	2.90	0.06	7.52E-01	9.21E-01	ZNF660	zinc finger protein 660	chr3p21.32	1561361_at	NM_173658																				
2.21	2.15	0.06	7.53E-01	9.21E-01	---	---	---	1557511_at	---																				
2.58	2.54	0.04	7.53E-01	9.21E-01	---	---	---	1569764_at	---																				
7.02	6.87	0.15	7.53E-01	9.21E-01	FAM152A	family with sequence similarity 152, member A	chr1q44	212371_at	NM_016076																				
2.33	2.29	0.04	7.53E-01	9.21E-01	CLINT1	clathrin interactor 1	chr5q33.3	230609_at	NM_014666 /// XM_001715730 /// XM_001723151 /// XM_001725023																				
2.20	2.16	0.04	7.53E-01	9.21E-01	ORF1	hypothetical protein, clone pT-Adv JuaX22	chr18q23	234806_at	---																				
4.47	4.32	0.15	7.53E-01	9.21E-01	ELL2	elongation factor, RNA polymerase II, 2	chr5q15	226982_at	NM_012081																				
2.11	2.07	0.04	7.53E-01	9.21E-01	C1orf96	chromosome 1 open reading frame 96	chr1q42.13	1553698_a_at	NM_145257																				
3.90	3.86	0.04	7.53E-01	9.21E-01	---	---	---	240270_x_at	---																				
4.69	4.63	0.07	7.53E-01	9.21E-01	CUL1	Cullin 1	chr7q36.1	238509_at	NM_003592																				
2.29	2.26	0.04	7.53E-01	9.21E-01	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	chr1q32	1570145_at	NM_015984																				
2.01	1.98	0.03	7.53E-01	9.21E-01	---	---	---	241151_at	---																				
3.11	3.05	0.06	7.53E-01	9.21E-01	LCN8	lipocalin 8	chr9q34.3	239369_at	NM_178469																				
2.24	2.18	0.06	7.53E-01	9.21E-01	---	---	---	240364_at	---																				
3.82	3.76	0.06	7.53E-01	9.21E-01	---	---	---	216637_at	---																				
2.78	2.69	0.09	7.53E-01	9.21E-01	---	---	---	233713_at	---																				

2.82	2.75	0.07	7.53E-01	9.21E-01	ITPRIPL1	inositol 1,4,5-triphosphate receptor interacting protein-like 1	chr2q11.2	240037_at	NM_001008949 /// NM_178495																			
2.09	2.06	0.03	7.53E-01	9.21E-01	FAM164A	family with sequence similarity 164, member A	chr8q21.12	1560197_at	NM_016010																			
3.41	3.36	0.05	7.53E-01	9.21E-01	AFMID	arylformamidase	chr17q25.3	240318_at	NM_001010982																			
2.65	2.58	0.07	7.53E-01	9.21E-01	tcag7.1238	homeo box A11, antisense	chr7p15.2	239950_at	NR_002795																			
4.61	4.56	0.05	7.53E-01	9.21E-01	DEF6	differentially expressed in FDCP 6 homolog (mouse)	chr6p21.33-p21.1	221293_s_at	NM_022047																			
3.03	2.97	0.05	7.53E-01	9.21E-01	---	---	---	1570344_at	---																			
4.97	4.90	0.07	7.53E-01	9.21E-01	C1orf102	chromosome 1 open reading frame 102	chr1p34.3	227359_at	NM_145047 /// NM_206837																			
4.40	4.35	0.05	7.53E-01	9.21E-01	DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12	chr10q22.1	202865_at	NM_001002762 /// NM_017626																			
5.80	5.70	0.09	7.54E-01	9.21E-01	FNBP1	formin binding protein 1	chr9q34	213940_s_at	NM_015033																			
4.72	4.65	0.07	7.54E-01	9.21E-01	CUL4A	Cullin 4A	chr13q34	242194_at	NM_001008895 /// NM_003589																			
2.33	2.29	0.04	7.54E-01	9.21E-01	LOC285577	hypothetical protein LOC285577	chr5p15.33	1561251_at	XM_379309																			
2.47	2.42	0.05	7.54E-01	9.21E-01	FBXO22	F-box protein 22	chr15q24.2	219638_at	NM_012170 /// NM_147188																			
3.44	3.40	0.04	7.54E-01	9.21E-01	NCR3	natural cytotoxicity triggering receptor 3	chr6p21.3	211583_x_at	NM_147130																			
3.40	3.34	0.06	7.54E-01	9.21E-01	---	---	---	215899_at	---																			
6.42	6.36	0.07	7.54E-01	9.21E-01	WDR48	WD repeat domain 48	chr3p21.33	221735_at	NM_020839																			
2.29	2.24	0.05	7.54E-01	9.21E-01	---	---	---	1570484_at	---																			
4.06	4.02	0.04	7.54E-01	9.21E-01	PTPN2	Protein tyrosine phosphatase, non-receptor type 2	chr18p11.3-p11.2	241983_at	NM_002828 /// NM_080422 /// NM_080423																			
2.18	2.15	0.03	7.54E-01	9.21E-01	PPP2R3C	protein phosphatase 2 (formerly 2A), regulatory subunit B", gamma	chr14q13.2	1569894_at	NM_017917																			
4.30	4.24	0.06	7.54E-01	9.21E-01	ADAMTSL3	ADAMTS-like 3	chr15q25.2	1559748_at	NM_207517																			
2.71	2.66	0.05	7.54E-01	9.21E-01	---	---	---	241127_at	---																			
8.62	8.53	0.09	7.54E-01	9.21E-01	---	---	---	213757_at	---																			
2.54	2.50	0.05	7.54E-01	9.21E-01	LOC284570	hypothetical protein LOC284570	chr1q32.1	1558189_a_at	---																			
2.20	2.16	0.04	7.54E-01	9.21E-01	SYCP1	synaptonemal complex protein 1	chr1p13-p12	206740_x_at	NM_003176																			
5.07	4.98	0.09	7.54E-01	9.21E-01	PLEKHA4	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	chr19q13.33	219011_at	NM_020904																			
3.20	3.11	0.10	7.54E-01	9.21E-01	---	---	---	232796_at	---																			
2.16	2.12	0.04	7.54E-01	9.21E-01	---	---	---	1559062_at	---																			
6.51	6.44	0.07	7.54E-01	9.21E-01	MORN2	MORN repeat containing 2	chr2p22.1	226790_at	XR_041208 /// XR_041209 /// XR_041210																			
6.68	6.57	0.11	7.54E-01	9.21E-01	MTMR4	myotubularin related protein 4	chr17q22-q23	214268_s_at	NM_004687																			
2.31	2.27	0.04	7.55E-01	9.21E-01	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	chr22q13.3	217262_s_at	NM_014246																			
4.61	4.53	0.08	7.55E-01	9.21E-01	SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	chr1p21	206770_s_at	NM_012243																			
3.20	3.05	0.15	7.55E-01	9.21E-01	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	chr16p13.1	215559_at	NM_001079528 /// NM_001171																			
3.44	3.38	0.06	7.55E-01	9.21E-01	NEUROD2	neurogenic differentiation 2	chr17q12	1552953_a_at	NM_006160																			
2.05	2.01	0.04	7.55E-01	9.21E-01	---	---	---	242250_at	---																			
2.69	2.64	0.05	7.55E-01	9.21E-01	MDFIC	MyoD family inhibitor domain containing	chr7q31.1-q31.2	239172_x_at	NM_199072																			
2.63	2.60	0.04	7.55E-01	9.21E-01	SBNO1	Strawberry notch homolog 1 (Drosophila)	chr12q24.31	216162_at	NM_018183																			
5.49	5.40	0.09	7.55E-01	9.21E-01	FERMT3	fermitin family homolog 3 (Drosophila)	chr11q13.1	223303_at	NM_031471 /// NM_178443																			
6.97	6.89	0.07	7.55E-01	9.21E-01	GRSF1	G-rich RNA sequence binding factor 1	chr4q13	201501_s_at	NM_001098477 /// NM_002092																			
2.10	2.06	0.03	7.55E-01	9.21E-01	---	---	---	242676_at	---																			
2.30	2.24	0.05	7.55E-01	9.21E-01	SLC35F5	solute carrier family 35, member F5	chr2q14.1	220123_at	NM_025181																			
2.15	2.11	0.05	7.55E-01	9.21E-01	ZIM3	zinc finger, imprinted 3	---	1553022_at	NM_052882																			
5.51	5.39	0.11	7.55E-01	9.21E-01	FAM13C1	family with sequence similarity 13, member C1	chr10q21.1	1554547_at	NM_001001971 /// NM_198215																			
6.69	6.61	0.08	7.55E-01	9.21E-01	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	chr2p22-p21	213294_at	NM_002759																			
4.65	4.57	0.08	7.55E-01	9.21E-01	ZNF558	zinc finger protein 558	chr19p13.2	227810_at	NM_144693																			
5.91	5.85	0.07	7.55E-01	9.21E-01	CYB5D1	cytochrome b5 domain containing 1	chr17p13.1	226833_at	NM_144607																			

7.38	7.31	0.07	7.55E-01	9.21E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	209939_x_at	NM_001127183 /// NM_001127184 /// NM_003879																			
3.96	3.88	0.08	7.55E-01	9.21E-01	GNRH2	gonadotropin-releasing hormone 2	chr20p13	208519_x_at	NM_001501 /// NM_178331 /// NM_178332																			
4.93	4.89	0.03	7.55E-01	9.21E-01	FLJ42627	hypothetical LOC645644	chr16p13.3	220352_x_at	NM_001039907																			
1.94	1.90	0.04	7.55E-01	9.21E-01	---	---	---	215653_at	---																			
2.48	2.43	0.05	7.55E-01	9.22E-01	UGT2B28	UDP glucuronosyltransferase 2 family, polypeptide B28	chr4q13.2	211682_x_at	NM_053039																			
2.11	2.08	0.03	7.56E-01	9.22E-01	---	---	---	232100_at	---																			
3.85	3.81	0.04	7.56E-01	9.22E-01	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	chr11q13	214367_at	NM_001098670 /// NM_001098671 /// NM_153819																			
4.90	4.81	0.09	7.56E-01	9.22E-01	MAST3	microtubule associated serine/threonine kinase 3	chr19p13.11	213045_at	NM_015016																			
2.96	2.92	0.04	7.56E-01	9.22E-01	OSGIN2	oxidative stress induced growth inhibitor family member 2	chr8q21	204024_at	NM_001126111 /// NM_004337																			
11.45	11.41	0.05	7.56E-01	9.22E-01	LOC727762 /// NDUFB4	similar to NADH:ubiquinone oxidoreductase B15 subunit /// NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	chr3q13.33	218226_s_at	NM_004547 /// XM_001125915																			
2.21	2.16	0.05	7.56E-01	9.22E-01	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	chr11q12.1	232725_s_at	NM_022349 /// NM_152851 /// NM_152852																			
4.77	4.67	0.10	7.56E-01	9.22E-01	---	---	---	217416_x_at	---																			
2.23	2.19	0.04	7.56E-01	9.22E-01	---	---	---	1569306_at	---																			
3.91	3.84	0.07	7.56E-01	9.22E-01	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	chr13q33	219479_at	NM_024089																			
3.67	3.62	0.05	7.56E-01	9.22E-01	SIP1	survival of motor neuron protein interacting protein 1	chr14q13	211114_x_at	NM_001009182 /// NM_001009183 /// NM_003616																			
6.15	6.04	0.11	7.56E-01	9.22E-01	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	chr7p14-p13	210849_s_at	NM_014396 /// NM_080631																			
6.46	6.41	0.05	7.56E-01	9.22E-01	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	chr22q13.2	225678_at	NM_001018050 /// NM_001018052 /// NM_138338																			
2.26	2.22	0.04	7.56E-01	9.22E-01	---	---	---	1568899_at	---																			
5.20	5.11	0.09	7.56E-01	9.22E-01	ZBTB47	zinc finger and BTB domain containing 47	chr3p22.1	226484_at	NM_145166																			
7.21	7.11	0.10	7.57E-01	9.22E-01	DDEFL1	development and differentiation enhancing factor-like 1	chr1p36.12	222236_s_at	NM_017707																			
2.41	2.36	0.05	7.57E-01	9.22E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	1558607_at	NM_002581																			
2.76	2.72	0.04	7.57E-01	9.22E-01	KIF6	kinesin family member 6	chr6p21.2	1556232_at	NM_145027																			
2.66	2.62	0.04	7.57E-01	9.22E-01	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	chr20q13.3	205737_at	NM_004518 /// NM_172106 /// NM_172107 /// NM_172108 /// NM_172109																			
3.62	3.56	0.06	7.57E-01	9.22E-01	DGKQ	diacylglycerol kinase, theta 110kDa	chr4p16.3	207562_at	NM_001347																			
9.91	9.87	0.03	7.57E-01	9.22E-01	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	chr5q35.2	200096_s_at	NM_003945																			
4.51	4.43	0.07	7.57E-01	9.22E-01	ASTE1	asteroid homolog 1 (Drosophila)	chr3q22.1	221135_s_at	NM_014065																			
2.49	2.44	0.05	7.57E-01	9.22E-01	---	---	---	1570567_at	---																			
2.55	2.50	0.05	7.57E-01	9.22E-01	RBPMS	RNA binding protein with multiple splicing	chr8p12-p11	207837_at	NM_001008710 /// NM_001008711 /// NM_001008712 /// NM_006867																			

8.55	8.45	0.11	7.57E-01	9.22E-01	PAM	peptidylglycine alpha-amidating monooxygenase	chr5q14-q21	212958_x_at	NM_000919 /// NM_138766 /// NM_138821 /// NM_138822																				
3.32	3.26	0.06	7.58E-01	9.22E-01	ERCC6	excision repair cross-complementing rodent repair deficiency, complementation group 6	chr10q11.23	207347_at	NM_000124																				
5.28	5.22	0.06	7.58E-01	9.22E-01	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	chrXp11.22	205010_at	NM_019067																				
2.34	2.29	0.04	7.58E-01	9.22E-01	---	---	---	1557780_at	---																				
2.26	2.22	0.04	7.58E-01	9.22E-01	ZNF585A	zinc finger protein 585A	chr19q13.12	1554824_at	NM_152655 /// NM_199126																				
2.78	2.72	0.06	7.58E-01	9.22E-01	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	chr10q24.3-qter	209975_at	NM_000773																				
2.39	2.35	0.04	7.58E-01	9.22E-01	C3orf44	chromosome 3 open reading frame 44	chr3q25.1	240729_at	NM_152394																				
2.65	2.59	0.06	7.58E-01	9.23E-01	---	---	---	221642_at	---																				
3.14	3.08	0.06	7.58E-01	9.23E-01	LOC100133474	hypothetical protein LOC100133474	---	236601_at	XM_001715715																				
3.07	3.01	0.06	7.58E-01	9.23E-01	NARG1L	NMDA receptor regulated 1-like	chr13q14.11	1555450_a_at	NM_001110798 /// NM_018527 /// NM_024561																				
2.49	2.43	0.07	7.58E-01	9.23E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	206615_s_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723																				
2.46	2.42	0.04	7.58E-01	9.23E-01	CTNND2	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	chr5p15.2	1566440_at	NM_001332																				
7.91	7.84	0.07	7.58E-01	9.23E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	208634_s_at	NM_012090 /// NM_033044																				
5.82	5.76	0.06	7.58E-01	9.23E-01	ATP5SL	ATP5S-like	chr19q13.2	218038_at	NM_018035																				
2.77	2.73	0.04	7.58E-01	9.23E-01	---	---	---	1556952_at	---																				
2.40	2.37	0.04	7.58E-01	9.23E-01	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	chr2q33.3-q34	233498_at	NM_001042599 /// NM_005235																				
3.23	3.17	0.06	7.59E-01	9.23E-01	ZNF827	Zinc finger protein 827	chr4q31.22	231902_at	NM_178835																				
4.13	4.06	0.07	7.59E-01	9.23E-01	CCDC6	coiled-coil domain containing 6	chr10q21	204716_at	NM_005436																				
2.70	2.65	0.05	7.59E-01	9.23E-01	FLJ30430	hypothetical protein FLJ30430	chr1q42.2	1552942_at	XR_017769 /// XR_017770 /// XR_042001																				
5.13	5.08	0.05	7.59E-01	9.23E-01	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	chr9q34.13	219328_at	NM_022779 /// NM_138620																				
8.45	8.36	0.09	7.59E-01	9.23E-01	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	chr4p16	212432_at	NM_025196																				
2.77	2.71	0.05	7.59E-01	9.23E-01	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	chr5q31.1	210229_s_at	NM_000758																				
6.90	6.83	0.07	7.59E-01	9.23E-01	IPO7	Importin 7	chr11p15.4	200994_at	NM_006391																				
4.46	4.41	0.06	7.59E-01	9.23E-01	---	---	---	229549_at	---																				
8.88	8.81	0.07	7.59E-01	9.23E-01	STUB1	STIP1 homology and U-box containing protein 1	chr16p13.3	233049_x_at	NM_005861																				
2.30	2.24	0.06	7.59E-01	9.23E-01	EED	embryonic ectoderm development	chr11q14.2-q22.3	210656_at	NM_003797 /// NM_152991																				
7.43	7.33	0.10	7.59E-01	9.23E-01	UTP18	UTP18, small subunit (SSU) processome component, homolog (yeast)	chr17q21.33	203721_s_at	NM_016001																				
2.10	2.06	0.04	7.59E-01	9.23E-01	AQP4	aquaporin 4	chr18q11.2-q12.1	210068_s_at	NM_001650 /// NM_004028																				
2.48	2.44	0.05	7.60E-01	9.23E-01	GLB1L3	galactosidase, beta 1-like 3	chr11q25	1562888_at	NM_001080407																				
2.63	2.59	0.05	7.60E-01	9.23E-01	---	---	---	243007_at	---																				
2.66	2.62	0.04	7.60E-01	9.23E-01	CASR	calcium-sensing receptor	chr3q13	211384_s_at	NM_000388																				
2.06	2.03	0.04	7.60E-01	9.23E-01	LOC100128176	hypothetical protein LOC100128176	chr6q25.1	1557741_at	XM_001718081 /// XM_001719798																				
6.91	6.82	0.09	7.60E-01	9.23E-01	FAM8A1	family with sequence similarity 8, member A1	chr6p22-p23	203420_at	NM_016255																				
2.29	2.25	0.04	7.60E-01	9.23E-01	MYH15	myosin, heavy chain 15	chr3q13.13	215331_at	NM_014981																				
5.48	5.41	0.07	7.60E-01	9.23E-01	LYAR	Ly1 antibody reactive homolog (mouse)	chr4p16.2	223414_s_at	NM_017816																				

2.21	2.16	0.05	7.60E-01	9.23E-01	---	---	---	1556459_at	---
3.35	3.28	0.06	7.60E-01	9.23E-01	OVOL1	ovo-like 1(Drosophila)	chr11q13	229396_at	NM_004561
6.31	6.23	0.08	7.60E-01	9.23E-01	SP3	Sp3 transcription factor	chr2q31	213168_at	NM_001017371 /// NM_003111
6.39	6.31	0.08	7.60E-01	9.23E-01	C7orf36	chromosome 7 open reading frame 36	chr7p14.1	223433_at	NM_020192
8.60	8.56	0.04	7.60E-01	9.23E-01	ARPC5L	actin related protein 2/3 complex, subunit 5-like	chr9q33.3	220966_x_at	NM_030978
8.97	8.88	0.08	7.60E-01	9.23E-01	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	chr3q26.2-q27	200893_at	NM_004593
2.07	2.03	0.03	7.60E-01	9.23E-01	COL10A1	collagen, type X, alpha 1	chr6q21-q22	217428_s_at	NM_000493
2.23	2.19	0.04	7.60E-01	9.23E-01	MTRF1	mitochondrial translational release factor 1	chr13q14.1-q14.3	244763_at	NM_004294
9.05	9.01	0.04	7.60E-01	9.23E-01	REEP5	receptor accessory protein 5	chr5q22-q23	208872_s_at	NM_005669
2.87	2.81	0.06	7.60E-01	9.23E-01	MLL	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	244110_at	NM_005933
7.92	7.73	0.19	7.60E-01	9.23E-01	LIMCH1	LIM and calponin homology domains 1	chr4p13	212328_at	NM_001112717 /// NM_001112718 /// NM_001112719 /// NM_001112720 /// NM_014988
2.16	2.11	0.05	7.60E-01	9.23E-01	---	---	---	244602_at	---
3.27	3.22	0.06	7.60E-01	9.23E-01	TM2D1	TM2 domain containing 1	chr1p31.3	212963_at	NM_032027
2.77	2.71	0.06	7.60E-01	9.23E-01	LOC729723	Hypothetical LOC729723	chr2p23.3	239325_at	XM_001721511 /// XM_001723129 /// XM_001726782
1.93	1.89	0.03	7.60E-01	9.23E-01	---	---	---	1565877_at	---
1.87	1.84	0.03	7.60E-01	9.23E-01	LOC100129620	similar to hCG2028334	chr1p21.3	1563904_at	XM_001720058 /// XM_001720783 /// XM_001726877
5.89	5.77	0.12	7.60E-01	9.23E-01	CPM	carboxypeptidase M	chr12q14.3	235019_at	NM_001005502 /// NM_001874 /// NM_198320
2.60	2.55	0.05	7.60E-01	9.23E-01	MAGEA1	melanoma antigen family A, 1 (directs expression of antigen MZ2-E)	chrXq28	207325_x_at	NM_004988
2.25	2.22	0.03	7.60E-01	9.23E-01	---	---	---	1555163_at	---
3.80	3.71	0.09	7.60E-01	9.23E-01	STX17	syntaxin 17	chr9q31.1	226662_at	NM_017919
1.98	1.95	0.03	7.60E-01	9.23E-01	---	---	---	1562902_at	---
3.36	3.27	0.09	7.60E-01	9.23E-01	---	---	---	1569500_at	---
3.31	3.26	0.05	7.60E-01	9.24E-01	OPTC	opticin	chr1q32.1	223884_at	NM_014359
2.40	2.36	0.05	7.61E-01	9.24E-01	---	---	---	234778_at	---
2.28	2.23	0.05	7.61E-01	9.24E-01	TMC5	transmembrane channel-like 5	chr16p12.3	222904_s_at	NM_001105248 /// NM_001105249 /// NM_024780
2.31	2.27	0.04	7.61E-01	9.24E-01	LRIT1	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	chr10q23	211353_at	NM_015613
5.50	5.42	0.08	7.61E-01	9.24E-01	SPNS2	spinster homolog 2 (Drosophila)	chr17p13.2	225671_at	NM_001124758 /// XM_001719788 /// XM_001723978 /// XM_001725485
6.70	6.64	0.06	7.61E-01	9.24E-01	FBXO42	F-box protein 42	chr1p36.23-p36.11	221813_at	NM_018994
3.05	3.00	0.05	7.61E-01	9.24E-01	PCNT	pericentrin	chr21q22.3	233387_s_at	NM_006031
4.14	4.03	0.11	7.61E-01	9.24E-01	MMRN2	multimerin 2	chr10q23.2	236262_at	NM_024756
2.78	2.73	0.04	7.61E-01	9.24E-01	ZNF41	zinc finger protein 41	chrXp11.23	214904_at	NM_007130 /// NM_153380
6.77	6.69	0.08	7.61E-01	9.24E-01	SLC4A2	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	chr7q35-q36	202111_at	NM_003040
2.26	2.22	0.04	7.61E-01	9.24E-01	SH2D1B	SH2 domain containing 1B	chr1q23.3	1553176_at	NM_053282
2.26	2.20	0.06	7.61E-01	9.24E-01	LASS6	LAG1 homolog, ceramide synthase 6	chr2q24.3	242019_at	NM_203463

7.70	7.62	0.08	7.61E-01	9.24E-01	ENY2	enhancer of yellow 2 homolog (Drosophila)	chr8q23.1	218482_at	NM_020189
2.10	2.06	0.04	7.61E-01	9.24E-01	---	---	---	242468_at	---
3.01	2.96	0.05	7.61E-01	9.24E-01	---	---	---	1562346_at	---
4.58	4.48	0.10	7.62E-01	9.24E-01	IFNGR1	interferon gamma receptor 1	chr6q23.3	242903_at	NM_000416
10.52	10.44	0.08	7.62E-01	9.24E-01	HNRNPK	heterogeneous nuclear ribonucleoprotein K	chr9q21.32-q21.33	200775_s_at	NM_002140 /// NM_031262 /// NM_031263
3.73	3.67	0.06	7.62E-01	9.24E-01	TRAK1	trafficking protein, kinesin binding 1	chr3p25.3-p24.1	201283_s_at	NM_001042646 /// NM_014965
2.27	2.23	0.04	7.62E-01	9.24E-01	---	---	---	236191_at	---
3.27	3.20	0.07	7.62E-01	9.24E-01	CNR2	cannabinoid receptor 2 (macrophage)	chr1p36.11	206586_at	NM_001841
2.31	2.26	0.05	7.62E-01	9.24E-01	LOC121952	hypothetical protein LOC121952	chr13q33.1	1560646_at	XR_015288 /// XR_015298 /// XR_041167
2.94	2.90	0.04	7.62E-01	9.24E-01	ASB1	ankyrin repeat and SOCS box-containing 1	chr2q37	212819_at	NM_001040445
3.24	3.19	0.06	7.62E-01	9.24E-01	---	---	---	1557688_at	---
1.92	1.89	0.03	7.62E-01	9.24E-01	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	chr10q11.2-q21	215957_at	NM_003338
4.06	3.99	0.07	7.62E-01	9.24E-01	WNK2	WNK lysine deficient protein kinase 2	chr9q22.3	1562026_at	NM_006648
2.30	2.26	0.04	7.62E-01	9.24E-01	---	---	---	1561915_at	---
5.48	5.43	0.05	7.62E-01	9.24E-01	RAX2	retina and anterior neural fold homeobox 2	chr19p13.3	1552311_a_at	NM_032753
4.45	4.37	0.08	7.62E-01	9.24E-01	PRF1	perforin 1 (pore forming protein)	chr10q22	214617_at	NM_001083116 /// NM_005041
1.97	1.93	0.04	7.62E-01	9.24E-01	ZNF354C	zinc finger protein 354C	chr5q35	234409_at	NM_014594
2.78	2.74	0.04	7.62E-01	9.24E-01	---	---	---	238942_at	---
4.11	4.07	0.04	7.63E-01	9.24E-01	LOC100128003	hypothetical protein LOC100128003	chr1p36.33	1562675_at	XM_001715367 /// XM_001718749 /// XM_001724970
2.89	2.86	0.03	7.63E-01	9.24E-01	---	---	---	1560094_at	---
2.51	2.46	0.05	7.63E-01	9.24E-01	LOC389247	hypothetical gene supported by BC038563	chr4q35.1	1560841_at	---
2.32	2.28	0.04	7.63E-01	9.24E-01	---	---	---	1562643_at	---
2.35	2.32	0.04	7.63E-01	9.25E-01	PHF8	PHD finger protein 8	chrXp11.22	215065_at	NM_015107
2.80	2.76	0.04	7.63E-01	9.25E-01	PLA2G5	phospholipase A2, group V	chr1p36-p34	215871_at	NM_000929
2.50	2.43	0.07	7.63E-01	9.25E-01	---	---	---	242276_at	---
3.86	3.69	0.16	7.63E-01	9.25E-01	JOSD3	Josephin domain containing 3	chr11q21	222728_s_at	NM_024116
4.01	3.95	0.06	7.63E-01	9.25E-01	WDR51B	WD repeat domain 51B	chr12q21.33	226283_at	NM_172240
2.80	2.69	0.11	7.63E-01	9.25E-01	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	chr12q13.13	228935_at	NM_001039960 /// NM_004858
4.79	4.72	0.07	7.63E-01	9.25E-01	RELA	V-rel reticuloendotheliosis viral oncogene homolog A (avian)	chr11q13	230202_at	NM_021975
2.08	2.04	0.04	7.63E-01	9.25E-01	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	chr9p21	208427_s_at	NM_004432
2.63	2.60	0.04	7.63E-01	9.25E-01	RAP1A	RAP1A, member of RAS oncogene family	chr1p13.3	1555340_x_at	NM_001010935 /// NM_002884
3.05	2.99	0.06	7.63E-01	9.25E-01	EXOSC3	Exosome component 3	chr9p11	227912_s_at	NM_001002269 /// NM_016042
2.68	2.64	0.04	7.63E-01	9.25E-01	STK17A	serine/threonine kinase 17a	chr7p12-p14	202694_at	NM_004760
2.60	2.55	0.05	7.63E-01	9.25E-01	---	---	---	216225_at	---
2.47	2.43	0.04	7.63E-01	9.25E-01	MORN2	MORN repeat containing 2	chr2p22.1	1556881_at	XR_041208 /// XR_041209 /// XR_041210
2.46	2.42	0.04	7.63E-01	9.25E-01	CLIC6	chloride intracellular channel 6	chr21q22.12	242913_at	NM_053277
7.36	7.27	0.08	7.64E-01	9.25E-01	---	---	---	226742_at	---
3.71	3.62	0.09	7.64E-01	9.25E-01	RNASE4	ribonuclease, RNase A family, 4	chr14q11.1	213397_x_at	NM_002937 /// NM_194431
8.55	8.46	0.09	7.64E-01	9.25E-01	SYNPO	synaptopodin	chr5q33.1	202796_at	NM_001109974 /// NM_007286
2.36	2.32	0.03	7.64E-01	9.25E-01	KRTDAP	keratinocyte differentiation-associated protein	chr19q13.12	230835_at	NM_207392
2.52	2.48	0.04	7.64E-01	9.25E-01	GKAP1	G kinase anchoring protein 1	chr9q21.32	229311_at	NM_025211
2.64	2.61	0.03	7.64E-01	9.25E-01	---	---	---	1564259_at	---

2.06	2.03	0.04	7.64E-01	9.25E-01	KYNU	Kynureninase (L-kynurenine hydrolase)	chr2q22.2	241305_at	NM_001032998 /// NM_003937																				
2.03	2.00	0.03	7.64E-01	9.25E-01	KLRF1	killer cell lectin-like receptor subfamily F, member 1	chr12p13.2-p12.3	220646_s_at	NM_016523																				
1.89	1.85	0.03	7.64E-01	9.25E-01	---	---	---	1555926_a_at	---																				
2.51	2.47	0.03	7.64E-01	9.25E-01	---	---	---	1566853_at	---																				
3.13	3.06	0.07	7.64E-01	9.25E-01	---	---	---	1568633_a_at	---																				
4.60	4.54	0.06	7.64E-01	9.25E-01	C11orf73	chromosome 11 open reading frame 73	chr11q14.2	219979_s_at	NM_016401																				
4.29	4.23	0.06	7.64E-01	9.25E-01	RRP7A /// RRP7B	ribosomal RNA processing 7 homolog A (S. cerevisiae) /// ribosomal RNA processing 7 homolog B (S. cerevisiae)	chr22q13.2 /// chr22q13.2-q13.31	202938_x_at	NM_015703 /// NR_002184																				
4.02	3.97	0.05	7.64E-01	9.25E-01	DYSFIP1	dysferlin interacting protein 1	chr17q25.3	1557480_a_at	NM_001007533																				
2.01	1.97	0.04	7.64E-01	9.25E-01	WNK1	WNK lysine deficient protein kinase 1	chr12p13.3	1555068_at	NM_018979																				
3.32	3.24	0.08	7.64E-01	9.25E-01	FRMD8	FERM domain containing 8	chr11q13	1554905_x_at	NM_031904																				
2.49	2.45	0.05	7.64E-01	9.25E-01	FLJ90757	hypothetical protein LOC440465	chr17q25.3	1566555_at	XR_017883 /// XR_017982 /// XR_040055																				
5.85	5.73	0.12	7.64E-01	9.25E-01	CLUAP1	clusterin associated protein 1	chr16p13.3	204576_s_at	NM_015041 /// NM_024793																				
1.98	1.95	0.04	7.64E-01	9.25E-01	ARL14	ADP-ribosylation factor-like 14	chr3q26.1	220468_at	NM_025047																				
9.93	9.83	0.10	7.64E-01	9.25E-01	APOC1	apolipoprotein C-I	chr19q13.2	213553_x_at	NM_001645																				
3.10	3.07	0.04	7.64E-01	9.25E-01	---	---	---	236980_at	---																				
3.40	3.35	0.05	7.65E-01	9.25E-01	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	chr19q13.4	211102_s_at	NM_001130917 /// NM_006866																				
4.29	4.18	0.10	7.65E-01	9.25E-01	TIAM2	T-cell lymphoma invasion and metastasis 2	chr6q25.2	222942_s_at	NM_001010927 /// NM_012454																				
3.06	3.00	0.07	7.65E-01	9.25E-01	RC3H2	ring finger and CCCH-type zinc finger domains 2	chr9q34	230133_at	NM_001100588 /// NM_018835																				
2.94	2.88	0.06	7.65E-01	9.25E-01	LOC400794	hypothetical gene supported by BC030596	chr1q23.2	1557761_s_at	---																				
2.24	2.21	0.04	7.65E-01	9.25E-01	---	---	---	1561625_at	---																				
2.55	2.51	0.04	7.65E-01	9.25E-01	---	---	---	1558007_s_at	---																				
2.74	2.69	0.05	7.65E-01	9.25E-01	FRMPD3	FERM and PDZ domain containing 3	chrXq22	236688_at	XM_001714381 /// XM_042978 /// XM_937007																				
2.30	2.26	0.05	7.65E-01	9.25E-01	MOXD1	monooxygenase, DBH-like 1	chr6q23.1-q23.3	243697_at	NM_015529																				
2.10	2.06	0.03	7.65E-01	9.25E-01	---	---	---	1559336_at	---																				
4.17	4.08	0.09	7.65E-01	9.25E-01	ABHD2	abhydrolase domain containing 2	chr15q26.1	87100_at	NM_007011 /// NM_152924																				
2.08	2.04	0.04	7.65E-01	9.25E-01	---	---	---	1559069_at	---																				
2.12	2.09	0.04	7.65E-01	9.25E-01	ARHGAP22	Rho GTPase activating protein 22	chr10q11.22	1560821_at	NM_021226																				
2.05	2.01	0.03	7.65E-01	9.25E-01	---	---	---	238901_at	---																				
4.06	3.99	0.08	7.65E-01	9.25E-01	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	chr20q13.33	232517_s_at	NM_001037335 /// NM_033405																				
5.44	5.32	0.12	7.65E-01	9.25E-01	---	---	---	239227_at	---																				
5.79	5.74	0.05	7.65E-01	9.25E-01	PRDM4	PR domain containing 4	chr12q23-q24.1	49485_at	NM_012406																				
4.43	4.35	0.09	7.65E-01	9.25E-01	ETNK1	ethanolamine kinase 1	chr12p12.1	225290_at	NM_001039481 /// NM_018638																				
5.58	5.49	0.09	7.65E-01	9.25E-01	WWOX	WW domain containing oxidoreductase	chr16q23.3-q24.1	219077_s_at	NM_016373 /// NM_130791 /// NM_130844																				
1.94	1.90	0.04	7.65E-01	9.25E-01	---	---	---	1561467_at	---																				
3.12	3.08	0.04	7.65E-01	9.25E-01	---	---	---	1562158_at	---																				
1.92	1.89	0.03	7.66E-01	9.25E-01	LOC339622	hypothetical protein LOC339622	chr21q21.1-q21.2	1561290_at	---																				
6.94	6.87	0.07	7.66E-01	9.25E-01	KIAA0652	KIAA0652	chr11p11.2	203364_s_at	NM_014741																				
2.30	2.27	0.03	7.66E-01	9.25E-01	ITSN1	intersectin 1 (SH3 domain protein)	chr21q22.1-q22.2	207322_at	NM_001001132 /// NM_003024																				
3.64	3.55	0.08	7.66E-01	9.25E-01	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	chr20q12-q13.1	205243_at	NM_001011554 /// NM_022829																				

3.35	3.31	0.04	7.66E-01	9.25E-01	MYOZ3	myozenin 3	chr5q33.1	213955_at	NM_001122853 /// NM_133371
3.10	3.05	0.05	7.66E-01	9.25E-01	CAPNS2	calpain, small subunit 2	chr16q12.2	223832_s_at	NM_032330
7.91	7.80	0.12	7.66E-01	9.25E-01	GLG1	golgi apparatus protein 1	chr16q22-q23	214730_s_at	NM_012201
7.44	7.28	0.16	7.66E-01	9.25E-01	S100A16	S100 calcium binding protein A16	chr1q21	227998_at	NM_080388
2.04	2.01	0.03	7.66E-01	9.25E-01	---	---	---	1564772_at	---
4.50	4.38	0.12	7.66E-01	9.25E-01	SLC22A17	solute carrier family 22, member 17	chr14q11.2	218675_at	NM_016609 /// NM_020372
3.18	3.12	0.06	7.66E-01	9.25E-01	SLA2	Src-like-adaptor 2	chr20q11.23	232234_at	NM_032214 /// NM_175077
1.97	1.93	0.04	7.66E-01	9.25E-01	DAB2	Disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	chr5p13	1559370_at	NM_001343
2.27	2.23	0.04	7.66E-01	9.25E-01	FGF18	Fibroblast growth factor 18	chr5q34	231382_at	NM_003862
3.33	3.28	0.05	7.66E-01	9.25E-01	---	---	---	1558568_a_at	---
2.54	2.50	0.03	7.66E-01	9.25E-01	LOC100132345	Hypothetical protein LOC100132345	chr3p24.3	241634_at	XM_001716679
4.51	4.46	0.05	7.66E-01	9.25E-01	C2orf34	chromosome 2 open reading frame 34	chr2p21	219617_at	NM_024766
3.99	3.94	0.06	7.66E-01	9.25E-01	---	---	---	239373_at	---
5.51	5.42	0.09	7.66E-01	9.25E-01	RAD17	RAD17 homolog (S. pombe)	chr5q13	210826_x_at	NM_002873 /// NM_133338 /// NM_133339 /// NM_133340 /// NM_133341 /// NM_133342 /// NM_133343 /// NM_133344
3.10	3.05	0.05	7.66E-01	9.25E-01	---	---	---	242966_x_at	---
2.85	2.78	0.07	7.66E-01	9.25E-01	CPXM2	carboxypeptidase X (M14 family), member 2	chr10q26.13	1570026_at	NM_198148
2.71	2.67	0.04	7.66E-01	9.25E-01	---	---	---	232853_at	---
3.07	2.97	0.10	7.67E-01	9.25E-01	STEAP1	six transmembrane epithelial antigen of the prostate 1	chr7q21	205542_at	NM_012449
2.86	2.81	0.05	7.67E-01	9.25E-01	LOC728799 /// LRRC27	similar to leucine rich repeat containing 27 /// leucine rich repeat containing 27	chr10q26.3	228884_at	NM_030626 /// XM_001132728
3.56	3.51	0.06	7.67E-01	9.25E-01	TMCO4	transmembrane and coiled-coil domains 4	chr1p36.13	1560292_a_at	NM_181719
2.91	2.83	0.08	7.67E-01	9.25E-01	TCF20	transcription factor 20 (AR1)	chr22q13.3|22q13.3	215511_at	NM_005650 /// NM_181492
2.46	2.40	0.05	7.67E-01	9.26E-01	41339	membrane-associated ring finger (C3HC4) 6	chr5p15.2	215512_at	NM_005885
4.79	4.73	0.06	7.67E-01	9.26E-01	---	---	---	1570143_at	---
1.94	1.92	0.03	7.67E-01	9.26E-01	PPEF2	protein phosphatase, EF-hand calcium binding domain 2	chr4q21.1	208411_x_at	NM_006239
7.34	7.24	0.10	7.67E-01	9.26E-01	CSK	c-src tyrosine kinase	chr15q23-q25	202329_at	NM_001127190 /// NM_004383
2.11	2.08	0.03	7.67E-01	9.26E-01	BEST3	bestrophin 3	chr12q14.2-q15	1555492_a_at	NM_032735 /// NM_152439
2.35	2.31	0.05	7.67E-01	9.26E-01	---	---	---	1561012_at	---
2.77	2.72	0.05	7.67E-01	9.26E-01	---	---	---	1566779_at	---
3.35	3.27	0.08	7.67E-01	9.26E-01	---	---	---	244382_at	---
2.10	2.06	0.04	7.67E-01	9.26E-01	XIRP2	xin actin-binding repeat containing 2	chr2q24.3	228794_at	NM_001079810 /// NM_152381
4.21	4.13	0.08	7.67E-01	9.26E-01	RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	chr2p11.2	212478_at	NM_022780
2.86	2.81	0.05	7.67E-01	9.26E-01	---	---	---	1561561_x_at	---
4.13	4.06	0.07	7.68E-01	9.26E-01	C3orf19	chromosome 3 open reading frame 19	chr3p25.1	223787_s_at	NM_016474
5.46	5.39	0.07	7.68E-01	9.26E-01	ZDHHC3	zinc finger, DHHC-type containing 3	chr3p21.31	218077_s_at	NM_016598
6.95	6.82	0.13	7.68E-01	9.26E-01	ANKMY2	ankyrin repeat and MYND domain containing 2	chr7p21	212798_s_at	NM_020319
6.28	6.22	0.06	7.68E-01	9.26E-01	TPP1	tripeptidyl peptidase I	chr11p15	214196_s_at	NM_000391
2.82	2.76	0.06	7.68E-01	9.26E-01	EMID1	EMI domain containing 1	chr22q12.2	1564251_at	NM_133455
3.11	3.07	0.04	7.68E-01	9.26E-01	GATAD2A	GATA zinc finger domain containing 2A	chr19p13.11	236932_s_at	NM_017660
6.37	6.30	0.07	7.68E-01	9.26E-01	ZDHHC9	zinc finger, DHHC-type containing 9	chrXq26.1	222451_s_at	NM_001008222 /// NM_016032
4.28	4.19	0.10	7.68E-01	9.26E-01	ZFX	zinc finger protein, X-linked	chrXp21.3	207920_x_at	NM_003410
4.02	3.97	0.06	7.68E-01	9.26E-01	RPPH1	ribonuclease P RNA component H1	chr14q11.2	1556684_at	NR_002312

2.14	2.10	0.04	7.68E-01	9.26E-01	HFM1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)	chr1p22.2	1564285_at	NM_001017975
4.40	4.35	0.04	7.68E-01	9.26E-01	---	---	---	230620_at	---
2.51	2.43	0.08	7.68E-01	9.26E-01	OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	chr12p13.2-p12.3	210004_at	NM_002543
5.09	5.00	0.09	7.68E-01	9.26E-01	LOC100128653	hypothetical LOC100128653	chr7p22.3	236053_at	XM_001716784 /// XM_001720879 /// XM_001721042
2.43	2.39	0.04	7.68E-01	9.26E-01	---	---	---	1561103_at	---
2.89	2.84	0.06	7.68E-01	9.26E-01	---	---	---	225054_x_at	---
3.70	3.62	0.07	7.69E-01	9.27E-01	HPD	4-hydroxyphenylpyruvate dioxygenase	chr12q24-qter	206024_at	NM_002150
2.89	2.83	0.05	7.69E-01	9.27E-01	IFNA17	interferon, alpha 17	chr9p22	211405_x_at	NM_021268
2.03	1.99	0.03	7.69E-01	9.27E-01	---	---	---	231383_at	---
6.40	6.31	0.08	7.69E-01	9.27E-01	MRC2	mannose receptor, C type 2	chr17q23.2	37408_at	NM_006039
4.17	4.03	0.14	7.69E-01	9.27E-01	AKAP10	A kinase (PRKA) anchor protein 10	chr17p11.1	205045_at	NM_007202
2.18	2.14	0.04	7.69E-01	9.27E-01	---	---	---	1569809_at	---
7.85	7.77	0.08	7.69E-01	9.27E-01	FOXN3	forkhead box N3	chr14q31.3	205022_s_at	NM_001085471 /// NM_005197
2.99	2.92	0.07	7.69E-01	9.27E-01	C14orf23	chromosome 14 open reading frame 23	chr14q12	243061_at	XM_001720615 /// XM_370758 /// XM_940323
2.14	2.11	0.03	7.69E-01	9.27E-01	C10orf46	Chromosome 10 open reading frame 46	chr10q26.11	227137_at	NM_153810
3.08	3.03	0.05	7.69E-01	9.27E-01	---	---	---	238491_at	---
2.73	2.67	0.05	7.69E-01	9.27E-01	SNW1	SNW domain containing 1	chr14q24.3	222183_x_at	NM_012245
2.81	2.76	0.06	7.69E-01	9.27E-01	LOC126661	hypothetical protein LOC126661	chr1p34.1	1559003_a_at	NM_001102601
10.37	10.29	0.08	7.69E-01	9.27E-01	NAP1L1	nucleosome assembly protein 1-like 1	chr12q21.2	212967_x_at	NM_004537 /// NM_139207
2.92	2.85	0.07	7.70E-01	9.27E-01	OTUD7B	OTU domain containing 7B	chr1q21.2	1555139_a_at	NM_020205
3.40	3.36	0.04	7.70E-01	9.27E-01	NAV1	neuron navigator 1	chr1q32.3	233870_at	NM_020443
1.81	1.78	0.03	7.70E-01	9.27E-01	---	---	---	243436_at	---
2.75	2.72	0.03	7.70E-01	9.27E-01	GALR2	galanin receptor 2	chr17q25.3	211226_at	NM_003857
2.01	1.97	0.04	7.70E-01	9.27E-01	MOP-1	MOP-1	chr4q21.22	224277_at	XR_041844 /// XR_041845 /// XR_041846
4.62	4.57	0.06	7.70E-01	9.27E-01	---	---	---	238913_at	---
3.86	3.82	0.04	7.70E-01	9.27E-01	CRIPAK	cysteine-rich PAK1 inhibitor	chr4p16.3	241408_at	NM_175918
5.19	5.02	0.18	7.70E-01	9.27E-01	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	chr8q23-q24	208608_s_at	NM_021021
6.22	6.16	0.06	7.70E-01	9.27E-01	GLRX2	glutaredoxin 2	chr1q31.2-q31.3	219933_at	NM_016066 /// NM_197962
2.74	2.66	0.08	7.70E-01	9.27E-01	---	---	---	1559348_a_at	---
3.34	3.30	0.05	7.70E-01	9.27E-01	CACNB4	calcium channel, voltage-dependent, beta 4 subunit	chr2q22-q23	207693_at	NM_000726 /// NM_001005746 /// NM_001005747
3.28	3.23	0.05	7.70E-01	9.27E-01	RBBP6	Retinoblastoma binding protein 6	chr16p12.2	227635_at	NM_006910 /// NM_018703 /// NM_032626
3.87	3.81	0.06	7.70E-01	9.27E-01	---	---	---	241783_at	---
7.83	7.72	0.11	7.70E-01	9.27E-01	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	chr2p15-p13	209610_s_at	NM_003038
6.20	6.12	0.07	7.70E-01	9.27E-01	C19orf60	chromosome 19 open reading frame 60	chr19p13.11	218958_at	NM_001100418 /// NM_001100419
3.02	2.97	0.05	7.70E-01	9.27E-01	---	---	---	233024_at	---
3.87	3.81	0.06	7.70E-01	9.27E-01	KIAA1688	KIAA1688 protein	chr8q24.3	227876_at	NM_025251
2.14	2.10	0.04	7.71E-01	9.27E-01	C6orf147 /// KHDC1	chromosome 6 open reading frame 147 /// KH homology domain containing 1	chr6q13	241024_at	NM_030568
6.40	6.30	0.10	7.71E-01	9.27E-01	CUL4A	cullin 4A	chr13q34	201423_s_at	NM_001008895 /// NM_003589

2.90	2.84	0.06	7.71E-01	9.27E-01	---	---	---	222184_at	---
2.56	2.49	0.06	7.71E-01	9.27E-01	CYP2B7P1	cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1	chr19q13.2	210272_at	NR_001278
2.39	2.34	0.05	7.71E-01	9.27E-01	---	---	---	242382_at	---
2.20	2.17	0.04	7.71E-01	9.27E-01	---	---	---	208421_at	---
4.91	4.86	0.06	7.71E-01	9.27E-01	PML	promyelocytic leukemia	chr15q22	235508_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250
3.35	3.28	0.06	7.71E-01	9.27E-01	C2orf56	chromosome 2 open reading frame 56	chr2p22.2	230379_x_at	NM_001083946 /// NM_144736
3.66	3.59	0.07	7.71E-01	9.27E-01	---	---	---	233243_at	---
1.97	1.94	0.03	7.71E-01	9.27E-01	---	---	---	234134_at	---
2.98	2.93	0.05	7.71E-01	9.28E-01	TNF	tumor necrosis factor (TNF superfamily, member 2)	chr6p21.3	207113_s_at	NM_000594
3.69	3.61	0.08	7.71E-01	9.28E-01	ZDHHC13	zinc finger, DHHC-type containing 13	chr11p15.1	219296_at	NM_001001483 /// NM_019028
2.20	2.16	0.04	7.71E-01	9.28E-01	---	---	---	242096_at	---
2.54	2.50	0.04	7.71E-01	9.28E-01	---	---	---	1563102_at	---
2.73	2.68	0.05	7.71E-01	9.28E-01	---	---	---	235376_at	---
7.52	7.47	0.05	7.71E-01	9.28E-01	MYH9	myosin, heavy chain 9, non-muscle	chr22q13.1	211926_s_at	NM_002473
2.46	2.42	0.04	7.71E-01	9.28E-01	---	---	---	1570102_at	---
5.46	5.37	0.09	7.71E-01	9.28E-01	FARS2	phenylalanyl-tRNA synthetase 2, mitochondrial	chr6p25.1	204283_at	NM_006567
6.49	6.45	0.03	7.71E-01	9.28E-01	LOC222070	hypothetical protein LOC222070	chr7p13	51774_s_at	---
3.12	3.07	0.05	7.72E-01	9.28E-01	LOC283481	hypothetical protein LOC283481	chr13q33.1	243225_at	XM_001128325 /// XM_001133584 /// XM_001719299
4.80	4.75	0.05	7.72E-01	9.28E-01	KIAA0090	KIAA0090	chr1p36.13	212394_at	NM_015047
2.30	2.25	0.05	7.72E-01	9.28E-01	LOC100133105	hypothetical protein LOC100133105	chr12q21.2	214090_at	XM_001714552 /// XM_001718272 /// XM_001718327
6.65	6.55	0.10	7.72E-01	9.28E-01	C9orf80	chromosome 9 open reading frame 80	chr9q32	223559_s_at	NM_021218
6.97	6.90	0.07	7.72E-01	9.28E-01	TMEM9B	TMEM9 domain family, member B	chr11p15.3	218065_s_at	NM_020644
2.58	2.54	0.05	7.72E-01	9.28E-01	C2orf61	chromosome 2 open reading frame 61	chr2p21	1553460_at	NM_173649
3.42	3.37	0.05	7.72E-01	9.28E-01	---	---	---	244200_at	---
9.31	9.24	0.07	7.72E-01	9.28E-01	HLA-F	major histocompatibility complex, class I, F	chr6p21.3	221875_x_at	NM_001098478 /// NM_001098479 /// NM_018950
4.48	4.41	0.06	7.72E-01	9.28E-01	TSPAN1	tetraspanin 1	chr1p34.1	209114_at	NM_005727
2.69	2.64	0.05	7.72E-01	9.28E-01	PES1	pescadillo homolog 1, containing BRCT domain (zebrafish)	chr22q12.1	236434_at	NM_014303

2.49	2.45	0.05	7.72E-01	9.28E-01	CSH1 /// CSH2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// growth hormone 1	chr17q24.2	205840_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645																				
5.69	5.64	0.05	7.72E-01	9.28E-01	ZC3H7B	zinc finger CCCH-type containing 7B	chr22q13.2	206169_x_at	NM_017590																				
2.92	2.89	0.03	7.72E-01	9.28E-01	---	---	---	244274_at	---																				
3.41	3.33	0.08	7.72E-01	9.28E-01	TLN2	talin 2	chr15q15-q21	212701_at	NM_015059																				
5.86	5.79	0.07	7.72E-01	9.28E-01	PTPRM	protein tyrosine phosphatase, receptor type, M	chr18p11.2	1555579_s_at	NM_001105244 /// NM_002845																				
1.99	1.96	0.03	7.72E-01	9.28E-01	---	---	---	1566437_at	---																				
6.24	6.18	0.06	7.72E-01	9.28E-01	GCDH	glutaryl-Coenzyme A dehydrogenase	chr19p13.2	203500_at	NM_000159 /// NM_013976																				
5.62	5.43	0.18	7.72E-01	9.28E-01	LAMC3	laminin, gamma 3	chr9q31-q34	219407_s_at	NM_006059																				

6.77	6.71	0.06	7.72E-01	9.28E-01	HNRNPA1 /// HNRPA1L-2 /// LOC100128836 /// LOC120364 /// LOC391670 /// LOC402112 /// LOC440125 /// LOC642817 /// LOC643033 /// LOC644037 /// LOC645001 /// LOC728170 /// LOC728643 /// LOC728732 /// LOC729102 /// LOC729366 /// LOC730246 /// RP11-78J21.1	heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1 pseudogene /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC642817 /// similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed) /// hypothetical LOC644037 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1 pseudogene /// hypothetical LOC728732 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC730246 /// heterogeneous nuclear ribonucleoprotein A1-like	chr10q11.22 /// chr11p15.4 /// chr11q23.1 /// chr12q13.1 /// chr12q22 /// chr13q12.11 /// chr13q14.3 /// chr19p13.2 /// chr19q13.2 /// chr1q32.1 /// chr2q31.1 /// chr2q33.3 /// chr3p22.1 /// chr4q21.1 /// chr5q14.1 /// chr6p25.1 /// chr8q21.13 /// chrXq24	216559_x_at	NM_001011724 /// NM_001011725 /// NM_002136 /// NM_031157 /// NR_002944 /// NR_003277 /// XM_001718684 /// XM_062025 /// XM_937967 /// XR_015330 /// XR_015514 /// XR_015658 /// XR_015746 /// XR_015895 /// XR_015958 /// XR_015974 /// XR_016080 /// XR_016093 /// XR_016314 /// XR_016373 /// XR_016388 /// XR_017084 /// XR_017337 /// XR_017501 /// XR_018564 /// XR_019025 /// XR_019262 /// XR_019573 /// XR_038280 /// XR_038288 /// XR_038331 /// XR_038689 /// XR_038697 /// XR_038725 /// XR_038755 /// XR_038765 /// XR_038785 /// XR_038911 /// XR_039047 /// XR_039155 /// XR_039380 /// XR_039402 /// XR_039425 /// XR_039446 /// XR_039541
2.47	2.43	0.04	7.72E-01	9.28E-01	ZNF367	zinc finger protein 367	chr9q22|9q22.32	229551_x_at	NM_153695
2.46	2.42	0.03	7.72E-01	9.28E-01	MED12L	mediator complex subunit 12-like	chr3q25.1	232114_at	NM_053002
2.06	2.02	0.04	7.72E-01	9.28E-01	SEMA3E	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	chr7q21.11	206941_x_at	NM_012431
7.69	7.63	0.05	7.73E-01	9.28E-01	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	chr2q37.3	202141_s_at	NM_006710 /// NM_198189
7.05	6.95	0.11	7.73E-01	9.28E-01	C1orf54	chromosome 1 open reading frame 54	chr1q21.2	219506_at	NM_024579
2.56	2.51	0.05	7.73E-01	9.28E-01	---	---	---	230850_at	---
6.25	6.15	0.10	7.73E-01	9.28E-01	ATG9A	ATG9 autophagy related 9 homolog A (S. cerevisiae)	chr2q35	202492_at	NM_001077198 /// NM_024085
10.56	10.42	0.14	7.73E-01	9.28E-01	ALAS1	aminolevulinate, delta-, synthase 1	chr3p21.1	205633_s_at	NM_000688 /// NM_199166
3.36	3.29	0.07	7.73E-01	9.28E-01	NAAA	N-acylethanolamine acid amidase	chr4q21.1	215178_x_at	NM_001042402 /// NM_014435
3.20	3.10	0.10	7.73E-01	9.28E-01	ADAM28	ADAM metallopeptidase domain 28	chr8p21.2	205997_at	NM_014265 /// NM_021777
2.24	2.20	0.03	7.73E-01	9.28E-01	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)	chr5q31.2	1564911_at	NR_003141
3.60	3.57	0.03	7.73E-01	9.28E-01	BC036928	hypothetical protein BC036928	chr19q13.43	238708_at	---
2.07	2.03	0.03	7.73E-01	9.29E-01	EPAG	early lymphoid activation protein	chrXq21.33	217245_at	XM_926826 /// XM_938050

5.46	5.39	0.08	7.73E-01	9.29E-01	TMEM144	transmembrane protein 144	chr4q32.1	228624_at	NM_018342
3.81	3.74	0.07	7.73E-01	9.29E-01	TTC7A	tetratricopeptide repeat domain 7A	chr2p21	224924_at	NM_020458
3.35	3.25	0.10	7.73E-01	9.29E-01	---	---	---	227140_at	---
4.94	4.86	0.08	7.73E-01	9.29E-01	MAN2C1	mannosidase, alpha, class 2C, member 1	chr15q11-q13	238089_at	NM_006715
6.98	6.72	0.26	7.73E-01	9.29E-01	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	chr3q25.31	212665_at	NM_015508
5.87	5.82	0.06	7.74E-01	9.29E-01	SIPA1	signal-induced proliferation-associated gene 1	chr11q13	204164_at	NM_006747 /// NM_153253
2.33	2.28	0.04	7.74E-01	9.29E-01	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	chr6p21.3	1566302_at	NM_021959
3.84	3.78	0.06	7.74E-01	9.29E-01	---	---	---	243992_at	---
2.34	2.31	0.04	7.74E-01	9.29E-01	CLIC5 /// LOC100131610	chloride intracellular channel 5 /// similar to chloride intracellular channel 5	chr6p21.1-p12.1	234329_at	NM_001114086 /// NM_016929 /// XM_001723558
2.42	2.38	0.04	7.74E-01	9.29E-01	---	---	---	244776_at	---
2.53	2.48	0.05	7.74E-01	9.29E-01	SPAG11A /// SPAG11B	sperm associated antigen 11A /// sperm associated antigen 11B	chr8p23-p22 /// chr8p23.1	1553582_a_at	NM_001081552 /// NM_016512 /// NM_058200 /// NM_058201 /// NM_058202 /// NM_058203 /// NM_058206 /// NM_058207 /// XM_001713749
2.39	2.34	0.04	7.74E-01	9.29E-01	LOC400456	hypothetical gene supported by BC040875	chr15q26.2	1562901_at	XM_001128315 /// XM_001716048 /// XM_944056
2.86	2.82	0.04	7.74E-01	9.29E-01	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	chr17q21	210632_s_at	NM_000023
3.19	3.13	0.07	7.74E-01	9.29E-01	LOC100130417	similar to hCG1995469	---	1555979_at	XM_001714163 /// XM_001718964
6.26	6.19	0.06	7.74E-01	9.29E-01	KIFC3	kinesin family member C3	chr16q13-q21	209661_at	NM_001130099 /// NM_001130100 /// NM_005550
7.07	6.92	0.15	7.74E-01	9.29E-01	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	chr12q24.11	225213_at	NM_139283
7.59	7.52	0.08	7.74E-01	9.29E-01	SRM	spermidine synthase	chr1p36-p22	201516_at	NM_003132
3.13	3.08	0.05	7.74E-01	9.29E-01	FAM110B	family with sequence similarity 110, member B	chr8q12.1	228790_at	NM_147189
4.24	4.17	0.07	7.74E-01	9.29E-01	HLA-DOA	major histocompatibility complex, class II, DO alpha	chr6p21.3	206313_at	NM_002119
2.72	2.68	0.03	7.75E-01	9.29E-01	---	---	---	1559668_s_at	---
2.87	2.83	0.04	7.75E-01	9.29E-01	RAB7B	RAB7B, member RAS oncogene family	chr1q32	1553982_a_at	NM_177403
2.63	2.59	0.04	7.75E-01	9.29E-01	RBM33	RNA binding motif protein 33	chr7q36.3	238801_at	NM_001008408 /// NM_053043
3.20	3.11	0.09	7.75E-01	9.29E-01	SSPN	sarcospan (Kras oncogene-associated gene)	chr12p11.2	204963_at	NM_005086
4.27	4.20	0.07	7.75E-01	9.29E-01	MTHFSD	methenyltetrahydrofolate synthetase domain containing	chr16q24.1	222769_at	NM_022764
1.87	1.84	0.03	7.75E-01	9.29E-01	---	---	---	1555925_at	---
2.00	1.97	0.03	7.75E-01	9.29E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	1559833_at	NM_015313
5.42	5.30	0.12	7.75E-01	9.29E-01	SDC1	syndecan 1	chr2p24.1	201286_at	NM_001006946 /// NM_002997
3.12	3.06	0.06	7.75E-01	9.29E-01	TMEM107	transmembrane protein 107	chr17p13.1	224496_s_at	NM_032354 /// NM_183065
8.59	8.32	0.27	7.75E-01	9.29E-01	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	chr9q31	202491_s_at	NM_003640

2.00	1.97	0.03	7.75E-01	9.29E-01	IRGM	immunity-related GTPase family, M	chr5q33.1	1563335_at	XR_040407 /// XR_040408 /// XR_040409																				
7.48	7.41	0.07	7.75E-01	9.29E-01	DAP3	death associated protein 3	chr1q21-q22	208822_s_at	NM_004632 /// NM_033657																				
3.59	3.54	0.05	7.75E-01	9.29E-01	SALL4	sal-like 4 (Drosophila)	chr20q13.13-q13.2	229661_at	NM_020436																				
4.35	4.31	0.04	7.75E-01	9.29E-01	SENP1	SUMO1/sentrin specific peptidase 1	chr12q13.1	226619_at	NM_014554																				
9.16	9.09	0.07	7.75E-01	9.29E-01	RPL7L1	ribosomal protein L7-like 1	chr6p21.1	224738_x_at	NM_198486																				
2.64	2.59	0.05	7.75E-01	9.29E-01	RP4-724E16.2	hypothetical protein FLJ14031	chr20q13.13-q13.2	215861_at	---																				
6.04	5.96	0.08	7.75E-01	9.29E-01	SLC35C1	solute carrier family 35, member C1	chr11p11.2	222647_at	NM_018389																				
7.39	7.34	0.05	7.75E-01	9.29E-01	DULLARD	dullard homolog (Xenopus laevis)	chr17p13	200035_at	NM_015343																				
1.96	1.93	0.03	7.75E-01	9.29E-01	---	---	---	1561529_at	---																				
3.72	3.67	0.05	7.76E-01	9.29E-01	MSRB2	methionine sulfoxide reductase B2	chr10p12	219451_at	NM_012228																				
3.59	3.52	0.07	7.76E-01	9.30E-01	PSAPL1	prosaposin-like 1	chr4p16.1	1564333_a_at	NM_001085382																				
1.93	1.90	0.03	7.76E-01	9.30E-01	KLRC4	killer cell lectin-like receptor subfamily C, member 4	chr12p13.2-p12.3	210690_at	NM_013431																				
3.45	3.40	0.05	7.76E-01	9.30E-01	PRKX /// PRKY	protein kinase, X-linked /// protein kinase, Y-linked	chrXp22.3 /// chrYp11.2	204060_s_at	NM_002760 /// NM_005044																				
2.23	2.20	0.03	7.76E-01	9.30E-01	TPCN2	two pore segment channel 2	chr11q13.2	231978_at	NM_139075																				
2.42	2.38	0.04	7.76E-01	9.30E-01	HIPK1	homeodomain interacting protein kinase 1	chr1p13.2	1552515_at	NM_152696 /// NM_181358 /// NM_198268 /// NM_198269																				
2.96	2.93	0.04	7.76E-01	9.30E-01	APOC3	Apolipoprotein C-III	chr11q23.1-q23.2	231587_at	NM_000040																				
4.32	4.20	0.11	7.76E-01	9.30E-01	---	---	---	230618_s_at	---																				
3.02	2.97	0.05	7.76E-01	9.30E-01	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	chr21q22.3	211626_x_at	NM_004449 /// NM_182918																				
2.14	2.09	0.05	7.76E-01	9.30E-01	GOLGA6	golgi autoantigen, golgin subfamily a, 6	chr15q24.1	207575_at	NM_001038640																				
2.19	2.16	0.04	7.76E-01	9.30E-01	---	---	---	233826_at	---																				
6.63	6.55	0.09	7.76E-01	9.30E-01	CRYL1	crystallin, lambda 1	chr13q12.11	220753_s_at	NM_015974																				
2.33	2.29	0.05	7.76E-01	9.30E-01	---	---	---	1562935_at	---																				
2.56	2.52	0.04	7.77E-01	9.30E-01	SIRPB1	signal-regulatory protein beta 1	chr20p13	206934_at	NM_001083910 /// NM_006065																				
2.93	2.89	0.04	7.77E-01	9.30E-01	OTUD7A	OTU domain containing 7A	chr15q13.3	1553351_at	NM_130901																				
4.28	4.23	0.05	7.77E-01	9.30E-01	FKBP1B	FK506 binding protein 1B, 12.6 kDa	chr2p23.3	209931_s_at	NM_004116 /// NM_054033																				
2.36	2.33	0.04	7.77E-01	9.30E-01	FOXP2	forkhead box P2	chr7q31	1555647_a_at	NM_014491 /// NM_148898 /// NM_148899																				
5.53	5.47	0.06	7.77E-01	9.30E-01	SLCO2B1	solute carrier organic anion transporter family, member 2B1	chr11q13	211557_x_at	NM_007256																				
4.06	3.99	0.08	7.77E-01	9.30E-01	GPR146	G protein-coupled receptor 146	chr7p22.3	228770_at	NM_138445																				
4.32	4.26	0.06	7.77E-01	9.30E-01	IL27	interleukin 27	---	1552995_at	NM_145659																				
2.31	2.27	0.04	7.77E-01	9.30E-01	---	---	---	1561036_at	---																				
1.86	1.83	0.03	7.77E-01	9.30E-01	---	---	---	1558957_s_at	---																				
2.29	2.23	0.06	7.77E-01	9.30E-01	ARMC8	armadillo repeat containing 8	chr3q22.3	219094_at	NM_014154 /// NM_015396 /// NM_213654																				
2.52	2.48	0.03	7.77E-01	9.30E-01	---	---	---	237063_at	---																				
9.25	9.19	0.06	7.77E-01	9.30E-01	LONP1	lon peptidase 1, mitochondrial	chr19p13.2	209017_s_at	NM_004793																				
7.10	6.99	0.10	7.77E-01	9.30E-01	RAB11A	RAB11A, member RAS oncogene family	chr15q21.3-q22.31	200864_s_at	NM_004663																				
2.75	2.72	0.04	7.77E-01	9.30E-01	IL22	interleukin 22	chr12q15	221165_s_at	NM_020525																				
2.67	2.64	0.03	7.77E-01	9.30E-01	---	---	---	240896_at	---																				
3.26	3.21	0.05	7.77E-01	9.30E-01	---	---	---	1566535_at	---																				
2.11	2.07	0.04	7.77E-01	9.30E-01	ZSCAN4	zinc finger and SCAN domain containing 4	chr19q13.43	1552851_at	NM_152677																				
2.21	2.18	0.03	7.77E-01	9.30E-01	POU2F3	POU class 2 homeobox 3	chr11q23.3	215355_at	NM_014352																				
3.03	2.99	0.04	7.77E-01	9.30E-01	---	---	---	1564798_at	---																				

2.46	2.40	0.06	7.77E-01	9.30E-01	TRIM5	tripartite motif-containing 5	chr11p15	223830_s_at	NM_033034 /// NM_033092 /// NM_033093																				
2.11	2.07	0.04	7.78E-01	9.30E-01	---	---	---	244510_at	---																				
3.05	2.99	0.06	7.78E-01	9.30E-01	---	---	---	235646_at	---																				
5.15	5.07	0.08	7.78E-01	9.30E-01	LAMP2	lysosomal-associated membrane protein 2	chrXq24	200821_at	NM_001122606 /// NM_002294 /// NM_013995																				
6.46	6.37	0.09	7.78E-01	9.30E-01	---	---	---	225886_at	---																				
2.65	2.58	0.07	7.78E-01	9.30E-01	BCL2L11	BCL2-like 11 (apoptosis facilitator)	chr2q13	208536_s_at	NM_006538 /// NM_138621 /// NM_207002																				
4.49	4.44	0.05	7.78E-01	9.30E-01	ZDHHC11	zinc finger, DHHC-type containing 11	chr5p15.33	221646_s_at	NM_024786																				
4.69	4.59	0.09	7.78E-01	9.30E-01	CCNT2	cyclin T2	chr2q21.3	204645_at	NM_001241 /// NM_058241																				
4.72	4.68	0.04	7.78E-01	9.30E-01	GINS2	GINS complex subunit 2 (Psf2 homolog)	chr16q24.1	1557595_at	NM_016095																				
4.05	4.00	0.04	7.78E-01	9.30E-01	NTN1	Netrin 1	chr17p13-p12	237847_at	NM_004822																				
5.36	5.26	0.10	7.78E-01	9.30E-01	ZBTB11	zinc finger and BTB domain containing 11	chr3q12.3	204847_at	NM_014415																				
3.17	3.10	0.07	7.78E-01	9.30E-01	---	---	---	230017_at	---																				
2.27	2.24	0.03	7.78E-01	9.30E-01	---	---	---	1570024_at	---																				
2.84	2.78	0.05	7.78E-01	9.30E-01	---	---	---	242253_at	---																				
2.87	2.84	0.04	7.78E-01	9.31E-01	---	---	---	1559426_at	---																				
3.88	3.82	0.06	7.78E-01	9.31E-01	DKFZp779M0652	hypothetical protein DKFZp779M0652	chr11p11.2	230115_at	XM_001721936 /// XM_001724399 /// XM_001724581																				
4.84	4.79	0.05	7.78E-01	9.31E-01	FOXO1	forkhead box O1	chr13q14.1	202723_s_at	NM_002015																				
2.02	1.99	0.03	7.79E-01	9.31E-01	PLSCR1	phospholipid scramblase 1	chr3q23	244315_at	NM_021105																				
2.09	2.04	0.05	7.79E-01	9.31E-01	---	---	---	1559497_at	---																				
1.78	1.75	0.03	7.79E-01	9.31E-01	C5orf36	chromosome 5 open reading frame 36	chr5q15	1553868_a_at	NM_173665																				
5.59	5.53	0.06	7.79E-01	9.31E-01	GLP-1	GATA like protein-1	chr19p13.2	239720_at	NM_001103167																				
3.61	3.57	0.04	7.79E-01	9.31E-01	---	---	---	222677_x_at	---																				
2.16	2.12	0.04	7.79E-01	9.31E-01	RTCD1	RNA terminal phosphate cyclase domain 1	chr1p21.2	215351_at	NM_001130841 /// NM_003729																				
3.09	3.05	0.04	7.79E-01	9.31E-01	ZCCHC5	zinc finger, CCHC domain containing 5	chrXq21.1	1552935_at	NM_152694																				
3.54	3.50	0.04	7.79E-01	9.31E-01	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	chr1p36.13-q31.3	237327_at	NM_001077628 /// NM_016022																				
2.12	2.08	0.04	7.79E-01	9.31E-01	ZCWPW2	zinc finger, CW type with PWWP domain 2	chr3p24.1	243863_at	NM_001040432																				
5.67	5.61	0.06	7.79E-01	9.31E-01	WDR48	WD repeat domain 48	chr3p21.33	65591_at	NM_020839																				
3.38	3.33	0.05	7.79E-01	9.31E-01	CCDC33	coiled-coil domain containing 33	chr15q24.1	220908_at	NM_025055 /// NM_182791																				
2.43	2.39	0.04	7.79E-01	9.31E-01	LOC440131	similar to bA90M5.1 (novel protein)	chr13q12.3	233804_at	NM_001010918																				
2.90	2.86	0.04	7.79E-01	9.31E-01	CCDC70	coiled-coil domain containing 70	chr13q14.3	221167_s_at	NM_031290																				
4.94	4.88	0.06	7.79E-01	9.31E-01	PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	chr1p36.31	227142_at	NM_001042663 /// NM_001042664 /// NM_001042665 /// NM_020631 /// NM_198681																				
6.58	6.51	0.07	7.79E-01	9.31E-01	ZSWIM6	zinc finger, SWIM-type containing 6	chr5q12.1	226208_at	XM_001716154 /// XM_035299 /// XM_936273																				
2.74	2.69	0.06	7.79E-01	9.31E-01	TUBGCP3	tubulin, gamma complex associated protein 3	chr13q34	215739_s_at	NM_006322																				
2.69	2.65	0.04	7.79E-01	9.31E-01	PTGIS	prostaglandin I2 (prostacyclin) synthase	chr20q13.13	210702_s_at	NM_000961																				
4.44	4.38	0.05	7.79E-01	9.31E-01	SPATA21	spermatogenesis associated 21	chr1p36.13	1570242_x_at	NM_198546																				
5.41	5.36	0.06	7.79E-01	9.31E-01	TMEM86A	transmembrane protein 86A	chr11p15.1	227570_at	NM_153347																				

7.13	7.03	0.10	7.80E-01	9.31E-01	ADNP	activity-dependent neuroprotector homeobox	chr20q13.13	201773_at	NM_015339 /// NM_181442
2.35	2.31	0.04	7.80E-01	9.31E-01	GPR110	G protein-coupled receptor 110	chr6p12.3	238689_at	NM_025048 /// NM_153840
2.04	2.00	0.04	7.80E-01	9.31E-01	PRKCI	protein kinase C, iota	chr3q26.3	209677_at	NM_002740
5.70	5.61	0.08	7.80E-01	9.31E-01	GCLC	glutamate-cysteine ligase, catalytic subunit	chr6p12	202922_at	NM_001498
1.95	1.91	0.04	7.80E-01	9.31E-01	---	---	---	240970_x_at	---
2.86	2.80	0.06	7.80E-01	9.31E-01	---	---	---	1557164_a_at	---
2.26	2.22	0.04	7.80E-01	9.31E-01	---	---	---	1562161_at	---
2.09	2.06	0.03	7.80E-01	9.31E-01	SPZ1	spermatogenic leucine zipper 1	chr5q14.1	224167_at	NM_032567
1.92	1.88	0.03	7.80E-01	9.31E-01	---	---	---	237991_at	---
2.70	2.66	0.04	7.80E-01	9.31E-01	---	---	---	1570382_at	---
5.63	5.59	0.03	7.80E-01	9.31E-01	DUS2L	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	chr16q22.1	219486_at	NM_017803
2.02	1.98	0.03	7.80E-01	9.31E-01	DLX6	distal-less homeobox 6	chr7q22	242940_x_at	NM_005222
2.04	1.99	0.05	7.80E-01	9.31E-01	---	---	---	1561242_at	---
4.14	4.09	0.05	7.80E-01	9.31E-01	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	chr11p11.2-p11.1	205567_at	NM_003654
2.45	2.40	0.04	7.80E-01	9.31E-01	CCDC17	coiled-coil domain containing 17	chr1p34.1	236320_at	NM_001114938 /// NM_152500
2.11	2.08	0.03	7.80E-01	9.32E-01	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	chr8p11	216361_s_at	NM_001099412 /// NM_001099413 /// NM_006766
2.32	2.28	0.05	7.81E-01	9.32E-01	CHD7	chromodomain helicase DNA binding protein 7	chr8q12.2	220619_at	NM_017780
2.85	2.80	0.05	7.81E-01	9.32E-01	---	---	---	220882_at	---
5.37	5.28	0.08	7.81E-01	9.32E-01	AKAP10	A kinase (PRKA) anchor protein 10	chr17p11.1	236007_at	NM_007202
1.92	1.88	0.04	7.81E-01	9.32E-01	LOC388907 /// LOC647436 /// RPL5 /// SNORA66	similar to MSTP030 /// similar to ribosomal protein L5 /// ribosomal protein L5 /// small nucleolar RNA, H/ACA box 66	chr1p22.1 /// chr22q13.2	210035_s_at	NM_000969 /// NR_002444 /// XM_001722636 /// XM_001722638 /// XM_001724883 /// XM_937113 /// XR_017615 /// XR_037140 /// XR_039555
6.01	5.96	0.05	7.81E-01	9.32E-01	XPO5	exportin 5	chr6p21.1	223056_s_at	NM_020750
4.34	4.27	0.07	7.81E-01	9.32E-01	DSCR3	Down syndrome critical region gene 3	chr21q22.2	217309_s_at	NM_006052
1.92	1.88	0.03	7.81E-01	9.32E-01	---	---	---	241557_x_at	---
7.79	7.69	0.10	7.81E-01	9.32E-01	MEIS1	Meis homeobox 1	chr2p14-p13	204069_at	NM_002398
2.31	2.28	0.03	7.81E-01	9.32E-01	LOC284632	hypothetical protein LOC284632	chr1p36.11	1562716_at	---
6.30	6.23	0.07	7.81E-01	9.32E-01	DHDDS	dehydrodolichyl diphosphate synthase	chr1p36.11	218547_at	NM_024887 /// NM_205861
6.30	6.24	0.06	7.81E-01	9.32E-01	41338	membrane-associated ring finger (C3HC4) 5	chr10q23.32	218582_at	NM_017824
2.62	2.57	0.04	7.81E-01	9.32E-01	MGC14436	hypothetical protein MGC14436	chr12q24.12	1553811_at	---
2.77	2.72	0.05	7.81E-01	9.32E-01	---	---	---	1562631_at	---
5.01	4.80	0.21	7.81E-01	9.32E-01	CXCL14	chemokine (C-X-C motif) ligand 14	chr5q31	218002_s_at	NM_004887
2.05	2.02	0.03	7.81E-01	9.32E-01	---	---	---	217537_x_at	---
2.58	2.53	0.05	7.81E-01	9.32E-01	SNORA68	small nucleolar RNA, H/ACA box 68	chr19p13	1566403_at	NR_000012
2.47	2.43	0.04	7.81E-01	9.32E-01	---	---	---	215998_at	---
4.73	4.62	0.11	7.81E-01	9.32E-01	RIT1	Ras-like without CAAX 1	chr1q22	209882_at	NM_006912
2.88	2.84	0.05	7.81E-01	9.32E-01	TLR6	toll-like receptor 6	chr4p14	207446_at	NM_006068
1.88	1.85	0.03	7.81E-01	9.32E-01	---	---	---	215542_at	---
5.06	4.98	0.08	7.81E-01	9.32E-01	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	chr2p22.1	213420_at	NM_198963
5.32	5.25	0.07	7.81E-01	9.32E-01	MGC16385	hypothetical protein MGC16385	chr16q24.3	223728_at	NM_145039
2.36	2.32	0.04	7.82E-01	9.32E-01	CENTD1	centaurin, delta 1	chr4p14	213618_at	NM_015230 /// NM_139182
6.51	6.43	0.08	7.82E-01	9.32E-01	RPUSD3	RNA pseudouridylate synthase domain containing 3	chr3p25.3	1555916_at	NM_173659
2.34	2.30	0.03	7.82E-01	9.32E-01	SLITRK3	SLIT and NTRK-like family, member 3	chr3q26.1	206732_at	NM_014926
2.05	2.02	0.04	7.82E-01	9.32E-01	RP2	retinitis pigmentosa 2 (X-linked recessive)	chrXp11.4-p11.21	1568782_at	NM_006915

7.13	7.00	0.13	7.82E-01	9.32E-01	MGST1	Microsomal glutathione S-transferase 1	chr12p12.3-p12.1	239001_at	NM_020300 /// NM_145764 /// NM_145791 /// NM_145792
2.44	2.40	0.04	7.82E-01	9.32E-01	PCDHGB8P	protocadherin gamma subfamily B, 8 pseudogene	chr5q31	234029_at	NR_001297
2.22	2.19	0.04	7.82E-01	9.32E-01	---	---	---	241971_at	---
2.24	2.21	0.03	7.82E-01	9.32E-01	C13orf38	chromosome 13 open reading frame 38	chr13q13.3	234085_at	XM_001130109 /// XM_001133689 /// XM_001719885
2.00	1.96	0.04	7.82E-01	9.32E-01	AKR1C1	Aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	chr10p15-p14	1562102_at	NM_001353 /// XM_001724839
4.45	4.38	0.07	7.82E-01	9.32E-01	---	---	---	238700_at	---
3.29	3.23	0.06	7.82E-01	9.32E-01	GPR137	G protein-coupled receptor 137	chr11cen-q22.3	219430_at	NM_020155
5.55	5.49	0.06	7.82E-01	9.32E-01	GHR	growth hormone receptor	chr5p13-p12	205498_at	NM_000163
3.31	3.25	0.06	7.82E-01	9.32E-01	C14orf106	chromosome 14 open reading frame 106	chr14q21.3	226630_at	NM_018353
2.68	2.63	0.05	7.83E-01	9.32E-01	---	---	---	1557665_at	---
2.20	2.15	0.05	7.83E-01	9.32E-01	TASP1	taspase, threonine aspartase, 1	chr20p12.1	233719_s_at	NM_017714
2.27	2.23	0.04	7.83E-01	9.32E-01	C15orf44	chromosome 15 open reading frame 44	chr15q22.31	1568801_at	NM_030800
8.84	8.78	0.05	7.83E-01	9.32E-01	WDR1	WD repeat domain 1	chr4p16.1	200609_s_at	NM_005112 /// NM_017491
2.58	2.53	0.04	7.83E-01	9.32E-01	---	---	---	241214_at	---
3.22	3.15	0.07	7.83E-01	9.32E-01	GIN1	gypsy retrotransposon integrase 1	chr5q21.1	1554345_a_at	NM_017676
3.33	3.28	0.04	7.83E-01	9.32E-01	ANKH	ankylosis, progressive homolog (mouse)	chr5p15.1	229176_at	NM_054027
3.51	3.46	0.05	7.83E-01	9.32E-01	LOC286068	hypothetical protein LOC286068	chr8q11.21	1561988_at	---
6.86	6.78	0.08	7.83E-01	9.32E-01	PARVA	parvin, alpha	chr11p15.3	217890_s_at	NM_018222
3.11	3.05	0.06	7.83E-01	9.32E-01	TMPRSS2	transmembrane protease, serine 2	chr21q22.3	226553_at	NM_005656 /// XM_001717226 /// XM_001722209 /// XM_001726078
2.69	2.64	0.04	7.83E-01	9.32E-01	HIST3H2A	Histone cluster 3, H2a	chr1q42.13	231681_x_at	NM_033445
3.68	3.63	0.05	7.83E-01	9.32E-01	SOX2	SRY (sex determining region Y)-box 2	chr3q26.3-q27	213721_at	NM_003106
2.87	2.82	0.05	7.83E-01	9.32E-01	---	---	---	236470_at	---
12.47	12.43	0.04	7.83E-01	9.32E-01	RPL31	ribosomal protein L31	chr2q11.2	200963_x_at	NM_000993 /// NM_001098577 /// NM_001099693
6.01	5.96	0.05	7.83E-01	9.32E-01	C15orf57	chromosome 15 open reading frame 57	chr15q15.1	225397_at	NM_001080791 /// NM_001080792 /// NM_052849
2.64	2.61	0.03	7.83E-01	9.32E-01	ROS1	c-ros oncogene 1 , receptor tyrosine kinase	chr6q22	207569_at	NM_002944
2.28	2.25	0.03	7.83E-01	9.32E-01	---	---	---	1559007_s_at	---
4.75	4.71	0.04	7.83E-01	9.33E-01	ZCWPW1	zinc finger, CW type with PWWP domain 1	chr7q22.1	220618_s_at	NM_017984
2.04	2.00	0.03	7.83E-01	9.33E-01	DPY19L1	dpy-19-like 1 (C. elegans)	chr7p14.3	1570355_a_at	NM_015283
6.02	5.83	0.19	7.83E-01	9.33E-01	CHD1	chromodomain helicase DNA binding protein 1	chr5q15-q21	204258_at	NM_001270
5.51	5.46	0.06	7.83E-01	9.33E-01	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	chr1p22.1	209188_x_at	NM_001938
1.90	1.87	0.03	7.83E-01	9.33E-01	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	chr1p34	234904_x_at	NM_021952
2.63	2.59	0.04	7.84E-01	9.33E-01	---	---	---	1560638_a_at	---
4.29	4.26	0.03	7.84E-01	9.33E-01	---	---	---	243467_at	---
3.12	3.07	0.05	7.84E-01	9.33E-01	RP1-21O18.1	kazrin	chr1p36.21	213752_at	NM_001017999 /// NM_001018000 /// NM_001018001 /// NM_015209 /// NM_201628
1.91	1.87	0.04	7.84E-01	9.33E-01	---	---	---	1566749_at	---

3.15	3.08	0.06	7.84E-01	9.33E-01	PYHIN1	pyrin and HIN domain family, member 1	chr1q23.1	216748_at	NM_152501 /// NM_198928 /// NM_198929 /// NM_198930																				
2.30	2.26	0.04	7.84E-01	9.33E-01	C6orf155	chromosome 6 open reading frame 155	chr6q13	220324_at	XR_040926 /// XR_040927 /// XR_040928																				
6.14	6.07	0.07	7.84E-01	9.33E-01	ABI2	abl interactor 2	chr2q33	225098_at	NM_005759																				
2.77	2.73	0.04	7.84E-01	9.33E-01	NR2C2	nuclear receptor subfamily 2, group C, member 2	chr3p25	206038_s_at	NM_003298																				
4.95	4.91	0.05	7.84E-01	9.33E-01	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	chr1q31	207931_s_at	NM_001018053 /// NM_006212																				
2.54	2.41	0.13	7.84E-01	9.33E-01	---	---	---	227952_at	---																				
5.13	4.97	0.17	7.84E-01	9.33E-01	GUCY1A3	Guanylate cyclase 1, soluble, alpha 3	chr4q31.3-q33|4q31.1-q31.2	227235_at	NM_000856 /// NM_001130682 /// NM_001130683 /// NM_001130684 /// NM_001130685 /// NM_001130686 /// NM_001130687																				
3.07	3.02	0.05	7.84E-01	9.33E-01	C1QTNF2	C1q and tumor necrosis factor related protein 2	chr5q33.3	223749_at	NM_031908																				
3.03	2.99	0.05	7.84E-01	9.33E-01	LRRK2	leucine-rich repeat kinase 2	chr12q12	229584_at	NM_198578																				
5.75	5.69	0.06	7.84E-01	9.33E-01	---	---	---	235474_at	---																				
3.63	3.58	0.05	7.84E-01	9.33E-01	ITGA9	integrin, alpha 9	chr3p21.3	1555336_a_at	NM_002207																				
2.47	2.42	0.04	7.84E-01	9.33E-01	WDR60	WD repeat domain 60	chr7q36.3	229008_at	NM_018051																				
4.27	4.12	0.15	7.84E-01	9.33E-01	C4orf33	chromosome 4 open reading frame 33	chr4q28.2	1552370_at	NM_001099783 /// NM_173487																				
2.36	2.32	0.04	7.85E-01	9.33E-01	C21orf34	chromosome 21 open reading frame 34	chr21q21.1	1559412_at	NM_001005732 /// NM_001005733 /// NM_001005734																				
2.25	2.21	0.04	7.85E-01	9.33E-01	C8orf54	chromosome 8 open reading frame 54	chr8q24.13	1553443_at	NM_001038706																				
5.41	5.29	0.12	7.85E-01	9.33E-01	DMXL1	Dmx-like 1	chr5q22	203791_at	NM_005509																				
4.32	4.28	0.05	7.85E-01	9.33E-01	HOXD9	homeobox D9	chr2q31.1	205605_at	NM_014213																				

10.03	9.94	0.09	7.85E-01	9.33E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	204670_x_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447
2.85	2.82	0.03	7.85E-01	9.33E-01	HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	chr9q22	206985_at	NM_000197
7.31	7.27	0.04	7.85E-01	9.33E-01	MBD2	methyl-CpG binding domain protein 2	chr18q21	202484_s_at	NM_003927 /// NM_015832
6.78	6.68	0.10	7.85E-01	9.33E-01	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	chr3q26.2-q27	200892_s_at	NM_004593
5.07	4.99	0.08	7.85E-01	9.33E-01	PACS2	phosphofurin acidic cluster sorting protein 2	chr14q32.33	212778_at	NM_001100913 /// NM_015197
2.50	2.45	0.05	7.85E-01	9.33E-01	---	---	---	232511_at	---
4.09	3.94	0.15	7.85E-01	9.33E-01	SCAMP1	secretory carrier membrane protein 1	chr5q13.3-q14.1	1552978_a_at	NM_004866
2.17	2.14	0.04	7.85E-01	9.33E-01	RNF103	ring finger protein 103	chr2p11.2	1568665_at	NM_005667
3.81	3.75	0.05	7.86E-01	9.33E-01	ZNF605	zinc finger protein 605	chr12q24.33	227822_at	NM_183238
3.83	3.71	0.11	7.86E-01	9.33E-01	---	---	---	235470_at	---
5.16	5.03	0.13	7.86E-01	9.33E-01	CDC14B /// CDC14C	CDC14 cell division cycle 14 homolog B (S. cerevisiae) /// CDC14 cell division cycle 14 homolog C (S. cerevisiae)	chr7p12.3 /// chr9q22.33	221556_at	NM_001077181 /// NM_003671 /// NM_033331 /// NR_003595
6.00	5.94	0.06	7.86E-01	9.33E-01	RAB35	RAB35, member RAS oncogene family	chr12q24.31	225620_at	NM_006861
2.05	2.01	0.05	7.86E-01	9.34E-01	OLFM4	olfactomedin 4	chr13q21.1	212768_s_at	NM_006418
5.68	5.64	0.04	7.86E-01	9.34E-01	KPNA6	karyopherin alpha 6 (importin alpha 7)	chr1p35.1-p34.3	226976_at	NM_012316
3.55	3.51	0.04	7.86E-01	9.34E-01	PHOSPHO1	phosphatase, orphan 1	chr17q21.32	236218_at	NM_178500
2.24	2.21	0.03	7.86E-01	9.34E-01	CYLC1	cylicin, basic protein of sperm head cytoskeleton 1	chrXq21.1	216779_at	NM_021118
2.29	2.26	0.03	7.86E-01	9.34E-01	---	---	---	242460_at	---

2.26	2.22	0.04	7.86E-01	9.34E-01	TRPM3	transient receptor potential cation channel, subfamily M, member 3	chr9q21.11-q21.12	216489_at	NM_001007470 /// NM_001007471 /// NM_020952 /// NM_024971 /// NM_206944 /// NM_206945 /// NM_206946 /// NM_206947 /// NM_206948																			
2.30	2.26	0.04	7.86E-01	9.34E-01	LOC100128663	similar to PRO3077	chr10p12.1	224089_at	XM_001721882 /// XM_001722440 /// XM_001725958																			
3.69	3.65	0.04	7.86E-01	9.34E-01	---	---	---	228503_at	---																			
2.62	2.58	0.04	7.86E-01	9.34E-01	---	---	---	241262_at	---																			
2.57	2.49	0.08	7.86E-01	9.34E-01	---	---	---	237839_at	---																			
3.37	3.32	0.05	7.86E-01	9.34E-01	---	---	---	230277_at	---																			
2.62	2.58	0.04	7.87E-01	9.34E-01	C2orf50	chromosome 2 open reading frame 50	chr2p25.1	1563814_at	NM_182500																			
6.08	5.88	0.20	7.87E-01	9.34E-01	RPS23	ribosomal protein S23	chr5q14.2	227722_at	NM_001025																			
6.80	6.74	0.05	7.87E-01	9.34E-01	RALY	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))	chr20q11.21-q11.23	201271_s_at	NM_007367 /// NM_016732																			
9.47	9.29	0.19	7.87E-01	9.34E-01	PDGFD	platelet derived growth factor D	chr11q22.3	219304_s_at	NM_025208 /// NM_033135																			
2.27	2.23	0.04	7.87E-01	9.34E-01	---	---	---	228604_at	---																			
2.04	2.00	0.05	7.87E-01	9.34E-01	---	---	---	1563061_at	---																			
3.13	3.07	0.06	7.87E-01	9.34E-01	TMEM43	Transmembrane protein 43	chr3p25.1	233480_at	NM_024334																			
6.83	6.74	0.09	7.87E-01	9.34E-01	LDOC1	leucine zipper, down-regulated in cancer 1	chrXq27	204454_at	NM_012317																			
2.42	2.39	0.04	7.87E-01	9.34E-01	---	---	---	1561739_at	---																			
2.27	2.24	0.03	7.87E-01	9.34E-01	---	---	---	239988_at	---																			
6.14	6.04	0.10	7.87E-01	9.34E-01	COG3	component of oligomeric golgi complex 3	chr13q14.12	223450_s_at	NM_031431																			
2.34	2.30	0.03	7.87E-01	9.34E-01	TIGD1L	tigger transposable element derived 1-like	chr6p21.3	216459_x_at	---																			
2.88	2.84	0.04	7.87E-01	9.34E-01	---	---	---	241922_at	---																			
6.16	6.06	0.10	7.87E-01	9.34E-01	FLJ35348	FLJ35348	chr9q34	203245_s_at	XR_041460 /// XR_041461 /// XR_041462																			
5.39	5.32	0.07	7.87E-01	9.34E-01	PHTF2	putative homeodomain transcription factor 2	chr7q11.23-q21	209780_at	NM_001127357 /// NM_001127358 /// NM_001127359 /// NM_001127360 /// NM_020432																			
3.84	3.74	0.09	7.87E-01	9.34E-01	CD9	CD9 molecule	chr12p13.3	233317_at	NM_001769																			
2.41	2.36	0.05	7.87E-01	9.34E-01	---	---	---	1560582_a_at	---																			
2.60	2.56	0.04	7.87E-01	9.34E-01	GTSE1	G-2 and S-phase expressed 1	chr22q13.2-q13.3	204315_s_at	NM_016426																			
2.97	2.91	0.05	7.87E-01	9.34E-01	MARVELD2	MARVEL domain containing 2	chr5q13.2	235141_at	NM_001038603 /// NM_144724																			
3.99	3.93	0.06	7.87E-01	9.34E-01	---	---	---	241689_at	---																			
2.14	2.11	0.03	7.87E-01	9.34E-01	SPAG16	sperm associated antigen 16	chr2q34	1560174_at	NM_001025436 /// NM_024532																			
8.45	8.39	0.06	7.87E-01	9.34E-01	IGBP1	immunoglobulin (CD79A) binding protein 1	chrXq13.1-q13.3	202105_at	NM_001551																			
2.58	2.54	0.04	7.88E-01	9.34E-01	LCT	lactase	chr2q21	206945_at	NM_002299																			
2.09	2.06	0.03	7.88E-01	9.34E-01	RANBP3L	RAN binding protein 3-like	chr5p13.2	1553147_at	NM_145000																			
1.96	1.93	0.04	7.88E-01	9.34E-01	---	---	---	1562579_at	---																			
5.08	4.97	0.11	7.88E-01	9.34E-01	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	chr5q12-q13	218769_s_at	NM_023039																			
5.21	5.08	0.14	7.88E-01	9.34E-01	---	---	---	243338_at	---																			
3.95	3.89	0.06	7.88E-01	9.34E-01	TTBK1	tau tubulin kinase 1	chr6p21.1	230191_at	NM_032538																			
2.47	2.43	0.04	7.88E-01	9.34E-01	KIAA1586	KIAA1586	chr6p12.1	231869_at	NM_020931																			

3.46	3.41	0.05	7.88E-01	9.34E-01	---	---	---	1566231_at	---
3.17	3.12	0.05	7.88E-01	9.34E-01	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	chr12q21.2	232441_at	NM_007043
2.07	2.04	0.04	7.88E-01	9.34E-01	---	---	---	241247_at	---
5.21	5.13	0.08	7.88E-01	9.34E-01	COX5B	Cytochrome c oxidase subunit Vb	chr2cen-q13	213736_at	NM_001862
4.23	4.12	0.11	7.88E-01	9.34E-01	RSPRY1	ring finger and SPRY domain containing 1	chr16q13	225774_at	NM_133368
2.35	2.32	0.03	7.88E-01	9.34E-01	TMPRSS2	transmembrane protease, serine 2	chr21q22.3	211689_s_at	NM_005656 /// XM_001717226 /// XM_001722209 /// XM_001726078
4.59	4.54	0.06	7.88E-01	9.34E-01	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	chr6q15	217824_at	NM_016021
2.19	2.17	0.03	7.88E-01	9.34E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1553076_at	NM_153003
4.49	4.37	0.12	7.88E-01	9.34E-01	HBG1 /// HBG2	hemoglobin, gamma A /// hemoglobin, gamma G	chr11p15.5	204848_x_at	NM_000184 /// NM_000559
4.62	4.47	0.15	7.88E-01	9.34E-01	SNAP23	synaptosomal-associated protein, 23kDa	chr15q15.1	209131_s_at	NM_003825 /// NM_130798
6.36	6.32	0.03	7.88E-01	9.34E-01	CCDC88B	coiled-coil domain containing 88B	chr11q12.3	223663_at	NM_032251
1.87	1.84	0.03	7.88E-01	9.34E-01	BCL2L14	BCL2-like 14 (apoptosis facilitator)	chr12p13-p12	1569719_at	NM_030766 /// NM_138722 /// NM_138723 /// NM_138724
11.83	11.80	0.03	7.88E-01	9.34E-01	ACTG1	actin, gamma 1	chr17q25	221607_x_at	NM_001614
3.04	2.99	0.05	7.88E-01	9.34E-01	---	---	---	1555429_at	---
5.07	5.01	0.06	7.88E-01	9.34E-01	KIAA0240	KIAA0240	chr6p21.1	38892_at	NM_015349
3.23	3.19	0.04	7.88E-01	9.34E-01	CXCL17	chemokine (C-X-C motif) ligand 17	chr19q13.2	226960_at	NM_198477
1.92	1.90	0.03	7.88E-01	9.34E-01	---	---	---	1568487_x_at	---
5.89	5.80	0.09	7.88E-01	9.34E-01	SETD5	SET domain containing 5	chr3p25.3	1569105_at	NM_001080517
7.46	7.32	0.14	7.88E-01	9.34E-01	GTF2B	general transcription factor IIB	chr1p22-p21	208066_s_at	NM_001514
9.31	9.26	0.05	7.88E-01	9.34E-01	EDF1	endothelial differentiation-related factor 1	chr9q34.3	209058_at	NM_003792 /// NM_153200
2.49	2.46	0.03	7.89E-01	9.34E-01	NRG3	neuregulin 3	chr10q22-q23	229233_at	NM_001010848
6.07	5.98	0.08	7.89E-01	9.34E-01	FIP1L1	FIP1 like 1 (S. cerevisiae)	chr4q12	221007_s_at	NM_030917
2.07	2.04	0.03	7.89E-01	9.34E-01	---	---	---	238713_at	---
2.73	2.68	0.05	7.89E-01	9.34E-01	FCRLB	Fc receptor-like B	chr1q23.3	238452_at	NM_001002901
3.38	3.32	0.06	7.89E-01	9.34E-01	GUCA1B	guanylate cyclase activator 1B (retina)	chr6p21.1	235528_at	NM_002098
5.18	5.12	0.06	7.89E-01	9.34E-01	---	---	---	243801_x_at	---
3.52	3.48	0.04	7.89E-01	9.34E-01	RNF207	ring finger protein 207	chr1p36.31	1568728_s_at	NM_207396 /// XM_001716213 /// XM_001718203 /// XM_001719665
2.29	2.25	0.04	7.89E-01	9.34E-01	---	---	---	241022_at	---
10.04	9.94	0.09	7.89E-01	9.35E-01	C9orf16	chromosome 9 open reading frame 16	chr9q34.1	204480_s_at	NM_024112
11.81	11.77	0.03	7.89E-01	9.35E-01	ACTG1	actin, gamma 1	chr17q25	224585_x_at	NM_001614
5.57	5.44	0.12	7.89E-01	9.35E-01	ZNF24	zinc finger protein 24	chr18q12	203248_at	NM_006965
1.86	1.83	0.03	7.89E-01	9.35E-01	LOC93463	hypothetical protein LOC93463	chr2q37.3	234861_at	XM_376186 /// XM_940178
4.99	4.92	0.08	7.89E-01	9.35E-01	ZNF211	zinc finger protein 211	chr19q13.4	205437_at	NM_006385 /// NM_198855
2.97	2.93	0.04	7.89E-01	9.35E-01	KRTAP4-5	keratin associated protein 4-5	chr17q12-q21	234637_at	NM_033188
2.48	2.45	0.03	7.89E-01	9.35E-01	OR7A5	olfactory receptor, family 7, subfamily A, member 5	chr19p13.1	208285_at	NM_017506
2.28	2.22	0.06	7.89E-01	9.35E-01	---	---	---	226341_at	---
3.16	3.12	0.04	7.89E-01	9.35E-01	TBX6	T-box 6	chr16p11.2	215122_at	NM_004608 /// NM_080758

2.54	2.49	0.05	7.89E-01	9.35E-01	SEPP1	Selenoprotein P, plasma, 1	chr5q31	229620_at	NM_001085486 /// NM_001093726 /// NM_005410																				
2.40	2.36	0.03	7.89E-01	9.35E-01	---	---	---	243962_at	---																				
6.18	6.14	0.04	7.89E-01	9.35E-01	C9orf37	chromosome 9 open reading frame 37	chr9q34.3	223390_at	NM_032937																				
5.79	5.72	0.07	7.89E-01	9.35E-01	SLC38A7	solute carrier family 38, member 7	chr16q21	56821_at	NM_018231																				
7.49	7.42	0.07	7.90E-01	9.35E-01	RBM9	RNA binding motif protein 9	chr22q13.1	212104_s_at	NM_001031695 /// NM_001082576 /// NM_001082577 /// NM_001082578 /// NM_001082579 /// NM_014309																				
3.76	3.72	0.04	7.90E-01	9.35E-01	ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	chr11p13	232624_at	NM_145804																				
2.71	2.67	0.04	7.90E-01	9.35E-01	DKFZP564C196	DKFZP564C196 protein	chr1q25.3	215953_at	XM_001134212 /// XM_001134393																				
2.16	2.13	0.03	7.90E-01	9.35E-01	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	chr9q22.1	236095_at	NM_001007097 /// NM_001018064 /// NM_001018065 /// NM_001018066 /// NM_006180																				
2.93	2.89	0.04	7.90E-01	9.35E-01	---	---	---	240680_at	---																				
3.68	3.59	0.09	7.90E-01	9.35E-01	LACTB	lactamase, beta	chr15q22.1	1552486_s_at	NM_032857 /// NM_171846																				
2.71	2.66	0.05	7.90E-01	9.35E-01	---	---	---	215251_at	---																				
3.35	3.30	0.05	7.90E-01	9.35E-01	NKX2-1	NK2 homeobox 1	chr14q13	210673_x_at	NM_001079668 /// NM_003317																				
7.10	7.02	0.08	7.90E-01	9.35E-01	EHD2	EH-domain containing 2	chr19q13.3	45297_at	NM_014601																				
2.35	2.31	0.03	7.90E-01	9.35E-01	---	---	---	1569975_at	---																				
2.03	1.98	0.04	7.90E-01	9.35E-01	LOC644624	Hypothetical LOC644624	chr4q28.1	1563462_at	XM_001718304 /// XM_934131 /// XM_943172																				
4.40	4.33	0.07	7.90E-01	9.35E-01	CLEC16A	C-type lectin domain family 16, member A	chr16p13.13	212786_at	NM_015226																				
2.26	2.22	0.03	7.90E-01	9.35E-01	LOC348808	BC048124	chr3q22.1	1569882_at	NR_002811																				
4.09	4.05	0.05	7.90E-01	9.35E-01	PKD1	polycystic kidney disease 1 (autosomal dominant)	chr16p13.3	216949_s_at	NM_000296 /// NM_001009944																				
2.35	2.31	0.04	7.90E-01	9.35E-01	GPR132	G protein-coupled receptor 132	chr14q32.3	223887_at	NM_013345																				
2.74	2.65	0.08	7.90E-01	9.35E-01	BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	chr21q22.11	210818_s_at	NM_001011545 /// NM_001186 /// NM_206866																				
6.74	6.67	0.07	7.90E-01	9.35E-01	FBXL11	F-box and leucine-rich repeat protein 11	chr11q13.1	208987_s_at	NM_012308																				
1.87	1.84	0.03	7.90E-01	9.35E-01	---	---	---	1560980_a_at	---																				
3.31	3.27	0.03	7.91E-01	9.35E-01	---	---	---	215907_at	---																				
4.81	4.76	0.05	7.91E-01	9.35E-01	HHAT	hedgehog acyltransferase	chr1q32	219687_at	NM_001122834 /// NM_018194																				
2.00	1.97	0.03	7.91E-01	9.35E-01	ARHGAP5	Rho GTPase activating protein 5	chr14q12	233872_x_at	NM_001030055 /// NM_001173																				
9.09	9.03	0.06	7.91E-01	9.35E-01	ATP6V0B	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	chr1p32.3	200078_s_at	NM_001039457 /// NM_004047																				
2.03	1.99	0.04	7.91E-01	9.35E-01	---	---	---	238162_at	---																				
6.52	6.47	0.06	7.91E-01	9.35E-01	LRRC42	leucine rich repeat containing 42	chr1p33-p32.1	215084_s_at	NM_052940																				

8.07	7.94	0.13	7.91E-01	9.35E-01	NQO1	NAD(P)H dehydrogenase, quinone 1	chr16q22.1	201468_s_at	NM_000903 /// NM_001025433 /// NM_001025434																			
4.78	4.72	0.06	7.91E-01	9.35E-01	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	chr12q24.2	218400_at	NM_006187																			
7.40	7.35	0.05	7.91E-01	9.35E-01	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	chr19q13	202264_s_at	NM_001128916 /// NM_001128917 /// NM_006114																			
3.18	3.13	0.05	7.91E-01	9.35E-01	---	---	---	244860_at	---																			
4.48	4.44	0.04	7.91E-01	9.35E-01	---	---	---	1562849_at	---																			
2.18	2.15	0.04	7.91E-01	9.35E-01	---	---	---	239927_at	---																			
7.03	6.84	0.19	7.91E-01	9.35E-01	ZNF295	zinc finger protein 295	chr21q22.3	233952_s_at	NM_001098402 /// NM_001098403 /// NM_020727																			
5.38	5.27	0.11	7.91E-01	9.35E-01	TRAPPC6B	trafficking protein particle complex 6B	chr14q21.1	225537_at	NM_001079537 /// NM_177452																			
3.48	3.38	0.10	7.91E-01	9.35E-01	FRMD4B	FERM domain containing 4B	chr3p14.1	213056_at	NM_015123																			
4.26	4.13	0.13	7.91E-01	9.35E-01	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	chr1q41-q42	239930_at	NM_004481																			
6.14	6.11	0.03	7.91E-01	9.35E-01	R3HDM1	R3H domain containing 1	chr2q21.3	202754_at	NM_015361																			
5.38	5.30	0.08	7.91E-01	9.35E-01	SLC38A7	solute carrier family 38, member 7	chr16q21	218727_at	NM_018231																			
13.02	12.99	0.03	7.91E-01	9.35E-01	hCG_16001 /// RPL23A	similar to ribosomal protein L23A /// ribosomal protein L23a	chr17q11 /// chr3q26.1	213084_x_at	NM_000984 /// NM_001093758																			
2.41	2.37	0.04	7.91E-01	9.35E-01	SLC30A8	solute carrier family 30 (zinc transporter), member 8	chr8q24.11	1552985_at	NM_173851																			
2.73	2.64	0.08	7.91E-01	9.35E-01	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	chr13q12	213262_at	NM_014363																			
5.26	5.20	0.06	7.92E-01	9.35E-01	RAD17	RAD17 homolog (S. pombe)	chr5q13	207405_s_at	NM_002873 /// NM_133338 /// NM_133339 /// NM_133340 /// NM_133341 /// NM_133342 /// NM_133343 /// NM_133344																			
3.35	3.29	0.06	7.92E-01	9.35E-01	SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	chr5q33.1	1553272_at	NM_078483																			
2.08	2.03	0.05	7.92E-01	9.35E-01	---	---	---	1558387_at	---																			
7.07	7.01	0.06	7.92E-01	9.35E-01	CTCF	CCCTC-binding factor (zinc finger protein)	chr16q21-q22.3	202521_at	NM_006565																			
5.76	5.67	0.09	7.92E-01	9.35E-01	LOC90784	hypothetical protein LOC90784	chr2p11.2	228515_at	---																			
2.09	2.06	0.03	7.92E-01	9.35E-01	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	chr5q33-q34	205044_at	NM_014211																			
2.69	2.65	0.04	7.92E-01	9.35E-01	EXOSC3	Exosome component 3	chr9p11	227913_at	NM_001002269 /// NM_016042																			
2.95	2.92	0.03	7.92E-01	9.35E-01	CNTD1	cyclin N-terminal domain containing 1	chr17q21.31	231463_at	NM_173478																			
1.97	1.94	0.03	7.92E-01	9.35E-01	---	---	---	1570205_at	---																			
3.96	3.90	0.06	7.92E-01	9.36E-01	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	chr2q32.3	222872_x_at	NM_001031716																			
5.71	5.62	0.09	7.92E-01	9.36E-01	C15orf39	chromosome 15 open reading frame 39	chr15q24.2	204495_s_at	NM_015492																			
2.78	2.73	0.05	7.92E-01	9.36E-01	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	chr3q27-q28	214971_s_at	NM_003032 /// NM_173216 /// NM_173217																			
2.24	2.19	0.04	7.92E-01	9.36E-01	KLHL6	kelch-like 6 (Drosophila)	---	228167_at	NM_130446																			
3.52	3.47	0.04	7.92E-01	9.36E-01	KIR3DL2 /// LOC727787	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 /// similar to killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I NK cell receptor) (Natural killer-associated transcript 4) (NKAT-4) (p70 natural killer cell receptor clone CL-5) (CD158k antigen)	chr19q13.4	207313_x_at	NM_006737 /// XM_001718625																			
3.07	3.03	0.03	7.92E-01	9.36E-01	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	chr11q13.4	224510_s_at	NM_030813																			
2.52	2.47	0.04	7.92E-01	9.36E-01	---	---	---	231451_s_at	---																			

2.77	2.74	0.03	7.92E-01	9.36E-01	SV2B	synaptic vesicle glycoprotein 2B	chr15q26.1	232426_at	NM_014848
2.03	2.00	0.03	7.92E-01	9.36E-01	---	---	---	1561322_at	---
2.03	2.00	0.03	7.92E-01	9.36E-01	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	chr17q11.1-q12	241811_x_at	NM_001045
6.68	6.63	0.06	7.92E-01	9.36E-01	STIP1	stress-induced-phosphoprotein 1	chr11q13	212009_s_at	NM_006819
3.42	3.38	0.04	7.92E-01	9.36E-01	ASB7	ankyrin repeat and SOCS box-containing 7	---	219996_at	NM_024708 /// NM_198243
8.17	8.05	0.12	7.93E-01	9.36E-01	SFRS3	splicing factor, arginine/serine-rich 3	chr6p21	202899_s_at	NM_003017
2.95	2.91	0.04	7.93E-01	9.36E-01	CUL4A	Cullin 4A	chr13q34	232466_at	NM_001008895 /// NM_003589
6.70	6.63	0.06	7.93E-01	9.36E-01	KIAA0391	KIAA0391	chr14q13.2	202713_s_at	NM_014672
3.93	3.89	0.04	7.93E-01	9.36E-01	FLJ35773	hypothetical protein FLJ35773	chr17p13.1	1552432_at	NM_152599
1.99	1.97	0.03	7.93E-01	9.36E-01	---	---	---	216795_at	---
7.82	7.71	0.11	7.93E-01	9.36E-01	STAMBPL1	STAM binding protein-like 1	chr10q23.31	227607_at	NM_020799
3.51	3.48	0.03	7.93E-01	9.36E-01	---	---	---	1569188_s_at	---
4.66	4.57	0.09	7.93E-01	9.36E-01	TSHZ3	teashirt zinc finger homeobox 3	chr19q12	223393_s_at	NM_020856
2.62	2.58	0.05	7.93E-01	9.36E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	217150_s_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833
2.65	2.60	0.05	7.93E-01	9.36E-01	ZNF124	zinc finger protein 124	chr1q44	206928_at	NM_003431
5.96	5.87	0.08	7.93E-01	9.36E-01	TMEM159	transmembrane protein 159	chr16p12	213272_s_at	NM_020422
2.33	2.28	0.04	7.93E-01	9.36E-01	ERC2	ELKS/RAB6-interacting/CAST family member 2	chr3p14.3	213938_at	NM_015576
3.90	3.81	0.10	7.93E-01	9.36E-01	NHLRC3	NHL repeat containing 3	chr13q13.3	239314_at	NM_001012754 /// NM_001017370
4.03	3.96	0.07	7.93E-01	9.36E-01	FLT3LG	fms-related tyrosine kinase 3 ligand	chr19q13.3	206980_s_at	NM_001459
2.02	1.99	0.03	7.93E-01	9.36E-01	---	---	---	243984_at	---
3.08	3.03	0.05	7.93E-01	9.36E-01	C1orf96	chromosome 1 open reading frame 96	chr1q42.13	1555145_at	NM_145257
4.81	4.76	0.05	7.93E-01	9.36E-01	ZMYM2	zinc finger, MYM-type 2	chr13q11-q12	226512_at	NM_003453 /// NM_197968
2.56	2.53	0.03	7.93E-01	9.36E-01	LOC729397	hypothetical LOC729397	chr1q42.3	236899_at	XM_001716181 /// XM_001716365
6.57	6.51	0.07	7.93E-01	9.36E-01	DHX33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	chr17p13.2	222875_at	NM_020162
5.65	5.47	0.18	7.93E-01	9.36E-01	MSI2	Musashi homolog 2 (Drosophila)	chr17q22	239232_at	NM_138962 /// NM_170721
2.77	2.73	0.04	7.93E-01	9.36E-01	SDK2	sidekick homolog 2 (chicken)	chr17q25.1	242064_at	NM_019064
2.37	2.34	0.03	7.94E-01	9.36E-01	---	---	---	208849_at	---
2.62	2.57	0.05	7.94E-01	9.36E-01	---	---	---	236595_at	---
4.55	4.44	0.11	7.94E-01	9.36E-01	LOC440345 /// LOC641298	hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1	chr16p12.1 /// chr16p12.2	231989_s_at	XR_015786 /// XR_041850
6.53	6.48	0.05	7.94E-01	9.36E-01	SYS1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	chr20q13.12	224670_at	NM_033542
2.12	2.09	0.03	7.94E-01	9.36E-01	---	---	---	244770_at	---

3.26	3.21	0.05	7.94E-01	9.36E-01	TCL1B /// TCL6	T-cell leukemia/lymphoma 1B /// T-cell leukemia/lymphoma 6	chr14q32.1	206413_s_at	NM_004918 /// NM_012468 /// NM_014418 /// NM_020550 /// NM_020552 /// NM_020553 /// NM_020554 /// NM_199206																				
2.59	2.55	0.04	7.94E-01	9.36E-01	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	chr15q21.1	220574_at	NM_020858 /// NM_024966 /// NM_153616 /// NM_153617 /// NM_153618 /// NM_153619																				
2.06	2.03	0.03	7.94E-01	9.36E-01	HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	chrXq24	207307_at	NM_000868																				
6.97	6.78	0.18	7.94E-01	9.36E-01	C10orf116	chromosome 10 open reading frame 116	chr10q23.2	203571_s_at	NM_006829																				
2.03	1.99	0.04	7.94E-01	9.36E-01	AASDHPPT	Aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	chr11q22	224313_at	NM_015423																				
8.09	8.06	0.03	7.94E-01	9.36E-01	SHB /// TOMM5	Src homology 2 domain containing adaptor protein B /// translocase of outer mitochondrial membrane 5 homolog (yeast)	chr9p13.2 /// chr9p13.2-p13.1	225036_at	NM_001001790 /// NM_001134484 /// NM_001134485 /// NM_003028																				
2.99	2.95	0.04	7.94E-01	9.36E-01	---	---	---	240021_at	---																				
4.98	4.92	0.05	7.94E-01	9.36E-01	ZFYVE26	zinc finger, FYVE domain containing 26	chr14q24.1	37943_at	NM_015346																				
2.01	1.98	0.03	7.94E-01	9.36E-01	FLJ21511	hypothetical protein FLJ21511	chr4p12-p11	220724_at	NM_025087																				
8.08	8.04	0.05	7.94E-01	9.36E-01	AFF1	AF4/FMR2 family, member 1	chr4q21	201924_at	NM_005935																				
4.96	4.79	0.17	7.94E-01	9.36E-01	---	---	---	230680_at	---																				
5.54	5.48	0.06	7.95E-01	9.36E-01	SNF1LK2	SNF1-like kinase 2	chr11q23.1	223430_at	NM_015191																				
3.18	3.12	0.05	7.95E-01	9.36E-01	GCC1	GRIP and coiled-coil domain containing 1	chr7q32.1	243306_s_at	NM_024523																				
5.54	5.44	0.10	7.95E-01	9.36E-01	SPIRE1	spire homolog 1 (Drosophila)	chr18p11.21	225018_at	NM_001128626 /// NM_001128627 /// NM_020148																				
6.42	6.36	0.06	7.95E-01	9.36E-01	TPCN1	two pore segment channel 1	chr12q24.13	1557186_s_at	NM_017901																				
8.08	7.98	0.09	7.95E-01	9.36E-01	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	chr7q32	222420_s_at	NM_003344 /// NM_182697																				
6.76	6.66	0.10	7.95E-01	9.36E-01	ZNF330	zinc finger protein 330	chr4q31.1|4q31.1-q31.2	209814_at	NM_014487																				
2.87	2.80	0.07	7.95E-01	9.37E-01	KPNA5	karyopherin alpha 5 (importin alpha 6)	chr6q22.2	206241_at	NM_002269																				
3.47	3.42	0.05	7.95E-01	9.37E-01	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	chr2q35	205852_at	NM_003936																				
2.04	2.00	0.03	7.95E-01	9.37E-01	LAYN	Layilin	chr11q23.1	1556885_at	NM_178834																				
10.70	10.64	0.06	7.95E-01	9.37E-01	FAM20B /// HLA-B /// HLA-C /// LOC730410 /// MICA /// XXbac-BPG181B23.1	family with sequence similarity 20, member B /// major histocompatibility complex, class I, B /// major histocompatibility complex, class I, C /// similar to HLA class I histocompatibility antigen, B-18 alpha chain precursor (MHC class I antigen B*18) /// MHC class I polypeptide-related sequence A /// MHC class I polypeptide-related sequence A	chr1q25 /// chr6p21.3 /// chr6p21.33	211911_x_at	NM_000247 /// NM_002117 /// NM_005514 /// NM_014864 /// XM_001713607 /// XM_001715881 /// XM_001717045 /// XM_001719879 /// XR_037663																				
2.36	2.32	0.05	7.95E-01	9.37E-01	CYP4F8	cytochrome P450, family 4, subfamily F, polypeptide 8	chr19p13.1	210576_at	NM_007253																				

5.23	5.19	0.03	7.95E-01	9.37E-01	---	---	---	227073_at	---
4.63	4.54	0.09	7.95E-01	9.37E-01	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	chr1q32.1	1556203_a_at	NM_001042758 /// NM_015326
1.97	1.94	0.03	7.95E-01	9.37E-01	---	---	---	1563477_at	---
4.60	4.52	0.08	7.95E-01	9.37E-01	TMED7	transmembrane emp24 protein transport domain containing 7	chr5q22.3	214658_at	NM_181836
7.62	7.56	0.06	7.95E-01	9.37E-01	RYBP	RING1 and YY1 binding protein	chr3p13	201846_s_at	NM_012234
3.85	3.79	0.06	7.95E-01	9.37E-01	---	---	---	1556479_at	---
6.43	6.38	0.05	7.95E-01	9.37E-01	UFM1	ubiquitin-fold modifier 1	chr13q13.3	218050_at	NM_016617
2.00	1.96	0.04	7.95E-01	9.37E-01	---	---	---	1561164_at	---
2.24	2.19	0.05	7.95E-01	9.37E-01	DRD3	dopamine receptor D3	chr3q13.3	211625_s_at	NM_000796 /// NM_033663
2.11	2.07	0.03	7.95E-01	9.37E-01	---	---	---	1562406_at	---
5.24	5.17	0.06	7.95E-01	9.37E-01	TRIM61	tripartite motif-containing 61	chr4q32.3	240342_at	NM_001012414
4.64	4.59	0.06	7.96E-01	9.37E-01	SRBD1	S1 RNA binding domain 1	chr2p21	219055_at	NM_018079
1.99	1.96	0.03	7.96E-01	9.37E-01	KCNMB2	potassium large conductance calcium-activated channel, subfamily M, beta member 2	chr3q26.2-q27.1	223823_at	NM_005832 /// NM_181361
4.24	4.16	0.08	7.96E-01	9.37E-01	IL16	interleukin 16 (lymphocyte chemoattractant factor)	chr15q26.3	209827_s_at	NM_004513 /// NM_172217
3.75	3.67	0.09	7.96E-01	9.37E-01	---	---	---	229190_at	---
4.33	4.29	0.04	7.96E-01	9.37E-01	COL7A1	collagen, type VII, alpha 1	chr3p21.1	204136_at	NM_000094
8.05	7.99	0.06	7.96E-01	9.37E-01	FLNA	filamin A, alpha (actin binding protein 280)	chrXq28	200859_x_at	NM_001110556 /// NM_001456
2.39	2.34	0.05	7.96E-01	9.37E-01	LMAN2	Lectin, mannose-binding 2	chr5q35.3	215656_at	NM_006816
2.45	2.42	0.03	7.96E-01	9.37E-01	FLJ41757	Hypothetical gene supported by AF086285; AK123751	chr2p21	1557372_at	---
2.16	2.12	0.04	7.96E-01	9.37E-01	---	---	---	1564964_at	---
2.50	2.43	0.07	7.96E-01	9.37E-01	---	---	---	244434_at	---
2.50	2.45	0.05	7.96E-01	9.37E-01	GABRA4	gamma-aminobutyric acid (GABA) A receptor, alpha 4	chr4p12	208463_at	NM_000809
4.21	4.17	0.04	7.96E-01	9.37E-01	ANKRD24	ankyrin repeat domain 24	chr19p13.3	1558400_x_at	NM_133475
2.42	2.38	0.04	7.96E-01	9.37E-01	GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	chr12p12	206312_at	NM_004963
6.82	6.70	0.12	7.96E-01	9.37E-01	CBX3 /// LOC653972	chromobox homolog 3 (HP1 gamma homolog, Drosophila) /// similar to chromobox homolog 3	chr7p15.2	201091_s_at	NM_007276 /// NM_016587 /// XM_938779
4.55	4.47	0.08	7.96E-01	9.37E-01	RND2	Rho family GTPase 2	chr17q21	213467_at	NM_005440
4.29	4.20	0.09	7.96E-01	9.37E-01	LPCAT4	lysophosphatidylcholine acyltransferase 4	chr15q14	40472_at	NM_153613
7.62	7.53	0.08	7.96E-01	9.37E-01	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	chr1q32.1	212765_at	NM_203459
5.91	5.84	0.07	7.96E-01	9.37E-01	STOML1	stomatin (EPB72)-like 1	chr15q24-q25	33736_at	NM_004809
1.95	1.92	0.03	7.96E-01	9.37E-01	LIPJ	lipase, family member J	chr10q23.31	1569571_at	NM_001010939
2.91	2.88	0.03	7.97E-01	9.37E-01	---	---	---	233515_at	---
2.43	2.39	0.04	7.97E-01	9.37E-01	PCDHGC4	protocadherin gamma subfamily C, 4	chr5q31	231754_at	NM_018928 /// NM_032406
10.76	10.71	0.05	7.97E-01	9.37E-01	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	chr19p13.3	201106_at	NM_001039847 /// NM_001039848 /// NM_002085
4.07	4.02	0.05	7.97E-01	9.37E-01	ANAPC7	anaphase promoting complex subunit 7	chr12q24.11	225521_at	NM_016238
2.77	2.73	0.04	7.97E-01	9.37E-01	---	---	---	1556958_at	---
2.84	2.77	0.07	7.97E-01	9.37E-01	ANUBL1	AN1, ubiquitin-like, homolog (Xenopus laevis)	chr10q11.21	223624_at	NM_001128324 /// NM_174890
2.32	2.27	0.04	7.97E-01	9.37E-01	---	---	---	1563165_at	---
3.05	3.00	0.05	7.97E-01	9.37E-01	ZSCAN10	zinc finger and SCAN domain containing 10	chr16p13.3	1553875_s_at	NM_032805
4.51	4.46	0.05	7.97E-01	9.37E-01	C2orf68	chromosome 2 open reading frame 68	chr2p11.2	221878_at	NM_001013649
5.30	5.22	0.08	7.97E-01	9.37E-01	ALG1	asparagine-linked glycosylation 1 homolog (S. cerevisiae, beta-1,4-mannosyltransferase)	chr16p13.3	223355_at	NM_019109
5.48	5.38	0.09	7.97E-01	9.37E-01	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	chr4q22-q23	223197_s_at	NM_001128429 /// NM_001128430 /// NM_020159
7.52	7.41	0.11	7.97E-01	9.37E-01	AK1	adenylate kinase 1	chr9q34.1	202587_s_at	NM_000476
2.36	2.32	0.04	7.97E-01	9.37E-01	---	---	---	1560264_at	---
2.85	2.81	0.04	7.97E-01	9.37E-01	---	---	---	233674_at	---
3.05	3.01	0.04	7.97E-01	9.37E-01	---	---	---	1557713_at	---

2.41	2.36	0.05	7.97E-01	9.37E-01	NCRNA00052	non-protein coding RNA 52	chr15q25.3	1553226_at	XR_017697 /// XR_017978 /// XR_040916																				
2.15	2.12	0.03	7.97E-01	9.37E-01	---	---	---	242166_at	---																				
2.97	2.94	0.04	7.97E-01	9.37E-01	CENPJ	centromere protein J	chr13q12.12	220885_s_at	NM_018451																				
3.45	3.40	0.05	7.97E-01	9.37E-01	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	chr4p14-p13	40148_at	NM_173075																				
5.25	5.13	0.13	7.97E-01	9.37E-01	ARHGAP5	Rho GTPase activating protein 5	chr14q12	217936_at	NM_001030055 /// NM_001173																				
5.04	4.94	0.10	7.97E-01	9.37E-01	---	---	---	242775_at	---																				
2.17	2.13	0.04	7.97E-01	9.37E-01	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	chr17q23.3	231799_at	NM_025185																				
8.23	8.07	0.17	7.97E-01	9.37E-01	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	chr8q22.1	222572_at	NM_018444																				
2.65	2.62	0.03	7.97E-01	9.37E-01	RASEF	RAS and EF-hand domain containing	chr9q21.32	1553986_at	NM_152573																				
3.88	3.84	0.04	7.98E-01	9.37E-01	---	---	---	241059_at	---																				
2.75	2.70	0.04	7.98E-01	9.37E-01	AGXT	alanine-glyoxylate aminotransferase	chr2q36-q37	210327_s_at	NM_000030																				
3.95	3.88	0.07	7.98E-01	9.37E-01	FNDC5	fibronectin type III domain containing 5	chr1p35.1	226097_at	NM_153756																				
2.96	2.90	0.05	7.98E-01	9.37E-01	ZCCHC3	Zinc finger, CCHC domain containing 3	chr20p13-p12.2	229993_at	NM_033089																				
2.28	2.25	0.03	7.98E-01	9.37E-01	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	chr2q36-q37	216367_at	NM_000091 /// NM_031362 /// NM_031365 /// NM_031366																				
6.78	6.73	0.04	7.98E-01	9.37E-01	C11orf51	chromosome 11 open reading frame 51	chr11q13.4	204218_at	NM_014042																				
3.05	3.00	0.05	7.98E-01	9.37E-01	IMPACT	Impact homolog (mouse)	chr18q11.2-q12.1	218637_at	NM_018439																				
3.24	3.19	0.05	7.98E-01	9.38E-01	WFDC2	WAP four-disulfide core domain 2	chr20q12-q13.2	1552261_at	NM_006103																				
2.06	2.03	0.03	7.98E-01	9.38E-01	---	---	---	1570291_at	---																				
3.46	3.43	0.03	7.98E-01	9.38E-01	DLX2	distal-less homeobox 2	chr2q32	215685_s_at	NM_004405																				
2.51	2.46	0.04	7.98E-01	9.38E-01	HTR1D	5-hydroxytryptamine (serotonin) receptor 1D	chr1p36.3-p34.3	207368_at	NM_000864																				
2.17	2.12	0.05	7.99E-01	9.38E-01	PIK3C2A	Phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	1569588_x_at	NM_002645																				
2.53	2.48	0.05	7.99E-01	9.38E-01	GPM6B	glycoprotein M6B	chrXp22.2	209169_at	NM_001001994 /// NM_001001995 /// NM_001001996 /// NM_005278																				
2.61	2.57	0.04	7.99E-01	9.38E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	1558768_at	NM_015512																				
3.05	3.02	0.03	7.99E-01	9.38E-01	TFDP3	transcription factor Dp family, member 3	chrXq26.2	207385_at	NM_016521																				
4.18	4.01	0.16	7.99E-01	9.38E-01	---	---	---	237849_at	---																				
4.31	4.23	0.09	7.99E-01	9.38E-01	PROX1	prospero homeobox 1	chr1q32.2-q32.3	207401_at	NM_002763																				
4.83	4.54	0.29	7.99E-01	9.38E-01	TSPAN12	tetraspanin 12	chr7q31.31	230626_at	NM_012338																				
2.18	2.14	0.04	7.99E-01	9.38E-01	YAF2	YY1 associated factor 2	chr12q12	244783_at	NM_005748																				
2.31	2.27	0.04	7.99E-01	9.38E-01	TTC22	tetratricopeptide repeat domain 22	chr1p32.3	215107_s_at	NM_001114108 /// NM_017904																				
7.17	7.09	0.08	7.99E-01	9.38E-01	TLK1	tousled-like kinase 1	chr2q31.1	202606_s_at	NM_012290																				
3.09	3.03	0.05	7.99E-01	9.38E-01	---	---	---	216173_at	---																				
5.36	5.29	0.07	7.99E-01	9.38E-01	---	---	---	1568408_x_at	---																				
7.47	7.40	0.07	7.99E-01	9.38E-01	ATRIP /// TREX1	ATR interacting protein /// three prime repair exonuclease 1	chr3p21.31	34689_at	NM_016381 /// NM_032166 /// NM_033629 /// NM_130384																				
2.18	2.15	0.03	7.99E-01	9.38E-01	---	---	---	1570465_at	---																				
2.50	2.46	0.04	7.99E-01	9.38E-01	KIAA0774	KIAA0774	chr13q12.3	1554755_a_at	NM_001033602 /// NM_015233																				
2.04	2.01	0.03	7.99E-01	9.38E-01	---	---	---	242820_at	---																				
3.29	3.24	0.05	7.99E-01	9.38E-01	LOC27320 /// TNRC18	hypothetical protein LOC27320 /// trinucleotide repeat containing 18	chr7p22.1 /// chr7q11.21	242187_s_at	NM_001080495 /// XM_376618 /// XM_499300																				
9.26	9.22	0.04	7.99E-01	9.38E-01	PTTG1IP	pituitary tumor-transforming 1 interacting protein	chr21q22.3	200677_at	NM_004339																				
4.50	4.44	0.06	8.00E-01	9.38E-01	---	---	---	241721_at	---																				
2.70	2.65	0.06	8.00E-01	9.38E-01	FRAS1	Fraser syndrome 1	chr4q21.21	1552503_at	NM_025074																				

2.82	2.78	0.04	8.00E-01	9.38E-01	KRT73	keratin 73	chr12q13.3	237507_at	NM_175068
3.61	3.58	0.03	8.00E-01	9.38E-01	GPR172B	G protein-coupled receptor 172B	chr17p13.2	220756_s_at	NM_001104577 /// NM_017986
3.49	3.45	0.04	8.00E-01	9.39E-01	---	---	---	1562586_at	---
2.60	2.56	0.04	8.00E-01	9.39E-01	---	---	---	230209_at	---
7.85	7.74	0.11	8.00E-01	9.39E-01	CHMP5	chromatin modifying protein 5	chr9p13.3	219356_s_at	NM_016410
2.33	2.30	0.03	8.00E-01	9.39E-01	SLC38A9	Solute carrier family 38, member 9	chr5q11.2	242330_at	NM_173514
2.15	2.12	0.03	8.00E-01	9.39E-01	---	---	---	1570629_at	---
6.69	6.61	0.08	8.00E-01	9.39E-01	STYXL1	serine/threonine/tyrosine interacting-like 1	chr7q11.23	218321_x_at	NM_016086
2.74	2.71	0.03	8.00E-01	9.39E-01	LOC100132319	hypothetical LOC100132319	chr3q28	224526_at	XM_001720974 /// XM_001726632 /// XM_001726742
1.92	1.88	0.04	8.00E-01	9.39E-01	---	---	---	243289_at	---
4.15	4.10	0.05	8.00E-01	9.39E-01	C2orf67	chromosome 2 open reading frame 67	chr2q34	231252_at	NM_152519
8.23	8.18	0.05	8.01E-01	9.39E-01	CHURC1	churchill domain containing 1	chr14q23.3	233268_s_at	NM_145165
7.18	7.13	0.05	8.01E-01	9.39E-01	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	chr3q27.3	223054_at	NM_016306
4.15	4.05	0.10	8.01E-01	9.39E-01	C3orf41	chromosome 3 open reading frame 41	chr3p22.1	228721_at	XM_934352 /// XM_942129
3.51	3.47	0.04	8.01E-01	9.39E-01	CD8B	CD8b molecule	chr2p12	207979_s_at	NM_004931 /// NM_172099 /// NM_172101 /// NM_172102 /// NM_172213
2.14	2.11	0.03	8.01E-01	9.39E-01	---	---	---	1561100_at	---
3.06	3.00	0.06	8.01E-01	9.39E-01	RORB	RAR-related orphan receptor B	chr9q22	206443_at	NM_006914
3.71	3.67	0.04	8.01E-01	9.39E-01	CDK5RAP2	CDK5 regulatory subunit associated protein 2	chr9q33.2	243153_at	NM_001011649 /// NM_018249
1.83	1.80	0.03	8.01E-01	9.39E-01	SLITRK6	SLIT and NTRK-like family, member 6	chr13q31.1	235976_at	NM_032229
5.92	5.84	0.07	8.01E-01	9.39E-01	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	chr1p36.13	206469_x_at	NM_012067
4.67	4.59	0.08	8.01E-01	9.39E-01	---	---	---	236989_at	---
6.13	6.03	0.10	8.01E-01	9.39E-01	PARS2	prolyl-tRNA synthetase 2, mitochondrial (putative)	chr1p32.2	227348_at	NM_152268
3.18	3.13	0.05	8.01E-01	9.39E-01	---	---	---	235078_at	---
3.10	3.05	0.06	8.02E-01	9.39E-01	ZNF267	zinc finger protein 267	chr16p11.2	219540_at	NM_003414
3.38	3.34	0.04	8.02E-01	9.39E-01	ZFP41	zinc finger protein 41 homolog (mouse)	chr8q24.3	237362_at	NM_173832
3.47	3.42	0.05	8.02E-01	9.39E-01	LOC127841	hypothetical protein LOC127841	chr1q32.1	1565554_at	---
2.77	2.73	0.04	8.02E-01	9.39E-01	LIMK2	LIM domain kinase 2	chr22q12.2	217475_s_at	NM_001031801 /// NM_005569 /// NM_016733
2.59	2.55	0.04	8.02E-01	9.39E-01	---	---	---	1559017_at	---
2.80	2.76	0.04	8.02E-01	9.40E-01	---	---	---	1563776_at	---
2.16	2.13	0.03	8.02E-01	9.40E-01	---	---	---	1562036_at	---
2.92	2.87	0.05	8.02E-01	9.40E-01	TCP11L2	T-complex 11 (mouse)-like 2	chr12q23.3	1565000_a_at	NM_152772
5.35	5.28	0.07	8.02E-01	9.40E-01	NR2F2	nuclear receptor subfamily 2, group F, member 2	chr15q26	215073_s_at	NM_021005
2.71	2.68	0.04	8.02E-01	9.40E-01	---	---	---	1559063_at	---
6.52	6.46	0.06	8.03E-01	9.40E-01	PCTK2	PCTAIRE protein kinase 2	chr12q23.1	221918_at	NM_002595
2.14	2.10	0.04	8.03E-01	9.40E-01	SLC25A4	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	chr4q35	1557631_at	NM_001151
4.09	3.98	0.11	8.03E-01	9.40E-01	ETNK1	ethanolamine kinase 1	chr12p12.1	226432_at	NM_001039481 /// NM_018638
2.29	2.26	0.03	8.03E-01	9.40E-01	---	---	---	1563557_at	---
2.56	2.53	0.04	8.03E-01	9.40E-01	---	---	---	1561029_at	---
2.22	2.20	0.03	8.03E-01	9.40E-01	HEPH	hephaestin	chrXq11-q12	203902_at	NM_001130860 /// NM_014799 /// NM_138737
3.84	3.80	0.04	8.03E-01	9.40E-01	C13orf33	Chromosome 13 open reading frame 33	chr13q12.3	1565765_x_at	NM_032849
5.99	5.90	0.09	8.03E-01	9.40E-01	DDHD2	DDHD domain containing 2	chr8p12	212690_at	NM_015214
2.56	2.50	0.05	8.03E-01	9.40E-01	LOC283693 /// LOC648921	actin, gamma pseudogene /// similar to LOC283693 protein	chr15q25.2	1569368_at	XM_001715629 /// XM_001720571 /// XR_018520

2.28	2.25	0.03	8.03E-01	9.40E-01	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	chr4q12	214664_at	NM_001079524 /// NM_001079525 /// NM_006452
5.73	5.44	0.28	8.03E-01	9.40E-01	TSPAN12	tetraspanin 12	chr7q31.31	219274_at	NM_012338
6.35	6.27	0.08	8.03E-01	9.40E-01	MYO1C	myosin IC	chr17p13	225080_at	NM_001080779 /// NM_001080950 /// NM_033375
6.67	6.62	0.04	8.03E-01	9.40E-01	NLN	Neurolysin (metallopeptidase M3 family)	chr5q12.3	234762_x_at	NM_020726
2.50	2.45	0.04	8.03E-01	9.40E-01	LOC642776	hypothetical protein LOC642776	chrXq23	233551_at	XM_001714063 /// XM_001714656 /// XM_001714780
1.88	1.85	0.03	8.04E-01	9.40E-01	---	---	---	1563001_at	---
2.20	2.16	0.04	8.04E-01	9.40E-01	IFNA14	interferon, alpha 14	chr9p22	208182_x_at	NM_002172
4.52	4.46	0.06	8.04E-01	9.40E-01	---	---	---	228963_at	---
6.06	6.02	0.05	8.04E-01	9.40E-01	PINX1	PIN2-interacting protein 1	chr8p23	223907_s_at	NM_017884
2.74	2.69	0.05	8.04E-01	9.40E-01	USP22	Ubiquitin specific peptidase 22	chr17p11.2	216964_at	NM_015276
2.17	2.14	0.03	8.04E-01	9.40E-01	---	---	---	217090_at	---
2.31	2.27	0.04	8.04E-01	9.40E-01	---	---	---	236790_s_at	---
4.91	4.85	0.06	8.04E-01	9.40E-01	MIER2	mesoderm induction early response 1, family member 2	chr19p13.3	44822_s_at	NM_017550
4.56	4.45	0.10	8.04E-01	9.40E-01	MSI2	musashi homolog 2 (Drosophila)	chr17q22	225238_at	NM_138962 /// NM_170721
6.14	6.09	0.05	8.04E-01	9.40E-01	FAM104A	family with sequence similarity 104, member A	chr17q25.1	225319_s_at	NM_001098832 /// NM_032837
6.21	6.14	0.07	8.04E-01	9.40E-01	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	chr1p36.3-p36.2	203508_at	NM_001066
2.37	2.33	0.04	8.04E-01	9.40E-01	---	---	---	236158_at	---
2.03	2.00	0.02	8.04E-01	9.40E-01	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	chr16q12.2	217214_s_at	NM_001043
2.77	2.72	0.05	8.04E-01	9.40E-01	ZNF654	zinc finger protein 654	chr3p11.2	222851_at	NM_018293
3.06	3.00	0.07	8.04E-01	9.40E-01	MAGEL2	MAGE-like 2	chr15q11-q12	219894_at	NM_019066
2.07	2.04	0.04	8.04E-01	9.40E-01	LOC283585	hypothetical LOC283585	chr14q31.3	1561442_at	XR_041535 /// XR_041536 /// XR_041537
5.98	5.84	0.14	8.04E-01	9.40E-01	CXorf15	chromosome X open reading frame 15	chrXp22.2	1557954_at	NM_018360
2.32	2.29	0.03	8.05E-01	9.41E-01	TLR10	toll-like receptor 10	chr4p14	223750_s_at	NM_001017388 /// NM_030956
2.47	2.43	0.04	8.05E-01	9.41E-01	RNASET2	ribonuclease T2	chr6q27	232722_at	NM_003730
2.51	2.47	0.03	8.05E-01	9.41E-01	PMP22CD	PMP22 claudin domain-containing protein	chr11q24.1	244460_at	NM_001013743
4.33	4.26	0.07	8.05E-01	9.41E-01	EWSR1	Ewing sarcoma breakpoint region 1	chr22q12.2	229966_at	NM_005243 /// NM_013986
4.33	4.27	0.06	8.05E-01	9.41E-01	AP4E1	adaptor-related protein complex 4, epsilon 1 subunit	chr15q21.2	228164_at	NM_007347
3.47	3.41	0.06	8.05E-01	9.41E-01	LMX1A	LIM homeobox transcription factor 1, alpha	chr1q22-q23	237595_at	NM_001033507 /// NM_177398 /// NM_177399
1.78	1.75	0.03	8.05E-01	9.41E-01	---	---	---	220837_at	---
4.13	4.04	0.09	8.05E-01	9.41E-01	TSHZ3	teashirt zinc finger homeobox 3	chr19q12	223392_s_at	NM_020856
10.46	10.39	0.07	8.05E-01	9.41E-01	NAP1L1	nucleosome assembly protein 1-like 1	chr12q21.2	208752_x_at	NM_004537 /// NM_139207
2.02	1.99	0.03	8.05E-01	9.41E-01	MYT1L	myelin transcription factor 1-like	chr2p25.3	216672_s_at	NM_015025
4.98	4.83	0.15	8.05E-01	9.41E-01	PLCL2	phospholipase C-like 2	chr3p24.3	216218_s_at	NM_015184
2.19	2.16	0.04	8.05E-01	9.41E-01	SEC61B	Sec61 beta subunit	chr9q22.32-q31.3	244700_at	NM_006808
5.79	5.74	0.05	8.05E-01	9.41E-01	LOC202051	hypothetical protein LOC202051	chr5q31.2	1558641_at	XM_001721173 /// XM_114430 /// XM_940745
1.87	1.84	0.03	8.05E-01	9.41E-01	---	---	---	1558225_at	---
2.21	2.17	0.03	8.05E-01	9.41E-01	USP42	Ubiquitin specific peptidase 42	chr7p22.1	226172_at	NM_032172
4.17	4.12	0.04	8.05E-01	9.41E-01	IGHMBP2	immunoglobulin mu binding protein 2	chr11q13.3	215980_s_at	NM_002180

2.20	2.18	0.02	8.05E-01	9.41E-01	PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	chr7p21-p11.2	224208_at	NM_032639
6.85	6.76	0.09	8.05E-01	9.41E-01	MFAP1	microfibrillar-associated protein 1	chr15q15-q21	203406_at	NM_005926
4.78	4.70	0.07	8.06E-01	9.41E-01	RNPC3	RNA-binding region (RNP1, RRM) containing 3	chr1p21	229903_x_at	NM_017619
3.69	3.64	0.05	8.06E-01	9.41E-01	C1orf183	chromosome 1 open reading frame 183	chr1p13.2	229608_at	NM_019099 /// NM_198926
3.09	3.06	0.04	8.06E-01	9.41E-01	LMX1B	LIM homeobox transcription factor 1, beta	chr9q34	208487_at	NM_002316
4.85	4.77	0.08	8.06E-01	9.41E-01	---	---	---	244574_at	---
3.60	3.57	0.04	8.06E-01	9.41E-01	---	---	---	231605_at	---
2.30	2.27	0.03	8.06E-01	9.41E-01	---	---	---	1560877_a_at	---
2.01	1.98	0.03	8.06E-01	9.41E-01	---	---	---	237836_at	---
2.33	2.30	0.04	8.06E-01	9.41E-01	---	---	---	237415_at	---
3.81	3.71	0.10	8.06E-01	9.41E-01	NUCKS1	Nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	222027_at	NM_022731
3.39	3.33	0.06	8.06E-01	9.41E-01	CALCA	calcitonin-related polypeptide alpha	chr11p15.2-p15.1	217495_x_at	NM_001033952 /// NM_001033953 /// NM_001741
2.23	2.19	0.04	8.06E-01	9.41E-01	---	---	---	1562094_at	---
4.16	4.07	0.09	8.06E-01	9.41E-01	SLC4A3	solute carrier family 4, anion exchanger, member 3	chr2q36	205918_at	NM_005070 /// NM_201574
2.76	2.73	0.03	8.06E-01	9.41E-01	---	---	---	1562056_at	---
2.45	2.42	0.03	8.06E-01	9.41E-01	---	---	---	237301_at	---
3.13	3.08	0.05	8.06E-01	9.41E-01	LOC643749	hypothetical LOC643749	chr6q21	236555_at	XR_041901 /// XR_041902 /// XR_041903
8.93	8.87	0.06	8.06E-01	9.41E-01	PDHB	pyruvate dehydrogenase (lipoamide) beta	chr3p21.1-p14.2	211023_at	NM_000925
5.27	5.16	0.11	8.06E-01	9.41E-01	HIST2H2BE	histone cluster 2, H2be	chr1q21-q23	202708_s_at	NM_003528
1.97	1.94	0.03	8.06E-01	9.41E-01	SUSD5	sushi domain containing 5	chr3p22.3	214954_at	NM_015551
6.29	6.23	0.06	8.06E-01	9.41E-01	ZNF394	zinc finger protein 394	chr7q22.1	214714_at	NM_032164
2.07	2.03	0.04	8.06E-01	9.41E-01	IFI6	Coiled-coil domain containing 42	chr1p35	224533_s_at	NM_002038 /// NM_022872 /// NM_022873
7.31	7.27	0.04	8.07E-01	9.41E-01	ARL2 /// SNX15	ADP-ribosylation factor-like 2 /// sorting nexin 15	chr11q12 /// chr11q13	202564_x_at	NM_001667 /// NM_013306 /// NM_147777
2.57	2.53	0.03	8.07E-01	9.41E-01	ADAM6	ADAM metallopeptidase domain 6	chr14q32.33	237909_at	NR_002224
2.93	2.89	0.04	8.07E-01	9.41E-01	SLC19A1	solute carrier family 19 (folate transporter), member 1	chr21q22.3	209776_s_at	NM_194255
2.22	2.18	0.03	8.07E-01	9.41E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	210771_at	NM_001001928 /// NM_005036
3.96	3.89	0.07	8.07E-01	9.41E-01	RP11-167P23.2	XAGE-4 protein	chrXp11.21	1565454_at	XR_015427 /// XR_040957 /// XR_040958
3.04	2.99	0.06	8.07E-01	9.41E-01	EOMES	eomesodermin homolog (Xenopus laevis)	chr3p21.3-p21.2	231776_at	NM_005442
4.26	4.22	0.04	8.07E-01	9.41E-01	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	chr6p22.3-p22.1	228542_at	NM_020662
2.46	2.43	0.03	8.07E-01	9.41E-01	---	---	---	1557338_x_at	---
5.25	5.16	0.09	8.07E-01	9.41E-01	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	chr12q13	203123_s_at	NM_000617
2.05	2.02	0.03	8.07E-01	9.41E-01	LOC728883	Hypothetical LOC728883	chr10q11.22	1563254_a_at	XM_001127767 /// XM_001128700 /// XM_001715110
2.22	2.18	0.04	8.07E-01	9.41E-01	IPP	intracisternal A particle-promoted polypeptide	chr1p34-p32	1554739_at	NM_005897
5.73	5.66	0.07	8.07E-01	9.41E-01	SLC46A1	solute carrier family 46 (folate transporter), member 1	chr17q11.2	1552279_a_at	NM_080669
4.13	4.03	0.09	8.07E-01	9.41E-01	ADAM17	ADAM metallopeptidase domain 17	chr2p25	205746_s_at	NM_003183
3.24	3.19	0.05	8.07E-01	9.41E-01	CD79B	CD79b molecule, immunoglobulin-associated beta	chr17q23	1555746_at	NM_000626 /// NM_001039933 /// NM_021602
6.25	6.18	0.07	8.07E-01	9.41E-01	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	chr20q13.33	224612_s_at	NM_025219
2.73	2.69	0.04	8.07E-01	9.42E-01	COL4A4	Collagen, type IV, alpha 4	chr2q35-q37	241565_at	NM_000092

2.67	2.62	0.04	8.07E-01	9.42E-01	GTSE1	G-2 and S-phase expressed 1	chr22q13.2-q13.3	204318_s_at	NM_016426																				
4.06	4.00	0.06	8.07E-01	9.42E-01	---	---	---	235437_at	---																				
2.69	2.65	0.04	8.08E-01	9.42E-01	---	---	---	239379_at	---																				
4.73	4.67	0.06	8.08E-01	9.42E-01	LOC27320 /// TNRC18	hypothetical protein LOC27320 /// trinucleotide repeat containing 18	chr7p22.1 /// chr7q11.21	1562896_at	NM_001080495 /// XM_376618 /// XM_499300																				
2.23	2.19	0.04	8.08E-01	9.42E-01	LOC285548	hypothetical LOC285548	chr4p15.33	236112_at	XM_001721233 /// XM_001722093 /// XM_001723165																				
2.33	2.30	0.04	8.08E-01	9.42E-01	---	---	---	237966_at	---																				
4.15	4.11	0.04	8.08E-01	9.42E-01	QSOX2	quiescin Q6 sulfhydryl oxidase 2	chr9q34.3	235239_at	NM_181701																				
6.04	5.92	0.11	8.08E-01	9.42E-01	CDKN1C	Cyclin-dependent kinase inhibitor 1C (p57, Kip2)	chr11p15.5	213183_s_at	NM_000076 /// NM_001122630 /// NM_001122631																				
2.11	2.07	0.03	8.08E-01	9.42E-01	---	---	---	233659_at	---																				
2.44	2.40	0.04	8.08E-01	9.42E-01	---	---	---	242934_at	---																				
2.49	2.45	0.05	8.08E-01	9.42E-01	KCNN3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	chr1q21.3	205903_s_at	NM_002249 /// NM_170782																				
6.07	6.01	0.06	8.08E-01	9.42E-01	YIPF5	Yip1 domain family, member 5	chr5q32	224953_at	NM_001024947 /// NM_030799																				
2.75	2.71	0.04	8.08E-01	9.42E-01	ZNF366	zinc finger protein 366	chr5q13.2|5q13.2	236570_at	NM_152625																				
4.21	4.13	0.08	8.08E-01	9.42E-01	ECSM2	endothelial cell-specific molecule 2	chr5q31.2	228339_at	NM_001077693																				
8.31	8.26	0.06	8.08E-01	9.42E-01	GAS5	growth arrest-specific 5 (non-protein coding)	chr1q25.1	224841_x_at	NR_002578																				
7.29	7.21	0.08	8.08E-01	9.42E-01	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	chr5q11.2-q13.1	202168_at	NM_001015891 /// NM_001015892 /// NM_003187 /// NM_016283																				
2.56	2.51	0.05	8.08E-01	9.42E-01	TM9SF3	Transmembrane 9 superfamily member 3	chr10q24.1	228610_at	NM_020123																				
4.15	4.09	0.07	8.08E-01	9.42E-01	ZNF709	zinc finger protein 709	chr19p13.2	242028_at	NM_152601																				
4.24	4.20	0.05	8.09E-01	9.42E-01	C1orf190	chromosome 1 open reading frame 190	chr1p34	235214_at	NM_001013615																				
3.59	3.55	0.03	8.09E-01	9.42E-01	ADCY5	Adenylate cyclase 5	chr3q13.2-q21	242891_at	NM_183357																				
7.42	7.35	0.07	8.09E-01	9.42E-01	RAD21	RAD21 homolog (S. pombe)	chr8q24	200608_s_at	NM_006265																				
3.71	3.64	0.07	8.09E-01	9.42E-01	ZNF839	Zinc finger protein 839	chr14q32.31	230223_at	NM_018335																				
4.59	4.54	0.05	8.09E-01	9.42E-01	ZSWIM3	zinc finger, SWIM-type containing 3	chr20q13.12	228223_at	NM_080752																				
2.50	2.47	0.03	8.09E-01	9.42E-01	---	---	---	1569666_s_at	---																				
5.48	5.43	0.05	8.09E-01	9.42E-01	AP3D1	adaptor-related protein complex 3, delta 1 subunit	chr19p13.3	208710_s_at	NM_001077523 /// NM_003938																				
3.82	3.78	0.04	8.09E-01	9.42E-01	---	---	---	232086_at	---																				
3.37	3.33	0.04	8.09E-01	9.42E-01	KLHL17	kelch-like 17 (Drosophila)	chr1p36.33	1555650_at	NM_198317																				
2.31	2.28	0.03	8.09E-01	9.42E-01	---	---	---	231439_at	---																				
1.93	1.91	0.03	8.09E-01	9.42E-01	---	---	---	1560890_at	---																				
2.26	2.23	0.03	8.09E-01	9.42E-01	FGFBP2	fibroblast growth factor binding protein 2	chr4p16	223836_at	NM_031950																				
3.11	3.07	0.04	8.10E-01	9.42E-01	RNF112	ring finger protein 112	chr17p11.2	223603_at	NM_007148																				
2.58	2.52	0.05	8.10E-01	9.42E-01	KRTCAP2	keratinocyte associated protein 2	chr1q22	233122_at	NM_173852																				
3.05	3.02	0.03	8.10E-01	9.42E-01	CIB2	calcium and integrin binding family member 2	chr15q24	214065_s_at	NM_006383																				
10.30	10.25	0.04	8.10E-01	9.42E-01	MTCH1	mitochondrial carrier homolog 1 (C. elegans)	chr6pter-p24.1	221619_s_at	NM_014341																				
2.36	2.32	0.03	8.10E-01	9.42E-01	WFDC9	WAP four-disulfide core domain 9	chr20q12-q13.1	1552415_a_at	NM_147198																				
2.22	2.19	0.03	8.10E-01	9.42E-01	---	---	---	243903_at	---																				
2.34	2.30	0.03	8.10E-01	9.42E-01	LOC100131402	hypothetical protein LOC100131402	chr1q32.1	1565867_a_at	XM_001725069 /// XM_001726819																				
5.73	5.64	0.09	8.10E-01	9.42E-01	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	chr17q11.2	224956_at	NM_020772																				
2.22	2.19	0.04	8.10E-01	9.42E-01	KIAA1430	KIAA1430	chr4q35.1	230567_at	NM_020827																				
3.93	3.87	0.05	8.10E-01	9.43E-01	MBIP	MAP3K12 binding inhibitory protein 1	chr14q13.3	218411_s_at	NM_016586																				
5.37	5.33	0.04	8.10E-01	9.43E-01	LRFN4	leucine rich repeat and fibronectin type III domain containing 4	chr11q13.1	219491_at	NM_024036																				
3.52	3.44	0.08	8.10E-01	9.43E-01	DOK3	docking protein 3	chr5q35.3	223553_s_at	NM_024872																				

2.54	2.51	0.03	8.10E-01	9.43E-01	IKZF2	IKAROS family zinc finger 2 (Helios)	chr2q34	220567_at	NM_001079526 /// NM_016260																				
8.69	8.56	0.12	8.10E-01	9.43E-01	CD46	CD46 molecule, complement regulatory protein	chr1q32	208783_s_at	NM_002389 /// NM_153826 /// NM_172350 /// NM_172351 /// NM_172352 /// NM_172353 /// NM_172354 /// NM_172355 /// NM_172356 /// NM_172357 /// NM_172358 /// NM_172359 /// NM_172360 /// NM_172361																		
3.88	3.85	0.03	8.10E-01	9.43E-01	LOC644450	hypothetical protein LOC644450	chr1q12	215625_at	XM_927590																				
2.02	1.99	0.03	8.10E-01	9.43E-01	---	---	---	1554865_at	---																				
6.33	6.27	0.06	8.11E-01	9.43E-01	MTO1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	chr6q13	218716_x_at	NM_001123226 /// NM_012123 /// NM_133645																				
4.85	4.70	0.15	8.11E-01	9.43E-01	EML4	echinoderm microtubule associated protein like 4	chr2p22-p21	220386_s_at	NM_019063																				
2.50	2.45	0.05	8.11E-01	9.43E-01	ARHGAP8 /// LOC553158 /// PRR5	Rho GTPase activating protein 8 /// PRR5-ARHGAP8 fusion /// proline rich 5 (renal)	chr22q13 /// chr22q13.31	205980_s_at	NM_001017526 /// NM_001017528 /// NM_001017529 /// NM_001017530 /// NM_015366 /// NM_181333 /// NM_181334 /// NM_181335																				
2.76	2.72	0.04	8.11E-01	9.43E-01	IQCF3	IQ motif containing F3	chr3p21.1	1555235_s_at	NM_001085479																				
2.05	2.03	0.03	8.11E-01	9.43E-01	COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	chr4q21.22	237649_at	NM_016129																				
1.94	1.91	0.03	8.11E-01	9.43E-01	---	---	---	1569494_at	---																				
3.13	3.09	0.04	8.11E-01	9.43E-01	BREA2	breast cancer estrogen-induced apoptosis 2	chr8q24.3	241475_at	XR_040172 /// XR_040173 /// XR_040174																				
11.72	11.69	0.03	8.11E-01	9.43E-01	ACTG1	actin, gamma 1	chr17q25	213214_x_at	NM_001614																				
3.31	3.21	0.09	8.11E-01	9.43E-01	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	chr18q12.2	1555202_a_at	NM_018170																				
5.05	5.01	0.04	8.11E-01	9.43E-01	PRKCI	protein kinase C, iota	chr3q26.3	213518_at	NM_002740																				
2.10	2.06	0.04	8.11E-01	9.43E-01	---	---	---	237841_at	---																				
2.41	2.37	0.03	8.11E-01	9.43E-01	---	---	---	216259_at	---																				

3.28	3.24	0.04	8.11E-01	9.43E-01	GAGE1 /// GAGE12F /// GAGE12G /// GAGE12I /// GAGE12J /// GAGE2A /// GAGE2B /// GAGE2E /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7	G antigen 1 /// G antigen 12F /// G antigen 12G /// G antigen 12I /// G antigen 12J /// G antigen 2A /// G antigen 2B /// G antigen 2E /// G antigen 4 /// G antigen 5 /// G antigen 6 /// G antigen 7	chrXp11.23 /// chrXp11.4-p11.2	208155_x_at	NM_001040663 /// NM_001098405 /// NM_001098406 /// NM_001098409 /// NM_001098411 /// NM_001127200 /// NM_001127212 /// NM_001468 /// NM_001474 /// NM_001475 /// NM_001476 /// NM_001477 /// NM_021123 /// XM_001130991																			
3.83	3.76	0.07	8.11E-01	9.43E-01	FXYD3	FXYD domain containing ion transport regulator 3	chr19q13.11-q13.12	202488_s_at	NM_005971 /// NM_021910																				
4.61	4.56	0.05	8.11E-01	9.43E-01	TRIM3	tripartite motif-containing 3	chr11p15.5	213885_at	NM_006458 /// NM_033278																				
2.01	1.98	0.03	8.11E-01	9.43E-01	RP11-756A22.3	Hypothetical LOC646405	chr13q12.12-q12.13	1562582_at	NM_001126062 /// XM_001722635 /// XM_929331 /// XM_940374																				
3.04	2.99	0.05	8.12E-01	9.43E-01	---	---	---	244474_at	---																				
3.10	3.07	0.03	8.12E-01	9.43E-01	CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11p11	235865_at	NM_001025596 /// NM_006560 /// NM_198700																				
2.93	2.89	0.03	8.12E-01	9.43E-01	---	---	---	217382_at	---																				
2.05	2.02	0.03	8.12E-01	9.43E-01	---	---	---	234289_x_at	---																				
1.97	1.94	0.03	8.12E-01	9.43E-01	FLJ30838	hypothetical gene supported by AL832565	chr2p16.1	1557472_a_at	XM_379096 /// XM_934421 /// XM_945691 /// XM_945693																				
4.75	4.67	0.07	8.12E-01	9.44E-01	LHFP	Lipoma HMGIC fusion partner	chr13q12	231411_at	NM_005780																				
2.84	2.80	0.04	8.12E-01	9.44E-01	---	---	---	222058_at	---																				
4.79	4.71	0.08	8.12E-01	9.44E-01	VPS37A	vacuolar protein sorting 37 homolog A (S. cerevisiae)	chr8p22	225378_at	NM_152415																				
2.79	2.75	0.04	8.12E-01	9.44E-01	---	---	---	1557810_at	---																				
2.21	2.18	0.03	8.12E-01	9.44E-01	LOC100132025	Putative transmembrane domain-containing protein ENSP00000320207	chr15q11.2	1561170_at	XM_001723658																				
2.05	2.01	0.03	8.12E-01	9.44E-01	---	---	---	1559685_at	---																				
3.81	3.75	0.06	8.13E-01	9.44E-01	PKN3	protein kinase N3	chr9q34.11	226299_at	NM_013355																				
3.20	3.12	0.08	8.13E-01	9.44E-01	LOC100131741	hypothetical protein LOC100131741	chr19q13.12	242462_at	XM_001720402 /// XM_001722412																				
4.84	4.80	0.04	8.13E-01	9.44E-01	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	chr15q24	218964_at	NM_006465																				
4.52	4.48	0.04	8.13E-01	9.44E-01	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	chr13q14.2	219347_at	NM_018283																				
3.23	3.20	0.03	8.13E-01	9.44E-01	---	---	---	1566268_at	---																				
2.23	2.21	0.03	8.13E-01	9.44E-01	---	---	---	1563170_at	---																				
3.44	3.40	0.03	8.13E-01	9.44E-01	---	---	---	243604_at	---																				
2.75	2.73	0.03	8.13E-01	9.44E-01	---	---	---	243866_x_at	---																				

3.90	3.85	0.05	8.13E-01	9.44E-01	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	chr1q32.1	214398_s_at	NM_014002																				
1.96	1.94	0.03	8.13E-01	9.44E-01	---	---	---	1561789_at	---																				
4.07	4.04	0.03	8.13E-01	9.44E-01	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	chr3p21.3	205455_at	NM_002447																				
7.42	7.34	0.08	8.13E-01	9.44E-01	LIMA1	LIM domain and actin binding 1	chr12q13	217892_s_at	NM_001113546 /// NM_001113547 /// NM_016357																				
2.44	2.40	0.04	8.13E-01	9.44E-01	RP1-27O5.1	zinc finger and BTB domain containing 8-like	chr1p35.1	1563770_at	XR_040711 /// XR_040712 /// XR_040713																				
1.92	1.90	0.03	8.13E-01	9.44E-01	WDR49	WD repeat domain 49	chr3q26.1	1554298_a_at	NM_178824																				
3.49	3.46	0.03	8.13E-01	9.44E-01	TFDP1	transcription factor Dp-1	chr13q34	242939_at	NM_007111																				
3.80	3.75	0.05	8.13E-01	9.44E-01	ADCY2 /// LOC100133953	adenylate cyclase 2 (brain) /// similar to adenylate cyclase 2	chr5p15.3	213217_at	NM_020546 /// XM_001717432																				
4.33	4.28	0.05	8.13E-01	9.44E-01	---	---	---	1566195_at	---																				
2.61	2.58	0.03	8.13E-01	9.44E-01	---	---	---	232703_at	---																				
5.35	5.27	0.08	8.13E-01	9.44E-01	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	chr12q24.12-q24.13	212871_at	NM_003668 /// NM_139078																				
5.04	4.98	0.06	8.13E-01	9.44E-01	EIF4E	eukaryotic translation initiation factor 4E	chr4q21-q25	201437_s_at	NM_001130678 /// NM_001130679 /// NM_001968																				
1.95	1.92	0.03	8.13E-01	9.44E-01	CSMD3	CUB and Sushi multiple domains 3	chr8q23.3	240228_at	NM_052900 /// NM_198123 /// NM_198124																				
11.29	11.25	0.03	8.14E-01	9.44E-01	RPL13	ribosomal protein L13	chr16q24.3|17p11.2	212933_x_at	NM_000977 /// NM_033251																				
1.94	1.91	0.03	8.14E-01	9.44E-01	---	---	---	1564547_x_at	---																				
4.79	4.74	0.05	8.14E-01	9.44E-01	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	chr12q24	1555323_at	NM_019624 /// NM_019625 /// NM_203444																				
2.38	2.33	0.05	8.14E-01	9.44E-01	SSFA2	sperm specific antigen 2	chr2q31.3	236207_at	NM_001130445 /// NM_006751																				
5.37	5.30	0.07	8.14E-01	9.44E-01	SH3BP5L	SH3-binding domain protein 5-like	chr1q44	223265_at	NM_030645																				
2.70	2.67	0.03	8.14E-01	9.44E-01	---	---	---	227503_at	---																				
3.82	3.77	0.04	8.14E-01	9.44E-01	SNX25	sorting nexin 25	chr4q35.1	1555388_s_at	NM_031953																				
2.86	2.82	0.04	8.14E-01	9.44E-01	---	---	---	1563019_at	---																				
5.17	5.12	0.05	8.14E-01	9.44E-01	C16orf7	chromosome 16 open reading frame 7	chr16q24	205781_at	NM_004913																				
2.05	2.01	0.03	8.14E-01	9.44E-01	ENPP6	ectonucleotide pyrophosphatase/phosphodiesterase 6	chr4q35.1	229916_at	NM_153343																				
3.30	3.25	0.05	8.14E-01	9.45E-01	GFRA3	GDNF family receptor alpha 3	chr5q31.1-q31.3	229936_at	NM_001496																				
3.52	3.48	0.04	8.14E-01	9.45E-01	RNF215	ring finger protein 215	chr22q12.2	234461_at	NM_001017981																				
2.76	2.71	0.04	8.14E-01	9.45E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	224016_at	NM_001113239 /// NM_022740																				
3.40	3.35	0.05	8.14E-01	9.45E-01	LOC401351	hypothetical gene supported by BC040831	chr7q11.21	240999_at	XM_379843 /// XM_926596 /// XM_935479 /// XM_935792 /// XM_938438 /// XM_943672																				
12.85	12.83	0.03	8.14E-01	9.45E-01	TPT1	tumor protein, translationally-controlled 1	chr13q12-q14	216520_s_at	NM_003295																				

3.11	3.05	0.05	8.14E-01	9.45E-01	SNX16	sorting nexin 16	chr8q21.13	229618_at	NM_022133 /// NM_152836 /// NM_152837																				
2.37	2.34	0.03	8.14E-01	9.45E-01	---	---	---	AFFX-TrpnX-M_at	---																				
3.09	3.05	0.04	8.14E-01	9.45E-01	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	chr3q28-q29	1556538_at	NM_005929 /// NM_033316																				
4.83	4.77	0.05	8.14E-01	9.45E-01	CCDC126	coiled-coil domain containing 126	chr7p15.3	228087_at	NM_138771																				
2.14	2.10	0.04	8.14E-01	9.45E-01	FAM9A	family with sequence similarity 9, member A	chrXp22.32	1555133_at	NM_174951																				
2.06	2.03	0.03	8.15E-01	9.45E-01	---	---	---	243419_at	---																				
2.80	2.77	0.03	8.15E-01	9.45E-01	KLHL22	Kelch-like 22 (Drosophila)	chr22q11.21	221948_s_at	NM_032775																				
2.41	2.38	0.04	8.15E-01	9.45E-01	C21orf123	chromosome 21 open reading frame 123	chr21q22.3	1564017_at	NM_199175																				
2.88	2.83	0.05	8.15E-01	9.45E-01	SLFN5	schlafen family member 5	chr17q12	1553055_a_at	NM_144975																				
5.42	5.32	0.10	8.15E-01	9.45E-01	---	---	---	233506_at	---																				
2.34	2.31	0.03	8.15E-01	9.45E-01	---	---	---	234563_at	---																				
2.69	2.65	0.04	8.15E-01	9.45E-01	ZNF654	zinc finger protein 654	chr3p11.2	241348_at	NM_018293																				
2.24	2.21	0.03	8.15E-01	9.45E-01	DPY19L2 /// DPY19L2P1 /// DPY19L2P2 /// DPY19L2P4	dpy-19-like 2 (C. elegans) /// dpy-19-like 2 pseudogene 1 (C. elegans) /// dpy-19-like 2 pseudogene 2 (C. elegans) /// dpy-19-like 2 pseudogene 4 (C. elegans)	chr12q14.2 /// chr7p14.2 /// chr7q21.13 /// chr7q22.1	1557290_at	NM_173812 /// NR_002833 /// NR_003551 /// NR_003561																			
2.31	2.28	0.03	8.15E-01	9.45E-01	---	---	---	244714_at	---																				
4.95	4.91	0.04	8.15E-01	9.45E-01	WDR55	WD repeat domain 55	chr5q31.3	223833_at	NM_017706																				
2.29	2.26	0.03	8.15E-01	9.45E-01	NUP153	nucleoporin 153kDa	chr6p22.3	239948_at	NM_005124																				
6.64	6.59	0.05	8.15E-01	9.45E-01	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	chr7q22	202185_at	NM_001084																				
9.42	9.37	0.05	8.15E-01	9.45E-01	DCTN2	dynactin 2 (p50)	chr12q13.2-q13.3	200932_s_at	NM_006400																				
3.28	3.24	0.04	8.15E-01	9.45E-01	---	---	---	241491_at	---																				
2.42	2.38	0.04	8.15E-01	9.45E-01	RASGEF1B	RasGEF domain family, member 1B	chr4q21.21-q21.22	1554999_at	NM_152545																				
4.58	4.51	0.07	8.15E-01	9.45E-01	MLH3	mutL homolog 3 (E. coli)	chr14q24.3	204838_s_at	NM_001040108 /// NM_014381																				
1.96	1.93	0.03	8.15E-01	9.45E-01	FLJ37644	Hypothetical gene supported by AK094963	chr17q24.3	1564466_at	XM_001126807 /// XM_001134151 /// XM_001725777																				
1.84	1.81	0.02	8.15E-01	9.45E-01	ZNF292	zinc finger protein 292	chr6q15	1562991_at	NM_015021																				
2.20	2.16	0.04	8.15E-01	9.45E-01	VSTM2A	V-set and transmembrane domain containing 2A	chr7p11.2	1554530_at	NM_182546																				
7.87	7.82	0.06	8.15E-01	9.45E-01	TMEM165	transmembrane protein 165	chr4q12	226825_s_at	NM_018475																				
5.45	5.38	0.08	8.16E-01	9.45E-01	EXOSC8	exosome component 8	chr13q13.1	215136_s_at	NM_181503																				
2.39	2.34	0.05	8.16E-01	9.45E-01	OR2A20P /// OR2A5 /// OR2A9P	olfactory receptor, family 2, subfamily A, member 20 pseudogene /// olfactory receptor, family 2, subfamily A, member 5 /// olfactory receptor, family 2, subfamily A, member 9 pseudogene	chr7q35	223971_at	NM_012365 /// NR_002157 /// NR_002158																				
2.55	2.51	0.04	8.16E-01	9.45E-01	---	---	---	240558_at	---																				
1.97	1.94	0.03	8.16E-01	9.45E-01	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	chrXq26.2	230030_at	NM_001077188 /// NM_147175																				
4.70	4.62	0.08	8.16E-01	9.45E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	208234_x_at	NM_000141 /// NM_022970																				
6.40	6.33	0.07	8.16E-01	9.45E-01	WDR12	WD repeat domain 12	chr2q33.1	218512_at	NM_018256																				
6.18	6.11	0.07	8.16E-01	9.45E-01	FBXO11	F-box protein 11	chr2p16.3	222119_s_at	NM_012167 /// NM_018693 /// NM_025133																				
3.10	3.03	0.07	8.16E-01	9.45E-01	---	---	---	240195_at	---																				
3.50	3.41	0.09	8.16E-01	9.45E-01	SP1	Sp1 transcription factor	chr12q13.1	1553685_s_at	NM_138473																				
5.24	5.20	0.05	8.16E-01	9.45E-01	GFOD2	glucose-fructose oxidoreductase domain containing 2	chr16q22.1	221028_s_at	NM_030819																				
1.96	1.93	0.03	8.16E-01	9.45E-01	AQP4	aquaporin 4	chr18q11.2-q12.1	210066_s_at	NM_001650 /// NM_004028																				
1.98	1.96	0.02	8.16E-01	9.45E-01	EIF1B	Eukaryotic translation initiation factor 1B	chr3p22.1	237988_at	NM_005875																				
2.31	2.28	0.03	8.17E-01	9.46E-01	EPHA5	EPH receptor A5	chr4q13.1	215664_s_at	NM_004439 /// NM_182472																				
8.15	7.65	0.50	8.17E-01	9.46E-01	XIST	X (inactive)-specific transcript (non-protein coding)	chrXq13.2	224588_at	NR_001564																				

4.75	4.70	0.05	8.17E-01	9.46E-01	EBP	emopamil binding protein (sterol isomerase)	chrXp11.23-p11.22	231320_at	NM_006579
3.04	2.99	0.05	8.17E-01	9.46E-01	---	---	---	1566924_at	---
3.09	3.07	0.03	8.17E-01	9.46E-01	---	---	---	1570013_at	---
2.23	2.20	0.03	8.17E-01	9.46E-01	---	---	---	232668_at	---
4.57	4.47	0.10	8.17E-01	9.46E-01	MYEF2	myelin expression factor 2	chr15q21.1	222771_s_at	NM_016132
2.15	2.12	0.02	8.17E-01	9.46E-01	NPVF	neuropeptide VF precursor	chr7p21-p15	221322_at	NM_022150
2.95	2.92	0.04	8.17E-01	9.46E-01	---	---	---	235662_at	---
3.06	3.02	0.04	8.17E-01	9.46E-01	---	---	---	1566278_at	---
2.08	2.05	0.03	8.17E-01	9.46E-01	COL2A1	collagen, type II, alpha 1	chr12q13.11	213492_at	NM_001844 /// NM_033150
2.24	2.20	0.04	8.17E-01	9.46E-01	---	---	---	1569785_at	---
7.52	7.44	0.08	8.17E-01	9.46E-01	EPM2AIP1	EPM2A (laforin) interacting protein 1	chr3p22.1	227847_at	NM_014805
2.03	2.01	0.02	8.17E-01	9.46E-01	IDS	iduronate 2-sulfatase	chrXq28	211782_at	NM_000202 /// NM_006123
4.21	4.17	0.03	8.18E-01	9.46E-01	FAM125B	family with sequence similarity 125, member B	chr9q33.3	221687_s_at	NM_001011703 /// NM_033446
2.62	2.58	0.04	8.18E-01	9.46E-01	---	---	---	227206_at	---
3.21	3.18	0.04	8.18E-01	9.46E-01	HIST1H4L	histone cluster 1, H4l	chr6p22-p21.3	214562_at	NM_003546
4.66	4.60	0.06	8.18E-01	9.46E-01	---	---	---	226855_at	---
5.53	5.49	0.04	8.18E-01	9.46E-01	SLC35C1	solute carrier family 35, member C1	chr11p11.2	218485_s_at	NM_018389
2.41	2.38	0.03	8.18E-01	9.46E-01	BMP15	bone morphogenetic protein 15	chrXp11.2	221332_at	NM_005448
3.01	2.97	0.04	8.18E-01	9.46E-01	MYH11	myosin, heavy chain 11, smooth muscle	chr16p13.11	228134_at	NM_001040113 /// NM_001040114 /// NM_002474 /// NM_022844
2.35	2.31	0.04	8.18E-01	9.46E-01	---	---	---	1557515_at	---
5.19	5.13	0.06	8.18E-01	9.46E-01	KIAA2018	KIAA2018	chr3q13.2	227433_at	NM_001009899
5.42	5.37	0.05	8.18E-01	9.46E-01	HIST1H2BD	histone cluster 1, H2bd	chr6p21.3	222067_x_at	NM_021063 /// NM_138720
1.92	1.90	0.03	8.18E-01	9.46E-01	SLC26A7	solute carrier family 26, member 7	chr8q23	239006_at	NM_052832 /// NM_134266
4.06	4.01	0.04	8.18E-01	9.46E-01	TBL1X	transducin (beta)-like 1X-linked	chrXp22.3	201867_s_at	NM_005647
6.61	6.55	0.06	8.18E-01	9.46E-01	RAB3D	RAB3D, member RAS oncogene family	chr19p13.2	225001_at	NM_004283
6.24	6.18	0.06	8.18E-01	9.46E-01	SURF6	surfeit 6	chr9q34.2	225038_s_at	NM_006753
3.44	3.41	0.03	8.18E-01	9.46E-01	---	---	---	1566473_a_at	---
2.39	2.36	0.03	8.18E-01	9.46E-01	---	---	---	222296_at	---
4.02	3.98	0.04	8.18E-01	9.46E-01	LOC653390 /// RRN3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene /// RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	chr16p11.2 /// chr16p12	230328_at	NM_018427 /// NR_003369
8.30	8.25	0.05	8.18E-01	9.46E-01	CAPZB	capping protein (actin filament) muscle Z-line, beta	chr1p36.1	201949_x_at	NM_004930
2.76	2.72	0.04	8.18E-01	9.46E-01	CD5L	CD5 molecule-like	chr1q21-q23	206680_at	NM_005894
3.16	3.12	0.04	8.18E-01	9.46E-01	---	---	---	241294_at	---
2.22	2.19	0.03	8.18E-01	9.46E-01	---	---	---	241901_at	---
4.17	4.07	0.10	8.18E-01	9.46E-01	---	---	---	225567_at	---
2.59	2.54	0.05	8.18E-01	9.46E-01	GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	chr19q13.1-qter	207036_x_at	NM_000836
3.92	3.88	0.05	8.18E-01	9.46E-01	SNRP70	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	chr19q13.3	213121_at	NM_003089
2.29	2.25	0.04	8.18E-01	9.46E-01	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)	chr7q31.3	210536_s_at	NM_003117 /// NM_153189
2.43	2.40	0.03	8.18E-01	9.46E-01	KRT6B	keratin 6B	chr12q12-q13	213680_at	NM_005555
1.97	1.94	0.03	8.18E-01	9.46E-01	---	---	---	237961_at	---
5.61	5.54	0.08	8.18E-01	9.46E-01	SLC4A1AP	solute carrier family 4 (anion exchanger), member 1, adaptor protein	chr2p23.2	1558201_s_at	NM_018158
2.09	2.07	0.03	8.18E-01	9.46E-01	SMR3A /// SMR3B	submaxillary gland androgen regulated protein 3A /// submaxillary gland androgen regulated protein 3B	chr4q13.3	214566_at	NM_006685 /// NM_012390
2.62	2.59	0.04	8.18E-01	9.46E-01	---	---	---	239239_at	---
2.83	2.80	0.03	8.18E-01	9.46E-01	DPYSL5	dihydropyrimidinase-like 5	chr2p23.3	222797_at	NM_020134
2.70	2.67	0.04	8.18E-01	9.46E-01	CCDC11	coiled-coil domain containing 11	chr18q21.1	1552326_a_at	NM_145020
4.68	4.62	0.05	8.19E-01	9.46E-01	POLR1A	polymerase (RNA) I polypeptide A, 194kDa	chr2p11.2	222704_at	NM_015425
1.98	1.95	0.03	8.19E-01	9.46E-01	---	---	---	234014_at	---
4.24	4.19	0.05	8.19E-01	9.46E-01	---	---	---	1570569_at	---
2.90	2.85	0.04	8.19E-01	9.46E-01	---	---	---	243369_at	---
2.27	2.25	0.03	8.19E-01	9.46E-01	---	---	---	1570537_a_at	---
3.46	3.42	0.03	8.19E-01	9.46E-01	FLOT1	Flotillin 1	chr6p21.3	213819_s_at	NM_005803

2.49	2.46	0.03	8.19E-01	9.46E-01	UBE3B	Ubiquitin protein ligase E3B	chr12q24.11	227914_s_at	NM_130466 /// NM_183415
4.15	4.11	0.04	8.19E-01	9.46E-01	---	---	---	220905_at	---
4.11	4.06	0.05	8.19E-01	9.46E-01	LOC340107	hypothetical protein LOC340107	chr5p14.1	1557008_at	---
3.04	2.97	0.08	8.19E-01	9.46E-01	CA12	carbonic anhydrase XII	chr15q22	203963_at	NM_001218 /// NM_206925
2.22	2.19	0.03	8.19E-01	9.46E-01	LOC731477	hypothetical protein LOC731477	---	237312_at	XM_001133171 /// XM_001724134
3.16	3.07	0.09	8.19E-01	9.46E-01	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15q22.1	207016_s_at	NM_003888 /// NM_170696 /// NM_170697
2.09	2.05	0.04	8.19E-01	9.46E-01	ADRB1	adrenergic, beta-1-, receptor	chr10q24-q26	229309_at	NM_000684
10.23	10.15	0.07	8.19E-01	9.46E-01	C9orf16	chromosome 9 open reading frame 16	chr9q34.1	41047_at	NM_024112
2.63	2.60	0.03	8.19E-01	9.46E-01	KCNE3	potassium voltage-gated channel, Isk-related family, member 3	chr11q13-q14	222922_at	NM_005472
2.34	2.31	0.03	8.19E-01	9.46E-01	C9orf100	chromosome 9 open reading frame 100	chr9p13.3	230521_at	NM_032818
1.98	1.95	0.02	8.19E-01	9.46E-01	---	---	---	1560899_at	---
5.51	5.47	0.04	8.20E-01	9.46E-01	C20orf166	chromosome 20 open reading frame 166	chr20q13.33	232892_at	NM_178463
7.15	7.09	0.06	8.20E-01	9.46E-01	HIST1H2BK	histone cluster 1, H2bk	chr6p21.33	209806_at	NM_080593
3.66	3.59	0.07	8.20E-01	9.46E-01	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	chr3q12.1	213355_at	NM_006100
2.45	2.41	0.05	8.20E-01	9.46E-01	LAMP3	lysosomal-associated membrane protein 3	chr3q26.3-q27	205569_at	NM_014398
1.92	1.90	0.02	8.20E-01	9.46E-01	---	---	---	1560791_at	---
10.96	10.92	0.04	8.20E-01	9.46E-01	HLA-C	major histocompatibility complex, class I, C	chr6p21.3	208812_x_at	NM_002117 /// XM_001715881 /// XM_001717045 /// XM_001719879
3.42	3.35	0.07	8.20E-01	9.46E-01	TEK	TEK tyrosine kinase, endothelial	chr9p21	217711_at	NM_000459
5.94	5.88	0.06	8.20E-01	9.46E-01	JARID1B	jumonji, AT rich interactive domain 1B	chr1q32.1	201548_s_at	NM_006618
2.66	2.63	0.03	8.20E-01	9.46E-01	---	---	---	240944_at	---
2.11	2.08	0.03	8.20E-01	9.47E-01	---	---	---	1566582_x_at	---
2.31	2.28	0.02	8.20E-01	9.47E-01	PHLDB2 /// PLCXD2	pleckstrin homology-like domain, family B, member 2 /// phosphatidylinositol-specific phospholipase C, X domain containing 2	chr3q13.2	238419_at	NM_001134437 /// NM_001134438 /// NM_001134439 /// NM_001134478 /// NM_145753 /// NM_153268
2.57	2.54	0.03	8.20E-01	9.47E-01	---	---	---	216146_at	---
5.61	5.53	0.08	8.20E-01	9.47E-01	BLOC1S3	biogenesis of lysosomal organelles complex-1, subunit 3	chr19q13.32	228244_at	NM_212550
2.32	2.28	0.04	8.21E-01	9.47E-01	C8orf83	chromosome 8 open reading frame 83	chr8q22.1	224158_s_at	NR_015339 /// XR_041349 /// XR_041350 /// XR_041351
3.23	3.20	0.03	8.21E-01	9.47E-01	---	---	---	231580_at	---
2.13	2.10	0.03	8.21E-01	9.47E-01	---	---	---	241678_at	---
2.59	2.57	0.03	8.21E-01	9.47E-01	---	---	---	243517_at	---
7.12	7.00	0.12	8.21E-01	9.47E-01	---	---	---	238619_at	---
5.32	5.24	0.08	8.21E-01	9.47E-01	---	---	---	242972_at	---
6.78	6.74	0.04	8.21E-01	9.47E-01	RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr15q15.1	212302_at	NM_015138
2.99	2.95	0.04	8.21E-01	9.47E-01	---	---	---	1559205_s_at	---
6.15	6.11	0.04	8.21E-01	9.47E-01	FLJ20021	hypothetical LOC90024	chr4q23	228832_at	XM_001717455 /// XM_028217 /// XM_944210
7.47	7.44	0.03	8.21E-01	9.47E-01	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	chrXq13	204571_x_at	NM_006223
5.53	5.40	0.13	8.21E-01	9.47E-01	FNDC5	fibronectin type III domain containing 5	chr1p35.1	226096_at	NM_153756
5.58	5.46	0.12	8.21E-01	9.47E-01	WBP4	WW domain binding protein 4 (formin binding protein 21)	chr13q14.11	203599_s_at	NM_007187

2.42	2.38	0.04	8.21E-01	9.47E-01	SOX14	SRY (sex determining region Y)-box 14	chr3q22-q23	208574_at	NM_004189
3.19	3.16	0.03	8.21E-01	9.47E-01	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	chr1q25.2	232112_at	NM_018037 /// NM_152663
3.68	3.63	0.05	8.21E-01	9.47E-01	OLFM2	olfactomedin 2	chr19p13.2	223601_at	NM_058164
6.67	6.59	0.08	8.21E-01	9.47E-01	TMEM204	transmembrane protein 204	chr16p13.3	219315_s_at	NM_024600
3.82	3.75	0.07	8.21E-01	9.47E-01	---	---	---	235093_at	---
2.52	2.47	0.05	8.21E-01	9.47E-01	PFN4	profilin family, member 4	chr2p23.3	1557476_at	NM_199346
2.59	2.54	0.05	8.21E-01	9.47E-01	FZD8	frizzled homolog 8 (Drosophila)	chr10p11.21	224325_at	NM_031866
9.51	9.46	0.05	8.21E-01	9.47E-01	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	chr7cen-q22	209036_s_at	NM_005918
2.09	2.06	0.03	8.21E-01	9.47E-01	---	---	---	234420_at	---
5.34	5.29	0.05	8.21E-01	9.47E-01	---	---	---	229121_at	---
3.29	3.26	0.03	8.21E-01	9.47E-01	---	---	---	241422_at	---
1.96	1.93	0.03	8.21E-01	9.47E-01	---	---	---	1566487_at	---
5.08	4.97	0.11	8.22E-01	9.47E-01	---	---	---	242907_at	---
2.26	2.23	0.03	8.22E-01	9.47E-01	LAMA1	laminin, alpha 1	chr18p11.31	227048_at	NM_005559
2.41	2.38	0.04	8.22E-01	9.47E-01	C1orf46	chromosome 1 open reading frame 46	chr1q21.3	216718_at	---
2.07	2.04	0.02	8.22E-01	9.47E-01	ARHGAP27 /// LOC201175	Rho GTPase activating protein 27 /// hypothetical protein LOC201175	chr17q21.31	1554594_at	NM_174919 /// NM_199282
2.32	2.28	0.04	8.22E-01	9.47E-01	FASTKD2	FAST kinase domains 2	chr2q33.3	205976_at	NM_014929
6.38	6.32	0.07	8.22E-01	9.47E-01	---	---	---	226343_at	---
2.30	2.27	0.03	8.22E-01	9.47E-01	RNASE7	ribonuclease, RNase A family, 7	chr14q11.2	234700_s_at	NM_032572
7.34	7.23	0.11	8.22E-01	9.47E-01	PRSS23	protease, serine, 23	chr11q14.1	202458_at	NM_007173
2.46	2.43	0.03	8.22E-01	9.47E-01	RNASET2	ribonuclease T2	chr6q27	1568977_at	NM_003730
3.77	3.71	0.05	8.22E-01	9.47E-01	RUNX3	runt-related transcription factor 3	chr1p36	204198_s_at	NM_001031680 /// NM_004350
2.42	2.38	0.04	8.22E-01	9.47E-01	CNOT4	CCR4-NOT transcription complex, subunit 4	chr7q22-qter	210866_s_at	NM_001008225 /// NM_013316
2.45	2.42	0.03	8.22E-01	9.47E-01	ZCCHC4	zinc finger, CCHC domain containing 4	chr4p15.2	220472_at	NM_024936
2.38	2.35	0.03	8.23E-01	9.47E-01	---	---	---	215234_at	---
5.00	4.93	0.07	8.23E-01	9.47E-01	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	chr6p22.3-p22.1	218538_s_at	NM_020662
6.50	6.44	0.06	8.23E-01	9.47E-01	KIAA0652	KIAA0652	chr11p11.2	209021_x_at	NM_014741
6.76	6.72	0.05	8.23E-01	9.47E-01	GBA /// GBAP	glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid, pseudogene	chr1q21	210589_s_at	NM_000157 /// NM_001005741 /// NM_001005742 /// NM_001005749 /// NM_001005750 /// NR_002188 /// XR_042183
4.36	4.30	0.06	8.23E-01	9.47E-01	---	---	---	222284_at	---
7.15	7.11	0.04	8.23E-01	9.47E-01	CCDC127	coiled-coil domain containing 127	chr5p15.33	226515_at	NM_145265
2.65	2.62	0.03	8.23E-01	9.47E-01	FKBP15	FK506 binding protein 15, 133kDa	chr9q32	76897_s_at	NM_015258
6.41	6.37	0.05	8.23E-01	9.47E-01	ZC3H7B	zinc finger CCCH-type containing 7B	chr22q13.2	205877_s_at	NM_017590
3.41	3.34	0.07	8.23E-01	9.48E-01	RBM6	RNA binding motif protein 6	chr3p21.3	230742_at	NM_005777
2.84	2.80	0.03	8.23E-01	9.48E-01	LOC339524	hypothetical protein LOC339524	chr1p22.3	235870_at	XR_039940 /// XR_039941 /// XR_039942
3.49	3.46	0.03	8.23E-01	9.48E-01	SLC1A7	solute carrier family 1 (glutamate transporter), member 7	chr1p32.3	243623_at	NM_006671
2.28	2.25	0.03	8.23E-01	9.48E-01	COL2A1	collagen, type II, alpha 1	chr12q13.11	217404_s_at	NM_001844 /// NM_033150
2.43	2.39	0.04	8.23E-01	9.48E-01	ZNF507	zinc finger protein 507	chr19q13.11	206225_at	NM_014910
2.99	2.95	0.04	8.23E-01	9.48E-01	ZMAT4	zinc finger, matrin type 4	chr8p11.21	219877_at	NM_024645
2.43	2.40	0.03	8.23E-01	9.48E-01	XKRX	XK, Kell blood group complex subunit-related, X-linked	chrXq22.1	230349_at	NM_212559
2.35	2.33	0.02	8.23E-01	9.48E-01	---	---	---	237130_at	---
3.29	3.22	0.07	8.23E-01	9.48E-01	GPR160	G protein-coupled receptor 160	chr3q26.2-q27	223423_at	NM_014373

2.22	2.19	0.03	8.23E-01	9.48E-01	AURKA	aurora kinase A	chr20q13.2-q13.3	208080_at	NM_003600 /// NM_198433 /// NM_198434 /// NM_198435 /// NM_198436 /// NM_198437																				
2.07	2.04	0.03	8.23E-01	9.48E-01	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	chr6p22.3-p22.2	215554_at	NM_001503 /// NM_177483																				
2.21	2.18	0.03	8.24E-01	9.48E-01	ARMC2	armadillo repeat containing 2	chr6q21	223866_at	NM_032131																				
3.88	3.85	0.03	8.24E-01	9.48E-01	FAM27E1 /// FAM27E2 /// FAM27E3	family with sequence similarity 27, member E1 /// family with sequence similarity 27, member E2 /// family with sequence similarity 27, member E3	chr9p11.2 /// chr9q12	1553590_at	NM_001013404 /// NM_001024608 /// XM_001720463																				
3.72	3.68	0.04	8.24E-01	9.48E-01	TSSK3	Testis-specific serine kinase 3	chr1p35-p34	228451_at	NM_052841																				
1.97	1.95	0.02	8.24E-01	9.48E-01	AQP4	aquaporin 4	chr18q11.2-q12.1	210906_x_at	NM_001650 /// NM_004028																				
3.40	3.35	0.05	8.24E-01	9.48E-01	LOC730236	hypothetical LOC730236	chr13q21.32	241471_at	XM_001133153 /// XM_001714412 /// XM_001715647																				
2.13	2.09	0.04	8.24E-01	9.48E-01	TMEM156	transmembrane protein 156	chr4p14	241844_x_at	NM_024943																				
2.34	2.31	0.03	8.24E-01	9.48E-01	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	chr1p36.1	235780_at	NM_002731 /// NM_182948 /// NM_207578																				
2.06	2.04	0.03	8.24E-01	9.48E-01	---	---	---	241562_x_at	---																				
2.39	2.35	0.03	8.24E-01	9.48E-01	USPL1	ubiquitin specific peptidase like 1	chr13q12-q14	1562238_at	NM_005800																				
4.67	4.62	0.05	8.24E-01	9.48E-01	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	chr16p12.1	238995_at	NM_001055 /// NM_177529 /// NM_177530 /// NM_177534 /// NM_177536																				
2.70	2.67	0.03	8.24E-01	9.48E-01	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	chr10q22.2	229701_at	NM_015190																				
2.29	2.26	0.03	8.24E-01	9.48E-01	---	---	---	1562165_at	---																				
2.26	2.23	0.03	8.24E-01	9.48E-01	TRIM7	tripartite motif-containing 7	chr5q35.3	239694_at	NM_033342 /// NM_203293 /// NM_203294 /// NM_203295 /// NM_203296 /// NM_203297																				
2.16	2.14	0.02	8.24E-01	9.48E-01	---	---	---	236202_at	---																				
2.63	2.60	0.04	8.24E-01	9.48E-01	SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	chr10q25	205857_at	NM_003054																				
3.24	3.19	0.05	8.24E-01	9.48E-01	RP11-345P4.4 /// SLC35E2	similar to solute carrier family 35, member E2 /// solute carrier family 35, member E2	chr1p36.33	215169_at	NM_001110781 /// NM_182838 /// XM_001717735																				
5.40	5.35	0.05	8.25E-01	9.48E-01	CTF1	cardiotrophin 1	chr16p11.2-p11.1	206813_at	NM_001330																				
5.49	5.42	0.07	8.25E-01	9.48E-01	CD2AP	CD2-associated protein	chr6p12	203593_at	NM_012120																				

2.77	2.73	0.04	8.25E-01	9.48E-01	CSHL1	chorionic somatomammotropin hormone-like 1	chr17q24.2	208295_x_at	NM_001318 /// NM_022579 /// NM_022580 /// NM_022581																				
6.41	6.26	0.16	8.25E-01	9.48E-01	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	chr5q23.1	215028_at	NM_020796																				
4.19	4.16	0.03	8.25E-01	9.48E-01	LOC647310	Hypothetical LOC647310	chr14q32.33	1558581_at	XM_930381																				
3.02	2.97	0.05	8.25E-01	9.48E-01	FAM44A	family with sequence similarity 44, member A	chr4p16.1	242594_at	NM_148894																				
4.29	4.20	0.09	8.25E-01	9.48E-01	---	---	---	226311_at	---																				
2.71	2.68	0.03	8.25E-01	9.48E-01	---	---	---	238745_at	---																				
3.73	3.68	0.05	8.25E-01	9.48E-01	DGCR6L	DiGeorge syndrome critical region gene 6-like	chr22q11	214024_s_at	NM_033257																				
4.42	4.37	0.05	8.25E-01	9.48E-01	---	---	---	230039_at	---																				
6.33	6.25	0.08	8.25E-01	9.48E-01	CD47	CD47 molecule	chr3q13.1-q13.2	226016_at	NM_001025079 /// NM_001777 /// NM_198793																				
4.61	4.56	0.05	8.25E-01	9.48E-01	---	---	---	241215_at	---																				
5.62	5.50	0.12	8.25E-01	9.48E-01	PRAGMIN	homolog of rat pragma of Rnd2	chr8p23.1	235085_at	NM_001080826																				
2.51	2.47	0.04	8.25E-01	9.48E-01	ZNF673 /// ZNF674	zinc finger family member 673 /// zinc finger family member 674	chrXp11.3	1554465_s_at	NM_001039891 /// NM_001129898 /// NM_001129899 /// NM_001129900 /// NM_017776																				
2.69	2.65	0.04	8.25E-01	9.48E-01	LOC642808	similar to RAD52 motif 1	chr17q12-q21.2	1564050_at	XM_926215																				
2.27	2.24	0.03	8.25E-01	9.48E-01	LOC727842	hypothetical LOC727842	chr6p11.1	217015_at	XR_015140 /// XR_037713 /// XR_037796																				
3.93	3.89	0.04	8.25E-01	9.48E-01	TTLL3	tubulin tyrosine ligase-like family, member 3	chr3p25.3	1555475_x_at	NM_001025930 /// NM_015644																				
3.14	3.11	0.03	8.25E-01	9.48E-01	GPR52	G protein-coupled receptor 52	chr1q24	221313_at	NM_005684																				
2.18	2.14	0.05	8.26E-01	9.48E-01	---	---	---	239539_at	---																				
2.10	2.08	0.02	8.26E-01	9.48E-01	---	---	---	1567333_at	---																				
2.11	2.08	0.03	8.26E-01	9.48E-01	---	---	---	241271_at	---																				
2.66	2.63	0.03	8.26E-01	9.48E-01	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	chrXp22.1-p21.3	222963_s_at	NM_014271																				
5.77	5.70	0.08	8.26E-01	9.48E-01	TP53	tumor protein p53	chr17p13.1	201746_at	NM_000546 /// NM_001126112 /// NM_001126113 /// NM_001126114 /// NM_001126115 /// NM_001126116 /// NM_001126117																				
4.88	4.85	0.03	8.26E-01	9.48E-01	TGFBRAP1	transforming growth factor, beta receptor associated protein 1	chr2q12.1-q12.2	205210_at	NM_004257																				
2.03	2.00	0.03	8.26E-01	9.48E-01	BRCA2	breast cancer 2, early onset	chr13q12.3	214727_at	NM_000059																				
3.25	3.21	0.03	8.26E-01	9.48E-01	---	---	---	1566955_at	---																				
3.83	3.74	0.08	8.26E-01	9.48E-01	PAPOLG	poly(A) polymerase gamma	chr2p16.1	224427_s_at	NM_022894																				
3.07	3.02	0.05	8.26E-01	9.48E-01	LOC388630	hypothetical LOC388630	chr1p33	244472_at	XM_001132797 /// XM_001717552 /// XM_371250																				
2.95	2.91	0.04	8.26E-01	9.48E-01	DOPEY1	dopey family member 1	chr6q15	40612_at	NM_015018																				
2.54	2.50	0.04	8.26E-01	9.48E-01	---	---	---	1558122_s_at	---																				
3.16	3.11	0.05	8.26E-01	9.49E-01	COL18A1	collagen, type XVIII, alpha 1	chr21q22.3	1555953_at	NM_030582 /// NM_130445																				

4.83	4.76	0.06	8.26E-01	9.49E-01	RFX2	regulatory factor X, 2 (influences HLA class II expression)	chr19p13.3-p13.2	208031_s_at	NM_000635 /// NM_134433																				
4.91	4.84	0.07	8.26E-01	9.49E-01	SIGIRR	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	chr11p15.5	52940_at	NM_021805																				
5.96	5.91	0.05	8.26E-01	9.49E-01	E2F4	E2F transcription factor 4, p107/p130-binding	chr16q21-q22	202248_at	NM_001950																				
8.05	7.97	0.08	8.26E-01	9.49E-01	GABARAPL1 /// GABARAPL3	GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associated protein like 3 (pseudogene)	chr12p13.2 /// chr15q26.1	211458_s_at	NM_031412																				
7.48	7.39	0.09	8.26E-01	9.49E-01	KLHL7	kelch-like 7 (Drosophila)	chr7p15.3	223250_at	NM_001031710 /// NM_018846																				
3.05	2.99	0.06	8.26E-01	9.49E-01	---	---	---	243303_at	---																				
2.54	2.52	0.02	8.26E-01	9.49E-01	LOC340074	hypothetical protein LOC340074	chr5q31.1	1562617_at	---																				
2.58	2.53	0.04	8.26E-01	9.49E-01	SFTPD	surfactant protein D	chr10q22.2-q23.1	214199_at	NM_003019																				
4.70	4.64	0.06	8.26E-01	9.49E-01	SRP72	signal recognition particle 72kDa	chr4q11	208802_at	NM_006947																				
2.30	2.27	0.03	8.26E-01	9.49E-01	CRABP1	Cellular retinoic acid binding protein 1	chr15q24	1563897_at	NM_004378																				
3.98	3.89	0.09	8.26E-01	9.49E-01	RNFT1	ring finger protein, transmembrane 1	chr17q23.1	221194_s_at	NM_016125																				
2.90	2.84	0.05	8.26E-01	9.49E-01	---	---	---	242440_at	---																				
3.89	3.84	0.05	8.26E-01	9.49E-01	CEP57	centrosomal protein 57kDa	chr11q21	203493_s_at	NM_014679																				
2.67	2.64	0.03	8.27E-01	9.49E-01	C21orf22	chromosome 21 open reading frame 22	chr21q22.3	1560881_a_at	NR_024028																				
3.25	3.22	0.04	8.27E-01	9.49E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	1563809_a_at	NM_001112732 /// NM_024979																				
2.37	2.34	0.03	8.27E-01	9.49E-01	LOC645513	Hypothetical LOC645513	chr4q26-q27	1561761_x_at	XM_001714125 /// XM_001714854 /// XM_001717939																				
2.68	2.65	0.04	8.27E-01	9.49E-01	FLJ39061	hypothetical protein FLJ39061	chr2q33.1	1564193_at	XR_040657 /// XR_040658 /// XR_040659																				
4.71	4.66	0.05	8.27E-01	9.49E-01	NFYC	nuclear transcription factor Y, gamma	chr1p32|1p32	1559218_s_at	NM_014223																				
1.75	1.72	0.03	8.27E-01	9.49E-01	---	---	---	234601_x_at	---																				
3.20	3.14	0.06	8.27E-01	9.49E-01	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	chr12q	204817_at	NM_012291																				
4.76	4.70	0.06	8.27E-01	9.49E-01	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	chr20q11.22-q11.23	217094_s_at	NM_031483																				
7.11	7.04	0.07	8.27E-01	9.49E-01	---	---	---	225725_at	---																				
2.57	2.54	0.03	8.27E-01	9.49E-01	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	chr15q15	203755_at	NM_001211																				
2.19	2.17	0.02	8.27E-01	9.49E-01	OTX2	orthodenticle homeobox 2	chr14q21-q22	231731_at	NM_021728 /// NM_172337																				
2.40	2.37	0.03	8.27E-01	9.49E-01	---	---	---	231515_at	---																				
1.95	1.92	0.03	8.27E-01	9.49E-01	DMBX1	diencephalon/mesencephalon homeobox 1	chr1p33	234776_at	NM_147192 /// NM_172225																				
4.82	4.76	0.06	8.27E-01	9.49E-01	KLF12	Kruppel-like factor 12	chr13q22	227261_at	NM_007249																				
3.82	3.77	0.05	8.27E-01	9.49E-01	METTL3	methyltransferase like 3	chr14q11.1	242111_at	NM_019852																				
5.99	5.90	0.09	8.27E-01	9.49E-01	REPS2	RALBP1 associated Eps domain containing 2	chrXp22.2	205645_at	NM_001080975 /// NM_004726																				
2.19	2.17	0.02	8.27E-01	9.49E-01	---	---	---	1562893_at	---																				
2.28	2.25	0.03	8.27E-01	9.49E-01	ACOT6	acyl-CoA thioesterase 6	chr14q24.3	241949_at	NM_001037162																				
3.07	3.04	0.04	8.27E-01	9.49E-01	MKI67	antigen identified by monoclonal antibody Ki-67	chr10q25-qter	212021_s_at	NM_002417																				
1.99	1.96	0.02	8.27E-01	9.49E-01	---	---	---	1562122_at	---																				
5.16	5.10	0.06	8.27E-01	9.49E-01	REC8	REC8 homolog (yeast)	chr14q11.2-q12	218599_at	NM_001048205 /// NM_005132																				
4.88	4.83	0.05	8.27E-01	9.49E-01	TPSG1	tryptase gamma 1	chr16p13.3	220339_s_at	NM_012467																				
2.01	1.99	0.03	8.28E-01	9.49E-01	FCRL4	Fc receptor-like 4	chr1q21	224403_at	NM_031282																				
6.76	6.72	0.04	8.28E-01	9.49E-01	ITFG1	Integrin alpha FG-GAP repeat containing 1	chr16q12.1	1556151_at	NM_030790																				
7.04	6.97	0.08	8.28E-01	9.49E-01	ARL1	ADP-ribosylation factor-like 1	chr12q23.2	201659_s_at	NM_001177																				
2.54	2.51	0.03	8.28E-01	9.49E-01	FAM59B	family with sequence similarity 59, member B	chr2p23.3	232015_at	XR_041887 /// XR_041888 /// XR_041889																				
5.98	5.91	0.06	8.28E-01	9.49E-01	SASH1	SAM and SH3 domain containing 1	chr6q24.3	41644_at	NM_015278																				
4.81	4.77	0.05	8.28E-01	9.49E-01	PEX14	peroxisomal biogenesis factor 14	chr1p36.22	203503_s_at	NM_004565																				
5.32	5.25	0.07	8.28E-01	9.49E-01	SLC39A4	solute carrier family 39 (zinc transporter), member 4	chr8q24.3	219215_s_at	NM_017767 /// NM_130849																				

2.27	2.23	0.04	8.28E-01	9.49E-01	PPP3R2	protein phosphatase 3 (formerly 2B), regulatory subunit B, beta isoform	chr9q31.1	231304_at	NM_147180																				
2.34	2.31	0.03	8.28E-01	9.49E-01	WDR16	WD repeat domain 16	chr17p13.1	239916_at	NM_001080556 /// NM_145054																				
4.57	4.54	0.03	8.28E-01	9.49E-01	RG9MTD3	RNA (guanine-9-) methyltransferase domain containing 3	chr9p13.2	240166_x_at	NM_144964																				
8.83	8.78	0.05	8.28E-01	9.49E-01	LUZP6 /// MTPN	leucine zipper protein 6 /// myotrophin	chr7q33	224656_s_at	NM_001128619 /// NM_145808																				
2.09	2.06	0.03	8.28E-01	9.49E-01	---	---	---	242906_at	---																				
2.09	2.06	0.03	8.28E-01	9.49E-01	C1orf173	chromosome 1 open reading frame 173	chr1p31.1	243753_at	NM_001002912																				
4.24	4.21	0.04	8.28E-01	9.49E-01	---	---	---	231278_at	---																				
2.60	2.57	0.03	8.28E-01	9.49E-01	PDLIM7	PDZ and LIM domain 7 (enigma)	chr5q35.3	1569149_at	NM_005451 /// NM_203352 /// NM_213636																				
7.18	7.12	0.05	8.28E-01	9.49E-01	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	chr9q34	206452_x_at	NM_021131 /// NM_178000 /// NM_178001 /// NM_178003																				
2.17	2.15	0.02	8.28E-01	9.49E-01	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7	chr2q24.2	1555316_a_at	NM_033272 /// NM_173162																				
1.95	1.92	0.02	8.28E-01	9.49E-01	MEGF11	multiple EGF-like-domains 11	chr15q22.31	1552439_s_at	NM_032445																				
6.45	6.37	0.07	8.28E-01	9.49E-01	TMEM8	transmembrane protein 8 (five membrane-spanning domains)	chr16p13.3	221882_s_at	NM_021259																				
6.72	6.69	0.04	8.28E-01	9.49E-01	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	chr17q21	200987_x_at	NM_005789 /// NM_176863																				
1.94	1.92	0.02	8.29E-01	9.49E-01	---	---	---	243885_x_at	---																				
2.59	2.56	0.03	8.29E-01	9.49E-01	CREB3L2	CAMP responsive element binding protein 3-like 2	chr7q34	237819_at	NM_194071																				
5.51	5.42	0.09	8.29E-01	9.49E-01	TEAD2	TEA domain family member 2	chr19q13.3	226408_at	NM_003598																				
2.50	2.46	0.04	8.29E-01	9.49E-01	GTF2H1	General transcription factor IIH, polypeptide 1, 62kDa	chr11p15.1-p14	242656_at	NM_005316																				
1.99	1.96	0.03	8.29E-01	9.49E-01	---	---	---	241587_at	---																				
4.78	4.72	0.05	8.29E-01	9.49E-01	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	chr1q32.1	204549_at	NM_014002																				
3.18	3.14	0.03	8.29E-01	9.49E-01	PDCD2	Programmed cell death 2	chr6q27	213585_s_at	NM_002598 /// NM_144781																				
8.24	8.02	0.22	8.29E-01	9.49E-01	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	chr14q24.3	209189_at	NM_005252																				
2.52	2.48	0.03	8.29E-01	9.49E-01	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	chrXq21	220737_at	NM_014496																				
5.08	5.03	0.05	8.29E-01	9.50E-01	---	---	---	239549_at	---																				
2.70	2.67	0.03	8.29E-01	9.50E-01	LOC51233	hypothetical protein LOC51233	chr22q11.2	237325_at	NM_016449																				
5.93	5.87	0.06	8.30E-01	9.50E-01	PUSL1	pseudouridylate synthase-like 1	chr1p36.33	228733_at	NM_153339																				
2.62	2.60	0.03	8.30E-01	9.50E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	217260_x_at	---																				
2.38	2.35	0.03	8.30E-01	9.50E-01	---	---	---	213516_at	---																				
4.10	4.00	0.10	8.30E-01	9.50E-01	REG3G	regenerating islet-derived 3 gamma	chr2p12	231661_at	NM_001008387 /// NM_198448																				
4.54	4.45	0.10	8.30E-01	9.50E-01	IFI44	interferon-induced protein 44	chr1p31.1	214453_s_at	NM_006417																				
2.98	2.95	0.04	8.30E-01	9.50E-01	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	chr7p15.3	1555371_at	NM_178559																				
2.64	2.60	0.04	8.30E-01	9.50E-01	ACSM5	acyl-CoA synthetase medium-chain family member 5	chr16p12.3	1554514_at	NM_017888																				
2.27	2.24	0.03	8.30E-01	9.50E-01	PPEF1	protein phosphatase, EF-hand calcium binding domain 1	chrXp22.2-p22.1	206547_s_at	NM_006240 /// NM_152224 /// NM_152226																				
1.90	1.88	0.03	8.30E-01	9.50E-01	POU2F1	POU class 2 homeobox 1	chr1q22-q23	244006_at	NM_002697																				
2.93	2.89	0.03	8.30E-01	9.50E-01	TLR8	toll-like receptor 8	chrXp22	229560_at	NM_138636																				
2.30	2.27	0.03	8.30E-01	9.50E-01	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	chr10p12.1	1554571_at	NM_019043																				
4.16	4.12	0.04	8.30E-01	9.50E-01	PTPN21	protein tyrosine phosphatase, non-receptor type 21	chr14q31.3	226380_at	NM_007039																				
2.45	2.41	0.04	8.30E-01	9.50E-01	IQCF3	IQ motif containing F3	chr3p21.1	236871_s_at	NM_001085479																				
2.40	2.36	0.04	8.30E-01	9.50E-01	ASCL1	achaete-scute complex homolog 1 (Drosophila)	chr12q23.2	209988_s_at	NM_004316																				
2.27	2.25	0.02	8.30E-01	9.50E-01	---	---	---	243822_at	---																				
2.39	2.35	0.03	8.30E-01	9.50E-01	---	---	---	239956_at	---																				
3.92	3.88	0.04	8.31E-01	9.50E-01	HDAC5	histone deacetylase 5	chr17q21	229408_at	NM_001015053 /// NM_005474																				
4.98	4.94	0.04	8.31E-01	9.50E-01	---	---	---	1565662_at	---																				

2.16	2.14	0.02	8.31E-01	9.50E-01	---	---	---	244372_at	---
3.03	2.99	0.04	8.31E-01	9.50E-01	---	---	---	234404_at	---
3.36	3.33	0.03	8.31E-01	9.50E-01	PSCA	prostate stem cell antigen	chr8q24.2	205319_at	NM_005672
3.93	3.88	0.04	8.31E-01	9.50E-01	ICOSLG	inducible T-cell co-stimulator ligand	chr21q22.3	211197_s_at	NM_015259
2.38	2.36	0.03	8.31E-01	9.50E-01	---	---	---	239003_at	---
3.51	3.45	0.05	8.31E-01	9.50E-01	TRIM32	tripartite motif-containing 32	chr9q33.1	236233_at	NM_001099679 /// NM_012210
6.51	6.48	0.03	8.31E-01	9.50E-01	RP5-1077B9.4	invasion inhibitory protein 45	chr1p36.22	218551_at	NM_021933
2.14	2.12	0.02	8.31E-01	9.50E-01	POLR2B	Polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	chr4q12	1555836_at	NM_000938
4.40	4.35	0.05	8.31E-01	9.50E-01	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	chr2q33.1	222604_at	NM_012086
4.21	4.16	0.05	8.31E-01	9.50E-01	KIAA1908	KIAA1908 protein	chr7p22.3	1561666_a_at	NR_021487 /// XM_001716897 /// XM_001720885 /// XM_001721044 /// XM_001722511
7.07	6.97	0.10	8.31E-01	9.50E-01	ZNF521	zinc finger protein 521	chr18q11.2	226676_at	NM_015461
5.03	4.89	0.14	8.31E-01	9.50E-01	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	chr7q21.1	214235_at	NM_000777
2.02	1.99	0.02	8.31E-01	9.50E-01	KCNC1	potassium voltage-gated channel, Shaw-related subfamily, member 1	chr11p15	230547_at	NM_001112741 /// NM_004976
8.74	8.65	0.09	8.31E-01	9.50E-01	IMPAD1	inositol monophosphatase domain containing 1	chr8q12.1	224743_at	NM_017813
4.09	4.05	0.03	8.31E-01	9.50E-01	---	---	---	243576_at	---
3.58	3.52	0.06	8.31E-01	9.50E-01	---	---	---	238191_at	---
5.06	4.96	0.10	8.31E-01	9.50E-01	MIB1	mindbomb homolog 1 (Drosophila)	chr18q11.2	224720_at	NM_020774
6.63	6.56	0.07	8.31E-01	9.50E-01	SEC23A	Sec23 homolog A (S. cerevisiae)	chr14q21.1	212887_at	NM_006364
2.76	2.72	0.04	8.31E-01	9.50E-01	---	---	---	216157_at	---
9.10	9.05	0.05	8.32E-01	9.50E-01	PUM1	pumilio homolog 1 (Drosophila)	chr1p35.2	201166_s_at	NM_001020658 /// NM_014676
6.26	6.22	0.05	8.32E-01	9.50E-01	TM9SF4	transmembrane 9 superfamily protein member 4	chr20q11.21	212198_s_at	NM_014742
2.01	1.97	0.04	8.32E-01	9.50E-01	---	---	---	1569406_at	---
6.29	6.23	0.06	8.32E-01	9.50E-01	NUCB1	nucleobindin 1	chr19q13.2-q13.4	200646_s_at	NM_006184
2.48	2.46	0.02	8.32E-01	9.50E-01	DEPDC2	DEP domain containing 2	chr8q13.2	220732_at	NM_024870 /// NM_025170
2.11	2.08	0.03	8.32E-01	9.51E-01	MYO5A	myosin VA (heavy chain 12, myoxin)	chr15q21	217417_at	NM_000259
2.12	2.10	0.03	8.32E-01	9.51E-01	TUBA1B	tubulin, alpha 1b	chr12q13.12	1565668_at	NM_006082
2.36	2.33	0.03	8.32E-01	9.51E-01	ALOX12	arachidonate 12-lipoxygenase	chr17p13.1	207206_s_at	NM_000697
4.69	4.54	0.15	8.32E-01	9.51E-01	NRCAM	neuronal cell adhesion molecule	chr7q31.1-q31.2	216959_x_at	NM_001037132 /// NM_001037133 /// NM_005010
3.57	3.48	0.09	8.32E-01	9.51E-01	NCAM1	Neural cell adhesion molecule 1	chr11q23.1	231532_at	NM_000615 /// NM_001076682 /// NM_181351
3.11	3.07	0.03	8.32E-01	9.51E-01	TTC39B	Tetratricopeptide repeat domain 39B	chr9p22.3	236826_at	NM_152574
2.17	2.15	0.03	8.32E-01	9.51E-01	---	---	---	1567860_at	---
4.69	4.58	0.11	8.32E-01	9.51E-01	KIAA1468	KIAA1468	chr18q21.33	225508_at	NM_020854
2.84	2.81	0.03	8.32E-01	9.51E-01	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	chr2q35	217507_at	NM_000578
7.77	7.72	0.05	8.32E-01	9.51E-01	PFN2	profilin 2	chr3q25.1-q25.2	204992_s_at	NM_002628 /// NM_053024
4.35	4.31	0.04	8.32E-01	9.51E-01	---	---	---	1563425_at	---
6.86	6.82	0.04	8.33E-01	9.51E-01	SHISA4	shisa homolog 4 (Xenopus laevis)	chr1q32.1	226674_at	NM_198149
3.03	3.00	0.03	8.33E-01	9.51E-01	CCDC44	Coiled-coil domain containing 44	chr17q23.3	229680_at	NM_016360
6.19	6.12	0.07	8.33E-01	9.51E-01	GGT5	gamma-glutamyltransferase 5	chr22q11.23	205582_s_at	NM_001099781 /// NM_001099782 /// NM_004121

2.45	2.41	0.03	8.33E-01	9.51E-01	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6	chr15q13-q15	223596_at	NM_001042494 /// NM_001042495 /// NM_001042496 /// NM_001042497 /// NM_005135 /// NM_133647																				
4.47	4.42	0.06	8.33E-01	9.51E-01	IGF2 /// INS-IGF2	insulin-like growth factor 2 (somatomedin A) /// INS-IGF2	chr11p15.5	210881_s_at	NM_000612 /// NM_001007139 /// NM_001042376 /// NM_001127598 /// NR_003512																				
2.28	2.25	0.03	8.33E-01	9.51E-01	NLRP2	NLR family, pyrin domain containing 2	chr19q13.42	221690_s_at	NM_017852																				
6.63	6.57	0.06	8.33E-01	9.51E-01	TRA2A	transformer-2 alpha	chr7p15.3	204658_at	NM_013293																				
2.63	2.59	0.04	8.33E-01	9.51E-01	NUDT3	Nudix (nucleoside diphosphate linked moiety X)-type motif 3	chr6p21.2	226061_s_at	NM_006703																				
6.14	6.06	0.08	8.33E-01	9.51E-01	TRIM22	tripartite motif-containing 22	chr11p15	213293_s_at	NM_006074																				
2.27	2.25	0.03	8.33E-01	9.51E-01	---	---	---	1570215_at	---																				
2.23	2.21	0.02	8.33E-01	9.51E-01	---	---	---	215762_at	---																				
2.23	2.20	0.03	8.33E-01	9.51E-01	---	---	---	1560869_a_at	---																				
2.21	2.18	0.03	8.33E-01	9.51E-01	WDR27	WD repeat domain 27	chr6q27	238239_at	NM_182552																				
2.93	2.90	0.03	8.33E-01	9.51E-01	LOC153811	hypothetical protein LOC153811	chr5q35.3	232192_at	---																				
7.29	7.24	0.05	8.33E-01	9.51E-01	NUP62	nucleoporin 62kDa	chr19q13.33	202153_s_at	NM_012346 /// NM_016553 /// NM_153718 /// NM_153719																				
3.16	3.12	0.04	8.33E-01	9.51E-01	TIAM1	T-cell lymphoma invasion and metastasis 1	chr21q22.1|21q22.11	206409_at	NM_003253																				
3.54	3.51	0.03	8.33E-01	9.51E-01	VDR	Vitamin D (1,25- dihydroxyvitamin D3) receptor	chr12q13.11	213692_s_at	NM_000376 /// NM_001017535																				
2.46	2.43	0.03	8.33E-01	9.51E-01	DIO2	deiodinase, iodothyronine, type II	chr14q24.2-q24.3	203699_s_at	NM_000793 /// NM_001007023 /// NM_013989																				
2.52	2.46	0.06	8.33E-01	9.51E-01	MAP3K13	mitogen-activated protein kinase kinase kinase 13	chr3q27	211083_s_at	NM_004721																				
2.51	2.47	0.04	8.33E-01	9.51E-01	KRTAP1-5	keratin associated protein 1-5	chr17q12-q21	233533_at	NM_031957																				
2.88	2.84	0.04	8.34E-01	9.51E-01	---	---	---	1567319_at	---																				
3.01	2.97	0.05	8.34E-01	9.51E-01	SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	chr1p13.3	1569121_at	NM_013386 /// NM_213651																				
2.10	2.07	0.03	8.34E-01	9.51E-01	---	---	---	1562927_at	---																				
2.24	2.22	0.03	8.34E-01	9.51E-01	---	---	---	233457_at	---																				
4.19	4.15	0.03	8.34E-01	9.51E-01	---	---	---	1569765_at	---																				
4.13	4.07	0.06	8.34E-01	9.51E-01	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	chr6p21.3	225973_at	NM_000544 /// NM_018833																				
5.39	5.35	0.04	8.34E-01	9.51E-01	DDO	D-aspartate oxidase	chr6q21	207418_s_at	NM_003649 /// NM_004032																				
2.88	2.83	0.05	8.34E-01	9.51E-01	SNX25	sorting nexin 25	chr4q35.1	227311_at	NM_031953																				
2.56	2.53	0.03	8.34E-01	9.51E-01	---	---	---	244060_at	---																				
7.40	7.35	0.04	8.34E-01	9.51E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	215222_x_at	NM_012090 /// NM_033044																				
2.36	2.33	0.03	8.34E-01	9.51E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	214872_at	NM_018151																				
2.24	2.21	0.03	8.34E-01	9.51E-01	ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	chrXp22	219962_at	NM_021804																				
2.51	2.48	0.03	8.34E-01	9.51E-01	---	---	---	244267_at	---																				
6.28	6.23	0.04	8.34E-01	9.51E-01	---	---	---	227333_at	---																				

4.07	4.04	0.04	8.34E-01	9.51E-01	NFYA	nuclear transcription factor Y, alpha	chr6p21.3	215720_s_at	NM_002505 /// NM_021705 /// XM_001716589 /// XM_001717592 /// XM_001718396
5.01	4.97	0.04	8.34E-01	9.51E-01	---	---	---	232710_at	---
3.57	3.53	0.04	8.34E-01	9.51E-01	---	---	---	241298_x_at	---
3.16	3.12	0.04	8.34E-01	9.51E-01	---	---	---	234898_at	---
3.98	3.95	0.03	8.34E-01	9.51E-01	---	---	---	214395_x_at	---
6.15	6.06	0.09	8.35E-01	9.51E-01	H2AFV	H2A histone family, member V	chr7p13	212206_s_at	NM_012412 /// NM_138635 /// NM_201436 /// NM_201516 /// NM_201517
2.45	2.42	0.03	8.35E-01	9.51E-01	---	---	---	236021_at	---
3.34	3.29	0.05	8.35E-01	9.51E-01	LOC283663	hypothetical protein LOC283663	chr15q21.3	230245_s_at	XM_001133132 /// XM_001133281 /// XM_001726159
2.52	2.49	0.03	8.35E-01	9.51E-01	---	---	---	1563044_at	---
5.40	5.34	0.06	8.35E-01	9.52E-01	RABGGTB	Rab geranylgeranyltransferase, beta subunit	chr1p31	213704_at	NM_004582
2.08	2.06	0.02	8.35E-01	9.52E-01	COX8C	cytochrome c oxidase subunit 8C	chr14q32.13	231487_at	NM_182971
2.84	2.80	0.04	8.35E-01	9.52E-01	ZMYND10	zinc finger, MYND-type containing 10	chr3p21.3	216663_s_at	NM_015896
6.48	6.42	0.06	8.35E-01	9.52E-01	EDEM2	ER degradation enhancer, mannosidase alpha-like 2	chr20q11.22	218282_at	NM_018217
6.39	6.35	0.04	8.35E-01	9.52E-01	SNAPC5	small nuclear RNA activating complex, polypeptide 5, 19kDa	chr15q22.31	1554093_a_at	NM_006049
2.72	2.68	0.04	8.35E-01	9.52E-01	---	---	---	1552976_at	---
6.25	6.17	0.08	8.35E-01	9.52E-01	NGLY1	N-glycanase 1	chr3p24.2	220742_s_at	NM_018297
3.12	3.09	0.03	8.35E-01	9.52E-01	---	---	---	237724_at	---
2.66	2.62	0.04	8.35E-01	9.52E-01	---	---	---	234270_at	---
2.38	2.35	0.03	8.35E-01	9.52E-01	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	chr3q26.32-q26.33	223487_x_at	NM_021629
5.95	5.89	0.06	8.35E-01	9.52E-01	NCKAP1L	NCK-associated protein 1-like	chr12q13.1	209734_at	NM_005337
5.63	5.58	0.05	8.35E-01	9.52E-01	---	---	---	228196_s_at	---
3.74	3.70	0.03	8.35E-01	9.52E-01	ABCD1 /// LOC648897 /// LOC731915	ATP-binding cassette, sub-family D (ALD), member 1 /// similar to ALD protein (ALDP) /// similar to ATP-binding cassette sub-family D member 1 (Adrenoleukodystrophy protein) (ALDP)	chr10p11.1 /// chrXq28	216418_at	NM_000033 /// XM_001713924 /// XM_001716475 /// XM_001716991 /// XM_001717311
1.89	1.87	0.02	8.35E-01	9.52E-01	SLC17A1	Solute carrier family 17 (sodium phosphate), member 1	chr6p23-p21.3	1560884_at	NM_005074
2.12	2.09	0.03	8.36E-01	9.52E-01	---	---	---	216487_at	---
7.42	7.36	0.07	8.36E-01	9.52E-01	HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	chr19q13.33	228713_s_at	NM_016246
2.16	2.13	0.03	8.36E-01	9.52E-01	ATP6V1G3	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G3	chr1q31.3	230565_at	NM_133262 /// NM_133326
3.42	3.29	0.12	8.36E-01	9.52E-01	TMEM168	transmembrane protein 168	chr7q31.32	234726_s_at	NM_022484
2.38	2.35	0.02	8.36E-01	9.52E-01	---	---	---	1566965_at	---
2.19	2.16	0.03	8.36E-01	9.52E-01	ACOT12	acyl-CoA thioesterase 12	chr5q14.1	238160_at	NM_130767
2.94	2.91	0.03	8.36E-01	9.52E-01	SNX20	sorting nexin 20	chr16q12.1	236549_x_at	NM_182854
2.47	2.44	0.03	8.36E-01	9.52E-01	WNT2B	wingless-type MMTV integration site family, member 2B	chr1p13	206458_s_at	NM_004185 /// NM_024494
5.61	5.53	0.08	8.36E-01	9.52E-01	RAB27A	RAB27A, member RAS oncogene family	chr15q15-q21.1	209514_s_at	NM_004580 /// NM_183234 /// NM_183235 /// NM_183236

5.34	5.31	0.03	8.36E-01	9.52E-01	BCKDHA /// TMEM91	branched chain keto acid dehydrogenase E1, alpha polypeptide /// transmembrane protein 91	chr19q13.1-q13.2 /// chr19q13.2	229957_at	NM_000709 /// NM_001042595 /// NM_001098821 /// NM_001098822 /// NM_001098823 /// NM_001098824 /// NM_001098825																				
3.62	3.59	0.03	8.36E-01	9.52E-01	ERICH1	glutamate-rich 1	chr8p23.3	217611_at	NM_207332																				
7.53	7.49	0.04	8.36E-01	9.52E-01	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	chr21q22.3	225440_at	NM_001037553 /// NM_020132																				
3.43	3.40	0.03	8.36E-01	9.52E-01	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	chr1p36.23-p34.3	235682_s_at	NM_014424																				
2.87	2.84	0.03	8.36E-01	9.52E-01	NCAPH	non-SMC condensin I complex, subunit H	chr2q11.2	212949_at	NM_015341																				
2.62	2.60	0.03	8.36E-01	9.52E-01	LOC51336	mesenchymal stem cell protein DSCD28	chr1p32.3	208154_at	---																				
7.85	7.75	0.10	8.36E-01	9.52E-01	G0S2	G0/G1switch 2	chr1q32.2|1q32.2-q41	213524_s_at	NM_015714																				
5.86	5.80	0.07	8.36E-01	9.52E-01	PCYOX1L	prenylcysteine oxidase 1 like	chr5q33.1	218953_s_at	NM_024028																				
5.29	5.24	0.05	8.36E-01	9.52E-01	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	chrXq23	222808_at	NM_018466 /// XM_001713667 /// XM_001713668																				
3.92	3.87	0.05	8.36E-01	9.52E-01	ATP10A	ATPase, class V, type 10A	chr15q11.2	1568743_at	NM_024490																				
4.02	3.98	0.04	8.37E-01	9.52E-01	WDR27	WD repeat domain 27	chr6q27	235298_at	NM_182552																				
3.96	3.91	0.05	8.37E-01	9.52E-01	FLCN	folliculin	chr17p11.2	235250_at	NM_144606 /// NM_144997																				
2.22	2.19	0.04	8.37E-01	9.52E-01	---	---	---	1562364_at	---																				
2.22	2.18	0.03	8.37E-01	9.52E-01	MIDN	Midnolin	chr19p13.3	227398_s_at	NM_177401																				
6.72	6.68	0.04	8.37E-01	9.52E-01	JMJD3	jumonji domain containing 3, histone lysine demethylase	chr17p13.1	41387_r_at	NM_001080424																				
5.20	5.13	0.06	8.37E-01	9.52E-01	TMEM37	transmembrane protein 37	chr2q14.2	1554483_at	NM_183240																				
6.79	6.74	0.04	8.37E-01	9.52E-01	C1orf144	chromosome 1 open reading frame 144	chr1p36.13	212004_at	NM_001114600 /// NM_015609																				
2.22	2.19	0.03	8.37E-01	9.52E-01	C1orf101	chromosome 1 open reading frame 101	chr1q44	240771_at	NM_001130957 /// NM_173807																				
4.69	4.62	0.07	8.37E-01	9.52E-01	SMG6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr17p13.3	214940_s_at	NM_017575																				
3.44	3.39	0.05	8.37E-01	9.52E-01	BTNL9	Butyrophilin-like 9	chr5q35.3	229985_at	NM_152547																				
2.12	2.10	0.02	8.37E-01	9.52E-01	FLJ34048	hypothetical transcript	chr7q21.3	230882_at	XR_040145 /// XR_040146 /// XR_040147 /// XR_040148																				
6.77	6.71	0.06	8.37E-01	9.52E-01	SDSL	serine dehydratase-like	chr12q24.13	228274_at	NM_138432																				
4.15	4.11	0.04	8.37E-01	9.52E-01	---	---	---	1566848_x_at	---																				
4.12	4.07	0.05	8.37E-01	9.52E-01	BRWD3	bromodomain and WD repeat domain containing 3	chrXq21.1	244738_at	NM_153252																				
2.23	2.19	0.04	8.37E-01	9.52E-01	SLC25A45	solute carrier family 25, member 45	chr11q13.1	1563498_s_at	NM_001077241 /// NM_182556																				
1.87	1.85	0.02	8.37E-01	9.52E-01	ZFP1	zinc finger protein 1 homolog (mouse)	chr16q23.1	234455_at	NM_153688																				
5.95	5.91	0.04	8.37E-01	9.52E-01	UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative)	chr7p13	65521_at	NM_015983																				
2.39	2.36	0.04	8.37E-01	9.52E-01	MTMR7	myotubularin related protein 7	chr8p22	243804_at	NM_004686																				
2.88	2.84	0.04	8.37E-01	9.52E-01	---	---	---	216358_at	---																				
3.03	2.94	0.09	8.38E-01	9.52E-01	---	---	---	233479_at	---																				
4.01	3.82	0.19	8.38E-01	9.52E-01	ZFAND5	zinc finger, AN1-type domain 5	chr9q13-q21	217649_at	NM_001102420 /// NM_001102421 /// NM_006007																				
2.97	2.93	0.04	8.38E-01	9.52E-01	PHIP	pleckstrin homology domain interacting protein	chr6q14	1557362_at	NM_017934																				
2.07	2.05	0.03	8.38E-01	9.52E-01	---	---	---	1557856_at	---																				

2.55	2.52	0.02	8.38E-01	9.52E-01	LOC728678	Similar to p40	chr3p22.3	234263_at	XR_015757 /// XR_039160 /// XR_039547																			
5.27	5.19	0.08	8.38E-01	9.52E-01	CDC16	cell division cycle 16 homolog (S. cerevisiae)	chr13q34	202717_s_at	NM_001078645 /// NM_003903																			
6.98	6.94	0.04	8.38E-01	9.52E-01	ZNF358	zinc finger protein 358	---	219379_x_at	NM_018083																			
8.08	8.03	0.04	8.38E-01	9.52E-01	PITPNB	phosphatidylinositol transfer protein, beta	chr22q12.1	202522_at	NM_012399																			
2.42	2.39	0.03	8.38E-01	9.52E-01	PDE7A	phosphodiesterase 7A	chr8q13	224046_s_at	NM_002603 /// NM_002604																			
3.87	3.84	0.03	8.38E-01	9.52E-01	WDR68	WD repeat domain 68	chr17q23.3	233782_at	NM_005828																			
1.99	1.97	0.02	8.38E-01	9.52E-01	GAS2	growth arrest-specific 2	chr11p14.3-p15.2	205848_at	NM_005256 /// NM_177553																			
2.71	2.68	0.03	8.38E-01	9.52E-01	C3orf16	chromosome 3 open reading frame 16	chr3q25.1	1561928_s_at	XM_001131739 /// XM_001132074 /// XM_001717444																			
2.29	2.26	0.03	8.38E-01	9.53E-01	KIAA1967	KIAA1967	chr8p22	221070_s_at	NM_021174 /// NM_199205																			
2.20	2.18	0.03	8.38E-01	9.53E-01	---	---	---	1553398_at	---																			
6.84	6.80	0.04	8.38E-01	9.53E-01	SCNM1	sodium channel modifier 1	chr1q21.2	218672_at	NM_024041 /// XM_001721083																			
6.79	6.72	0.07	8.39E-01	9.53E-01	CMTM6	CKLF-like MARVEL transmembrane domain containing 6	chr3p22.3	223047_at	NM_017801																			
3.25	3.18	0.06	8.39E-01	9.53E-01	LIMS1	LIM and senescent cell antigen-like domains 1	chr2q12.3-q13	1566129_at	NM_004987																			
2.29	2.27	0.03	8.39E-01	9.53E-01	SDCCAG8	serologically defined colon cancer antigen 8	chr1q43-q44	1553034_at	NM_006642																			
2.07	2.05	0.03	8.39E-01	9.53E-01	ZBBX	zinc finger, B-box domain containing	chr3q26.1	220269_at	NM_024687																			
3.52	3.44	0.08	8.39E-01	9.53E-01	---	---	---	244265_at	---																			
8.36	8.25	0.10	8.39E-01	9.53E-01	SF3B1	splicing factor 3b, subunit 1, 155kDa	chr2q33.1	201071_x_at	NM_001005526 /// NM_012433																			
1.94	1.92	0.02	8.39E-01	9.53E-01	---	---	---	1556783_a_at	---																			
4.85	4.82	0.04	8.39E-01	9.53E-01	LOC442113	similar to protein-tyrosine phosphatase	chr4q21.22	241930_x_at	XR_015385 /// XR_016390																			
3.21	3.18	0.04	8.39E-01	9.53E-01	CARD9	caspase recruitment domain family, member 9	chr9q34.3	220162_s_at	NM_052813 /// NM_052814																			
2.89	2.85	0.04	8.39E-01	9.53E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	214099_s_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359																			
2.54	2.51	0.03	8.39E-01	9.53E-01	---	---	---	236610_at	---																			
3.55	3.52	0.04	8.39E-01	9.53E-01	C1orf86	chromosome 1 open reading frame 86	chr1p36.33	236498_s_at	NM_182533 /// XM_001718861																			
8.14	8.10	0.04	8.39E-01	9.53E-01	C22orf28	chromosome 22 open reading frame 28	chr22q12	200042_at	NM_014306																			
4.85	4.78	0.08	8.39E-01	9.53E-01	MAOA	monoamine oxidase A	chrXp11.3	204389_at	NM_000240																			
6.25	6.19	0.07	8.39E-01	9.53E-01	PAPD1	PAP associated domain containing 1	chr10p11.23	222794_x_at	NM_018109																			
1.91	1.89	0.02	8.39E-01	9.53E-01	ZNF846	zinc finger protein 846	chr19p13.2	1564331_at	NM_001077624																			
2.50	2.47	0.03	8.39E-01	9.53E-01	---	---	---	1562166_at	---																			
2.76	2.72	0.04	8.39E-01	9.53E-01	SETX	senataxin	chr9q34.13	232229_at	NM_015046																			
2.35	2.32	0.03	8.39E-01	9.53E-01	SGCZ	sarcoglycan zeta	chr8p22	1552971_at	NM_139167																			
7.04	6.99	0.05	8.39E-01	9.53E-01	LACTB	lactamase, beta	chr15q22.1	226354_at	NM_032857 /// NM_171846																			
2.86	2.83	0.03	8.39E-01	9.53E-01	---	---	---	238517_at	---																			

2.43	2.40	0.03	8.40E-01	9.53E-01	RAB3IP	RAB3A interacting protein (rabin3)	chr12q14.3	228432_at	NM_001024647 /// NM_022456 /// NM_175623 /// NM_175624 /// NM_175625
3.70	3.66	0.04	8.40E-01	9.53E-01	HOXB13	homeobox B13	chr17q21.2	209844_at	NM_006361
3.64	3.59	0.04	8.40E-01	9.53E-01	NCAPH2	non-SMC condensin II complex, subunit H2	chr22q13.33	221633_at	NM_014551 /// NM_152299
3.80	3.73	0.07	8.40E-01	9.53E-01	HDDC2	HD domain containing 2	chr6q13-q24.3	203260_at	NM_016063
2.02	2.00	0.02	8.40E-01	9.53E-01	ZNF804B	zinc finger protein 804B	chr7q21.13	1564022_at	NM_181646
3.18	3.14	0.04	8.40E-01	9.53E-01	---	---	---	1560625_s_at	---
1.98	1.96	0.03	8.40E-01	9.53E-01	---	---	---	1570168_at	---
1.93	1.91	0.02	8.40E-01	9.53E-01	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2	chr3q26.1-q26.2	206535_at	NM_000340
2.33	2.30	0.03	8.40E-01	9.53E-01	---	---	---	1566672_at	---
2.86	2.82	0.03	8.40E-01	9.53E-01	PHACTR1	phosphatase and actin regulator 1	chr6p24.1	232045_at	NM_030948
2.27	2.24	0.03	8.40E-01	9.53E-01	---	---	---	1553547_at	---
4.30	4.25	0.06	8.40E-01	9.53E-01	OGDHL	oxoglutarate dehydrogenase-like	chr10q11.23	219277_s_at	NM_018245
3.18	3.15	0.03	8.40E-01	9.53E-01	IL1F10	interleukin 1 family, member 10 (theta)	chr2q13	224262_at	NM_032556 /// NM_173161
2.34	2.31	0.03	8.40E-01	9.53E-01	C2orf82	chromosome 2 open reading frame 82	chr2q37.1	230244_at	NM_206895
4.52	4.48	0.04	8.40E-01	9.53E-01	---	---	---	229375_at	---
5.66	5.59	0.07	8.40E-01	9.53E-01	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	chr17p13	229100_s_at	NM_013337
4.20	4.10	0.10	8.40E-01	9.53E-01	LOC283551	hypothetical protein LOC283551	chr14q22.1	237460_x_at	NM_001012706
2.05	2.02	0.03	8.40E-01	9.53E-01	C1orf168	chromosome 1 open reading frame 168	chr1p32.2	238625_at	NM_001004303
2.44	2.41	0.03	8.40E-01	9.53E-01	ZNF79	zinc finger protein 79	chr9q34	216482_x_at	NM_007135
3.17	3.09	0.08	8.40E-01	9.53E-01	TNIK	TRAF2 and NCK interacting kinase	chr3q26.2-q26.31	213109_at	NM_015028
2.65	2.61	0.04	8.40E-01	9.53E-01	NUB1	negative regulator of ubiquitin-like proteins 1	chr7q36	234332_at	NM_016118
6.15	6.11	0.04	8.40E-01	9.53E-01	C7orf20	chromosome 7 open reading frame 20	chr7p22.3	223811_s_at	NM_015949
5.74	5.67	0.07	8.41E-01	9.53E-01	SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	chr3q27.2	218122_s_at	NM_021627
3.51	3.46	0.05	8.41E-01	9.53E-01	C5orf24	chromosome 5 open reading frame 24	chr5q31.1	1553108_at	NM_152409
2.12	2.10	0.02	8.41E-01	9.53E-01	---	---	---	AFFX-ThrX-M_at	---
2.39	2.36	0.03	8.41E-01	9.53E-01	---	---	---	242606_at	---
7.57	7.50	0.07	8.41E-01	9.53E-01	CCNC	cyclin C	chr6q21	201955_at	NM_001013399 /// NM_005190
5.71	5.65	0.06	8.41E-01	9.53E-01	THOC1	THO complex 1	chr18p11.32	204064_at	NM_005131
2.01	1.98	0.03	8.41E-01	9.53E-01	---	---	---	215312_at	---
2.43	2.41	0.02	8.41E-01	9.53E-01	---	---	---	234558_at	---
4.00	3.97	0.03	8.41E-01	9.54E-01	E2F5	E2F transcription factor 5, p130-binding	chr8q21.2	221586_s_at	NM_001083588 /// NM_001083589 /// NM_001951
4.13	4.10	0.03	8.41E-01	9.54E-01	ICHTHYIN	ichthyin protein	chr5q33.3	230188_at	NM_001099287
2.48	2.45	0.03	8.41E-01	9.54E-01	---	---	---	1569681_at	---
4.30	4.26	0.04	8.41E-01	9.54E-01	C16orf68	Chromosome 16 open reading frame 68	chr16p13.2	233742_at	NM_024109
2.31	2.27	0.04	8.41E-01	9.54E-01	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	chr14q32.12	243969_at	NM_153646 /// NM_153647 /// NM_153648
2.14	2.12	0.02	8.41E-01	9.54E-01	---	---	---	1561279_at	---
3.35	3.30	0.05	8.41E-01	9.54E-01	---	---	---	239559_at	---
2.18	2.16	0.02	8.41E-01	9.54E-01	ERAP1	endoplasmic reticulum aminopeptidase 1	chr5q15	214034_at	NM_001040458 /// NM_016442
3.75	3.71	0.04	8.41E-01	9.54E-01	PTGER4	prostaglandin E receptor 4 (subtype EP4)	chr5p13.1	204896_s_at	NM_000958
2.73	2.71	0.03	8.41E-01	9.54E-01	PDE3B	phosphodiesterase 3B, cGMP-inhibited	chr11p15.1	208591_s_at	NM_000922
2.20	2.18	0.03	8.41E-01	9.54E-01	DSCAML1	Down syndrome cell adhesion molecule like 1	chr11q23	232059_at	NM_020693
3.13	3.09	0.03	8.42E-01	9.54E-01	ICMT	isoprenylcysteine carboxyl methyltransferase	chr1p36.21	201610_at	NM_012405
2.43	2.41	0.03	8.42E-01	9.54E-01	LOC4951	parvalbumin	chr7q21.2	207944_at	NM_006188
4.25	4.19	0.07	8.42E-01	9.54E-01	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	chr19q13.3	206109_at	NM_000148

4.56	4.53	0.03	8.42E-01	9.54E-01	AZI1	5-azacytidine induced 1	chr17q25.3	214742_at	NM_001009811 /// NM_014984																				
4.48	4.41	0.07	8.42E-01	9.54E-01	---	---	---	226532_at	---																				
6.23	6.20	0.03	8.42E-01	9.54E-01	APH1B	anterior pharynx defective 1 homolog B (C. elegans)	chr15q22.2	221036_s_at	NM_031301																				
3.27	3.22	0.05	8.42E-01	9.54E-01	RHOH	ras homolog gene family, member H	chr4p13	204951_at	NM_004310																				
2.41	2.38	0.03	8.42E-01	9.54E-01	EFCAB4B	EF-hand calcium binding domain 4B	chr12p13.32	223955_at	NM_032680																				
2.52	2.49	0.02	8.42E-01	9.54E-01	THBS1	Thrombospondin 1	chr15q15	215775_at	NM_003246																				
3.20	3.17	0.04	8.42E-01	9.54E-01	TDP1	tyrosyl-DNA phosphodiesterase 1	chr14q32.11	226044_at	NM_001008744 /// NM_018319																				
2.71	2.67	0.04	8.42E-01	9.54E-01	FAM73A	family with sequence similarity 73, member A	chr1p31.1	243042_at	NM_198549																				
2.42	2.38	0.04	8.42E-01	9.54E-01	---	---	---	1561460_at	---																				
2.36	2.33	0.02	8.42E-01	9.54E-01	---	---	---	238279_x_at	---																				
4.42	4.39	0.03	8.42E-01	9.54E-01	SGK2	serum/glucocorticoid regulated kinase 2	chr20q13.2	220357_s_at	NM_016276 /// NM_170693																				
6.56	6.50	0.06	8.42E-01	9.54E-01	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	chr6q14.1	210970_s_at	NM_015525																				
6.66	6.61	0.05	8.42E-01	9.54E-01	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	chr8p11	226547_at	NM_001099412 /// NM_001099413 /// NM_006766																				
4.02	3.99	0.03	8.42E-01	9.54E-01	HBEGF	heparin-binding EGF-like growth factor	chr5q23	244857_at	NM_001945																				
5.70	5.60	0.10	8.43E-01	9.54E-01	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	chr5q23-q31	227314_at	NM_002203																				
2.88	2.72	0.15	8.43E-01	9.54E-01	CYorf15A	chromosome Y open reading frame 15A	chrYq11.222	236694_at	NM_001005852																				
3.97	3.93	0.04	8.43E-01	9.54E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	234923_at	NM_014990 /// NM_194301																				
5.68	5.59	0.09	8.43E-01	9.54E-01	---	---	---	231205_at	---																				
6.51	6.49	0.02	8.43E-01	9.54E-01	TCF20	transcription factor 20 (AR1)	chr22q13.3|22q13.3	212931_at	NM_005650 /// NM_181492																				
3.04	3.00	0.04	8.43E-01	9.54E-01	CXYorf2	chromosome X and Y open reading frame 2	chrXp22.33; Yp11.3	1552872_at	XR_040863 /// XR_040864																				
2.98	2.94	0.04	8.43E-01	9.54E-01	PURG	purine-rich element binding protein G	chr8p11	235634_at	NM_001015508 /// NM_013357																				
2.15	2.13	0.02	8.43E-01	9.54E-01	LOC100130476	Similar to hCG2036711	chr6q23.3	243871_at	XM_001723486 /// XM_001724879 /// XM_001726724																				
5.03	4.98	0.05	8.43E-01	9.54E-01	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	chr21q22.3	223184_s_at	NM_001037553 /// NM_020132																				
2.60	2.56	0.03	8.43E-01	9.54E-01	TCEA1	transcription elongation factor A (SII), 1	chr8q11.2	1566208_at	NM_006756 /// NM_201437																				
2.08	2.06	0.02	8.43E-01	9.54E-01	---	---	---	240992_at	---																				
2.25	2.23	0.02	8.43E-01	9.54E-01	---	---	---	243464_at	---																				
2.61	2.59	0.03	8.43E-01	9.54E-01	C21orf100	chromosome 21 open reading frame 100	chr21q21.3	1554405_a_at	XR_017892 /// XR_017991																				
4.15	4.08	0.08	8.43E-01	9.54E-01	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	chr3q26.1	1558956_s_at	NM_020800																				
2.76	2.72	0.05	8.43E-01	9.54E-01	RP4-692D3.1	hypothetical protein LOC728621	chr1p34.2	230897_at	NM_001080850																				
5.34	5.27	0.07	8.43E-01	9.54E-01	---	---	---	226910_at	---																				
3.96	3.90	0.06	8.43E-01	9.54E-01	BICD2	bicaudal D homolog 2 (Drosophila)	chr9q22.31	209203_s_at	NM_001003800 /// NM_015250																				

4.40	4.37	0.03	8.43E-01	9.54E-01	FLJ22795 /// LOC388152 /// LOC388161 /// LOC727751 /// LOC727849 /// LOC727994 /// LOC728125 /// LOC729353	hypothetical protein FLJ22795 /// hypothetical LOC388152 /// LOC388161 /// similar to cis-Golgi matrix protein GM130 /// similar to cis-Golgi matrix protein GM130 /// similar to colon cancer-associated antigen AgSK1-2HT-ECS /// similar to colon cancer-associated antigen AgSK1-2HT-ECS /// hypothetical LOC729353	chr15q25.2 /// chr15q25.3	220602_s_at	XM_001713899 /// XM_001717645 /// XM_001718554 /// XM_001722113 /// XR_015455 /// XR_040862 /// XR_040915 /// XR_041987
3.27	3.24	0.03	8.43E-01	9.54E-01	SCAMP1	secretory carrier membrane protein 1	chr5q13.3-q14.1	212425_at	NM_004866
4.17	4.11	0.05	8.43E-01	9.54E-01	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	chr7p22	217735_s_at	NM_001134335 /// NM_014413
2.99	2.95	0.05	8.43E-01	9.54E-01	---	---	---	1566138_at	---
3.46	3.41	0.05	8.43E-01	9.54E-01	---	---	---	1569527_at	---
2.01	1.99	0.02	8.43E-01	9.54E-01	FAM123A	family with sequence similarity 123A	chr13q12.13	230496_at	NM_152704 /// NM_199138
2.13	2.11	0.02	8.44E-01	9.54E-01	---	---	---	222326_at	---
3.79	3.76	0.03	8.44E-01	9.54E-01	NR2F2	nuclear receptor subfamily 2, group F, member 2	chr15q26	229092_at	NM_021005
5.00	4.95	0.05	8.44E-01	9.54E-01	MOSC1	MOCO sulphurase C-terminal domain containing 1	chr1q41	218865_at	NM_022746
7.34	7.29	0.06	8.44E-01	9.54E-01	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily C, 5	chr5q31	211066_x_at	NM_002588 /// NM_003735 /// NM_003736 /// NM_014004 /// NM_018912 /// NM_018913 /// NM_018914 /// NM_018915 /// NM_018916 /// NM_018917 /// NM_018918 /// NM_018919 /// NM_018920 /// NM_018921 /// NM_018922 /// NM_018923 /// NM_018924 /// NM_018925 /// NM_018926 /// NM_018927 /// NM_018928 /// NM_018929 /// NM_031993 /// NM_032009 /// NM_032011 /// NM_032053 /// NM_032054 /// NM_032086 /// NM_032087 /// NM_032088 /// NM_032089 /// NM_032090 /// NM_032091 /// NM_032092 /// NM_032094 /// NM_032095 /// NM_032096 /// NM_032097 /// NM_032098 /// NM_032099 /// NM_032100 /// NM_032101 /// NM_032402 /// NM_032403 /// NM_032406 /// NM_032407

6.71	6.66	0.05	8.44E-01	9.54E-01	ZSCAN18	zinc finger and SCAN domain containing 18	chr19q13.43	218312_s_at	NM_023926
2.72	2.64	0.08	8.44E-01	9.54E-01	P2RY12	purinergic receptor P2Y, G-protein coupled, 12	chr3q24-q25	235885_at	NM_022788 /// NM_176876
2.46	2.44	0.02	8.44E-01	9.54E-01	---	---	---	1566257_at	---
8.14	8.11	0.03	8.44E-01	9.54E-01	FTO	fat mass and obesity associated	chr16q12.2	209702_at	NM_001080432
2.43	2.41	0.02	8.44E-01	9.54E-01	WFDC9	WAP four-disulfide core domain 9	chr20q12-q13.1	1552414_at	NM_147198
4.25	4.22	0.03	8.44E-01	9.54E-01	---	---	---	237583_at	---
5.49	5.45	0.04	8.44E-01	9.54E-01	ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl	chr4p15.3	204242_s_at	NM_001101667 /// NM_003501
4.71	4.64	0.07	8.44E-01	9.54E-01	NKAP	NFKB activating protein	chrXq24	223439_at	NM_024528
2.79	2.76	0.02	8.44E-01	9.54E-01	LOC727944	similar to hCG2042412	chr2p25.3	231256_at	XM_001126199 /// XM_001126250 /// XM_001715287
2.83	2.80	0.03	8.44E-01	9.54E-01	CSH1	chorionic somatomammotropin hormone 1 (placental lactogen)	chr17q24.2	208357_x_at	NM_001317 /// NM_022640 /// NM_022641
5.11	5.04	0.07	8.44E-01	9.54E-01	---	---	---	238651_at	---
2.25	2.22	0.03	8.44E-01	9.54E-01	MDN1	MDN1, midasin homolog (yeast)	chr6q15	1569484_s_at	NM_014611
3.99	3.93	0.06	8.44E-01	9.54E-01	RAB11FIP3	RAB11 family interacting protein 3 (class II)	chr16p13.3	214999_s_at	NM_014700
5.25	5.15	0.10	8.44E-01	9.54E-01	RBMS3	RNA binding motif, single stranded interacting protein	chr3p24-p23	206767_at	NM_001003792 /// NM_001003793 /// NM_014483
3.33	3.30	0.03	8.45E-01	9.54E-01	LOC100132707	hypothetical LOC100132707	chr7q36.2	1569898_a_at	XM_001719292 /// XM_001720302 /// XM_001721385
1.88	1.86	0.02	8.45E-01	9.54E-01	---	---	---	1557475_at	---
2.82	2.78	0.04	8.45E-01	9.54E-01	OMD	osteomodulin	chr9q22.31	205908_s_at	NM_005014
2.10	2.08	0.03	8.45E-01	9.54E-01	---	---	---	216158_at	---
2.02	2.00	0.02	8.45E-01	9.54E-01	---	---	---	238914_at	---
2.16	2.13	0.03	8.45E-01	9.54E-01	LOC645984	hypothetical LOC645984	chr10p11.23	1560007_at	XM_001724778 /// XM_928946 /// XM_940362
2.25	2.23	0.02	8.45E-01	9.54E-01	FCAMR	Fc receptor, IgA, IgM, high affinity	chr1q32.1	231496_at	NM_001122979 /// NM_001122980 /// NM_032029 /// XM_001713738 /// XM_001713739 /// XM_001713740
3.06	3.02	0.04	8.45E-01	9.55E-01	C21orf49	chromosome 21 open reading frame 49	chr21q22.11	1559755_at	XR_017702 /// XR_017893 /// XR_041041
3.13	3.11	0.03	8.45E-01	9.55E-01	ATM	ataxia telangiectasia mutated	chr11q22-q23	1553387_at	NM_000051 /// NM_138292
3.04	2.98	0.06	8.45E-01	9.55E-01	HIF3A	hypoxia inducible factor 3, alpha subunit	chr19q13.32	1556069_s_at	NM_022462 /// NM_152794 /// NM_152795
2.35	2.32	0.03	8.45E-01	9.55E-01	FGF4	fibroblast growth factor 4	chr11q13.3	1552982_a_at	NM_002007
7.24	7.21	0.03	8.45E-01	9.55E-01	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7	chr2q37.3	201214_s_at	NM_002712

2.44	2.41	0.03	8.45E-01	9.55E-01	GRINL1A	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	chr15q22.1	239099_at	NM_001018102 /// NM_001018103 /// NM_015532																				
4.83	4.74	0.09	8.45E-01	9.55E-01	BAALC	brain and acute leukemia, cytoplasmic	chr8q22.3	222780_s_at	NM_001024372 /// NM_024812																				
2.07	2.04	0.02	8.45E-01	9.55E-01	FLG	filaggrin	chr1q21.3	215704_at	NM_002016																				
2.03	2.01	0.02	8.45E-01	9.55E-01	NMBR	neuromedin B receptor	chr6q21-qter	207333_at	NM_002511																				
3.36	3.31	0.05	8.45E-01	9.55E-01	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	chr12p11.23-p11.22	214374_s_at	NM_003622 /// NM_177444																				
4.63	4.58	0.06	8.46E-01	9.55E-01	ORC2L	origin recognition complex, subunit 2-like (yeast)	chr2q33	204853_at	NM_006190																				
6.02	5.94	0.09	8.46E-01	9.55E-01	HYMAI	hydatidiform mole associated and imprinted (non-protein coding)	chr6q24	215513_at	NR_002768																				
1.85	1.83	0.02	8.46E-01	9.55E-01	C4orf21	chromosome 4 open reading frame 21	chr4q25	231204_at	NM_018392																				
4.80	4.76	0.04	8.46E-01	9.55E-01	C19orf20	chromosome 19 open reading frame 20	chr19p13.3	227903_x_at	NM_033513																				
2.23	2.20	0.03	8.46E-01	9.55E-01	---	---	---	240232_at	---																				
4.38	4.33	0.05	8.46E-01	9.55E-01	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	210399_x_at	NM_000150 /// NM_001040701																				
2.52	2.49	0.03	8.46E-01	9.55E-01	---	---	---	239181_at	---																				
3.44	3.40	0.05	8.46E-01	9.55E-01	CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	chr2p16	235117_at	NM_001008708																				
4.77	4.71	0.06	8.46E-01	9.55E-01	FUSIP1	FUS interacting protein (serine/arginine-rich) 1	chr1p36.11	225348_at	NM_006625 /// NM_054016																				
2.87	2.84	0.03	8.46E-01	9.55E-01	---	---	---	237811_at	---																				
2.53	2.50	0.03	8.46E-01	9.55E-01	---	---	---	244064_at	---																				
5.19	5.11	0.08	8.46E-01	9.55E-01	NGFR	nerve growth factor receptor (TNFR superfamily, member 16)	chr17q21-q22	205858_at	NM_002507																				
2.65	2.62	0.03	8.46E-01	9.55E-01	CNTNAP2	contactin associated protein-like 2	chr7q35-q36	219301_s_at	NM_014141																				
1.97	1.95	0.02	8.46E-01	9.55E-01	---	---	---	244096_at	---																				
2.25	2.22	0.03	8.46E-01	9.55E-01	ZNF321	zinc finger protein 321	chr19q13.41	1558888_x_at	NM_203307																				
2.78	2.74	0.03	8.46E-01	9.55E-01	CDC2	cell division cycle 2, G1 to S and G2 to M	chr10q21.1	203213_at	NM_001130829 /// NM_001786 /// NM_033379																				
9.36	9.33	0.04	8.46E-01	9.55E-01	GLRX5	glutaredoxin 5	chr14q32.13	221932_s_at	NM_016417																				
2.21	2.18	0.03	8.46E-01	9.55E-01	---	---	---	236662_at	---																				
7.56	7.51	0.05	8.46E-01	9.55E-01	ACTN1	actinin, alpha 1	chr14q24.1-q24.2|14q24|14q22q24	208637_x_at	NM_001102 /// NM_001130004 /// NM_001130005																				
2.65	2.62	0.03	8.46E-01	9.55E-01	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	chr2q33.3	1553188_s_at	NM_057177 /// NM_152526 /// NM_205863																				
7.88	7.77	0.11	8.46E-01	9.55E-01	DUSP16	dual specificity phosphatase 16	chr12p13	224832_at	NM_030640																				
2.95	2.91	0.04	8.46E-01	9.55E-01	---	---	---	1564931_at	---																				
2.37	2.35	0.02	8.46E-01	9.55E-01	---	---	---	237663_at	---																				
2.03	2.00	0.03	8.46E-01	9.55E-01	---	---	---	238411_x_at	---																				
2.42	2.40	0.02	8.46E-01	9.55E-01	---	---	---	241684_at	---																				
2.35	2.33	0.03	8.46E-01	9.55E-01	---	---	---	231142_at	---																				
5.13	5.08	0.06	8.46E-01	9.55E-01	DOCK2	dedicator of cytokinesis 2	chr5q35.1	213160_at	NM_004946																				
2.49	2.46	0.03	8.47E-01	9.55E-01	---	---	---	240736_at	---																				
3.33	3.29	0.04	8.47E-01	9.55E-01	GFRA4	GDNF family receptor alpha 4	chr20p13-p12	221199_at	NM_022139 /// NM_145762																				
3.23	3.19	0.04	8.47E-01	9.55E-01	IGL@ /// IGLV3-19	immunoglobulin lambda locus /// immunoglobulin lambda variable 3-19	chr22q11.1-q11.2 /// chr22q11.2	216365_x_at	---																				
4.96	4.87	0.09	8.47E-01	9.55E-01	NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma	chr18p11.22	210048_at	NM_003826																				
3.34	3.30	0.04	8.47E-01	9.55E-01	C18orf56	chromosome 18 open reading frame 56	chr18p11.32	228989_at	NM_001012716																				
2.26	2.23	0.03	8.47E-01	9.55E-01	LOC100131138	similar to hCG2040918	chr12q24.11	230195_at	XM_001717925 /// XM_001722798 /// XM_001726259																				

10.65	10.63	0.02	8.47E-01	9.55E-01	GNAS	GNAS complex locus	chr20q13.3	211858_x_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259																				
3.40	3.36	0.05	8.47E-01	9.55E-01	TBX4	T-box 4	chr17q21-q22	220634_at	NM_018488																				
4.00	3.97	0.03	8.47E-01	9.55E-01	KLC3	kinesin light chain 3	chr19q13.2-q13.3	1570402_at	NM_177417																				
2.20	2.17	0.02	8.47E-01	9.55E-01	---	---	---	235905_at	---																				
2.01	1.99	0.02	8.47E-01	9.55E-01	---	---	---	243302_at	---																				
3.89	3.85	0.05	8.47E-01	9.55E-01	AFG3L1	AFG3 ATPase family gene 3-like 1 (S. cerevisiae)	chr16q24.3	1559863_a_at	NR_003226 /// NR_003227 /// NR_003228																				
6.28	6.22	0.06	8.47E-01	9.55E-01	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	chrXq28	209929_s_at	NM_001099856 /// NM_001099857 /// NM_003639																				
1.96	1.93	0.03	8.47E-01	9.55E-01	---	---	---	237100_at	---																				
2.52	2.50	0.02	8.47E-01	9.55E-01	---	---	---	237272_at	---																				
3.37	3.33	0.04	8.47E-01	9.55E-01	COX19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr7p22.3	235533_at	NM_001031617																				
3.46	3.43	0.02	8.47E-01	9.55E-01	CD1A	CD1a molecule	chr1q22-q23	210325_at	NM_001763																				
2.05	2.02	0.03	8.47E-01	9.55E-01	---	---	---	232754_at	---																				
5.94	5.84	0.09	8.48E-01	9.55E-01	C3orf59	chromosome 3 open reading frame 59	chr3q29	227599_at	NM_178496																				
2.54	2.51	0.02	8.48E-01	9.55E-01	GRM1	glutamate receptor, metabotropic 1	chr6q24	210939_s_at	NM_000838 /// NM_001114329																				
2.22	2.20	0.03	8.48E-01	9.55E-01	---	---	---	231456_at	---																				
6.05	5.98	0.06	8.48E-01	9.55E-01	TRIM37	tripartite motif-containing 37	chr17q23.2	213009_s_at	NM_001005207 /// NM_015294																				
2.56	2.53	0.04	8.48E-01	9.55E-01	LOC440888	ARP3 actin-related protein 3 homolog B pseudogene	chr2p11.1	224424_x_at	---																				
2.47	2.44	0.03	8.48E-01	9.56E-01	---	---	---	240309_at	---																				
2.83	2.79	0.03	8.48E-01	9.56E-01	MRO	maestro	chr18q21	224323_s_at	NM_001127174 /// NM_001127175 /// NM_001127176 /// NM_031939																				
2.40	2.37	0.03	8.48E-01	9.56E-01	IL17RD	interleukin 17 receptor D	chr3p14.3	229263_at	NM_001080973 /// NM_017563																				
6.06	6.01	0.05	8.48E-01	9.56E-01	ANAPC5	anaphase promoting complex subunit 5	chr12q24.31	208721_s_at	NM_016237																				
2.63	2.60	0.04	8.48E-01	9.56E-01	ANKLE1	ankyrin repeat and LEM domain containing 1	chr19p13.11	1553138_a_at	NM_152363																				
2.37	2.35	0.02	8.48E-01	9.56E-01	EBF3	early B-cell factor 3	chr10q26.3	1559796_at	NM_001005463																				
2.54	2.51	0.03	8.48E-01	9.56E-01	ZAR1	zygote arrest 1	chr4p11	1555775_a_at	NM_175619																				
4.88	4.83	0.04	8.48E-01	9.56E-01	CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	chr7p22.3	220562_at	NM_017781																				
2.94	2.90	0.04	8.48E-01	9.56E-01	---	---	---	1565734_at	---																				
7.49	7.43	0.06	8.48E-01	9.56E-01	FAM98A	family with sequence similarity 98, member A	chr2p22.3	212333_at	NM_015475																				
2.27	2.24	0.02	8.48E-01	9.56E-01	LOC151438	hypothetical protein LOC151438	chr2q12.1	1560679_at	---																				
2.35	2.32	0.03	8.48E-01	9.56E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	1555033_a_at	NM_002926 /// NM_198227 /// NM_198229																				
2.24	2.22	0.03	8.48E-01	9.56E-01	---	---	---	234825_at	---																				
3.13	3.06	0.07	8.49E-01	9.56E-01	SMYD2	SET and MYND domain containing 2	chr1q41	212921_at	NM_020197																				

4.53	4.48	0.05	8.49E-01	9.56E-01	PAX8	paired box 8	chr2q12-q14	209552_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992																			
5.93	5.87	0.06	8.49E-01	9.56E-01	CMIP	c-Maf-inducing protein	chr16q23	224991_at	NM_030629 /// NM_198390																			
2.35	2.32	0.03	8.49E-01	9.56E-01	C4A /// C4B	complement component 4A (Rodgers blood group) /// complement component 4B (Childo blood group)	chr6p21.3	1559036_at	NM_000592 /// NM_001002029 /// NM_007293																			
3.39	3.36	0.03	8.49E-01	9.56E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	232035_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054																			
2.83	2.81	0.02	8.49E-01	9.56E-01	IRGC	immunity-related GTPase family, cinema	chr19q13.31	214392_at	NM_019612																			
1.85	1.82	0.02	8.49E-01	9.56E-01	RASAL2	RAS protein activator like 2	chr1q24	217194_at	NM_004841 /// NM_170692																			
7.75	7.71	0.04	8.49E-01	9.56E-01	R3HCC1	R3H domain and coiled-coil containing 1	chr8p21.3	35156_at	XM_001716421 /// XM_114618 /// XM_939319																			
2.18	2.16	0.02	8.49E-01	9.56E-01	MMD2	monocyte to macrophage differentiation-associated 2	chr7p22.1	1569998_at	NM_001100600 /// NM_198403																			
2.32	2.29	0.03	8.49E-01	9.56E-01	---	---	---	237389_at	---																			
2.05	2.03	0.03	8.50E-01	9.56E-01	WDSOF1	WD repeats and SOF1 domain containing	chr8q22.3	1568840_at	NM_015420																			
3.00	2.96	0.04	8.50E-01	9.56E-01	---	---	---	1570631_at	---																			
6.22	6.16	0.05	8.50E-01	9.56E-01	BTBD1	BTB (POZ) domain containing 1	chr15q24	217945_at	NM_001011885 /// NM_025238																			
2.10	2.08	0.02	8.50E-01	9.56E-01	FLJ32810 /// LOC100129602	hypothetical protein FLJ32810 /// similar to hCG40515	chr11q22.1	1553383_at	XM_001127597 /// XM_001725369 /// XM_001725431 /// XM_001725432 /// XM_001726122 /// XM_001726124																			
3.78	3.74	0.05	8.50E-01	9.56E-01	LOC728448	peptidylprolyl isomerase E pseudogene	chr1p34.2	222054_at	NR_003929																			

2.73	2.69	0.04	8.50E-01	9.56E-01	CSH1 /// CSH2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// growth hormone 1	chr17q24.2	203807_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645
2.22	2.19	0.02	8.50E-01	9.56E-01	---	---	---	237632_at	---
2.31	2.28	0.03	8.50E-01	9.56E-01	LOC553137	hypothetical LOC553137	chr6q21	230432_at	NR_015365 /// XR_001059 /// XR_001268
3.24	3.21	0.03	8.50E-01	9.56E-01	NEUROG1	neurogenin 1	chr5q23-q31	208497_x_at	NM_006161
4.34	4.27	0.07	8.50E-01	9.56E-01	CCNT2	cyclin T2	chr2q21.3	213743_at	NM_001241 /// NM_058241
4.82	4.78	0.03	8.50E-01	9.56E-01	NIP7	nuclear import 7 homolog (S. cerevisiae)	chr16q22.1	219031_s_at	NM_016101
1.95	1.93	0.02	8.50E-01	9.56E-01	ACSM2A	acyl-CoA synthetase medium-chain family member 2A	chr16p12.3	230554_at	NM_001010845
2.96	2.91	0.05	8.50E-01	9.56E-01	PCTK2	PCTAIRE protein kinase 2	chr12q23.1	206474_at	NM_002595
3.84	3.77	0.08	8.50E-01	9.56E-01	SPATA6	spermatogenesis associated 6	chr1p33	220299_at	NM_019073
2.38	2.36	0.02	8.50E-01	9.56E-01	ZDHHC21	zinc finger, DHHC-type containing 21	chr9p22.3	233216_at	NM_178566
2.07	2.05	0.02	8.50E-01	9.56E-01	RUFY2	RUN and FYVE domain containing 2	chr10q21.3	1569630_a_at	NM_001042417 /// NM_017987
2.93	2.90	0.04	8.50E-01	9.56E-01	ZIC5	Zic family member 5 (odd-paired homolog, Drosophila)	chr13q32.3	1552938_at	NM_033132
2.05	2.02	0.02	8.50E-01	9.56E-01	---	---	---	1561362_at	---
3.05	3.01	0.05	8.50E-01	9.56E-01	---	---	---	1568611_at	---
2.09	2.06	0.02	8.51E-01	9.57E-01	---	---	---	241675_s_at	---
4.40	4.36	0.04	8.51E-01	9.57E-01	ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	chr9q34	220208_at	NM_139025 /// NM_139026 /// NM_139027
2.03	2.00	0.03	8.51E-01	9.57E-01	DSG4	desmoglein 4	chr18q12.1	1561330_at	NM_001134453 /// NM_177986
2.41	2.38	0.03	8.51E-01	9.57E-01	MDH1B	malate dehydrogenase 1B, NAD (soluble)	chr2q33.3	1558077_s_at	NM_001039845
3.21	3.18	0.03	8.51E-01	9.57E-01	DPEP3	dipeptidase 3	chr16q22.1	220179_at	NM_001129758 /// NM_022357
2.17	2.14	0.02	8.51E-01	9.57E-01	LOC148189	hypothetical protein LOC148189	chr19q12	1558256_at	---
2.14	2.11	0.03	8.51E-01	9.57E-01	KLHL22	kelch-like 22 (Drosophila)	chr22q11.21	222141_at	NM_032775
4.28	4.23	0.04	8.51E-01	9.57E-01	RBM38	RNA binding motif protein 38	chr20q13.31	212430_at	NM_017495 /// NM_183425
2.08	2.06	0.02	8.51E-01	9.57E-01	CXorf20	chromosome X open reading frame 20	chrXp22.13	1553842_at	NM_153346
3.11	3.08	0.03	8.51E-01	9.57E-01	LOC644538	hypothetical protein LOC644538	chrXq26.3	227976_at	XM_001715907 /// XM_927661 /// XM_939025
2.97	2.94	0.04	8.51E-01	9.57E-01	DIO3OS	DIO3 opposite strand (non-protein coding)	chr14q32.31	239727_at	NR_002770
4.79	4.72	0.07	8.51E-01	9.57E-01	ZNHIT6	zinc finger, HIT type 6	chr1p22.3	218932_at	NM_017953
5.59	5.54	0.05	8.51E-01	9.57E-01	FBXO16 /// ZNF395	F-box protein 16 /// zinc finger protein 395	chr8p21.1	232693_s_at	NM_018660 /// NM_172366
2.98	2.94	0.04	8.51E-01	9.57E-01	---	---	---	243680_at	---
3.92	3.89	0.03	8.51E-01	9.57E-01	---	---	---	1556345_s_at	---

2.59	2.56	0.03	8.51E-01	9.57E-01	UGT1A1 /// UGT1A10 /// UGT1A3 /// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 family, polypeptide A3 /// UDP glucuronosyltransferase 1 family, polypeptide A4 /// UDP glucuronosyltransferase 1 family, polypeptide A5 /// UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A7 /// UDP glucuronosyltransferase 1 family, polypeptide A8 /// UDP glucuronosyltransferase 1 family, polypeptide A9	chr2q37	215125_s_at	NM_000463 /// NM_001072 /// NM_007120 /// NM_019075 /// NM_019076 /// NM_019077 /// NM_019078 /// NM_019093 /// NM_021027 /// NM_205862
2.14	2.10	0.03	8.52E-01	9.57E-01	ZNF578	Zinc finger protein 578	chr19q13.41	1562245_a_at	NM_001099694
5.97	5.88	0.09	8.52E-01	9.57E-01	---	---	---	244185_at	---
2.30	2.27	0.03	8.52E-01	9.57E-01	SCGB2A1	secretoglobin, family 2A, member 1	chr11q13	205979_at	NM_002407
3.22	3.19	0.03	8.52E-01	9.57E-01	---	---	---	241333_x_at	---
2.57	2.55	0.03	8.52E-01	9.57E-01	LOC349114	hypothetical LOC349114	chr7p14.1	1558425_x_at	XR_040227 /// XR_040228 /// XR_040229 /// XR_040230
2.76	2.70	0.06	8.52E-01	9.57E-01	NUP160	nucleoporin 160kDa	chr11p11.2	212709_at	NM_015231
4.37	4.30	0.07	8.52E-01	9.57E-01	---	---	---	226192_at	---
2.59	2.57	0.02	8.52E-01	9.57E-01	IRAK3	Interleukin-1 receptor-associated kinase 3	chr12q14.3	1568830_at	NM_007199
2.91	2.87	0.04	8.52E-01	9.57E-01	FKSG2	apoptosis inhibitor	chr8p11.2	208588_at	NM_021631
2.09	2.07	0.02	8.52E-01	9.57E-01	---	---	---	242161_at	---
2.10	2.08	0.02	8.52E-01	9.57E-01	---	---	---	240739_at	---
2.38	2.35	0.03	8.52E-01	9.57E-01	CCDC132	coiled-coil domain containing 132	chr7q21.3	1554217_a_at	NM_017667 /// NM_024553
2.07	2.05	0.03	8.52E-01	9.57E-01	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	chr2q33.1	1569058_at	NM_012086
1.97	1.95	0.02	8.52E-01	9.57E-01	---	---	---	1561662_at	---
4.62	4.58	0.04	8.52E-01	9.57E-01	ST20	suppressor of tumorigenicity 20	chr15q25.1	210242_x_at	NM_001100879 /// NM_001100880
2.31	2.28	0.03	8.52E-01	9.57E-01	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	chr8p22-p21.3	207626_s_at	NM_001008539 /// NM_003046
5.31	5.25	0.05	8.52E-01	9.57E-01	WIPI2	WD repeat domain, phosphoinositide interacting 2	chr7p22.1	226986_at	NM_001033518 /// NM_001033519 /// NM_001033520 /// NM_015610 /// NM_016003
7.19	7.14	0.05	8.52E-01	9.57E-01	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	chr12q12-q13.11	225336_at	NM_004719
3.28	3.24	0.04	8.52E-01	9.57E-01	---	---	---	243735_at	---
4.77	4.71	0.06	8.52E-01	9.57E-01	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	chr8q12-q13	232149_s_at	NM_003580
3.84	3.78	0.05	8.52E-01	9.57E-01	LOC440104	Similar to RIKEN cDNA 1110012D08	chr12q13.2	1557124_at	XM_001721986 /// XM_001721988 /// XM_001721989 /// XM_001722083 /// XM_927712
2.59	2.57	0.03	8.52E-01	9.57E-01	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	chr12q24.31	1552923_a_at	NM_020845
7.88	7.84	0.04	8.53E-01	9.57E-01	---	---	---	229733_s_at	---
2.43	2.40	0.03	8.53E-01	9.57E-01	---	---	---	1561654_at	---
3.84	3.80	0.04	8.53E-01	9.57E-01	C1orf74	chromosome 1 open reading frame 74	chr1q32.2	229933_at	NM_152485
2.11	2.09	0.02	8.53E-01	9.57E-01	LOC285144	hypothetical protein LOC285144	chr2p25.3	1565685_at	---

2.41	2.38	0.03	8.53E-01	9.57E-01	---	---	---	243516_at	---
5.60	5.57	0.04	8.53E-01	9.57E-01	NFAM1	NFAT activating protein with ITAM motif 1	chr22q13.2	230322_at	NM_145912
2.15	2.13	0.02	8.53E-01	9.57E-01	---	---	---	240658_at	---
8.96	8.90	0.06	8.53E-01	9.57E-01	GHITM	growth hormone inducible transmembrane protein	chr10q23.1	209248_at	NM_014394
2.26	2.23	0.03	8.53E-01	9.57E-01	DNAH5	dynein, axonemal, heavy chain 5	chr5p15.2	243938_x_at	NM_001369
2.76	2.73	0.02	8.53E-01	9.57E-01	---	---	---	237197_at	---
2.50	2.48	0.03	8.53E-01	9.57E-01	LOC283435	hypothetical protein LOC283435	chr12q24.32	1561536_at	---
9.19	9.15	0.04	8.53E-01	9.57E-01	CFL1	cofilin 1 (non-muscle)	chr11q13	1555730_a_at	NM_005507
2.73	2.69	0.04	8.53E-01	9.57E-01	---	---	---	241337_at	---
4.52	4.48	0.04	8.53E-01	9.57E-01	CHAF1A	chromatin assembly factor 1, subunit A (p150)	chr19p13.3	203976_s_at	NM_005483
2.21	2.19	0.02	8.53E-01	9.57E-01	BRPF3	Bromodomain and PHD finger containing, 3	chr6p21	1565844_at	NM_015695
2.90	2.86	0.04	8.53E-01	9.58E-01	OR3A1	olfactory receptor, family 3, subfamily A, member 1	chr17p13.3	221353_at	NM_002550
2.08	2.06	0.02	8.54E-01	9.58E-01	---	---	---	241473_at	---
3.42	3.37	0.05	8.54E-01	9.58E-01	SENP5	SUMO1/sentrin specific peptidase 5	chr3q29	57703_at	NM_152699
2.81	2.78	0.04	8.54E-01	9.58E-01	---	---	---	242872_at	---
2.35	2.33	0.03	8.54E-01	9.58E-01	---	---	---	1559787_at	---
2.18	2.16	0.02	8.54E-01	9.58E-01	---	---	---	244553_at	---
6.06	6.02	0.04	8.54E-01	9.58E-01	---	---	---	226441_at	---
3.36	3.33	0.04	8.54E-01	9.58E-01	COX6B2	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	chr19q13.42	1553367_a_at	NM_144613
2.87	2.84	0.04	8.54E-01	9.58E-01	AIF1	allograft inflammatory factor 1	chr6p21.3	207823_s_at	NM_001623 /// NM_032955
2.41	2.38	0.03	8.54E-01	9.58E-01	---	---	---	1566709_at	---
2.17	2.15	0.03	8.54E-01	9.58E-01	WIPI2	WD repeat domain, phosphoinositide interacting 2	chr7p22.1	1570033_at	NM_001033518 /// NM_001033519 /// NM_001033520 /// NM_015610 /// NM_016003
6.44	6.41	0.03	8.54E-01	9.58E-01	TSPAN9	tetraspanin 9	chr12p13.33-p13.32	220968_s_at	NM_006675
5.13	5.07	0.06	8.54E-01	9.58E-01	---	---	---	239587_at	---
4.94	4.90	0.03	8.54E-01	9.58E-01	C9orf163	chromosome 9 open reading frame 163	chr9q34.3	1553642_at	NM_152571
3.08	3.04	0.03	8.55E-01	9.58E-01	---	---	---	231649_at	---
3.22	3.19	0.03	8.55E-01	9.58E-01	PSORS1C2	psoriasis susceptibility 1 candidate 2	chr6p21.3	220635_at	NM_014069
4.06	4.03	0.03	8.55E-01	9.58E-01	FOXN3	Forkhead box N3	chr14q31.3	229237_s_at	NM_001085471 /// NM_005197
2.58	2.55	0.03	8.55E-01	9.58E-01	---	---	---	1559538_at	---
2.27	2.24	0.03	8.55E-01	9.58E-01	---	---	---	215589_at	---
2.31	2.28	0.03	8.55E-01	9.58E-01	INDOL1	indoleamine-pyrrole 2,3 dioxygenase-like 1	chr8p11.21	1568638_a_at	NM_194294
3.21	3.18	0.03	8.55E-01	9.58E-01	---	---	---	236212_at	---
3.12	3.08	0.04	8.55E-01	9.58E-01	MSR1	macrophage scavenger receptor 1	chr8p22	211887_x_at	NM_002445 /// NM_138715 /// NM_138716
5.08	5.02	0.07	8.55E-01	9.58E-01	FAM122A	family with sequence similarity 122A	chr9q21.11	235043_at	NM_138333
3.09	3.05	0.04	8.55E-01	9.58E-01	---	---	---	216797_at	---
4.87	4.83	0.04	8.55E-01	9.58E-01	FLJ23185	hypothetical protein FLJ23185	chr22q11.22	207758_at	XR_040844 /// XR_040845 /// XR_040846
4.72	4.68	0.04	8.55E-01	9.58E-01	TUSC4	tumor suppressor candidate 4	chr3p21.3	210373_at	NM_006545
4.91	4.85	0.06	8.55E-01	9.58E-01	SPATA7	spermatogenesis associated 7	chr14q31.3	219583_s_at	NM_001040428 /// NM_018418
3.14	3.11	0.03	8.55E-01	9.58E-01	---	---	---	233966_at	---
1.88	1.86	0.02	8.55E-01	9.58E-01	---	---	---	1557692_a_at	---
2.09	2.07	0.02	8.55E-01	9.58E-01	---	---	---	243345_at	---
2.97	2.94	0.03	8.55E-01	9.58E-01	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	chr19q13.4	211245_x_at	NM_001080770 /// NM_001080772 /// NM_002255
2.14	2.12	0.02	8.55E-01	9.58E-01	---	---	---	217699_at	---
2.17	2.14	0.02	8.56E-01	9.59E-01	---	---	---	238318_at	---
2.79	2.77	0.02	8.56E-01	9.59E-01	C1orf49	chromosome 1 open reading frame 49	chr1q25.2	223938_at	NM_032126
3.07	3.04	0.03	8.56E-01	9.59E-01	---	---	---	1561484_at	---
2.62	2.60	0.02	8.56E-01	9.59E-01	---	---	---	239736_at	---
2.25	2.23	0.02	8.56E-01	9.59E-01	NFYB	nuclear transcription factor Y, beta	chr12q22-q23	244704_at	NM_006166
6.01	5.92	0.09	8.56E-01	9.59E-01	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	chr4q21.23	226185_at	NM_001263

2.88	2.86	0.03	8.56E-01	9.59E-01	CACNG7	calcium channel, voltage-dependent, gamma subunit 7	chr19q13.4	224137_at	NM_031896																			
3.27	3.23	0.04	8.56E-01	9.59E-01	---	---	---	217690_at	---																			
4.38	4.19	0.19	8.56E-01	9.59E-01	CD36	CD36 molecule (thrombospondin receptor)	chr7q11.2	228766_at	NM_000072 /// NM_001001547 /// NM_001001548 /// NM_001127443 /// NM_001127444																			
6.54	6.51	0.03	8.56E-01	9.59E-01	ABI2	abl interactor 2	chr2q33	225112_at	NM_005759																			
2.35	2.33	0.03	8.56E-01	9.59E-01	NR2E1	nuclear receptor subfamily 2, group E, member 1	chr6q21	207443_at	NM_003269																			
3.31	3.27	0.03	8.56E-01	9.59E-01	ZNF529	zinc finger protein 529	chr19q13.13	237453_at	NM_020951																			
6.62	6.57	0.05	8.56E-01	9.59E-01	GMFG	glia maturation factor, gamma	chr19q13.2	204220_at	NM_004877																			
6.72	6.67	0.06	8.56E-01	9.59E-01	C3orf17	chromosome 3 open reading frame 17	chr3q13.2	225281_at	NM_001025072 /// NM_001025073 /// NM_015412																			
2.50	2.47	0.04	8.56E-01	9.59E-01	RIBC1	RIB43A domain with coiled-coils 1	chrXp11.22	1553318_at	NM_001031745 /// NM_144968																			
4.66	4.62	0.04	8.56E-01	9.59E-01	LOC338799	hypothetical locus LOC338799	chr12q24.31	1556042_s_at	NR_002809																			
2.81	2.78	0.03	8.56E-01	9.59E-01	GINS4	GINS complex subunit 4 (Sld5 homolog)	chr8p11.21	211767_at	NM_032336																			
7.62	7.57	0.05	8.56E-01	9.59E-01	ICMT	isoprenylcysteine carboxyl methyltransferase	chr1p36.21	201609_x_at	NM_012405																			
4.01	3.98	0.03	8.56E-01	9.59E-01	---	---	---	233862_at	---																			
1.93	1.89	0.03	8.56E-01	9.59E-01	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	chr3p22	210286_s_at	NM_003615																			
2.32	2.30	0.02	8.56E-01	9.59E-01	ZNF831	zinc finger protein 831	chr20q13.32	1558826_at	NM_178457																			
6.55	6.52	0.03	8.56E-01	9.59E-01	MBD3	methyl-CpG binding domain protein 3	chr19p13.3	202463_s_at	NM_003926																			
3.66	3.62	0.04	8.57E-01	9.59E-01	NCKIPSD	NCK interacting protein with SH3 domain	chr3p21	216114_at	NM_016453 /// NM_184231																			
9.79	9.72	0.08	8.57E-01	9.59E-01	GPR98	G protein-coupled receptor 98	chr5q13	223582_at	NM_032119 /// NR_003149																			
2.66	2.63	0.03	8.57E-01	9.59E-01	ZNF300	zinc finger protein 300	chr5q33.1	228144_at	NM_052860																			
3.38	3.32	0.06	8.57E-01	9.59E-01	---	---	---	237216_at	---																			
2.18	2.16	0.02	8.57E-01	9.59E-01	TMEM67	transmembrane protein 67	chr8q22.1	1569377_at	NM_153704																			
2.88	2.86	0.02	8.57E-01	9.59E-01	C21orf84	chromosome 21 open reading frame 84	chr21q22.3	239968_at	XR_040120 /// XR_040121 /// XR_040122																			
5.39	5.35	0.04	8.57E-01	9.59E-01	SMOX	spermine oxidase	chr20p13	210357_s_at	NM_175839 /// NM_175840 /// NM_175841 /// NM_175842																			
2.98	2.93	0.04	8.57E-01	9.59E-01	DNAH17	dynein, axonemal, heavy chain 17	chr17q25.3	1553470_at	NM_173628																			

7.32	7.26	0.05	8.57E-01	9.59E-01	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily C, 5	chr5q31	215836_s_at	NM_002588 /// NM_003735 /// NM_003736 /// NM_014004 /// NM_018912 /// NM_018913 /// NM_018914 /// NM_018915 /// NM_018916 /// NM_018917 /// NM_018918 /// NM_018919 /// NM_018920 /// NM_018921 /// NM_018922 /// NM_018923 /// NM_018924 /// NM_018925 /// NM_018926 /// NM_018927 /// NM_018928 /// NM_018929 /// NM_031993 /// NM_032009 /// NM_032011 /// NM_032053 /// NM_032054 /// NM_032086 /// NM_032087 /// NM_032088 /// NM_032089 /// NM_032090 /// NM_032091 /// NM_032092 /// NM_032094 /// NM_032095 /// NM_032096 /// NM_032097 /// NM_032098 /// NM_032099 /// NM_032100 /// NM_032101 /// NM_032402 /// NM_032403 /// NM_032406 /// NM_032407																				
2.79	2.77	0.02	8.57E-01	9.59E-01	---	---	---	235161_at	---																				
3.81	3.77	0.04	8.57E-01	9.59E-01	NUP214	nucleoporin 214kDa	chr9q34.1	211261_at	NM_005085																				
2.18	2.15	0.03	8.57E-01	9.59E-01	RANBP10	RAN binding protein 10	chr16q22.1	232329_at	NM_020850																				
2.60	2.57	0.03	8.57E-01	9.59E-01	C20orf70	chromosome 20 open reading frame 70	chr20q11.21	237099_at	NM_080574																				
4.35	4.32	0.02	8.57E-01	9.59E-01	ORC6L	origin recognition complex, subunit 6 like (yeast)	chr16q12	219105_x_at	NM_014321																				
3.15	3.11	0.04	8.57E-01	9.59E-01	CHD1L	chromodomain helicase DNA binding protein 1-like	chr1q12	207645_s_at	NM_004284																				
2.92	2.87	0.05	8.57E-01	9.59E-01	---	---	---	230053_at	---																				
3.19	3.16	0.03	8.57E-01	9.59E-01	---	---	---	236252_at	---																				
2.17	2.16	0.02	8.58E-01	9.59E-01	AKAP14	A kinase (PRKA) anchor protein 14	chrXq24	242698_at	NM_001008534 /// NM_001008535 /// NM_178813																				
2.80	2.77	0.03	8.58E-01	9.59E-01	HRASLS2	HRAS-like suppressor 2	chr11q12.3	221122_at	NM_017878																				
3.08	3.06	0.02	8.58E-01	9.59E-01	FAM170B	family with sequence similarity 170, member B	chr10q11.22	1559828_at	XM_001715115 /// XM_096317 /// XM_937528																				
2.36	2.34	0.02	8.58E-01	9.59E-01	PIH1D2	PIH1 domain containing 2	chr11q23.1	235062_at	NM_001082619 /// NM_138789																				
3.81	3.76	0.05	8.58E-01	9.59E-01	CTPS2	CTP synthase II	chrXp22	219080_s_at	NM_019857 /// NM_175859																				
2.20	2.18	0.02	8.58E-01	9.59E-01	---	---	---	240580_at	---																				

8.41	8.35	0.06	8.58E-01	9.59E-01	LOC100129361	hypothetical protein LOC100129361	chr12p13.2	221847_at	XM_001721915 /// XM_001723199 /// XM_001723624																			
2.33	2.31	0.02	8.58E-01	9.59E-01	---	---	---	1561050_a_at	---																			
9.60	9.56	0.04	8.58E-01	9.59E-01	ZNF275	zinc finger protein 275	chrXq28	225382_at	NM_001080485																			
3.95	3.91	0.04	8.58E-01	9.59E-01	---	---	---	232478_at	---																			
3.73	3.70	0.03	8.58E-01	9.59E-01	BAIAP3	BAI1-associated protein 3	chr16p13.3	204874_x_at	NM_003933																			
1.95	1.92	0.02	8.58E-01	9.59E-01	PHIP	pleckstrin homology domain interacting protein	chr6q14	1557363_a_at	NM_017934																			
3.61	3.53	0.09	8.58E-01	9.59E-01	MUSTN1	musculoskeletal, embryonic nuclear protein 1	chr3p21.1	226856_at	NM_205853																			
5.13	5.10	0.03	8.58E-01	9.59E-01	PARVB	parvin, beta	chr22q13.2-q13.33	216253_s_at	NM_001003828 /// NM_013327																			
4.14	4.09	0.06	8.58E-01	9.59E-01	JARID1A	jumonji, AT rich interactive domain 1A	chr12p11	230226_s_at	NM_001042603 /// NM_005056																			
3.53	3.49	0.04	8.58E-01	9.59E-01	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	chr20q12	211573_x_at	NM_004613 /// NM_198951																			
2.30	2.27	0.03	8.58E-01	9.59E-01	---	---	---	1560306_at	---																			
2.17	2.14	0.03	8.58E-01	9.59E-01	---	---	---	1560979_a_at	---																			
3.33	3.25	0.08	8.58E-01	9.59E-01	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	chr12p12.3	235996_at	NM_007211																			
2.18	2.15	0.03	8.58E-01	9.59E-01	SV2C	synaptic vesicle glycoprotein 2C	chr5q13.3	1562372_at	NM_014979																			
5.72	5.68	0.04	8.58E-01	9.59E-01	NAPB	N-ethylmaleimide-sensitive factor attachment protein, beta	chr20p12.3-p11.21	225111_s_at	NM_022080																			
2.56	2.52	0.04	8.58E-01	9.59E-01	SETD5	SET domain containing 5	chr3p25.3	244691_at	NM_001080517																			
1.92	1.90	0.03	8.58E-01	9.59E-01	LHX8	LIM homeobox 8	chr1p31.1	1569469_a_at	NM_001001933																			
2.55	2.53	0.03	8.58E-01	9.59E-01	C14orf48	chromosome 14 open reading frame 48	chr14q32.13	1553053_at	NM_152777																			
2.21	2.19	0.02	8.58E-01	9.59E-01	---	---	---	1557993_at	---																			
5.75	5.72	0.03	8.59E-01	9.59E-01	LOC100131941	Hypothetical protein LOC100131941	chr13q14.3	1557817_a_at	XM_001714946 /// XM_001716781 /// XM_001718409																			
7.63	7.59	0.04	8.59E-01	9.59E-01	WDR22	WD repeat domain 22	chr14q23-q24.1	224703_at	NM_003861																			
4.62	4.56	0.07	8.59E-01	9.59E-01	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	chr17p11.2	228900_at	NM_001033553 /// NM_001033554 /// NM_001033555 /// NM_152904																			
2.85	2.81	0.03	8.59E-01	9.59E-01	XPO4	exportin 4	chr13q11	218479_s_at	NM_022459																			
2.86	2.82	0.04	8.59E-01	9.59E-01	C1orf183	chromosome 1 open reading frame 183	chr1p13.2	241809_at	NM_019099 /// NM_198926																			
3.76	3.73	0.04	8.59E-01	9.59E-01	---	---	---	1561107_at	---																			
1.96	1.94	0.02	8.59E-01	9.59E-01	---	---	---	1568784_at	---																			
5.66	5.61	0.05	8.59E-01	9.59E-01	MGC2752	hypothetical LOC65996	chr19q13.43	222694_at	XR_039990 /// XR_039991																			
7.57	7.51	0.06	8.59E-01	9.59E-01	TXNDC13	thioredoxin domain containing 13	chr20p12	201581_at	NM_021156																			
2.25	2.23	0.02	8.59E-01	9.59E-01	DMP1	dentin matrix acidic phosphoprotein 1	chr4q21	217067_s_at	NM_001079911 /// NM_004407																			
6.09	6.06	0.03	8.59E-01	9.59E-01	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	chr17q21	209853_s_at	NM_005789 /// NM_176863																			
2.44	2.42	0.02	8.59E-01	9.59E-01	GABRQ	gamma-aminobutyric acid (GABA) receptor, theta	chrXq28	220886_at	NM_018558																			
4.74	4.70	0.05	8.59E-01	9.59E-01	FAM80B	family with sequence similarity 80, member B	chr12p13.31	225978_at	NM_020734																			
2.71	2.68	0.03	8.59E-01	9.60E-01	CNTNAP2	contactin associated protein-like 2	chr7q35-q36	215145_s_at	NM_014141																			
4.70	4.67	0.04	8.59E-01	9.60E-01	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	chr18q23	210162_s_at	NM_006162 /// NM_172387 /// NM_172388 /// NM_172389 /// NM_172390																			

2.60	2.58	0.02	8.59E-01	9.60E-01	MERTK	c-mer proto-oncogene tyrosine kinase	chr2q14.1	211912_at	NM_006343
2.19	2.17	0.02	8.60E-01	9.60E-01	---	---	---	1557753_at	---
2.77	2.74	0.03	8.60E-01	9.60E-01	SOS2	Son of sevenless homolog 2 (Drosophila)	chr14q21	238830_at	NM_006939
2.25	2.23	0.02	8.60E-01	9.60E-01	FMN2	formin 2	chr1q43	1559244_at	NM_020066
10.00	9.97	0.04	8.60E-01	9.60E-01	LOC441533	60S ribosomal protein L26 pseudogene	chrYp11.2	222229_x_at	XR_016751 /// XR_038702
3.32	3.29	0.03	8.60E-01	9.60E-01	---	---	---	230428_at	---
7.99	7.96	0.03	8.60E-01	9.60E-01	HYPK	Huntingtin interacting protein K	chr15q15.3	233746_x_at	NM_016400
2.18	2.16	0.02	8.60E-01	9.60E-01	---	---	---	1562690_at	---
4.21	4.14	0.07	8.60E-01	9.60E-01	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	chr4p14-p12	213106_at	NM_001105529 /// NM_006095
3.76	3.72	0.05	8.60E-01	9.60E-01	---	---	---	238604_at	---
6.50	6.45	0.04	8.60E-01	9.60E-01	SERBP1	SERPINE1 mRNA binding protein 1	chr1p31	210076_x_at	NM_001018067 /// NM_001018068 /// NM_001018069 /// NM_015640
2.34	2.30	0.03	8.60E-01	9.60E-01	SCGB1D2	secretoglobin, family 1D, member 2	chr11q13	206799_at	NM_006551
2.83	2.80	0.03	8.60E-01	9.60E-01	CRHR2	corticotropin releasing hormone receptor 2	chr7p15.1	207897_at	NM_001883
4.10	4.06	0.04	8.60E-01	9.60E-01	---	---	---	227749_at	---
4.36	4.33	0.03	8.60E-01	9.60E-01	FGL1	fibrinogen-like 1	chr8p22|8p22-p21.3	205305_at	NM_004467 /// NM_147203 /// NM_201552 /// NM_201553 /// XM_001722880
6.15	6.12	0.02	8.60E-01	9.60E-01	GOLGA2	golgi autoantigen, golgin subfamily a, 2	chr9q34.11	35436_at	NM_004486
2.21	2.19	0.02	8.60E-01	9.60E-01	---	---	---	224034_at	---
5.19	5.16	0.03	8.60E-01	9.60E-01	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	chr14q22.3	212497_at	NM_144578
2.01	2.00	0.02	8.60E-01	9.60E-01	---	---	---	1556936_at	---
2.84	2.79	0.05	8.60E-01	9.60E-01	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	chr12q24.11	235744_at	NM_139283
5.22	5.14	0.08	8.61E-01	9.60E-01	HSF2	heat shock transcription factor 2	chr6q22.31	209657_s_at	NM_004506
3.84	3.77	0.07	8.61E-01	9.60E-01	FAM29A	family with sequence similarity 29, member A	chr9p22.1	222685_at	NM_017645
6.64	6.59	0.05	8.61E-01	9.60E-01	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	chr19p13.3	212518_at	NM_012398
2.78	2.74	0.04	8.61E-01	9.60E-01	---	---	---	1556650_at	---
6.32	6.22	0.10	8.61E-01	9.60E-01	---	---	---	240263_at	---
4.31	4.26	0.05	8.61E-01	9.60E-01	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	chr7q21-q22.1	211843_x_at	NM_000765
3.98	3.94	0.04	8.61E-01	9.60E-01	C2orf57	chromosome 2 open reading frame 57	chr2q37.1	238187_at	NM_152614
3.97	3.88	0.09	8.61E-01	9.60E-01	---	---	---	230764_at	---
2.45	2.43	0.02	8.61E-01	9.60E-01	---	---	---	235846_at	---
11.72	11.70	0.02	8.61E-01	9.60E-01	ACTG1	actin, gamma 1	chr17q25	211970_x_at	NM_001614
2.20	2.17	0.03	8.61E-01	9.60E-01	FRYL	FRY-like	chr4p12	1562625_at	NM_015030
2.29	2.27	0.02	8.61E-01	9.60E-01	---	---	---	244799_s_at	---
2.40	2.37	0.03	8.61E-01	9.60E-01	LOC283999	hypothetical protein LOC283999	chr17q25.3	1564040_a_at	XM_001726188 /// XM_211287 /// XM_941058
3.28	3.24	0.04	8.61E-01	9.60E-01	AMACR	alpha-methylacyl-CoA racemase	chr5p13	217113_at	NM_014324 /// NM_203382
2.33	2.30	0.03	8.61E-01	9.60E-01	DRD3	dopamine receptor D3	chr3q13.3	214559_at	NM_000796 /// NM_033663
5.59	5.51	0.08	8.61E-01	9.60E-01	C6orf120	chromosome 6 open reading frame 120	chr6q27	221787_at	NM_001029863
2.78	2.75	0.03	8.61E-01	9.60E-01	JMJD2B	Jumonji domain containing 2B	chr19p13.3	230126_s_at	NM_015015
2.71	2.68	0.03	8.61E-01	9.60E-01	---	---	---	229214_at	---
2.12	2.10	0.02	8.61E-01	9.60E-01	LPAR4	lysophosphatidic acid receptor 4	chrXq13-q21.1	206960_at	NM_005296
2.58	2.55	0.02	8.61E-01	9.60E-01	---	---	---	1570262_at	---
3.32	3.28	0.04	8.61E-01	9.60E-01	GSTA1	Glutathione S-transferase A1	chr6p12.1	215766_at	NM_145740
2.62	2.60	0.02	8.62E-01	9.60E-01	MOGAT1	monoacylglycerol O-acyltransferase 1	chr2q36.1	1553062_at	NM_058165
2.29	2.27	0.02	8.62E-01	9.60E-01	---	---	---	237476_at	---
2.66	2.63	0.04	8.62E-01	9.60E-01	ZNF623	zinc finger protein 623	chr8q24.3	206188_at	NM_001082480 /// NM_014789
3.22	3.19	0.04	8.62E-01	9.60E-01	---	---	---	244874_at	---
2.44	2.41	0.03	8.62E-01	9.60E-01	BMP7	bone morphogenetic protein 7	chr20q13	209591_s_at	NM_001719

5.04	5.01	0.02	8.62E-01	9.60E-01	IDS	iduronate 2-sulfatase	chrXq28	210666_at	NM_000202 /// NM_006123																				
9.61	9.57	0.04	8.62E-01	9.60E-01	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	chr11p15.3	200055_at	NM_006284																				
6.01	5.96	0.05	8.62E-01	9.60E-01	MFSD10	major facilitator superfamily domain containing 10	chr4p16.3	209215_at	NM_001120																				
2.29	2.26	0.03	8.62E-01	9.60E-01	---	---	---	240130_at	---																				
2.40	2.38	0.02	8.62E-01	9.60E-01	---	---	---	1566528_at	---																				
7.49	7.44	0.05	8.62E-01	9.60E-01	VEZF1	vascular endothelial zinc finger 1	chr17q22	202171_at	NM_007146																				
2.15	2.13	0.02	8.62E-01	9.60E-01	GSTK1	Glutathione S-transferase kappa 1	---	243325_at	NM_015917																				
7.35	7.30	0.05	8.62E-01	9.60E-01	ICMT	isoprenylcysteine carboxyl methyltransferase	chr1p36.21	201611_s_at	NM_012405																				
3.41	3.38	0.02	8.62E-01	9.60E-01	---	---	---	239709_at	---																				
8.07	8.03	0.04	8.62E-01	9.60E-01	UBE2R2	ubiquitin-conjugating enzyme E2R 2	chr9p13.3	223014_at	NM_017811																				
4.96	4.93	0.04	8.62E-01	9.60E-01	SLC34A3	solute carrier family 34 (sodium phosphate), member 3	chr9q34	1552510_at	NM_080877																				
2.31	2.29	0.02	8.62E-01	9.60E-01	---	---	---	231418_at	---																				
6.32	6.24	0.08	8.62E-01	9.60E-01	---	---	---	213396_s_at	---																				
5.35	5.19	0.16	8.62E-01	9.60E-01	SFRP2	secreted frizzled-related protein 2	chr4q31.3	223122_s_at	NM_003013																				
3.31	3.26	0.05	8.62E-01	9.60E-01	---	---	---	239489_at	---																				
6.21	6.13	0.08	8.62E-01	9.60E-01	SNAI2	snail homolog 2 (Drosophila)	chr8q11	213139_at	NM_003068																				
2.13	2.11	0.02	8.62E-01	9.60E-01	---	---	---	1569372_at	---																				
3.53	3.50	0.02	8.62E-01	9.60E-01	GSDMB	gasdermin B	chr17q12	219233_s_at	NM_001042471 /// NM_018530																				
2.09	2.06	0.03	8.62E-01	9.60E-01	KERA	keratocan	chr12q22	220504_at	NM_007035																				
9.20	9.11	0.09	8.63E-01	9.60E-01	GOLM1	golgi membrane protein 1	chr9q21.33	217771_at	NM_016548 /// NM_177937																				
3.87	3.83	0.04	8.63E-01	9.61E-01	ZNF25	zinc finger protein 25	chr10p11.21	228185_at	NM_145011																				
2.16	2.14	0.02	8.63E-01	9.61E-01	---	---	---	244241_x_at	---																				
2.80	2.76	0.04	8.63E-01	9.61E-01	---	---	---	242073_at	---																				
2.11	2.08	0.03	8.63E-01	9.61E-01	FKBP14	FK506 binding protein 14, 22 kDa	chr7p15.1	235311_at	NM_017946																				
2.16	2.14	0.02	8.63E-01	9.61E-01	---	---	---	237488_at	---																				
3.82	3.80	0.03	8.63E-01	9.61E-01	---	---	---	1562799_at	---																				
3.47	3.43	0.03	8.63E-01	9.61E-01	RAB21	RAB21, member RAS oncogene family	chr12q21.1	226268_at	NM_014999																				
2.57	2.54	0.02	8.63E-01	9.61E-01	HAPLN4 /// TM6SF2	hyaluronan and proteoglycan link protein 4 /// transmembrane 6 superfamily member 2	chr19p13.1 /// chr19p13.3-p12	234092_s_at	NM_001001524 /// NM_023002																				
3.14	3.11	0.03	8.63E-01	9.61E-01	PNMA3	paraneoplastic antigen MA3	chrXq28	223621_at	NM_013364																				
2.87	2.85	0.02	8.63E-01	9.61E-01	---	---	---	1561135_at	---																				
5.88	5.85	0.03	8.63E-01	9.61E-01	SYMPK	symplekin	chr19q13.3	202339_at	NM_004819																				
2.07	2.05	0.02	8.63E-01	9.61E-01	---	---	---	1554225_a_at	---																				
2.55	2.52	0.03	8.63E-01	9.61E-01	PDE12	Phosphodiesterase 12	chr3p14.3	214826_at	NM_177966																				
2.75	2.73	0.02	8.63E-01	9.61E-01	LOC100128098	hypothetical protein LOC100128098	chr10p12.33	242350_s_at	XM_001721625 /// XM_001722654 /// XM_001725654																				
2.55	2.52	0.03	8.63E-01	9.61E-01	HNMT	histamine N-methyltransferase	chr2q22.1	204110_at	NM_001024074 /// NM_001024075 /// NM_006895																				
2.65	2.63	0.02	8.63E-01	9.61E-01	LYPD6	LY6/PLAUR domain containing 6	chr2q23.2	239028_at	NM_194317																				
2.30	2.28	0.02	8.63E-01	9.61E-01	---	---	---	239199_at	---																				
8.44	8.42	0.03	8.63E-01	9.61E-01	VDAC1	voltage-dependent anion channel 1	chr5q31	212038_s_at	NM_003374																				
2.05	2.04	0.02	8.63E-01	9.61E-01	---	---	---	239767_at	---																				
2.37	2.34	0.02	8.63E-01	9.61E-01	VRK3	vaccinia related kinase 3	chr19q13	239190_at	NM_001025778 /// NM_016440																				
5.23	5.19	0.04	8.63E-01	9.61E-01	DMWD	dystrophia myotonica, WD repeat containing	chr19q13.3	1554429_a_at	NM_004943																				
2.87	2.84	0.03	8.64E-01	9.61E-01	---	---	---	1566837_at	---																				
2.46	2.43	0.03	8.64E-01	9.61E-01	---	---	---	1562720_at	---																				
5.18	5.12	0.07	8.64E-01	9.61E-01	C10orf18	chromosome 10 open reading frame 18	chr10p15.1	218331_s_at	NM_017782																				
2.30	2.29	0.02	8.64E-01	9.61E-01	---	---	---	240461_at	---																				
2.14	2.11	0.02	8.64E-01	9.61E-01	HUS1	HUS1 checkpoint homolog (S. pombe)	chr7p13-p12	204884_s_at	NM_004507																				
4.22	4.17	0.05	8.64E-01	9.61E-01	CD33	CD33 molecule	chr19q13.3	206120_at	NM_001082618 /// NM_001772																				
2.91	2.89	0.02	8.64E-01	9.61E-01	---	---	---	1556155_at	---																				
4.29	4.27	0.02	8.64E-01	9.61E-01	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	chr3q29	214739_at	NM_032773																				
2.27	2.24	0.03	8.64E-01	9.61E-01	SNF1LK2	SNF1-like kinase 2	chr11q23.1	215752_at	NM_015191																				
2.56	2.55	0.02	8.64E-01	9.61E-01	PABPC4L	poly(A) binding protein, cytoplasmic 4-like	chr4q28.3	238865_at	NM_001114734 /// NR_003550																				

2.41	2.39	0.02	8.64E-01	9.61E-01	C21orf128	chromosome 21 open reading frame 128	chr21q22.3	1553282_at	XR_040363 /// XR_040364 /// XR_040365																				
7.21	7.18	0.03	8.64E-01	9.61E-01	MSI2	musashi homolog 2 (Drosophila)	chr17q22	243579_at	NM_138962 /// NM_170721																				
4.62	4.58	0.05	8.64E-01	9.61E-01	---	---	---	242590_at	---																				
3.76	3.74	0.02	8.64E-01	9.61E-01	FLJ13769	hypothetical protein FLJ13769	chr12q24.31	220719_at	XR_040824 /// XR_040825 /// XR_040826																				
3.53	3.50	0.03	8.64E-01	9.61E-01	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	chr11q12.3	213210_at	NM_006473																				
5.49	5.39	0.10	8.64E-01	9.61E-01	HSPD1	heat shock 60kDa protein 1 (chaperonin)	chr2q33.1	241716_at	NM_002156 /// NM_199440																				
2.27	2.24	0.02	8.64E-01	9.61E-01	---	---	---	231156_at	---																				
2.36	2.35	0.02	8.64E-01	9.61E-01	---	---	---	236162_at	---																				
2.51	2.48	0.02	8.64E-01	9.61E-01	ZNF530	zinc finger protein 530	chr19q13.43	232228_at	NM_020880																				
3.15	3.13	0.02	8.64E-01	9.61E-01	TPPP	tubulin polymerization promoting protein	chr5p15.3	230104_s_at	NM_007030																				
8.18	8.16	0.03	8.64E-01	9.61E-01	SAMM50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	chr22q13.31	201570_at	NM_015380																				
4.67	4.58	0.09	8.64E-01	9.61E-01	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	chr15q24	201878_at	NM_005744																				
2.79	2.77	0.03	8.64E-01	9.61E-01	---	---	---	242667_at	---																				
5.04	5.00	0.04	8.64E-01	9.61E-01	C1orf127	chromosome 1 open reading frame 127	chr1p36.22	1553444_a_at	NM_173507																				
5.85	5.78	0.07	8.65E-01	9.61E-01	---	---	---	225412_at	---																				
6.08	6.04	0.04	8.65E-01	9.61E-01	SHROOM1	shroom family member 1	chr5q31.1	239435_x_at	NM_133456																				
2.68	2.64	0.03	8.65E-01	9.61E-01	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	chr12q12	234561_at	NM_052885																				
8.76	8.73	0.03	8.65E-01	9.61E-01	GNAS	GNAS complex locus	chr20q13.3	217673_x_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259																				
2.71	2.68	0.03	8.65E-01	9.61E-01	KRTAP9-2 /// KRTAP9-8	keratin associated protein 9-2 /// keratin associated protein 9-8	chr17q12-q21	233631_x_at	NM_031961 /// NM_031963																				
4.53	4.49	0.04	8.65E-01	9.61E-01	---	---	---	239133_at	---																				
3.38	3.34	0.04	8.65E-01	9.61E-01	LINS1	lines homolog 1 (Drosophila)	chr15q26.3	231976_at	NM_001040614 /// NM_001040615 /// NM_001040616 /// NM_018148																				
7.15	7.09	0.06	8.65E-01	9.61E-01	DEK	DEK oncogene	chr6p22.3	200934_at	NM_001134709 /// NM_003472																				
2.05	2.03	0.02	8.65E-01	9.61E-01	---	---	---	1562084_at	---																				
2.16	2.14	0.02	8.65E-01	9.61E-01	LOC644242	Hypothetical protein LOC644242	chr1p12	1558404_at	XM_927425																				
9.66	9.61	0.05	8.65E-01	9.61E-01	C1QC	complement component 1, q subcomponent, C chain	chr1p36.11	225353_s_at	NM_001114101 /// NM_172369																				
2.29	2.27	0.02	8.65E-01	9.61E-01	DNAH6	dynein, axonemal, heavy chain 6	---	1565338_x_at	NM_001370																				
2.09	2.07	0.02	8.65E-01	9.61E-01	---	---	---	1557739_at	---																				
4.64	4.59	0.05	8.65E-01	9.61E-01	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	chr11p15.3	212472_at	NM_014632																				
7.72	7.64	0.08	8.65E-01	9.61E-01	RHOBTB3	Rho-related BTB domain containing 3	chr5q15	202976_s_at	NM_014899																				

4.48	4.45	0.04	8.65E-01	9.61E-01	ATRIP /// TREX1	ATR interacting protein /// three prime repair exonuclease 1	chr3p21.31	1552937_s_at	NM_016381 /// NM_032166 /// NM_033629 /// NM_130384																			
2.13	2.11	0.02	8.65E-01	9.61E-01	---	---	---	1570639_at	---																			
9.93	9.91	0.03	8.65E-01	9.61E-01	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	chr21q21.1	202325_s_at	NM_001003696 /// NM_001003697 /// NM_001003701 /// NM_001003703 /// NM_001685																			
2.66	2.62	0.04	8.65E-01	9.61E-01	---	---	---	236626_at	---																			
2.14	2.12	0.02	8.66E-01	9.61E-01	FSD1L	fibronectin type III and SPRY domain containing 1-like	chr9q31	230904_at	NM_031919 /// NM_207647																			
7.77	7.70	0.07	8.66E-01	9.61E-01	CYR61	cysteine-rich, angiogenic inducer, 61	chr1p31-p22	201289_at	NM_001554																			
2.13	2.11	0.02	8.66E-01	9.61E-01	---	---	---	216444_at	---																			
2.24	2.22	0.03	8.66E-01	9.61E-01	---	---	---	230809_at	---																			
2.26	2.23	0.02	8.66E-01	9.61E-01	FLJ30403	hypothetical protein LOC729975	chr19q13.33	1559093_at	XM_001134208 /// XM_001134327 /// XM_001726038																			
2.49	2.47	0.02	8.66E-01	9.61E-01	TAS2R1	taste receptor, type 2, member 1	chr5p15	221324_at	NM_019599																			
5.98	5.91	0.08	8.66E-01	9.61E-01	RNF19A	ring finger protein 19A	chr8q22	223085_at	NM_015435 /// NM_183419																			
2.85	2.79	0.06	8.66E-01	9.61E-01	ZNF571	zinc finger protein 571	chr19q13.12	206648_at	NM_016536																			
3.57	3.54	0.04	8.66E-01	9.61E-01	---	---	---	237653_at	---																			
2.14	2.12	0.02	8.66E-01	9.61E-01	CEP290	centrosomal protein 290kDa	chr12q21.32	221683_s_at	NM_025114																			
2.26	2.24	0.02	8.66E-01	9.61E-01	TWF1	Twinfilin, actin-binding protein, homolog 1 (Drosophila)	chr12q12	214008_at	NM_002822																			
3.46	3.43	0.04	8.66E-01	9.62E-01	SLC1A7	solute carrier family 1 (glutamate transporter), member 7	chr1p32.3	207355_at	NM_006671																			
2.11	2.09	0.02	8.66E-01	9.62E-01	---	---	---	1563091_at	---																			
5.61	5.57	0.04	8.66E-01	9.62E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	209360_s_at	NM_001001890 /// NM_001122607 /// NM_001754																			
2.59	2.56	0.03	8.66E-01	9.62E-01	ICOSLG	inducible T-cell co-stimulator ligand	chr21q22.3	211199_s_at	NM_015259																			
2.15	2.12	0.02	8.66E-01	9.62E-01	C12orf33	chromosome 12 open reading frame 33	chr12p13.31	1555040_at	XR_041988 /// XR_041989 /// XR_041990																			
4.78	4.72	0.06	8.66E-01	9.62E-01	TMEM53	transmembrane protein 53	chr1p34.1	219462_at	NM_024587																			
3.37	3.34	0.03	8.67E-01	9.62E-01	---	---	---	211869_at	---																			
4.39	4.36	0.03	8.67E-01	9.62E-01	---	---	---	1566232_at	---																			
3.59	3.55	0.04	8.67E-01	9.62E-01	---	---	---	235875_at	---																			
2.36	2.34	0.02	8.67E-01	9.62E-01	ZNF594	zinc finger protein 594	chr17p13	235690_at	NM_032530																			
2.55	2.52	0.03	8.67E-01	9.62E-01	ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	chr4q21-q24|4q22	231675_s_at	NM_000670																			
4.54	4.50	0.04	8.67E-01	9.62E-01	ZNF318	zinc finger protein 318	chr6pter-p12.1	203520_s_at	NM_014345																			
3.90	3.84	0.06	8.67E-01	9.62E-01	LOC646576	hypothetical LOC646576	chr4q31.22	236632_at	XR_041422 /// XR_041423																			
2.82	2.75	0.07	8.67E-01	9.62E-01	ZNF638	zinc finger protein 638	chr2p13.2-p13.1	1554249_a_at	NM_001014972 /// NM_014497																			
2.68	2.66	0.03	8.67E-01	9.62E-01	CCNO	cyclin O	chr5p15.2-p13.1	210021_s_at	NM_021147																			
2.48	2.46	0.02	8.67E-01	9.62E-01	KCTD4	potassium channel tetramerisation domain containing 4	chr13q14.12	239787_at	NM_198404																			
1.77	1.75	0.02	8.67E-01	9.62E-01	---	---	---	241647_x_at	---																			
2.19	2.17	0.02	8.67E-01	9.62E-01	LOC100128687	Hypothetical protein LOC100128687	chr8q21.3	1558440_at	XM_001716979 /// XM_001717014 /// XM_001717131																			
4.26	4.24	0.03	8.67E-01	9.62E-01	ARVCF	Armadillo repeat gene deletes in velocardiofacial syndrome	chr22q11.21	216204_at	NM_001670																			
2.42	2.39	0.02	8.67E-01	9.62E-01	C9orf16	chromosome 9 open reading frame 16	chr9q34.1	222166_at	NM_024112																			

2.18	2.15	0.02	8.67E-01	9.62E-01	---	---	---	241089_at	---
3.17	3.14	0.03	8.67E-01	9.62E-01	FUT6	Fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	1565661_x_at	NM_000150 /// NM_001040701
7.47	7.35	0.12	8.67E-01	9.62E-01	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	chr13q32-q34	223502_s_at	NM_006573
3.66	3.63	0.03	8.67E-01	9.62E-01	KCNS1	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1	chr20q12	207366_at	NM_002251
5.03	4.97	0.06	8.67E-01	9.62E-01	TRIM38	tripartite motif-containing 38	chr6p21.3	203610_s_at	NM_006355
2.68	2.66	0.02	8.67E-01	9.62E-01	LOC283697	hypothetical protein LOC283697	chr15q13.1	1557406_s_at	---
3.27	3.25	0.02	8.67E-01	9.62E-01	---	---	---	1566186_at	---
2.95	2.92	0.03	8.68E-01	9.62E-01	ZCCHC14	zinc finger, CCHC domain containing 14	chr16q24.2	215426_at	NM_015144
3.01	2.99	0.02	8.68E-01	9.62E-01	CCDC147	coiled-coil domain containing 147	chr10q25.1	233131_at	NM_001008723
2.44	2.41	0.03	8.68E-01	9.62E-01	TRHR	thyrotropin-releasing hormone receptor	chr8q23	211438_at	NM_003301
4.23	4.19	0.04	8.68E-01	9.62E-01	CCDC102A	coiled-coil domain containing 102A	chr16q13	232051_at	NM_033212
2.19	2.17	0.02	8.68E-01	9.62E-01	TTC17	tetratricopeptide repeat domain 17	chr11p12-p11.2	244416_at	NM_018259
2.94	2.92	0.02	8.68E-01	9.62E-01	NAT8B	N-acetyltransferase 8B (gene/pseudogene)	chr2p13.2	206964_at	NM_016347
3.32	3.30	0.03	8.68E-01	9.62E-01	---	---	---	236958_at	---
7.26	7.22	0.04	8.68E-01	9.62E-01	PHLDB1	pleckstrin homology-like domain, family B, member 1	chr11q23.3	212134_at	NM_015157
2.76	2.74	0.02	8.68E-01	9.62E-01	MKL1	Megakaryoblastic leukemia (translocation) 1	chr22q13	1555763_x_at	NM_020831
5.71	5.69	0.02	8.68E-01	9.62E-01	TMEM19	transmembrane protein 19	chr12q21.1	229126_at	NM_018279
2.38	2.36	0.02	8.68E-01	9.62E-01	---	---	---	237170_at	---
3.37	3.33	0.04	8.68E-01	9.62E-01	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	chr10q11.2-q21	214590_s_at	NM_003338
4.18	4.09	0.09	8.68E-01	9.62E-01	TOR1AIP1	torsin A interacting protein 1	chr1q24.2	216100_s_at	NM_015602
2.73	2.69	0.03	8.68E-01	9.62E-01	---	---	---	1569832_at	---
2.05	2.03	0.02	8.69E-01	9.62E-01	FLJ35848	hypothetical protein FLJ35848	chr17q21.31	1562484_at	NM_001033659
2.51	2.48	0.03	8.69E-01	9.62E-01	GLS2	glutaminase 2 (liver, mitochondrial)	chr12q13	1564706_s_at	NM_013267
2.29	2.26	0.03	8.69E-01	9.62E-01	NEK3	NIMA (never in mitosis gene a)-related kinase 3	chr13q14.13	211089_s_at	NM_002498 /// NM_152720
3.51	3.48	0.03	8.69E-01	9.62E-01	EPHA1	EPH receptor A1	chr7q34	215804_at	NM_005232
2.56	2.52	0.04	8.69E-01	9.62E-01	LOX	lysyl oxidase	chr5q23.2	213640_s_at	NM_002317
2.12	2.09	0.03	8.69E-01	9.62E-01	ZNF157	zinc finger protein 157	chrXp11.2	208019_at	NM_003446
2.47	2.44	0.02	8.69E-01	9.63E-01	DNAH1	Dynein, axonemal, heavy chain 1	chr3p21.1	1566776_at	NM_015512
9.70	9.67	0.03	8.69E-01	9.63E-01	SEC11A	SEC11 homolog A (S. cerevisiae)	chr15q25.3	201290_at	NM_014300
2.24	2.22	0.02	8.69E-01	9.63E-01	---	---	---	1561144_at	---
2.62	2.60	0.02	8.69E-01	9.63E-01	LOC100133898	similar to anaphase promoting complex subunit 1	---	230037_at	XM_001726697
3.39	3.35	0.04	8.69E-01	9.63E-01	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	chr7q22	203730_s_at	NM_014569 /// NM_145102
5.14	5.10	0.04	8.69E-01	9.63E-01	LAT /// SPNS1	linker for activation of T cells /// spinster homolog 1 (Drosophila)	chr16p11.2	209881_s_at	NM_001014987 /// NM_001014988 /// NM_001014989 /// NM_014387 /// NM_032038
7.44	7.38	0.06	8.69E-01	9.63E-01	EPC1	enhancer of polycomb homolog 1 (Drosophila)	chr10p11	234969_s_at	NM_025209
2.08	2.06	0.02	8.70E-01	9.63E-01	---	---	---	1558651_at	---
2.15	2.12	0.03	8.70E-01	9.63E-01	---	---	---	1564430_at	---
2.73	2.71	0.03	8.70E-01	9.63E-01	---	---	---	238495_at	---
5.03	5.00	0.03	8.70E-01	9.63E-01	LOC203274	Hypothetical protein LOC203274	chr9q21.11	1554516_at	---
5.80	5.75	0.05	8.70E-01	9.63E-01	WDR20	WD repeat domain 20	chr14q32.31	227541_at	NM_144574 /// NM_181291 /// NM_181302 /// NM_181308
11.46	11.43	0.02	8.70E-01	9.63E-01	ACTB	actin, beta	chr7p15-p12	AFFX-HSAC07/X00351_M_at	NM_001101
5.59	5.56	0.03	8.70E-01	9.63E-01	---	---	---	227788_at	---
4.70	4.63	0.08	8.70E-01	9.63E-01	FLJ25076	similar to CG4502-PA	chr5p15.31	226612_at	XR_040585 /// XR_040586
3.65	3.61	0.04	8.70E-01	9.63E-01	---	---	---	1565802_at	---

2.26	2.24	0.02	8.70E-01	9.63E-01	TACC2	transforming, acidic coiled-coil containing protein 2	chr10q26	1570546_a_at	NM_006997 /// NM_206860 /// NM_206861 /// NM_206862
5.65	5.61	0.04	8.70E-01	9.63E-01	TRA2A	transformer-2 alpha	chr7p15.3	229574_at	NM_013293
5.57	5.53	0.04	8.70E-01	9.63E-01	ULBP2	UL16 binding protein 2	chr6q25	221291_at	NM_025217
6.11	6.07	0.03	8.70E-01	9.63E-01	AP3S2	adaptor-related protein complex 3, sigma 2 subunit	chr15q26.1	213215_at	NM_005829 /// NR_023361
2.20	2.18	0.02	8.70E-01	9.63E-01	BVES	blood vessel epicardial substance	chr6q21	223853_at	NM_007073 /// NM_147147
2.10	2.07	0.02	8.70E-01	9.63E-01	---	---	---	207879_at	---
3.13	3.10	0.02	8.70E-01	9.63E-01	---	---	---	243144_at	---
2.08	2.07	0.02	8.70E-01	9.63E-01	CCDC138	coiled-coil domain containing 138	chr2q13	235644_at	NM_144978
2.29	2.27	0.02	8.70E-01	9.63E-01	---	---	---	1569840_at	---
6.56	6.50	0.07	8.70E-01	9.63E-01	VEZT	vezatin, adherens junctions transmembrane protein	chr12q22	223090_x_at	NM_017599
2.82	2.79	0.02	8.70E-01	9.63E-01	LRRC50	leucine rich repeat containing 50	chr16q24.1	215173_at	NM_178452
2.06	2.04	0.02	8.70E-01	9.63E-01	CCDC152	coiled-coil domain containing 152	chr5p12	242519_at	XM_001714967 /// XM_001716661 /// XM_001717416
2.01	1.99	0.02	8.71E-01	9.63E-01	---	---	---	234692_at	---
6.38	6.33	0.05	8.71E-01	9.63E-01	WISP2	WNT1 inducible signaling pathway protein 2	chr20q12-q13.1	205792_at	NM_003881
4.20	4.15	0.05	8.71E-01	9.63E-01	ALOX15B	arachidonate 15-lipoxygenase, type B	chr17p13.1	206714_at	NM_001039130 /// NM_001039131 /// NM_001141
2.99	2.95	0.04	8.71E-01	9.63E-01	IGHG1 /// LOC100132941	immunoglobulin heavy constant gamma 1 (G1m marker) /// hypothetical protein LOC100132941	chr14q32.33 /// chr16p11.2	217369_at	XM_001718037
2.95	2.88	0.07	8.71E-01	9.63E-01	REEP3	receptor accessory protein 3	chr10q21.3	235016_at	NM_001001330
3.56	3.54	0.02	8.71E-01	9.63E-01	---	---	---	244693_at	---
2.44	2.42	0.02	8.71E-01	9.63E-01	N6AMT1	N-6 adenine-specific DNA methyltransferase 1 (putative)	chr21q21.3	234676_s_at	NM_013240 /// NM_182749
3.72	3.70	0.02	8.71E-01	9.63E-01	LRRC37A3	leucine rich repeat containing 37, member A3	chr17q24.1	229962_at	NM_199340
6.56	6.53	0.03	8.71E-01	9.63E-01	WDR32	WD repeat domain 32	chr9p13.2	222804_x_at	NM_024345
4.88	4.85	0.03	8.71E-01	9.63E-01	OBP2A	odorant binding protein 2A	chr9q34	220848_x_at	NM_014582
2.34	2.33	0.02	8.71E-01	9.63E-01	TRIM42	tripartite motif-containing 42	chr3q23	1566852_at	NM_152616
2.27	2.25	0.02	8.71E-01	9.63E-01	SLC30A4	solute carrier family 30 (zinc transporter), member 4	chr15q11.2-q21.3|15q21.1	207362_at	NM_013309
2.87	2.84	0.03	8.71E-01	9.63E-01	---	---	---	1556777_a_at	---
2.50	2.47	0.02	8.71E-01	9.63E-01	LOC100131311	hypothetical protein LOC100131311	chr1q21.2	227175_at	XM_001715386 /// XM_001717798 /// XM_001718187
3.32	3.27	0.05	8.71E-01	9.63E-01	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	chr3q26	214329_x_at	NM_003810
3.76	3.72	0.04	8.71E-01	9.63E-01	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	chr8p23.1	1552670_a_at	NM_024607
2.46	2.44	0.02	8.71E-01	9.63E-01	LOC646324	hypothetical LOC646324	chr2q35	1564200_at	XR_039807 /// XR_039808 /// XR_039809
8.43	8.37	0.06	8.71E-01	9.63E-01	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	chr8q23.1	200638_s_at	NM_003406 /// NM_145690
2.89	2.85	0.04	8.72E-01	9.63E-01	---	---	---	241841_at	---
4.63	4.56	0.07	8.72E-01	9.63E-01	KIAA0776	KIAA0776	chr6q16.1	212633_at	NM_015323
3.35	3.30	0.04	8.72E-01	9.63E-01	---	---	---	232903_at	---
2.67	2.65	0.02	8.72E-01	9.63E-01	SVIL	supervillin	chr10p11.2	217634_at	NM_003174 /// NM_021738
2.25	2.23	0.02	8.72E-01	9.63E-01	ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif, 19	chr5q31	1553179_at	NM_133638
4.10	4.07	0.03	8.72E-01	9.63E-01	EVL	Enah/Vasp-like	chr14q32.2	227232_at	NM_016337
3.48	3.40	0.08	8.72E-01	9.63E-01	---	---	---	243546_at	---

1.98	1.97	0.02	8.72E-01	9.63E-01	C9orf29	Chromosome 9 open reading frame 29	chr9q31.3	1562803_at	XR_042069 /// XR_042070 /// XR_042071																			
3.06	3.02	0.03	8.72E-01	9.63E-01	RNF170	ring finger protein 170	chr8p11.21	1554312_at	NM_030954																			
2.14	2.11	0.03	8.72E-01	9.63E-01	NR1I3	nuclear receptor subfamily 1, group I, member 3	chr1q23.3	1570188_at	NM_001077469 /// NM_001077470 /// NM_001077471 /// NM_001077472 /// NM_001077473 /// NM_001077474 /// NM_001077475 /// NM_001077476 /// NM_001077477 /// NM_001077478 /// NM_001077479 /// NM_001077480 /// NM_001077481 /// NM_001077482 /// NM_005122																			
2.49	2.47	0.02	8.72E-01	9.63E-01	---	---	---	228657_at	---																			
2.02	2.00	0.02	8.72E-01	9.63E-01	DLC1	deleted in liver cancer 1	chr8p22	242631_x_at	NM_006094 /// NM_024767 /// NM_182643																			
3.10	3.05	0.04	8.72E-01	9.63E-01	RNF38	ring finger protein 38	chr9p13	222660_s_at	NM_022781 /// NM_194328 /// NM_194329 /// NM_194330 /// NM_194332																			
2.53	2.51	0.03	8.72E-01	9.63E-01	LOC100144597	hypothetical transcript	---	1557893_a_at	---																			
4.49	4.45	0.04	8.72E-01	9.63E-01	TMEM63A	Transmembrane protein 63A	chr1q42.12	215583_at	NM_014698																			
2.74	2.72	0.02	8.72E-01	9.63E-01	ENG	Endoglin (Osler-Rendu-Weber syndrome 1)	chr9q33-q34.1	228586_at	NM_000118 /// NM_001114753																			
4.59	4.45	0.14	8.72E-01	9.63E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	228128_x_at	NM_002581																			
2.50	2.47	0.04	8.72E-01	9.63E-01	---	---	---	1568981_at	---																			
3.28	3.25	0.03	8.72E-01	9.63E-01	tAKR	aldo-keto reductase, truncated	chr10p15.1	224070_at	XM_001715222 /// XM_372302 /// XM_937939																			
4.21	4.16	0.05	8.72E-01	9.63E-01	C13orf1	chromosome 13 open reading frame 1	chr13q14	230151_at	NM_001127482 /// NM_020456 /// NR_023351																			
6.00	5.97	0.03	8.72E-01	9.63E-01	ZDHHC6	zinc finger, DHHC-type containing 6	chr10q25.2	218249_at	NM_022494																			
4.53	4.48	0.05	8.72E-01	9.63E-01	ARL17 /// ARL17P1	ADP-ribosylation factor-like 17 /// ADP-ribosylation factor-like 17 pseudogene 1	chr17q21.31 /// chr17q21.32	1554245_x_at	NM_001039083 /// NM_001103154 /// NM_001113738 /// NM_016632																			

6.39	6.31	0.08	8.72E-01	9.63E-01	CCBE1	collagen and calcium binding EGF domains 1	chr18q21.32	242324_x_at	NM_133459
2.27	2.26	0.02	8.72E-01	9.63E-01	KIAA1841	KIAA1841	chr2q14	243539_at	NM_001129993 /// NM_032506
2.21	2.19	0.02	8.72E-01	9.63E-01	KLHL6	kelch-like 6 (Drosophila)	---	1555275_a_at	NM_130446
2.25	2.23	0.02	8.72E-01	9.63E-01	---	---	---	242409_at	---
2.48	2.46	0.02	8.72E-01	9.63E-01	---	---	---	215876_at	---
6.55	6.51	0.05	8.73E-01	9.64E-01	VPS45	vacuolar protein sorting 45 homolog (S. cerevisiae)	chr1q21.2	209268_at	NM_007259
2.19	2.17	0.02	8.73E-01	9.64E-01	---	---	---	237462_at	---
2.89	2.84	0.04	8.73E-01	9.64E-01	WDFY3	WD repeat and FYVE domain containing 3	chr4q21.23	238660_at	NM_014991 /// NM_178583 /// NM_178585
2.42	2.38	0.05	8.73E-01	9.64E-01	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	chr1q25.2-q25.3	1554997_a_at	NM_000963
2.07	2.05	0.02	8.73E-01	9.64E-01	C9orf57	chromosome 9 open reading frame 57	chr9q21.13	240316_at	NM_001128618 /// XM_001714846 /// XM_059954 /// XM_937019
1.88	1.86	0.02	8.73E-01	9.64E-01	---	---	---	240787_at	---
5.60	5.55	0.05	8.73E-01	9.64E-01	RECQL	RecQ protein-like (DNA helicase Q1-like)	chr12p12	212918_at	NM_002907 /// NM_032941
2.39	2.36	0.03	8.73E-01	9.64E-01	FLJ31958	hypothetical protein FLJ31958	chr10q11.23	1553354_a_at	---
3.06	3.01	0.05	8.73E-01	9.64E-01	---	---	---	240170_at	---
5.93	5.88	0.05	8.73E-01	9.64E-01	ZNRF1	zinc and ring finger 1	chr16q23.1	223382_s_at	NM_032268
6.88	6.83	0.05	8.73E-01	9.64E-01	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	chr17q21.2	211989_at	NM_003079
4.03	3.97	0.06	8.73E-01	9.64E-01	S1PR3	sphingosine-1-phosphate receptor 3	chr9q22.1-q22.2	231741_at	NM_005226
2.10	2.08	0.02	8.73E-01	9.64E-01	---	---	---	1569858_at	---
2.00	1.98	0.02	8.73E-01	9.64E-01	CACNA1A	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	chr19p13.2-p13.1	1558945_s_at	NM_000068 /// NM_001127221 /// NM_001127222 /// NM_023035
2.10	2.08	0.02	8.73E-01	9.64E-01	---	---	---	1556694_a_at	---
2.42	2.39	0.03	8.73E-01	9.64E-01	KIF23	Kinesin family member 23	chr15q23	244427_at	NM_004856 /// NM_138555
3.44	3.41	0.03	8.74E-01	9.64E-01	USP15	ubiquitin specific peptidase 15	chr12q14	231990_at	NM_006313
8.85	8.80	0.05	8.74E-01	9.64E-01	TYROBP	TYRO protein tyrosine kinase binding protein	chr19q13.1	204122_at	NM_003332 /// NM_198125
2.97	2.93	0.04	8.74E-01	9.64E-01	---	---	---	230757_at	---
6.14	6.11	0.03	8.74E-01	9.64E-01	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	chr2q37.3	225783_at	NM_080678
2.41	2.38	0.02	8.74E-01	9.64E-01	---	---	---	233481_at	---
3.40	3.36	0.04	8.74E-01	9.64E-01	MGC16275	hypothetical protein MGC16275	chr17q25.2	1558166_at	---
2.51	2.49	0.02	8.74E-01	9.64E-01	---	---	---	231113_at	---
2.65	2.63	0.03	8.74E-01	9.64E-01	WTAP	Wilms tumor 1 associated protein	chr6q25-q27	241626_at	NM_004906 /// NM_152857 /// NM_152858
4.89	4.83	0.06	8.74E-01	9.64E-01	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	chr5q23.1	208296_x_at	NM_001077654 /// NM_014350
6.33	6.28	0.05	8.74E-01	9.64E-01	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	chr1p36	211552_s_at	NM_003748 /// NM_170726
2.09	2.07	0.02	8.74E-01	9.64E-01	FAM3C	family with sequence similarity 3, member C	chr7q31	236316_at	NM_001040020 /// NM_014888
2.98	2.96	0.03	8.74E-01	9.64E-01	---	---	---	229575_at	---
3.72	3.65	0.07	8.74E-01	9.64E-01	RNF12	ring finger protein 12	chrXq13-q21	222815_at	NM_016120 /// NM_183353
6.94	6.90	0.04	8.74E-01	9.64E-01	DHRS4 /// DHRS4L2	dehydrogenase/reductase (SDR family) member 4 /// dehydrogenase/reductase (SDR family) member 4 like 2	chr14q11.2	218021_at	NM_021004 /// NM_198083
2.12	2.10	0.02	8.74E-01	9.64E-01	---	---	---	1566267_at	---

2.09	2.07	0.02	8.74E-01	9.64E-01	GTPBP8	GTP-binding protein 8 (putative)	chr3q13.2	242685_at	NM_014170 /// NM_138485
3.56	3.50	0.05	8.74E-01	9.64E-01	RGNEF	Rho-guanine nucleotide exchange factor	chr5q13.2	1560348_at	NM_001080479
2.38	2.36	0.02	8.74E-01	9.64E-01	---	---	---	237410_x_at	---
3.41	3.35	0.05	8.75E-01	9.64E-01	C12orf29	chromosome 12 open reading frame 29	chr12q21.32	228378_at	NM_001009894
3.90	3.88	0.02	8.75E-01	9.64E-01	---	---	---	1560784_x_at	---
2.83	2.80	0.03	8.75E-01	9.64E-01	C21orf45	Chromosome 21 open reading frame 45	chr21q22.11	229671_s_at	NM_018944
3.30	3.27	0.03	8.75E-01	9.64E-01	RAB7A	RAB7A, member RAS oncogene family	chr3q21.3	227602_at	NM_004637
1.91	1.89	0.02	8.75E-01	9.64E-01	CCDC144A	coiled-coil domain containing 144A	chr17p11.2	1561477_at	NM_014695
6.81	6.76	0.05	8.75E-01	9.64E-01	GOLT1B	golgi transport 1 homolog B (S. cerevisiae)	chr12p12.1	222552_at	NM_016072
9.56	9.47	0.09	8.75E-01	9.64E-01	SLIT2	slit homolog 2 (Drosophila)	chr4p15.2	209897_s_at	NM_004787
2.68	2.65	0.03	8.75E-01	9.64E-01	GDF15	growth differentiation factor 15	chr19p13.11	221576_at	NM_004864
1.97	1.95	0.02	8.75E-01	9.64E-01	TMEM67	transmembrane protein 67	chr8q22.1	1569411_at	NM_153704
3.22	3.18	0.04	8.75E-01	9.64E-01	CDK6	cyclin-dependent kinase 6	chr7q21-q22	243000_at	NM_001259
4.54	4.46	0.08	8.75E-01	9.64E-01	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	chr15q15.3	223271_s_at	NM_016396
2.46	2.44	0.02	8.75E-01	9.64E-01	C12orf51	Chromosome 12 open reading frame 51	chr12q24.13	244378_at	NM_001109662
5.82	5.78	0.04	8.75E-01	9.64E-01	KIAA0240	KIAA0240	chr6p21.1	213208_at	NM_015349
5.44	5.41	0.03	8.75E-01	9.64E-01	ADCK1	aarF domain containing kinase 1	chr14q24.3	227482_at	NM_020421
1.98	1.96	0.02	8.75E-01	9.64E-01	SALL1	sal-like 1 (Drosophila)	chr16q12.1	229273_at	NM_001127892 /// NM_002968
2.64	2.61	0.02	8.75E-01	9.64E-01	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	chr1p35-p31.3	201249_at	NM_006516
2.62	2.58	0.04	8.75E-01	9.64E-01	---	---	---	1556923_at	---
2.50	2.48	0.02	8.76E-01	9.64E-01	---	---	---	231136_at	---
3.82	3.76	0.06	8.76E-01	9.64E-01	---	---	---	239086_at	---
4.48	4.46	0.02	8.76E-01	9.64E-01	SIPA1L3	signal-induced proliferation-associated 1 like 3	chr19q13.13	213600_at	NM_015073
2.67	2.65	0.02	8.76E-01	9.64E-01	---	---	---	237930_at	---
1.87	1.86	0.02	8.76E-01	9.64E-01	---	---	---	1556210_at	---
3.21	3.18	0.03	8.76E-01	9.64E-01	ZNF155	zinc finger protein 155	chr19q13.2-q13.32|19q13.2	221201_s_at	NM_003445 /// NM_198089
4.24	4.20	0.04	8.76E-01	9.64E-01	C14orf70	chromosome 14 open reading frame 70	chr14q32.2	1560198_at	NM_001007560 /// NR_024096
4.22	4.13	0.08	8.76E-01	9.64E-01	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	chr1p12	1557918_s_at	NM_003051
2.64	2.61	0.03	8.76E-01	9.64E-01	SVOPL	SVOP-like	chr7q34	1554300_a_at	NM_174959
3.97	3.93	0.04	8.76E-01	9.64E-01	IRAK4	interleukin-1 receptor-associated kinase 4	chr12q12	219618_at	NM_001114182 /// NM_016123
2.51	2.49	0.02	8.76E-01	9.64E-01	TRIM69	tripartite motif-containing 69	chr15q21.1	232792_at	NM_080745 /// NM_182985
3.38	3.36	0.02	8.76E-01	9.64E-01	ARHGAP26	Rho GTPase activating protein 26	chr5q31	205068_s_at	NM_015071
2.29	2.26	0.03	8.76E-01	9.64E-01	---	---	---	1561448_at	---
2.32	2.30	0.02	8.76E-01	9.64E-01	---	---	---	1561519_at	---
2.25	2.23	0.02	8.76E-01	9.64E-01	---	---	---	1558337_at	---
3.11	3.08	0.03	8.76E-01	9.65E-01	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	chr3q28	1554835_a_at	NM_032047
2.55	2.53	0.02	8.76E-01	9.65E-01	---	---	---	226186_at	---
4.25	4.19	0.05	8.76E-01	9.65E-01	---	---	---	213567_at	---
3.54	3.52	0.02	8.76E-01	9.65E-01	AKAP8L	A kinase (PRKA) anchor protein 8-like	chr19p13.12	227691_at	NM_014371
2.87	2.84	0.02	8.76E-01	9.65E-01	TLE6	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)	chr19p13.3	1553813_s_at	NM_024760
2.56	2.54	0.02	8.76E-01	9.65E-01	---	---	---	241178_at	---
2.46	2.43	0.02	8.76E-01	9.65E-01	---	---	---	1563612_at	---
2.04	2.02	0.02	8.77E-01	9.65E-01	RP1	retinitis pigmentosa 1 (autosomal dominant)	chr8q11-q13	224021_at	NM_006269
2.38	2.36	0.02	8.77E-01	9.65E-01	---	---	---	1559551_at	---
2.25	2.23	0.03	8.77E-01	9.65E-01	---	---	---	241615_x_at	---
2.79	2.76	0.03	8.77E-01	9.65E-01	---	---	---	242510_at	---
2.94	2.91	0.03	8.77E-01	9.65E-01	NHEDC2	Na+/H+ exchanger domain containing 2	chr4q24	1564746_at	NM_178833
3.53	3.50	0.03	8.77E-01	9.65E-01	ZNF397OS	Zinc finger protein 397 opposite strand	chr18q12.2	1557105_a_at	NM_001112734 /// XM_001720071 /// XM_001722380 /// XM_001723235
2.74	2.71	0.03	8.77E-01	9.65E-01	---	---	---	240828_at	---
2.83	2.81	0.03	8.77E-01	9.65E-01	A2ML1	alpha-2-macroglobulin-like 1	chr12p13.31	1553505_at	NM_144670

3.81	3.75	0.05	8.77E-01	9.65E-01	MIER3	mesoderm induction early response 1, family member 3	chr5q11.2	231975_s_at	NM_152622
2.19	2.17	0.02	8.77E-01	9.65E-01	C11orf67	chromosome 11 open reading frame 67	chr11q14.1	220268_at	NM_024684
2.64	2.62	0.02	8.77E-01	9.65E-01	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	chr2p22.1	244784_at	NM_198963
2.05	2.03	0.02	8.77E-01	9.65E-01	FOXA1	Forkhead box A1	chr14q12-q13	237086_at	NM_004496
5.11	5.05	0.05	8.77E-01	9.65E-01	RSBN1	round spermatid basic protein 1	chr1p13.2	222789_at	NM_018364
7.11	7.08	0.03	8.77E-01	9.65E-01	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	chr22q12.3	201020_at	NM_003405
2.46	2.44	0.03	8.77E-01	9.65E-01	C9orf117	chromosome 9 open reading frame 117	chr9q34.11	1557866_at	NM_001012502
4.75	4.70	0.05	8.77E-01	9.65E-01	PDLIM7	PDZ and LIM domain 7 (enigma)	chr5q35.3	214121_x_at	NM_005451 /// NM_203352 /// NM_213636
2.38	2.35	0.02	8.77E-01	9.65E-01	ZNF746	zinc finger protein 746	chr7q36.1	1570373_at	NM_152557
2.34	2.33	0.02	8.77E-01	9.65E-01	DEFB126	defensin, beta 126	chr20p13	221414_s_at	NM_030931
5.22	5.15	0.07	8.77E-01	9.65E-01	PDE8A	phosphodiesterase 8A	chr15q25.3	1552931_a_at	NM_002605 /// NM_173454
2.13	2.10	0.02	8.77E-01	9.65E-01	LOC653505 /// LOC653598 /// PPIAL4 /// RP6-206I17.5	similar to cyclophilin-LC (COAS2) /// similar to cyclophilin-LC (COAS2) /// peptidylprolyl isomerase A (cyclophilin A)-like 4 /// peptidylprolyl isomerase A (cyclophilin A)-like	chr1q21.1	217136_at	NM_001123068 /// NM_178230 /// XM_927706 /// XM_927767 /// XM_928338
2.03	2.01	0.02	8.77E-01	9.65E-01	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit	chr3p24-p21	220791_x_at	NM_014139
2.20	2.18	0.02	8.78E-01	9.65E-01	C6orf114	chromosome 6 open reading frame 114	chr6p23	1554486_a_at	NM_033069
6.44	6.40	0.05	8.78E-01	9.65E-01	CCDC86	coiled-coil domain containing 86	chr11q12.2	203119_at	NM_024098
8.00	7.96	0.04	8.78E-01	9.65E-01	DC2	DC2 protein	chr4q25	223001_at	NM_021227
4.44	4.42	0.02	8.78E-01	9.65E-01	B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	chr17q25.3	215055_at	NM_001009905
2.38	2.36	0.02	8.78E-01	9.65E-01	---	---	---	1568589_at	---
2.44	2.41	0.02	8.78E-01	9.65E-01	---	---	---	201265_at	---
1.99	1.96	0.03	8.78E-01	9.65E-01	PIK3R4	Phosphoinositide-3-kinase, regulatory subunit 4	chr3q22.1	216752_at	NM_014602
3.86	3.83	0.03	8.78E-01	9.65E-01	GGNBP2	gametogenetin binding protein 2	chr17q12	1554419_x_at	NM_024835
2.82	2.80	0.02	8.78E-01	9.65E-01	PAEP	progestagen-associated endometrial protein	chr9q34	206859_s_at	NM_001018049 /// NM_002571
6.47	6.43	0.04	8.78E-01	9.65E-01	SGK3	serum/glucocorticoid regulated kinase family, member 3	chr8q12.3-q13.1	227627_at	NM_001033578 /// NM_013257 /// NM_170709
2.39	2.37	0.02	8.78E-01	9.65E-01	LRRC37B2	leucine rich repeat containing 37, member B2	chr17q11.2	216149_at	NR_015341 /// XR_040942 /// XR_040943
2.45	2.42	0.03	8.78E-01	9.65E-01	ZNF497	zinc finger protein 497	chr19q13.43	230857_s_at	NM_198458
4.94	4.90	0.04	8.78E-01	9.65E-01	MRPL35	mitochondrial ribosomal protein L35	chr2p11.2	222775_s_at	NM_016622 /// NM_145644
2.88	2.85	0.03	8.78E-01	9.65E-01	SYN2	synapsin II	chr3p25	240197_at	NM_003178 /// NM_133625
2.56	2.53	0.03	8.78E-01	9.65E-01	LOC100133991	Similar to hCG1995169	---	1557783_at	XM_001721581
4.37	4.32	0.04	8.78E-01	9.65E-01	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	chr17p13.1	227645_at	NM_014308
3.23	3.21	0.02	8.79E-01	9.65E-01	SLAMF6	SLAM family member 6	chr1q23.2	1552497_a_at	NM_052931
6.02	5.91	0.12	8.79E-01	9.65E-01	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	chrXp11.3-p11.23	212514_x_at	NM_001356
2.26	2.24	0.02	8.79E-01	9.65E-01	---	---	---	230312_at	---
3.07	3.04	0.03	8.79E-01	9.65E-01	---	---	---	1562232_at	---
5.10	5.05	0.05	8.79E-01	9.65E-01	CLEC11A	C-type lectin domain family 11, member A	chr19q13.3	205131_x_at	NM_002975
2.19	2.16	0.02	8.79E-01	9.65E-01	---	---	---	1557865_at	---
2.10	2.08	0.02	8.79E-01	9.65E-01	TLL2	tolloid-like 2	chr10q23-q24	215008_at	NM_012465
2.25	2.23	0.02	8.79E-01	9.65E-01	---	---	---	240732_at	---
2.38	2.36	0.02	8.79E-01	9.66E-01	UBR4	ubiquitin protein ligase E3 component n-recognin 4	chr1p36.13	231889_at	NM_020765
2.84	2.82	0.02	8.79E-01	9.66E-01	C6orf52	chromosome 6 open reading frame 52	chr6p24.1	243943_x_at	XM_001718541 /// XM_371798 /// XM_938497

6.74	6.69	0.05	8.79E-01	9.66E-01	TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	chr7q11.21-q11.22	218347_at	NM_018264
2.93	2.90	0.02	8.79E-01	9.66E-01	---	---	---	1559188_x_at	---
3.87	3.83	0.04	8.79E-01	9.66E-01	PSMG4	proteasome (prosome, macropain) assembly chaperone 4	chr6p25.2	1561304_a_at	NM_001128591 /// NM_001128592 /// XR_017743 /// XR_017905 /// XR_041314
3.06	3.03	0.03	8.79E-01	9.66E-01	---	---	---	237714_at	---
3.53	3.50	0.03	8.79E-01	9.66E-01	---	---	---	243484_x_at	---
4.49	4.46	0.03	8.79E-01	9.66E-01	FLJ42875	hypothetical LOC440556	chr1p36.32	237108_x_at	XM_928346 /// XM_932794 /// XM_942662 /// XM_946195
6.39	6.34	0.05	8.79E-01	9.66E-01	PYGB	phosphorylase, glycogen; brain	chr20p11.2-p11.1	201481_s_at	NM_002862
3.71	3.66	0.05	8.79E-01	9.66E-01	LOC642980	hypothetical LOC642980	chrXq28	243129_at	XR_041043
2.06	2.04	0.02	8.79E-01	9.66E-01	FBXO4	F-box protein 4	chr5p12	220550_at	NM_012176 /// NM_033484
3.45	3.42	0.03	8.79E-01	9.66E-01	DBF4	DBF4 homolog (S. cerevisiae)	chr7q21.3	204244_s_at	NM_006716
2.15	2.13	0.02	8.79E-01	9.66E-01	---	---	---	1569917_at	---
2.01	1.99	0.02	8.80E-01	9.66E-01	MGC42157	hypothetical locus MGC42157	chr4p14	1552987_a_at	XR_017710 /// XR_017809 /// XR_041588
2.49	2.47	0.02	8.80E-01	9.66E-01	TARP /// TRGV3 /// TRGV5	TCR gamma alternate reading frame protein /// T cell receptor gamma variable 3 /// T cell receptor gamma variable 5	chr7p14 /// chr7p15-p14	217374_x_at	NM_001003799 /// NM_001003806
2.16	2.14	0.02	8.80E-01	9.66E-01	---	---	---	238137_at	---
1.95	1.93	0.02	8.80E-01	9.66E-01	---	---	---	1559515_at	---
2.33	2.31	0.02	8.80E-01	9.66E-01	---	---	---	1568904_at	---
2.19	2.17	0.02	8.80E-01	9.66E-01	C17orf98	chromosome 17 open reading frame 98	chr17q12	244316_at	NM_001080465
2.47	2.45	0.02	8.80E-01	9.66E-01	AGXT2L2	Alanine-glyoxylate aminotransferase 2-like 2	chr5q35.3	235669_at	NM_153373
5.76	5.70	0.06	8.80E-01	9.66E-01	LOC401504	Hypothetical gene supported by AK091718	chr9p13.2	225635_s_at	---
2.25	2.23	0.02	8.80E-01	9.66E-01	---	---	---	233705_at	---
4.27	4.23	0.04	8.80E-01	9.66E-01	MGC24975	hypothetical protein MGC24975	chr19p13.3	1552271_at	NM_001134316 /// NM_153359
2.56	2.54	0.03	8.80E-01	9.66E-01	---	---	---	241192_at	---
3.06	3.03	0.03	8.80E-01	9.66E-01	LOC100131701	hypothetical protein LOC100131701	---	238804_at	XM_001714073 /// XM_001714319
2.69	2.67	0.03	8.80E-01	9.66E-01	CNIH3	Cornichon homolog 3 (Drosophila)	chr1q42.12	238503_at	NM_152495
1.93	1.92	0.01	8.80E-01	9.66E-01	NAP5	Nck-associated protein 5	chr2q21.2	239650_at	NM_207363 /// NM_207481
2.40	2.35	0.04	8.80E-01	9.66E-01	---	---	---	222170_at	---
2.24	2.22	0.02	8.80E-01	9.66E-01	DXS542	putative X-linked retinopathy protein	chrXp11.3-q12	222247_at	---
2.09	2.08	0.02	8.80E-01	9.66E-01	---	---	---	234096_at	---
2.85	2.81	0.04	8.80E-01	9.66E-01	---	---	---	229129_at	---
5.76	5.70	0.06	8.81E-01	9.66E-01	---	---	---	236592_at	---
2.74	2.71	0.03	8.81E-01	9.66E-01	ABCC11	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	chr16q12.1	1554911_at	NM_032583 /// NM_033151 /// NM_145186
4.92	4.87	0.05	8.81E-01	9.66E-01	PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	chr17q23.2	204566_at	NM_003620
8.21	8.19	0.02	8.81E-01	9.66E-01	SURF4	surfeit 4	chr9q34.2	222977_at	NM_033161

2.52	2.49	0.03	8.81E-01	9.66E-01	C2orf21	chromosome 2 open reading frame 21	chr2q35	230220_at	NM_032504 /// NM_182587 /// XM_001715588 /// XM_001717212 /// XM_001717654																				
3.72	3.70	0.02	8.81E-01	9.66E-01	CRIP3	cysteine-rich protein 3	chr6p21.1	235720_at	NM_206922																				
2.82	2.80	0.02	8.81E-01	9.66E-01	SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	chr19q13.1	220135_s_at	NM_001126335 /// NM_014270																				
2.20	2.18	0.02	8.81E-01	9.66E-01	LOC201477	hypothetical protein LOC201477	chr18p11.31	1560522_at	---																				
5.48	5.45	0.03	8.81E-01	9.66E-01	PER3	period homolog 3 (Drosophila)	chr1p36.23	221045_s_at	NM_016831																				
3.84	3.81	0.03	8.81E-01	9.66E-01	LOC100129122	Hypothetical protein LOC100129122	chr13q32.3	231062_at	XM_001714405 /// XM_001714912 /// XM_001715622																				
5.80	5.76	0.04	8.81E-01	9.66E-01	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	chr15q22.2	218396_at	NM_001018088 /// NM_017684 /// NM_018080 /// NM_020821																				
2.51	2.49	0.02	8.81E-01	9.66E-01	---	---	---	1560463_at	---																				
1.98	1.96	0.02	8.81E-01	9.66E-01	---	---	---	234180_at	---																				
4.08	4.02	0.06	8.81E-01	9.66E-01	GALC	galactosylceramidase	chr14q31	211810_s_at	NM_000153 /// NM_001037525																				
4.23	4.20	0.03	8.81E-01	9.66E-01	C14orf65	chromosome 14 open reading frame 65	chr14q32.31	219018_s_at	XR_040689 /// XR_040690 /// XR_040691																				
3.73	3.69	0.05	8.81E-01	9.66E-01	MOSPD2	motile sperm domain containing 2	chrXp22.2	64883_at	NM_152581																				
2.73	2.71	0.02	8.81E-01	9.66E-01	GAB4	GRB2-associated binding protein family, member 4	chr22q11.1	1563816_at	NM_001037814																				
2.46	2.43	0.03	8.81E-01	9.66E-01	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	chr7p15.3	1561269_at	NM_012294																				
6.04	6.01	0.04	8.81E-01	9.66E-01	LARP1	La ribonucleoprotein domain family, member 1	chr5q33.2	212193_s_at	NM_015315 /// NM_033551																				
6.14	6.10	0.04	8.81E-01	9.66E-01	TLK2	tousled-like kinase 2	chr17q23	212997_s_at	NM_001112707 /// NM_006852																				
4.35	4.27	0.08	8.81E-01	9.66E-01	JUN	Jun oncogene	chr1p32-p31	213281_at	NM_002228																				
2.41	2.39	0.02	8.82E-01	9.66E-01	---	---	---	242270_at	---																				
2.19	2.17	0.02	8.82E-01	9.66E-01	---	---	---	1562543_at	---																				
4.26	4.23	0.03	8.82E-01	9.66E-01	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	chr13q22.1	214194_at	NM_001128226 /// NM_014953																				
2.74	2.71	0.03	8.82E-01	9.66E-01	HLA-DOA	major histocompatibility complex, class II, DO alpha	chr6p21.3	216946_at	NM_002119																				
5.38	5.31	0.08	8.82E-01	9.66E-01	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	chr15q24	201881_s_at	NM_005744																				
2.44	2.42	0.02	8.82E-01	9.66E-01	APOH	apolipoprotein H (beta-2-glycoprotein I)	chr17q23-qter	205216_s_at	NM_000042																				
2.32	2.30	0.02	8.82E-01	9.66E-01	KCNU1	potassium channel, subfamily U, member 1	chr8p12	237273_at	NM_001031836																				
2.67	2.65	0.02	8.82E-01	9.66E-01	SYCE2	synaptonemal complex central element protein 2	chr19p13.13	237304_at	NM_001105578																				
4.73	4.69	0.04	8.82E-01	9.66E-01	MERTK	c-mer proto-oncogene tyrosine kinase	chr2q14.1	233079_at	NM_006343																				
2.11	2.09	0.03	8.82E-01	9.66E-01	RBM26	RNA binding motif protein 26	chr13q31.1	215751_at	NM_022118																				
3.80	3.77	0.02	8.82E-01	9.66E-01	---	---	---	239925_at	---																				
2.07	2.06	0.02	8.82E-01	9.66E-01	ZFP14	zinc finger protein 14 homolog (mouse)	chr19q13.12	232911_at	NM_020917																				
6.69	6.67	0.02	8.82E-01	9.66E-01	OGFR	opioid growth factor receptor	chr20q13.3	202841_x_at	NM_007346																				
3.03	3.00	0.03	8.82E-01	9.66E-01	FAM160A1	family with sequence similarity 160, member A1	chr4q31.3	242687_at	NM_001109977 /// XM_001715912 /// XM_001715923 /// XM_001718535																				

3.56	3.52	0.04	8.82E-01	9.66E-01	---	---	---	231312_at	---
2.61	2.59	0.03	8.82E-01	9.66E-01	---	---	---	1559501_at	---
5.58	5.54	0.03	8.82E-01	9.66E-01	MECP2	methyl CpG binding protein 2 (Rett syndrome)	chrXq28	202617_s_at	NM_001110792 /// NM_004992
2.49	2.47	0.02	8.82E-01	9.66E-01	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	chr10p11.23	206780_at	NM_000818 /// NM_001134366
2.61	2.59	0.02	8.82E-01	9.66E-01	---	---	---	240272_at	---
4.84	4.80	0.03	8.82E-01	9.66E-01	PACS2	phosphofurin acidic cluster sorting protein 2	chr14q32.33	34406_at	NM_001100913 /// NM_015197
2.29	2.27	0.02	8.82E-01	9.66E-01	C21orf87	chromosome 21 open reading frame 87	chr21q22.2	1553069_at	XR_040389 /// XR_040390 /// XR_040391
2.87	2.84	0.03	8.83E-01	9.67E-01	---	---	---	213484_at	---
4.95	4.92	0.03	8.83E-01	9.67E-01	---	---	---	236804_at	---
2.01	2.00	0.02	8.83E-01	9.67E-01	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	chr7p14.3	234793_at	NM_015483
5.81	5.75	0.05	8.83E-01	9.67E-01	EFHC1	EF-hand domain (C-terminal) containing 1	chr6p12.3	225656_at	NM_018100
2.93	2.91	0.02	8.83E-01	9.67E-01	PHOSPHO2	phosphatase, orphan 2	chr2q31.1	230434_at	NM_001008489
7.77	7.71	0.07	8.83E-01	9.67E-01	EML4	echinoderm microtubule associated protein like 4	chr2p22-p21	223068_at	NM_019063
4.67	4.61	0.06	8.83E-01	9.67E-01	---	---	---	238714_at	---
3.33	3.31	0.03	8.83E-01	9.67E-01	SCUBE2	signal peptide, CUB domain, EGF-like 2	chr11p15.3	219197_s_at	NM_020974
4.75	4.72	0.02	8.83E-01	9.67E-01	---	---	---	239017_at	---
2.81	2.79	0.02	8.83E-01	9.67E-01	---	---	---	1566696_at	---
2.10	2.08	0.01	8.83E-01	9.67E-01	---	---	---	1568787_at	---
2.13	2.11	0.02	8.83E-01	9.67E-01	---	---	---	1562696_at	---
2.01	2.00	0.01	8.83E-01	9.67E-01	---	---	---	1562854_at	---
1.95	1.93	0.02	8.83E-01	9.67E-01	LOC100129038	PRO2812	chr16p13.12	224112_at	XM_001723300 /// XM_001723412 /// XM_001725474
2.64	2.61	0.02	8.83E-01	9.67E-01	---	---	---	234962_at	---
6.05	6.00	0.05	8.83E-01	9.67E-01	SMG7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr1q25	201794_s_at	NM_173156 /// NM_201568 /// NM_201569
2.26	2.25	0.02	8.83E-01	9.67E-01	---	---	---	1560893_at	---
2.48	2.46	0.03	8.83E-01	9.67E-01	MGC34800	hypothetical protein MGC34800	chr16p11.2	1553914_at	XR_017798 /// XR_041335 /// XR_041336
2.98	2.96	0.02	8.83E-01	9.67E-01	---	---	---	216461_at	---
1.98	1.97	0.02	8.83E-01	9.67E-01	---	---	---	1557597_at	---
2.43	2.40	0.03	8.83E-01	9.67E-01	TGIF2LY	TGFB-induced factor homeobox 2-like, Y-linked	chrYp11.2	233178_at	NM_139214
4.42	4.37	0.05	8.84E-01	9.67E-01	---	---	---	1557353_at	---
3.53	3.51	0.02	8.84E-01	9.67E-01	---	---	---	1570375_at	---
9.08	9.04	0.04	8.84E-01	9.67E-01	CD59	CD59 molecule, complement regulatory protein	chr11p13	200983_x_at	NM_000611 /// NM_001127223 /// NM_001127225 /// NM_001127226 /// NM_001127227 /// NM_203329 /// NM_203330 /// NM_203331
3.06	3.03	0.03	8.84E-01	9.67E-01	---	---	---	236991_at	---
2.77	2.75	0.02	8.84E-01	9.67E-01	MAP2K6	mitogen-activated protein kinase kinase 6	chr17q24.3	205699_at	NM_002758
6.88	6.84	0.04	8.84E-01	9.67E-01	ITSN2	intersectin 2	chr2pter-p25.1	209898_x_at	NM_006277 /// NM_019595 /// NM_147152

1.96	1.94	0.02	8.84E-01	9.67E-01	FGA	fibrinogen alpha chain	chr4q28	205649_s_at	NM_000508 /// NM_021871
3.39	3.35	0.03	8.84E-01	9.67E-01	---	---	---	1557276_at	---
7.55	7.52	0.03	8.84E-01	9.67E-01	NPLOC4	nuclear protein localization 4 homolog (S. cerevisiae)	chr17qter	217796_s_at	NM_017921
3.31	3.29	0.02	8.84E-01	9.67E-01	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	chr1p13.3	211827_s_at	NM_004980 /// NM_172198
2.04	2.02	0.02	8.84E-01	9.67E-01	CXorf61	chromosome X open reading frame 61	chrXq23	1559258_a_at	NM_001017978
5.23	5.20	0.03	8.84E-01	9.67E-01	NCAPH2	non-SMC condensin II complex, subunit H2	chr22q13.33	205086_s_at	NM_014551 /// NM_152299
2.32	2.30	0.02	8.84E-01	9.67E-01	---	---	---	216012_at	---
2.27	2.26	0.02	8.84E-01	9.67E-01	---	---	---	233187_s_at	---
2.28	2.26	0.02	8.84E-01	9.67E-01	CAMK4	calcium/calmodulin-dependent protein kinase IV	chr5q21.3	210349_at	NM_001744
4.39	4.36	0.04	8.85E-01	9.67E-01	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	chr5q31.1	1554894_a_at	NM_032151
2.08	2.07	0.02	8.85E-01	9.67E-01	---	---	---	1561191_at	---
3.27	3.19	0.07	8.85E-01	9.67E-01	---	---	---	230781_at	---
2.00	1.97	0.03	8.85E-01	9.67E-01	C21orf99	chromosome 21 open reading frame 99	chr21q11.2	1552895_a_at	XR_040882
3.11	3.09	0.02	8.85E-01	9.67E-01	WNT6	wingless-type MMTV integration site family, member 6	chr2q35	221608_at	NM_006522
6.02	5.97	0.05	8.85E-01	9.67E-01	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	chr1q23	203561_at	NM_021642
3.69	3.66	0.03	8.85E-01	9.67E-01	ZNF821	zinc finger protein 821	chr16q22.3	205494_at	NM_017530
2.83	2.80	0.03	8.85E-01	9.67E-01	---	---	---	238524_at	---
3.05	3.01	0.04	8.85E-01	9.67E-01	SENP6	SUMO1/sentrin specific peptidase 6	chr6q13-q14.3	202319_at	NM_001100409 /// NM_015571
3.52	3.49	0.04	8.85E-01	9.67E-01	LOC285550	hypothetical protein LOC285550	chr4p15.33-p15.32	227270_at	XR_017764 /// XR_017908 /// XR_040763
2.77	2.73	0.04	8.85E-01	9.67E-01	LRRC8C	leucine rich repeat containing 8 family, member C	chr1p22.2	1570007_at	NM_032270
2.26	2.24	0.02	8.85E-01	9.67E-01	---	---	---	241635_at	---
2.19	2.18	0.02	8.85E-01	9.67E-01	---	---	---	237009_at	---
8.57	8.53	0.04	8.85E-01	9.67E-01	TXN2	thioredoxin 2	chr22q13.1	209077_at	NM_012473
2.39	2.37	0.02	8.85E-01	9.67E-01	---	---	---	236476_at	---
3.72	3.68	0.04	8.85E-01	9.67E-01	ITGA7	integrin, alpha 7	chr12q13	209663_s_at	NM_002206
3.14	3.12	0.02	8.85E-01	9.67E-01	XIRP1	xin actin-binding repeat containing 1	chr3p22.2	235042_at	NM_194293
6.97	6.91	0.05	8.85E-01	9.67E-01	CPM	carboxypeptidase M	chr12q14.3	235706_at	NM_001005502 /// NM_001874 /// NM_198320
2.30	2.28	0.02	8.85E-01	9.67E-01	---	---	---	1564215_at	---
3.54	3.53	0.02	8.85E-01	9.67E-01	---	---	---	241222_at	---
2.08	2.06	0.02	8.85E-01	9.67E-01	NR2C1	nuclear receptor subfamily 2, group C, member 1	chr12q22	210531_at	NM_001032287 /// NM_001127362 /// NM_003297
3.55	3.53	0.02	8.85E-01	9.67E-01	LY6G6D /// LY6G6F	lymphocyte antigen 6 complex, locus G6D /// lymphocyte antigen 6 complex, locus G6F	chr6p21 /// chr6p21.3	234897_s_at	NM_001003693 /// NM_021246
1.84	1.83	0.02	8.85E-01	9.67E-01	---	---	---	208192_at	---
2.65	2.62	0.03	8.85E-01	9.67E-01	EXPH5	exophilin 5	chr11q22.3	214734_at	NM_015065
3.33	3.31	0.03	8.85E-01	9.67E-01	MOV10L1	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)	chr22q13.33	239257_at	NM_018995
2.71	2.67	0.04	8.85E-01	9.67E-01	---	---	---	237104_at	---
1.92	1.90	0.02	8.85E-01	9.67E-01	---	---	---	1562250_at	---
6.72	6.69	0.03	8.85E-01	9.67E-01	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	chr12q24.31	222104_x_at	NM_001516
3.98	3.96	0.02	8.85E-01	9.67E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	208229_at	NM_000141 /// NM_022970
6.97	6.94	0.03	8.85E-01	9.67E-01	KIF3B	kinesin family member 3B	chr20q11.21	225205_at	NM_004798
3.07	3.05	0.02	8.85E-01	9.67E-01	CIAPIN1	cytokine induced apoptosis inhibitor 1	chr16q13-q21	230838_s_at	NM_020313
2.46	2.43	0.03	8.86E-01	9.67E-01	C14orf64	chromosome 14 open reading frame 64	chr14q32.2	1559097_at	NR_015430
2.97	2.95	0.02	8.86E-01	9.68E-01	KRTAP5-10 /// KRTAP5-11 /// KRTAP5-2	keratin associated protein 5-10 /// keratin associated protein 5-11 /// keratin associated protein 5-2	chr11p15.5 /// chr11q13.4	1566218_at	NM_001004325 /// NM_001005405 /// NM_001012710
6.75	6.72	0.03	8.86E-01	9.68E-01	RABGAP1	RAB GTPase activating protein 1	chr9q33.2	213313_at	NM_012197

2.23	2.22	0.02	8.86E-01	9.68E-01	FLJ25694 /// LOC100128202	hypothetical protein FLJ25694 /// hypothetical protein LOC100128202	chr13q21.31	1553614_a_at	XM_001716986 /// XM_001721733 /// XM_001723719																			
5.23	5.07	0.16	8.86E-01	9.68E-01	CD36	CD36 molecule (thrombospondin receptor)	chr7q11.2	209555_s_at	NM_000072 /// NM_001001547 /// NM_001001548 /// NM_001127443 /// NM_001127444																			
2.33	2.30	0.02	8.86E-01	9.68E-01	---	---	---	229363_at	---																			
2.19	2.17	0.02	8.86E-01	9.68E-01	ATP13A4	ATPase type 13A4	chr3q29	1559571_a_at	NM_032279																			
3.40	3.37	0.03	8.86E-01	9.68E-01	AK2	adenylate kinase 2	chr1p34	212173_at	NM_001625 /// NM_013411																			
7.30	7.25	0.04	8.86E-01	9.68E-01	MBTPS2	membrane-bound transcription factor peptidase, site 2	chrXp22.13	226760_at	NM_015884																			
2.53	2.51	0.02	8.86E-01	9.68E-01	FKBP15	FK506 binding protein 15, 133kDa	chr9q32	1568717_a_at	NM_015258																			
2.33	2.31	0.02	8.86E-01	9.68E-01	KIF13A	kinesin family member 13A	chr6p23	223520_s_at	NM_001105566 /// NM_001105567 /// NM_001105568 /// NM_022113																			
2.34	2.33	0.01	8.86E-01	9.68E-01	ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13	chr21q11.2	1555265_at	NR_003087 /// NR_003088																			
2.68	2.65	0.03	8.86E-01	9.68E-01	ABHD1	abhydrolase domain containing 1	chr2p23.3	236461_at	NM_032604																			
3.59	3.51	0.08	8.86E-01	9.68E-01	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	chr9q21.31	216997_x_at	NM_007005																			
2.28	2.26	0.02	8.87E-01	9.68E-01	---	---	---	240422_at	---																			
7.65	7.62	0.02	8.87E-01	9.68E-01	PMVK	phosphomevalonate kinase	chr1q22	203515_s_at	NM_006556																			
4.11	4.08	0.03	8.87E-01	9.68E-01	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	chr10q25.1	209804_at	NM_014881																			
8.97	8.94	0.03	8.87E-01	9.68E-01	AURKAIP1	aurora kinase A interacting protein 1	chr1p36.33	225552_x_at	NM_001127229 /// NM_001127230 /// NM_017900																			
6.73	6.69	0.04	8.87E-01	9.68E-01	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	chr8q23.1	223342_at	NM_015713																			
5.21	5.17	0.04	8.87E-01	9.68E-01	---	---	---	238042_at	---																			
2.81	2.79	0.02	8.87E-01	9.68E-01	CHDH	choline dehydrogenase	chr3p21.1	229502_at	NM_018397																			
6.02	5.97	0.05	8.87E-01	9.68E-01	OFD1	oral-facial-digital syndrome 1	chrXp22	203569_s_at	NM_003611																			
2.11	2.09	0.02	8.87E-01	9.68E-01	C9orf122	chromosome 9 open reading frame 122	chr9p13.1	1557014_a_at	XR_041857																			
2.32	2.30	0.03	8.87E-01	9.68E-01	TAS1R1	taste receptor, type 1, member 1	chr1p36.23	1555417_a_at	NM_138697 /// NM_177539 /// NM_177540 /// NM_177541																			
5.09	5.07	0.02	8.87E-01	9.68E-01	TTC38	Tetratricopeptide repeat domain 38	chr22q13	216434_at	NM_017931																			
2.95	2.92	0.03	8.87E-01	9.68E-01	ZNF502	zinc finger protein 502	chr3p21.31	229532_at	NM_001134440 /// NM_001134441 /// NM_001134442 /// NM_033210																			
5.32	5.29	0.03	8.87E-01	9.68E-01	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	chr2q35	217473_x_at	NM_000578																			
3.08	3.05	0.03	8.87E-01	9.68E-01	---	---	---	242596_at	---																			
2.44	2.42	0.02	8.87E-01	9.68E-01	---	---	---	242501_at	---																			
3.27	3.23	0.04	8.87E-01	9.68E-01	---	---	---	240529_at	---																			
8.13	8.08	0.05	8.87E-01	9.68E-01	MATR3	matrin 3	chr5q31.2	200626_s_at	NM_018834 /// NM_199189																			
6.71	6.68	0.03	8.87E-01	9.68E-01	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	chr8q12-q13	203269_at	NM_003580																			
5.39	5.37	0.03	8.87E-01	9.68E-01	NR6A1	nuclear receptor subfamily 6, group A, member 1	chr9q33-q34.1	227494_at	NM_001489 /// NM_033334																			

3.28	3.24	0.03	8.87E-01	9.68E-01	---	---	---	231013_at	---
5.43	5.39	0.04	8.87E-01	9.68E-01	MAP1S	microtubule-associated protein 1S	chr19p13.11	218522_s_at	NM_018174
3.03	3.00	0.03	8.87E-01	9.68E-01	LOC339803	Hypothetical protein LOC339803	chr2p16.1	227940_at	---
2.71	2.67	0.03	8.87E-01	9.68E-01	---	---	---	243528_at	---
2.14	2.12	0.02	8.87E-01	9.68E-01	PAQR9	progestin and adipoQ receptor family member IX	chr3q23	1560467_at	NM_198504
2.38	2.36	0.02	8.87E-01	9.68E-01	KIAA0494	KIAA0494	chr1pter-p22.1	1559022_at	NM_014774
9.11	9.08	0.03	8.87E-01	9.68E-01	PIGP	phosphatidylinositol glycan anchor biosynthesis, class P	chr21q22.2	221689_s_at	NM_153681 /// NM_153682
2.77	2.74	0.03	8.87E-01	9.68E-01	FAM80B	Family with sequence similarity 80, member B	chr12p13.31	242870_at	NM_020734
3.32	3.29	0.03	8.88E-01	9.68E-01	PZP	pregnancy-zone protein	chr12p13-p12.2	207330_at	NM_002864
3.29	3.25	0.04	8.88E-01	9.68E-01	---	---	---	226637_at	---
2.30	2.28	0.02	8.88E-01	9.68E-01	LOC732087	hypothetical protein LOC732087	---	1559617_at	XM_001131817 /// XM_001716453
6.95	6.91	0.04	8.88E-01	9.68E-01	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	chr9q21.33	209273_s_at	NM_030940
7.70	7.67	0.04	8.88E-01	9.68E-01	EMD	emerin	chrXq28	209477_at	NM_000117
3.69	3.66	0.03	8.88E-01	9.68E-01	KIF9	kinesin family member 9	chr3p21.31	223778_at	NM_022342 /// NM_182902 /// NM_182903
4.21	4.19	0.02	8.88E-01	9.68E-01	ZNF554	zinc finger protein 554	chr19p13.3	242864_at	NM_001102651
1.92	1.91	0.01	8.88E-01	9.68E-01	FCRLA	Fc receptor-like A	chr1q23.3	235401_s_at	NM_032738
2.07	2.05	0.02	8.88E-01	9.68E-01	HORMAD2	HORMA domain containing 2	chr22q12.2	237781_at	NM_152510
4.00	3.97	0.03	8.88E-01	9.68E-01	RHOBTB2	Rho-related BTB domain containing 2	chr8p21.3	1554586_a_at	NM_015178
3.06	3.03	0.03	8.88E-01	9.68E-01	TTC26	tetratricopeptide repeat domain 26	chr7q34	233999_s_at	NM_024926
2.54	2.51	0.03	8.88E-01	9.68E-01	B3GAT2	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)	chr6q13	239144_at	NM_080742
6.96	6.90	0.06	8.88E-01	9.68E-01	LMBR1	limb region 1 homolog (mouse)	chr7q36	224410_s_at	NM_022458
3.23	3.21	0.02	8.88E-01	9.68E-01	LRRC1	leucine rich repeat containing 1	chr6p12.1	218816_at	NM_018214
1.93	1.92	0.02	8.88E-01	9.68E-01	CCDC39	coiled-coil domain containing 39	chr3q26.33	233326_at	NM_181426
4.70	4.67	0.02	8.88E-01	9.68E-01	LOC653419 /// NPB	similar to preproneuropeptide B /// neuropeptide B	chr17q25.3	1553663_a_at	NM_148896 /// XM_934478
8.93	8.86	0.07	8.89E-01	9.68E-01	QPRT	quinolinate phosphoribosyltransferase	chr16p11.2	242414_at	NM_014298
6.31	6.26	0.05	8.89E-01	9.68E-01	EMP1	epithelial membrane protein 1	chr12p12.3	201325_s_at	NM_001423
2.05	2.03	0.02	8.89E-01	9.68E-01	BLZF1	basic leucine zipper nuclear factor 1	chr1q24	210462_at	NM_003666
4.82	4.79	0.03	8.89E-01	9.68E-01	LOC645638	similar to WDNM1-like protein	chr17q23.1	229566_at	XR_040455 /// XR_040456 /// XR_040457
3.14	3.11	0.03	8.89E-01	9.68E-01	BEST3	bestrophin 3	chr12q14.2-q15	237003_at	NM_032735 /// NM_152439
7.16	7.11	0.04	8.89E-01	9.68E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	225097_at	NM_001113239 /// NM_022740
2.63	2.60	0.03	8.89E-01	9.68E-01	JAK1	Janus kinase 1 (a protein tyrosine kinase)	chr1p32.3-p31.3	239695_at	NM_002227
2.83	2.73	0.10	8.89E-01	9.68E-01	CYorf15A	chromosome Y open reading frame 15A	chrYq11.222	232618_at	NM_001005852
2.03	2.01	0.01	8.89E-01	9.68E-01	EXDL1	exonuclease 3'-5' domain-like 1	chr15q15.1	1553907_a_at	NM_152596
3.46	3.41	0.05	8.89E-01	9.68E-01	---	---	---	241387_at	---
4.46	4.42	0.04	8.89E-01	9.68E-01	---	---	---	233476_at	---
5.75	5.73	0.03	8.89E-01	9.68E-01	RC3H2	ring finger and CCCH-type zinc finger domains 2	chr9q34	225813_at	NM_001100588 /// NM_018835
3.24	3.19	0.05	8.89E-01	9.68E-01	LOC649305	hypothetical protein LOC649305	---	1568780_at	XM_001722373 /// XM_001726970
4.43	4.40	0.02	8.90E-01	9.69E-01	PGP	phosphoglycolate phosphatase	chr16p13.3	218410_s_at	NM_001042371
3.88	3.85	0.03	8.90E-01	9.69E-01	LOC285908	hypothetical protein LOC285908	chr7q11.21	235397_at	NM_181722
2.39	2.37	0.02	8.90E-01	9.69E-01	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	chr17q24	1565780_at	NM_007168
2.26	2.24	0.02	8.90E-01	9.69E-01	LOC100130460	hypothetical protein LOC100130460	chr11p15.4	237915_at	XM_001721426 /// XM_001721658 /// XM_001724829
3.30	3.26	0.05	8.90E-01	9.69E-01	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	chr18q11	206232_s_at	NM_004775

2.21	2.19	0.02	8.90E-01	9.69E-01	ESR1	estrogen receptor 1	chr6q25.1	215551_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742																			
4.49	4.46	0.03	8.90E-01	9.69E-01	CHD4	chromodomain helicase DNA binding protein 4	chr12p13	201182_s_at	NM_001273																			
2.44	2.41	0.03	8.90E-01	9.69E-01	ZNF460	zinc finger protein 460	chr19q13.4	233175_at	NM_006635																			
2.38	2.35	0.02	8.90E-01	9.69E-01	CASC5	cancer susceptibility candidate 5	chr15q14	228323_at	NM_144508 /// NM_170589																			
4.97	4.95	0.02	8.90E-01	9.69E-01	PPP4R1L	protein phosphatase 4, regulatory subunit 1-like	chr20q13.32	223733_s_at	NR_003505																			
4.72	4.69	0.03	8.90E-01	9.69E-01	USP12	ubiquitin specific peptidase 12	chr13q12.13	213327_s_at	NM_182488																			
4.10	4.07	0.03	8.90E-01	9.69E-01	CCDC123	Coiled-coil domain containing 123	chr19q13.11	232106_s_at	NM_032816																			
2.33	2.32	0.02	8.91E-01	9.69E-01	C1orf2	chromosome 1 open reading frame 2	chr1q21	1555515_a_at	NM_006589 /// NM_198264																			
2.71	2.69	0.02	8.91E-01	9.69E-01	---	---	---	236564_at	---																			
3.04	3.01	0.03	8.91E-01	9.69E-01	---	---	---	233652_at	---																			
2.40	2.38	0.02	8.91E-01	9.69E-01	FIBIN	fin bud initiation factor	chr11p14.2	231001_at	NM_203371																			
5.41	5.39	0.02	8.91E-01	9.69E-01	---	---	---	229167_at	---																			
2.02	2.01	0.02	8.91E-01	9.69E-01	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	chr6q22-q23	215152_at	NM_001130172 /// NM_001130173 /// NM_005375																			
2.29	2.27	0.02	8.91E-01	9.69E-01	---	---	---	232709_at	---																			
2.28	2.26	0.02	8.91E-01	9.69E-01	---	---	---	1559792_at	---																			
2.10	2.08	0.02	8.91E-01	9.69E-01	MYT1L	myelin transcription factor 1-like	chr2p25.3	1554633_a_at	NM_015025																			
2.99	2.97	0.03	8.91E-01	9.69E-01	ZNF41	zinc finger protein 41	chrXp11.23	1553216_at	NM_007130 /// NM_153380																			
2.72	2.70	0.02	8.91E-01	9.69E-01	---	---	---	243606_at	---																			
2.23	2.21	0.02	8.91E-01	9.69E-01	ZCCHC4	zinc finger, CCHC domain containing 4	chr4p15.2	220473_s_at	NM_024936																			
2.23	2.21	0.03	8.91E-01	9.69E-01	---	---	---	234176_at	---																			
2.07	2.04	0.03	8.91E-01	9.69E-01	IL1RAP	interleukin 1 receptor accessory protein	chr3q28	210233_at	NM_002182 /// NM_134470																			
4.16	4.12	0.04	8.91E-01	9.69E-01	EMID2	EMI domain containing 2	chr7q22.1	229080_at	NM_133457																			
2.50	2.47	0.02	8.91E-01	9.69E-01	---	---	---	243248_at	---																			
5.31	5.28	0.03	8.91E-01	9.69E-01	ASPSCR1	alveolar soft part sarcoma chromosome region, candidate 1	chr17q25	218908_at	NM_024083																			
12.72	12.70	0.01	8.92E-01	9.70E-01	TPT1	tumor protein, translationally-controlled 1	chr13q12-q14	212284_x_at	NM_003295																			
2.77	2.75	0.02	8.92E-01	9.70E-01	LOC283174	hypothetical LOC283174	chr11q25	232123_at	XR_017873 /// XR_017972 /// XR_039979																			
2.17	2.15	0.02	8.92E-01	9.70E-01	LOC151658	hypothetical LOC151658	chr3q13.12	238283_at	---																			
4.56	4.54	0.02	8.92E-01	9.70E-01	SLC22A5	solute carrier family 22 (organic cation/carnitine transporter), member 5	chr5q31	239615_at	NM_003060																			
4.17	4.14	0.03	8.92E-01	9.70E-01	---	---	---	1556852_a_at	---																			
4.55	4.53	0.02	8.92E-01	9.70E-01	---	---	---	230868_at	---																			
3.45	3.42	0.02	8.92E-01	9.70E-01	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	chr17q21.32	216956_s_at	NM_000419																			
7.18	7.13	0.05	8.92E-01	9.70E-01	NQO1	NAD(P)H dehydrogenase, quinone 1	chr16q22.1	201467_s_at	NM_000903 /// NM_001025433 /// NM_001025434																			
2.37	2.35	0.02	8.92E-01	9.70E-01	TSGA14	testis specific, 14	chr7q32	215637_at	NM_018718																			
1.98	1.96	0.02	8.92E-01	9.70E-01	ESX1	ESX homeobox 1	chrXq22.1	1552445_a_at	NM_153448																			
3.42	3.40	0.02	8.92E-01	9.70E-01	GTF2A1	general transcription factor IIA, 1, 19/37kDa	chr14q31.1	206521_s_at	NM_015859 /// NM_201595																			
8.39	8.36	0.03	8.92E-01	9.70E-01	TMCO1	transmembrane and coiled-coil domains 1	chr1q22-q25	208716_s_at	NM_019026																			

2.17	2.15	0.01	8.92E-01	9.70E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	1562270_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735
3.13	3.10	0.03	8.92E-01	9.70E-01	---	---	---	229149_at	---
2.59	2.57	0.02	8.92E-01	9.70E-01	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	chr10p14	230215_at	NM_018144
3.60	3.55	0.05	8.92E-01	9.70E-01	---	---	---	232354_at	---
2.08	2.06	0.02	8.93E-01	9.70E-01	AREG	Amphiregulin	chr4q13-q21	215564_at	NM_001657
1.89	1.88	0.02	8.93E-01	9.70E-01	TYR	tyrosinase (oculocutaneous albinism IA)	chr11q14-q21	1555504_at	NM_000372
2.01	1.99	0.02	8.93E-01	9.70E-01	KRTAP4-7	keratin associated protein 4-7	chr17q12-q21	216810_at	NM_033061
3.13	3.11	0.02	8.93E-01	9.70E-01	HLA-DOB	major histocompatibility complex, class II, DO beta	chr6p21.3	1554984_a_at	NM_002120
4.49	4.46	0.03	8.93E-01	9.70E-01	GRB2	growth factor receptor-bound protein 2	chr17q24-q25	228572_at	NM_002086 /// NM_203506
3.76	3.69	0.07	8.93E-01	9.70E-01	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	chr1p35	203649_s_at	NM_000300
2.02	2.00	0.01	8.93E-01	9.70E-01	---	---	---	1563149_at	---
3.27	3.25	0.02	8.93E-01	9.70E-01	KILLIN	killin protein	chr10q23	244431_at	NM_001126049
1.96	1.94	0.02	8.93E-01	9.70E-01	FGGY	FGGY carbohydrate kinase domain containing	chr1p32.1	232380_at	NM_001113411 /// NM_018291
5.15	5.12	0.03	8.93E-01	9.70E-01	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	chr15q25.1	220395_at	NM_001130182 /// NM_001130183 /// NM_018602
5.01	4.96	0.04	8.93E-01	9.70E-01	FLJ12993	hypothetical LOC441027	chr4q21.22	231923_at	NM_001080506
2.71	2.68	0.03	8.93E-01	9.70E-01	C14orf145	chromosome 14 open reading frame 145	chr14q31.1	1557755_at	NM_152446
2.03	2.02	0.02	8.93E-01	9.70E-01	C18orf58	chromosome 18 open reading frame 58	chr18p11.22	1564015_at	NM_173817
2.11	2.10	0.01	8.93E-01	9.70E-01	---	---	---	238632_at	---
2.12	2.10	0.02	8.93E-01	9.70E-01	---	---	---	240662_at	---
4.96	4.93	0.02	8.93E-01	9.70E-01	LENG1	leukocyte receptor cluster (LRC) member 1	chr19q13.4	232018_at	NM_024316
1.97	1.95	0.02	8.93E-01	9.70E-01	GRIK2	glutamate receptor, ionotropic, kainate 2	chr6q16.3-q21	1555375_at	NM_021956 /// NM_175768
2.24	2.22	0.02	8.93E-01	9.70E-01	WFDC8	WAP four-disulfide core domain 8	chr20q13.12	1554156_a_at	NM_130896 /// NM_181510
2.23	2.21	0.02	8.93E-01	9.70E-01	---	---	---	1563179_at	---
2.09	2.07	0.02	8.93E-01	9.70E-01	LILRB4	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	chr19q13.4	1569504_at	NM_001081438 /// NM_006847
2.70	2.68	0.02	8.93E-01	9.70E-01	LOC730441	similar to trypsin X5	---	1568828_at	XM_001125779
2.31	2.29	0.02	8.93E-01	9.70E-01	SYNE2	spectrin repeat containing, nuclear envelope 2	chr14q23.2	1558392_at	NM_015180 /// NM_182910 /// NM_182913 /// NM_182914
3.92	3.90	0.03	8.93E-01	9.70E-01	LOC100131512	hypothetical protein LOC100131512	chr7p21.1	239775_at	XM_001721163 /// XM_001722836 /// XM_001722891
3.24	3.20	0.04	8.93E-01	9.70E-01	COG2	component of oligomeric golgi complex 2	chr1q42.2	243608_at	NM_007357
1.95	1.94	0.01	8.93E-01	9.70E-01	LOC150005	hypothetical protein LOC150005	chr21q21.1	1561343_a_at	---
4.39	4.36	0.03	8.94E-01	9.70E-01	KIAA1310	KIAA1310	chr2p12-p11.2	220950_s_at	NM_001115016 /// NM_017991
2.48	2.46	0.02	8.94E-01	9.70E-01	---	---	---	239543_s_at	---
1.97	1.96	0.01	8.94E-01	9.70E-01	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	chr14q22.1	238799_at	NM_001003803 /// NM_001003805 /// NM_015684
2.16	2.14	0.02	8.94E-01	9.70E-01	C8orf34	chromosome 8 open reading frame 34	chr8q13	231380_at	NM_052958
2.02	2.00	0.02	8.94E-01	9.70E-01	LOC347475	hypothetical gene supported by BC017958	chrXq26.2	1563022_at	NM_001101357

2.73	2.71	0.02	8.94E-01	9.70E-01	PRR18	proline rich region 18	chr6q27	238008_at	NM_175922
4.69	4.66	0.03	8.94E-01	9.70E-01	DTX3	deltex 3 homolog (Drosophila)	chr12q13.3	49049_at	NM_178502
2.53	2.51	0.01	8.94E-01	9.70E-01	---	---	---	1565610_at	---
2.76	2.73	0.03	8.94E-01	9.70E-01	HABP2	hyaluronan binding protein 2	chr10q25.3	206010_at	NM_004132
3.12	3.07	0.04	8.94E-01	9.70E-01	P2RY12	purinergic receptor P2Y, G-protein coupled, 12	chr3q24-q25	224102_at	NM_022788 /// NM_176876
4.34	4.32	0.02	8.94E-01	9.70E-01	TMEM70	transmembrane protein 70	chr8q21.11	219448_at	NM_001040613 /// NM_017866
7.82	7.79	0.03	8.94E-01	9.70E-01	FAM14A	family with sequence similarity 14, member A	chr14q32.13	223626_x_at	NM_032036
5.11	5.09	0.02	8.94E-01	9.70E-01	SERF1A /// SERF1B	small EDRK-rich factor 1A (telomeric) /// small EDRK-rich factor 1B (centromeric)	chr5q12.2-q13.3 /// chr5q13.2	219982_s_at	NM_021967 /// NM_022968 /// NM_022978 /// XM_001713905 /// XM_001720851 /// XM_001720856
5.34	5.28	0.05	8.94E-01	9.70E-01	KLHL24	kelch-like 24 (Drosophila)	chr3q27.1	221985_at	NM_017644
5.50	5.48	0.02	8.94E-01	9.71E-01	C19orf21	chromosome 19 open reading frame 21	chr19p13.3	212925_at	NM_173481
5.94	5.90	0.04	8.94E-01	9.71E-01	KANK1	KN motif and ankyrin repeat domains 1	chr9p24.3	213005_s_at	NM_015158 /// NM_153186
2.43	2.41	0.02	8.94E-01	9.71E-01	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	chr1q41	216057_at	NM_012414
3.18	3.15	0.03	8.94E-01	9.71E-01	LOC550631	Hypothetical LOC550631	chr22q12.2	242949_x_at	NM_001017437
2.26	2.23	0.03	8.95E-01	9.71E-01	---	---	---	205955_at	---
5.44	5.39	0.05	8.95E-01	9.71E-01	UBXN8	UBX domain protein 8	chr8p12-p11.2	215983_s_at	NM_005671
6.78	6.72	0.06	8.95E-01	9.71E-01	RANBP2	RAN binding protein 2	chr2q12.3	201713_s_at	NM_006267
5.03	4.98	0.04	8.95E-01	9.71E-01	NRP2	neuropilin 2	chr2q33.3	229225_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279
6.27	6.25	0.03	8.95E-01	9.71E-01	ATF2	activating transcription factor 2	chr2q32	212984_at	NM_001880
2.99	2.97	0.02	8.95E-01	9.71E-01	GPR132	G protein-coupled receptor 132	chr14q32.3	221140_s_at	NM_013345
8.23	8.19	0.04	8.95E-01	9.71E-01	GBE1	glucan (1,4-alpha-), branching enzyme 1	chr3p12.3	203282_at	NM_000158
3.22	3.19	0.03	8.95E-01	9.71E-01	PILRA	paired immunoglobin-like type 2 receptor alpha	chr7q22.1	219788_at	NM_013439 /// NM_178272 /// NM_178273
5.71	5.68	0.04	8.95E-01	9.71E-01	TSPAN14	tetraspanin 14	chr10q23.1	223314_at	NM_001128309 /// NM_030927
2.84	2.82	0.02	8.95E-01	9.71E-01	LOC100131763	hypothetical LOC100131763	chr2q37.3	1563822_at	XM_001720360 /// XM_001722609
2.96	2.94	0.02	8.95E-01	9.71E-01	---	---	---	215369_at	---
1.98	1.97	0.01	8.95E-01	9.71E-01	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	chr15q15-q21.1	220281_at	NM_000338
2.54	2.52	0.02	8.95E-01	9.71E-01	PCNXL2	pecanex-like 2 (Drosophila)	chr1q42.2	220461_at	NM_014801
3.01	2.99	0.02	8.95E-01	9.71E-01	---	---	---	241945_at	---
6.77	6.72	0.05	8.95E-01	9.71E-01	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	chr5q32	1567628_at	NM_001025158 /// NM_001025159 /// NM_004355
2.33	2.31	0.01	8.95E-01	9.71E-01	---	---	---	237553_at	---
2.15	2.13	0.02	8.95E-01	9.71E-01	---	---	---	1562380_at	---
2.45	2.43	0.02	8.95E-01	9.71E-01	ZIC4	Zic family member 4	chr3q24	211463_at	NM_032153
2.64	2.63	0.02	8.95E-01	9.71E-01	---	---	---	233456_at	---
2.12	2.11	0.02	8.95E-01	9.71E-01	---	---	---	1562071_at	---
2.50	2.48	0.02	8.95E-01	9.71E-01	TMEM169	transmembrane protein 169	chr2q35	228981_at	NM_138390

2.33	2.31	0.02	8.95E-01	9.71E-01	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	chrXp11.4	238698_at	NM_001126054 /// NM_001126055 /// NM_003688																				
6.49	6.47	0.02	8.95E-01	9.71E-01	C14orf153	chromosome 14 open reading frame 153	chr14q32.33	225948_at	NM_032374																				
2.57	2.54	0.03	8.96E-01	9.71E-01	LOC553137	hypothetical LOC553137	chr6q21	235774_at	NR_015365 /// XR_001059 /// XR_001268																				
4.14	4.12	0.02	8.96E-01	9.71E-01	IGHE	immunoglobulin heavy constant epsilon	chr14q32.33	1558437_at	---																				
2.03	2.01	0.01	8.96E-01	9.71E-01	CCDC18	coiled-coil domain containing 18	chr1p22.1	236665_at	NM_206886																				
2.28	2.27	0.02	8.96E-01	9.71E-01	---	---	---	1563898_at	---																				
6.30	6.26	0.04	8.96E-01	9.71E-01	ZNF827	Zinc finger protein 827	chr4q31.22	228046_at	NM_178835																				
2.47	2.45	0.02	8.96E-01	9.71E-01	---	---	---	241217_x_at	---																				
1.95	1.93	0.02	8.96E-01	9.71E-01	EPHA7	EPH receptor A7	chr6q16.1	206852_at	NM_004440																				
2.15	2.13	0.02	8.96E-01	9.71E-01	ZBED2	zinc finger, BED-type containing 2	chr3q13.13	219836_at	NM_024508																				
2.05	2.04	0.02	8.96E-01	9.71E-01	C9orf152	chromosome 9 open reading frame 152	chr9q31.3	229964_at	NM_001012993																				
1.91	1.90	0.01	8.96E-01	9.71E-01	---	---	---	241545_x_at	---																				
2.50	2.47	0.02	8.96E-01	9.71E-01	LY6H	lymphocyte antigen 6 complex, locus H	chr8q24.3	206773_at	NM_001130478 /// NM_002347																				
6.59	6.54	0.05	8.96E-01	9.71E-01	SLU7	SLU7 splicing factor homolog (S. cerevisiae)	chr5q33.3	227990_at	NM_006425																				
2.31	2.29	0.02	8.96E-01	9.71E-01	41340	Membrane-associated ring finger (C3HC4) 7	chr2q24.2	232371_at	NM_022826																				
2.25	2.23	0.02	8.96E-01	9.71E-01	---	---	---	1566658_at	---																				
3.07	3.04	0.02	8.96E-01	9.71E-01	KALRN	Kalirin, RhoGEF kinase	chr3q21.1-q21.2	232756_at	NM_001024660 /// NM_003947 /// NM_007064																				
3.65	3.61	0.03	8.96E-01	9.71E-01	---	---	---	232923_at	---																				
2.88	2.84	0.03	8.96E-01	9.71E-01	---	---	---	1570339_x_at	---																				
3.52	3.50	0.02	8.96E-01	9.71E-01	C10orf53	chromosome 10 open reading frame 53	chr10q11.23	239998_at	NM_001042427 /// NM_182554																				
3.01	2.98	0.03	8.96E-01	9.71E-01	KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4	chr22q13.1	208359_s_at	NM_004981 /// NM_152868																				
8.11	8.09	0.02	8.96E-01	9.71E-01	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	chr2q31.3	203371_s_at	NM_002491																				
2.36	2.34	0.02	8.97E-01	9.71E-01	ARGLU1	arginine and glutamate rich 1	chr13q33.3	227448_at	NM_018011																				
5.60	5.56	0.05	8.97E-01	9.71E-01	MON2	MON2 homolog (S. cerevisiae)	chr12q14.1	212754_s_at	NM_015026																				
1.86	1.85	0.02	8.97E-01	9.71E-01	---	---	---	233372_at	---																				
6.88	6.85	0.04	8.97E-01	9.71E-01	NR2F1	nuclear receptor subfamily 2, group F, member 1	chr5q14	209506_s_at	NM_005654																				
6.21	6.16	0.04	8.97E-01	9.71E-01	LONP2	Lon peptidase 2, peroxisomal	chr16q12.1	221834_at	NM_031490																				
3.29	3.26	0.03	8.97E-01	9.71E-01	LOC202181	Hypothetical protein LOC202181	chr5q35.3	231375_at	XR_015120 /// XR_015544 /// XR_040243																				
2.48	2.46	0.02	8.97E-01	9.71E-01	MTHFSD	methenyltetrahydrofolate synthetase domain containing	chr16q24.1	1554495_s_at	NM_022764																				
5.61	5.58	0.03	8.97E-01	9.71E-01	---	---	---	229278_at	---																				
1.96	1.94	0.02	8.97E-01	9.71E-01	LOC401074	Hypothetical LOC401074	chr3p12.3	1564175_at	XM_001714392																				
3.02	2.99	0.03	8.97E-01	9.71E-01	CAPN5	calpain 5	chr11q14	205166_at	NM_004055																				
2.56	2.54	0.02	8.97E-01	9.71E-01	KREMEN1	kringle containing transmembrane protein 1	chr22q12.1	234843_s_at	NM_001039570 /// NM_001039571																				
6.01	5.99	0.03	8.97E-01	9.71E-01	RBM4	RNA binding motif protein 4	chr11q13	213718_at	NM_002896																				
3.30	3.27	0.03	8.97E-01	9.71E-01	CPSF3L	cleavage and polyadenylation specific factor 3-like	chr1p36.33	232437_at	NM_017871																				
4.09	4.07	0.03	8.97E-01	9.71E-01	FANCE	Fanconi anemia, complementation group E	chr6p22-p21	220255_at	NM_021922																				

2.27	2.25	0.02	8.97E-01	9.71E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	210767_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833																				
2.69	2.67	0.02	8.98E-01	9.71E-01	CFC1	cripto, FRL-1, cryptic family 1	chr2q21.1	223752_at	NM_032545																				
2.08	2.06	0.02	8.98E-01	9.71E-01	ABI3BP	ABI gene family, member 3 (NESH) binding protein	chr3q12	1559077_at	NM_015429																				
8.99	8.97	0.02	8.98E-01	9.72E-01	SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	chr5p15	201093_x_at	NM_004168																				
2.18	2.16	0.02	8.98E-01	9.72E-01	C10orf84	chromosome 10 open reading frame 84	chr10q26.11	218390_s_at	NM_001134672 /// NM_022063																				
3.59	3.57	0.02	8.98E-01	9.72E-01	---	---	---	243639_at	---																				
2.82	2.78	0.03	8.98E-01	9.72E-01	SKI	v-ski sarcoma viral oncogene homolog (avian)	chr1q22-q24	204270_at	NM_003036																				
4.98	4.94	0.04	8.98E-01	9.72E-01	WDR32	WD repeat domain 32	chr9p13.2	226511_at	NM_024345																				
2.57	2.55	0.02	8.98E-01	9.72E-01	PMS2L3	postmeiotic segregation increased 2-like 3	chr7q11.23	217488_x_at	NM_001003686 /// NM_005395 /// XM_001716315																				
7.70	7.63	0.07	8.98E-01	9.72E-01	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	chr18q11.2	203441_s_at	NM_001792																				
2.82	2.80	0.02	8.98E-01	9.72E-01	SLC37A1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	chr21q22.3	234754_at	NM_018964																				
2.16	2.14	0.02	8.98E-01	9.72E-01	OR2M4	olfactory receptor, family 2, subfamily M, member 4	chr1q44	1566288_at	NM_017504																				
3.14	3.11	0.02	8.98E-01	9.72E-01	---	---	---	234487_at	---																				
2.75	2.72	0.03	8.98E-01	9.72E-01	FAM98A	Family with sequence similarity 98, member A	chr2p22.3	239487_at	NM_015475																				
2.15	2.13	0.02	8.98E-01	9.72E-01	BRS3	bombesin-like receptor 3	chrXq26-q28	1552818_a_at	NM_001727																				
3.35	3.33	0.02	8.98E-01	9.72E-01	XAGE3	X antigen family, member 3	chrXp11.22-p11.21	236040_at	NM_130776 /// NM_133179																				
1.96	1.95	0.01	8.99E-01	9.72E-01	LHX9	LIM homeobox 9	chr1q31-q32	1562736_at	NM_001014434 /// NM_020204																				
2.90	2.89	0.01	8.99E-01	9.72E-01	---	---	---	242346_x_at	---																				
2.56	2.55	0.01	8.99E-01	9.72E-01	HUS1B	HUS1 checkpoint homolog b (S. pombe)	chr6p25.3	1553661_a_at	NM_148959																				
2.10	2.09	0.02	8.99E-01	9.72E-01	---	---	---	1561516_at	---																				
3.01	2.99	0.02	8.99E-01	9.72E-01	LOC339240	keratin pseudogene	chr17p11.2	241828_x_at	NR_001443 /// XR_042158																				
7.18	7.14	0.04	8.99E-01	9.72E-01	ZMYM2	zinc finger, MYM-type 2	chr13q11-q12	202778_s_at	NM_003453 /// NM_197968																				
3.48	3.46	0.02	8.99E-01	9.72E-01	LLGL1	lethal giant larvae homolog 1 (Drosophila)	chr17p11.2	206124_s_at	NM_004140																				
2.11	2.10	0.01	8.99E-01	9.72E-01	---	---	---	1560132_a_at	---																				
7.26	7.24	0.02	8.99E-01	9.72E-01	APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	chr22q13.1|22q13.1-q13.2	209584_x_at	NM_014508																				
2.04	2.02	0.02	8.99E-01	9.72E-01	---	---	---	1561158_at	---																				
2.88	2.87	0.02	8.99E-01	9.72E-01	ZNF44	zinc finger protein 44	chr19p13.2	233712_at	NM_016264 /// XM_001718561 /// XM_001719479 /// XM_001719639																				
7.10	7.06	0.05	8.99E-01	9.72E-01	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	chr4q23	217971_at	NM_021970																				
7.02	6.99	0.02	8.99E-01	9.72E-01	CRAT	carnitine acetyltransferase	chr9q34.1	205843_x_at	NM_000755 /// NM_004003																				
5.06	5.03	0.04	8.99E-01	9.72E-01	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	chr11q13.3	210235_s_at	NM_003626 /// NM_177423																				

1.93	1.91	0.02	8.99E-01	9.72E-01	C21orf100	chromosome 21 open reading frame 100	chr21q21.3	1552466_x_at	XR_017892 /// XR_017991
3.75	3.72	0.03	8.99E-01	9.72E-01	ALDH1L1	aldehyde dehydrogenase 1 family, member L1	chr3q21.2	215798_at	NM_012190
2.76	2.74	0.02	8.99E-01	9.72E-01	---	---	---	241232_x_at	---
3.86	3.83	0.04	8.99E-01	9.72E-01	ARID2	AT rich interactive domain 2 (ARID, RFX-like)	chr12q12	225486_at	NM_152641
6.44	6.41	0.03	8.99E-01	9.72E-01	RNASEN	ribonuclease type III, nuclear	chr5p13.3	218269_at	NM_001100412 /// NM_013235
6.12	6.06	0.06	8.99E-01	9.72E-01	LTBP2	latent transforming growth factor beta binding protein 2	chr14q24	204682_at	NM_000428
2.22	2.21	0.02	8.99E-01	9.72E-01	TMCO3	transmembrane and coiled-coil domains 3	chr13q34	220241_at	NM_017905
3.83	3.81	0.02	8.99E-01	9.72E-01	---	---	---	1555132_at	---
4.39	4.36	0.03	8.99E-01	9.72E-01	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	chr18q23	227204_at	NM_032510
2.19	2.18	0.02	8.99E-01	9.72E-01	---	---	---	244253_at	---
1.89	1.87	0.02	8.99E-01	9.72E-01	CENPJ	centromere protein J	chr13q12.12	234023_s_at	NM_018451
2.04	2.03	0.02	9.00E-01	9.72E-01	NCOR1	nuclear receptor co-repressor 1	chr17p11.2	234313_at	NM_006311
3.56	3.52	0.04	9.00E-01	9.72E-01	TMF1	TATA element modulatory factor 1	chr3p21-p12	227685_at	NM_007114
5.88	5.83	0.04	9.00E-01	9.72E-01	RPH3AL	rabphilin 3A-like (without C2 domains)	chr17p13.3	221614_s_at	NM_006987
3.95	3.92	0.03	9.00E-01	9.72E-01	KIAA0040	KIAA0040	chr1q24-q25	203143_s_at	NR_015350 /// XR_041163 /// XR_041164 /// XR_041165
2.20	2.19	0.01	9.00E-01	9.72E-01	SQSTM1	sequestosome 1	chr5q35	217252_at	NM_003900
3.22	3.20	0.02	9.00E-01	9.72E-01	CORO6	coronin 6	chr17q11.2	1552301_a_at	NM_032854
2.14	2.12	0.02	9.00E-01	9.72E-01	---	---	---	1569259_at	---
2.99	2.96	0.02	9.00E-01	9.72E-01	---	---	---	240400_at	---
1.92	1.91	0.01	9.00E-01	9.72E-01	KIAA1109	KIAA1109	chr4q27	1553792_at	NM_015312
2.66	2.63	0.02	9.00E-01	9.72E-01	GTPBP5	GTP binding protein 5 (putative)	chr20q13.33	1568822_at	NM_015666
2.33	2.32	0.02	9.00E-01	9.72E-01	MAGEA3	melanoma antigen family A, 3	chrXq28	209942_x_at	NM_005362
3.24	3.21	0.02	9.00E-01	9.72E-01	FAM100A	family with sequence similarity 100, member A	chr16p13.3	1558975_at	NM_145253
2.28	2.26	0.02	9.00E-01	9.72E-01	---	---	---	231353_at	---
2.70	2.67	0.02	9.00E-01	9.72E-01	BRMS1L	breast cancer metastasis-suppressor 1-like	chr14q13.2	224484_s_at	NM_032352
5.00	4.96	0.04	9.00E-01	9.72E-01	CC2D2A	coiled-coil and C2 domain containing 2A	chr4p15.33	234936_s_at	NM_001080522 /// NM_020785 /// NR_024098
2.53	2.51	0.02	9.00E-01	9.72E-01	FLJ39739	hypothetical FLJ39739	chr1q21.1	1556456_at	XR_039904 /// XR_039905
2.80	2.78	0.02	9.00E-01	9.72E-01	---	---	---	243132_at	---
8.16	8.12	0.04	9.00E-01	9.72E-01	SNX5	sorting nexin 5	chr20p11	229980_s_at	NM_014426 /// NM_152227
2.23	2.21	0.01	9.00E-01	9.72E-01	---	---	---	1568803_at	---
5.83	5.79	0.04	9.00E-01	9.72E-01	ANKRD49	ankyrin repeat domain 49	chr11q21	219069_at	NM_017704
3.81	3.77	0.04	9.00E-01	9.72E-01	---	---	---	244010_at	---
2.07	2.05	0.02	9.01E-01	9.72E-01	---	---	---	231633_at	---
4.51	4.49	0.03	9.01E-01	9.72E-01	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	chr19q13.4	207857_at	NM_001130917 /// NM_006866
2.81	2.79	0.02	9.01E-01	9.72E-01	SPEN	spen homolog, transcriptional regulator (Drosophila)	chr1p36.33-p36.11	1556058_s_at	NM_015001
2.92	2.90	0.02	9.01E-01	9.73E-01	LHX9	LIM homeobox 9	chr1q31-q32	1565407_at	NM_001014434 /// NM_020204
10.49	10.47	0.02	9.01E-01	9.73E-01	H3F3A /// H3F3B	H3 histone, family 3A /// H3 histone, family 3B (H3.3B)	chr17q25 /// chr1q41	211997_x_at	NM_002107 /// NM_005324
5.94	5.90	0.05	9.01E-01	9.73E-01	PKD2	polycystic kidney disease 2 (autosomal dominant)	chr4q21-q23	203688_at	NM_000297
1.96	1.95	0.02	9.01E-01	9.73E-01	LOC286002	hypothetical protein LOC286002	chr7q22.3	1557107_at	XM_001715026 /// XM_001718146 /// XM_001718326
3.52	3.51	0.01	9.01E-01	9.73E-01	---	---	---	216425_at	---
2.29	2.27	0.02	9.01E-01	9.73E-01	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	chr17q22	1553211_at	NM_153228
6.99	6.96	0.03	9.01E-01	9.73E-01	FAM14B	Family with sequence similarity 14, member B	chr14q32.13	230172_at	NM_145249 /// NM_206949
3.12	3.10	0.02	9.01E-01	9.73E-01	KIR2DS4	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	chr19q13.4	216552_x_at	NM_012314

2.91	2.90	0.02	9.01E-01	9.73E-01	FAM110B	family with sequence similarity 110, member B	chr8q12.1	227800_at	NM_147189
5.52	5.47	0.06	9.02E-01	9.73E-01	FAM92A1	family with sequence similarity 92, member A1	chr8q22.1	235391_at	NM_145269
2.97	2.95	0.02	9.02E-01	9.73E-01	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	chr6p21.3	204770_at	NM_000544 /// NM_018833
3.18	3.16	0.02	9.02E-01	9.73E-01	FLJ77644 /// TMEM106A	similar to transmembrane protein 106A /// transmembrane protein 106A	chr17q21.31	1552303_a_at	NM_145041 /// XM_001133074 /// XM_001722626
3.02	2.99	0.02	9.02E-01	9.73E-01	---	---	---	236691_at	---
4.43	4.40	0.02	9.02E-01	9.73E-01	FTCD	formiminotransferase cyclodeaminase	chr21q22.3	223979_x_at	NM_006657 /// NM_206965
2.20	2.19	0.01	9.02E-01	9.73E-01	---	---	---	1563721_at	---
7.76	7.73	0.03	9.02E-01	9.73E-01	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	chr11q24.2	203759_at	NM_006278 /// XM_001714343 /// XM_001726541 /// XM_001726562
2.78	2.76	0.01	9.02E-01	9.73E-01	TRIM50	Tripartite motif-containing 50	chr7q11.23	238941_at	NM_178125
1.82	1.81	0.01	9.02E-01	9.73E-01	---	---	---	234655_at	---
2.09	2.08	0.02	9.02E-01	9.73E-01	BLZF1	basic leucine zipper nuclear factor 1	chr1q24	1558560_s_at	NM_003666
2.87	2.85	0.02	9.02E-01	9.73E-01	MYOC	myocilin, trabecular meshwork inducible glucocorticoid response	chr1q23-q24	210155_at	NM_000261
5.44	5.41	0.03	9.02E-01	9.73E-01	APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	chr3p21.1-p14.3	218158_s_at	NM_012096
2.57	2.55	0.02	9.02E-01	9.73E-01	---	---	---	244668_at	---
3.71	3.67	0.04	9.02E-01	9.73E-01	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	chr21q22.3	213541_s_at	NM_004449 /// NM_182918
6.66	6.61	0.05	9.02E-01	9.73E-01	ABHD2	abhydrolase domain containing 2	chr15q26.1	63825_at	NM_007011 /// NM_152924
2.29	2.28	0.01	9.02E-01	9.73E-01	LOC145845	hypothetical protein LOC145845	chr15q14	233382_at	XR_040653 /// XR_040654 /// XR_040655
4.99	4.97	0.02	9.02E-01	9.73E-01	---	---	---	216694_at	---
7.15	7.11	0.04	9.02E-01	9.73E-01	RAD23B	RAD23 homolog B (S. cerevisiae)	chr9q31.2	201223_s_at	NM_002874
3.74	3.71	0.02	9.02E-01	9.73E-01	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	chr17q11.2	214883_at	NM_003250 /// NM_199334
2.43	2.41	0.02	9.02E-01	9.73E-01	PM20D2	Peptidase M20 domain containing 2	chr6q15	229495_at	NM_001010853
7.42	7.38	0.04	9.02E-01	9.73E-01	XPO1	exportin 1 (CRM1 homolog, yeast)	chr2p16	208775_at	NM_003400
2.99	2.97	0.02	9.03E-01	9.73E-01	CEP68	centrosomal protein 68kDa	chr2p14	1559159_at	NM_015147
2.26	2.24	0.02	9.03E-01	9.73E-01	---	---	---	216072_at	---
7.17	7.15	0.03	9.03E-01	9.73E-01	CCDC92	coiled-coil domain containing 92	chr12q24.31	218175_at	NM_025140
4.29	4.27	0.02	9.03E-01	9.73E-01	KLHDC10	kelch domain containing 10	chr7q32.2	209254_at	NM_014997
2.54	2.52	0.02	9.03E-01	9.73E-01	---	---	---	1561002_at	---
6.08	6.06	0.02	9.03E-01	9.73E-01	GATAD1	GATA zinc finger domain containing 1	chr7q21-q22	208503_s_at	NM_021167
2.02	2.00	0.02	9.03E-01	9.73E-01	---	---	---	1564468_at	---
4.93	4.89	0.03	9.03E-01	9.73E-01	ZNF85	zinc finger protein 85	chr19p13.1-p12	206572_x_at	NM_003429
4.25	4.23	0.02	9.03E-01	9.73E-01	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	chr16p11.2	229807_s_at	NM_001042539 /// NM_002383
2.67	2.65	0.02	9.03E-01	9.73E-01	---	---	---	235633_at	---
2.08	2.06	0.02	9.03E-01	9.73E-01	CCNB2	Cyclin B2	chr15q22.2	1560161_at	NM_004701
2.56	2.54	0.02	9.03E-01	9.73E-01	---	---	---	1559054_a_at	---
5.94	5.89	0.05	9.03E-01	9.73E-01	F8	coagulation factor VIII, procoagulant component	chrXq28	205756_s_at	NM_000132 /// NM_019863
2.29	2.28	0.01	9.03E-01	9.73E-01	---	---	---	215648_at	---

11.01	10.99	0.03	9.03E-01	9.73E-01	HNRNPA1 /// HNRPA1L-2 /// HNRPA1P5 /// LOC100128836 /// LOC391670 /// LOC402112 /// LOC440125 /// LOC642817 /// LOC643033 /// LOC644037 /// LOC645001 /// LOC728170 /// LOC728732 /// LOC729366 /// LOC729423 /// LOC730246 /// RP11-78J21.1	heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucleoprotein A1 pseudogene /// heterogeneous nuclear ribonucleoprotein A1 pseudogene 5 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC642817 /// similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed) /// hypothetical LOC644037 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC728732 /// similar to heterogeneous nuclear ribonucleoprotein A1 /// similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) (HDP) /// hypothetical LOC730246 /// heterogeneous nuclear ribonucleoprotein A1-like	chr11p15.4 /// chr12q13.1 /// chr12q22 /// chr13q12.11 /// chr13q14.3 /// chr19p13.2 /// chr19q13.2 /// chr1p32.2 /// chr1q32.1 /// chr2q31.1 /// chr2q33.3 /// chr4q21.1 /// chr5q14.1 /// chr6p25.1 /// chr8q21.13 /// chrXq22 /// chrXq24	213356_x_at	NM_001011724 /// NM_001011725 /// NM_002136 /// NM_031157 /// NR_002944 /// XM_001726305 /// XM_001726948 /// XM_001726952 /// XR_015330 /// XR_015514 /// XR_015658 /// XR_015746 /// XR_015958 /// XR_016080 /// XR_016093 /// XR_016314 /// XR_016373 /// XR_016388 /// XR_017084 /// XR_017337 /// XR_017501 /// XR_018564 /// XR_019025 /// XR_019262 /// XR_019573 /// XR_038280 /// XR_038288 /// XR_038331 /// XR_038689 /// XR_038697 /// XR_038725 /// XR_038755 /// XR_038765 /// XR_038785 /// XR_038911 /// XR_039047 /// XR_039155 /// XR_039380 /// XR_039425 /// XR_039446 /// XR_039541																				
3.76	3.72	0.03	9.03E-01	9.73E-01	LOC728842	hypothetical LOC728842	chr11q23.2	239807_at	XM_001128533 /// XM_001128599 /// XM_001718531																				
6.08	6.04	0.04	9.03E-01	9.73E-01	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	chr10q22.2	212462_at	NM_012330																				
2.05	2.03	0.01	9.03E-01	9.73E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	210516_at	NM_014612																				
3.11	3.07	0.04	9.03E-01	9.73E-01	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	chr12q24.2	204972_at	NM_001032731 /// NM_002535 /// NM_016817																				
1.85	1.84	0.01	9.03E-01	9.73E-01	---	---	---	233861_at	---																				
2.22	2.19	0.03	9.03E-01	9.73E-01	BOLA2	BolA homolog 2 (E. coli)	chr16p11.2	231500_s_at	NM_001031827																				
5.65	5.62	0.03	9.03E-01	9.73E-01	SHE	Src homology 2 domain containing E	chr1q21.3	229910_at	NM_001010846																				
3.16	3.13	0.02	9.03E-01	9.73E-01	STX11	syntaxin 11	chr6q24.2	210190_at	NM_003764																				
2.28	2.25	0.03	9.03E-01	9.73E-01	CLEC2B	C-type lectin domain family 2, member B	chr12p13-p12	1556209_at	NM_005127																				
5.78	5.74	0.04	9.03E-01	9.73E-01	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	chr6q15	217825_s_at	NM_016021																				

2.55	2.53	0.02	9.03E-01	9.73E-01	ANKRD60	Ankyrin repeat domain 60	chr20q13.32	230683_at	XM_001134442 /// XM_001134462 /// XM_001717339																			
6.68	6.65	0.03	9.03E-01	9.73E-01	Magmas	mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	chr16p13.3	218969_at	NM_016069																			
5.31	5.28	0.02	9.03E-01	9.73E-01	---	---	---	236867_at	---																			
2.16	2.14	0.02	9.03E-01	9.73E-01	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	chr1p34	238073_at	NM_021952																			
3.79	3.77	0.02	9.03E-01	9.73E-01	DLL3	delta-like 3 (Drosophila)	chr19q13	222898_s_at	NM_016941 /// NM_203486																			
6.32	6.27	0.05	9.03E-01	9.73E-01	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	chr17q23.1	226660_at	NM_003161																			
5.03	4.99	0.04	9.04E-01	9.73E-01	SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa	chr14q22	205443_at	NM_003082																			
2.05	2.04	0.02	9.04E-01	9.73E-01	BTG4	B-cell translocation gene 4	chr11q23	220766_at	NM_017589																			
1.95	1.94	0.01	9.04E-01	9.73E-01	FANCB	Fanconi anemia, complementation group B	chrXp22.2	1557217_a_at	NM_001018113 /// NM_152633																			
2.99	2.97	0.02	9.04E-01	9.73E-01	NAV1	neuron navigator 1	chr1q32.3	233567_at	NM_020443																			
2.17	2.16	0.02	9.04E-01	9.74E-01	CALCR	calcitonin receptor	chr7q21.3	207886_s_at	NM_001742																			
7.96	7.94	0.03	9.04E-01	9.74E-01	TMEM208	transmembrane protein 208	chr16q22.1	221597_s_at	NM_014187																			
3.24	3.21	0.03	9.04E-01	9.74E-01	---	---	---	215006_at	---																			
3.08	3.06	0.02	9.04E-01	9.74E-01	ODF1	outer dense fiber of sperm tails 1	chr8q22.3	214485_at	NM_024410																			
4.29	4.26	0.03	9.04E-01	9.74E-01	---	---	---	241568_at	---																			
2.35	2.33	0.02	9.04E-01	9.74E-01	LOC100132207	hypothetical LOC100132207	chr3q21.3	243019_at	XM_001723750 /// XM_001724482 /// XM_001725883																			
4.06	4.04	0.03	9.04E-01	9.74E-01	ZNF541	zinc finger protein 541	chr19q13.32	232604_at	XM_001716969 /// XM_001717930 /// XM_001718013																			
1.97	1.96	0.02	9.04E-01	9.74E-01	---	---	---	244367_at	---																			
2.41	2.39	0.02	9.04E-01	9.74E-01	---	---	---	216782_at	---																			
2.67	2.64	0.02	9.04E-01	9.74E-01	---	---	---	1560181_at	---																			
2.38	2.36	0.02	9.04E-01	9.74E-01	TSC22D3	TSC22 domain family, member 3	chrXq22.3	235364_at	NM_001015881 /// NM_004089 /// NM_198057																			
6.47	6.44	0.03	9.05E-01	9.74E-01	CNOT8	CCR4-NOT transcription complex, subunit 8	chr5q31-q33	202163_s_at	NM_004779																			
1.81	1.79	0.01	9.05E-01	9.74E-01	HEATR1	HEAT repeat containing 1	chr1q43	1556348_at	NM_018072																			
7.35	7.31	0.04	9.05E-01	9.74E-01	RIOK3	RIO kinase 3 (yeast)	chr18q11.2	202130_at	NM_003831																			
2.26	2.24	0.02	9.05E-01	9.74E-01	PIGM	phosphatidylinositol glycan anchor biosynthesis, class M	chr1q23.2	236622_at	NM_145167																			
3.37	3.35	0.02	9.05E-01	9.74E-01	KIAA1712	KIAA1712	chr4q34	231850_x_at	NM_001040157																			
3.60	3.58	0.02	9.05E-01	9.74E-01	C11orf30	chromosome 11 open reading frame 30	chr11q13.5	222806_s_at	NM_020193																			
2.29	2.28	0.02	9.05E-01	9.74E-01	---	---	---	237599_at	---																			
6.72	6.69	0.03	9.05E-01	9.74E-01	FXC1	fracture callus 1 homolog (rat)	chr11p15.5-p15.3	222481_at	NM_012192																			
3.40	3.38	0.02	9.05E-01	9.74E-01	---	---	---	1556747_a_at	---																			
2.28	2.26	0.01	9.05E-01	9.74E-01	CLEC4D	C-type lectin domain family 4, member D	chr12p13.31	1552772_at	NM_080387																			
5.08	5.05	0.02	9.05E-01	9.74E-01	LOC100128936 /// LOC728979 /// RPL10A	similar to ribosomal protein L10a /// similar to ribosomal protein L10a /// ribosomal protein L10a	chr3p14.2 /// chr5q14.3 /// chr6p21.3-p21.2	229562_at	NM_007104 /// XM_001721819 /// XM_001726108 /// XM_001726387 /// XR_015799 /// XR_038428 /// XR_038884																			
1.87	1.86	0.01	9.05E-01	9.74E-01	CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	chr18q11.2	224400_s_at	NM_031422																			
6.85	6.81	0.04	9.05E-01	9.74E-01	ZCCHC24	zinc finger, CCHC domain containing 24	chr10q22.3	212419_at	NM_153367																			
4.04	3.99	0.04	9.05E-01	9.74E-01	PTPN11	protein tyrosine phosphatase, non-receptor type 11	chr12q24	205868_s_at	NM_002834																			

4.51	4.49	0.02	9.06E-01	9.74E-01	ANK1	ankyrin 1, erythrocytic	chr8p11.1	208353_x_at	NM_000037 /// NM_020475 /// NM_020476 /// NM_020477 /// NM_020478 /// NM_020480																				
2.35	2.34	0.02	9.06E-01	9.74E-01	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	chr1q43	220794_at	NM_022469																				
2.35	2.33	0.01	9.06E-01	9.74E-01	ARSB	arylsulfatase B	chr5q11-q13	232197_x_at	NM_000046 /// NM_198709																				
4.48	4.44	0.05	9.06E-01	9.74E-01	RHOU	ras homolog gene family, member U	chr1q42.11-q42.3	223169_s_at	NM_021205																				
2.73	2.71	0.02	9.06E-01	9.74E-01	---	---	---	1561015_at	---																				
2.57	2.55	0.02	9.06E-01	9.74E-01	---	---	---	1562810_at	---																				
8.49	8.45	0.05	9.06E-01	9.74E-01	ARHGAP18	Rho GTPase activating protein 18	chr6q22.33	225171_at	NM_033515																				
6.37	6.33	0.04	9.06E-01	9.74E-01	ABHD10	abhydrolase domain containing 10	chr3q13.2	222697_s_at	NM_018394																				
2.50	2.48	0.02	9.06E-01	9.74E-01	---	---	---	1562943_at	---																				
3.15	3.13	0.02	9.06E-01	9.74E-01	RAB27B	RAB27B, member RAS oncogene family	chr18q21.2	207017_at	NM_004163																				
3.89	3.86	0.03	9.06E-01	9.74E-01	ERO1L	ERO1-like (S. cerevisiae)	chr14q22.1	218498_s_at	NM_014584																				
8.12	8.09	0.02	9.06E-01	9.74E-01	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	chr16p13.3	228301_x_at	NM_004548																				
2.74	2.72	0.01	9.06E-01	9.74E-01	NLRP1	NLR family, pyrin domain containing 1	chr17p13.2	211822_s_at	NM_001033053 /// NM_014922 /// NM_033004 /// NM_033006 /// NM_033007																				
3.05	3.03	0.01	9.07E-01	9.74E-01	---	---	---	234784_at	---																				
2.52	2.51	0.01	9.07E-01	9.74E-01	PTPN5	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	chr11p15.1	233471_at	NM_001039970 /// NM_006906 /// NM_032781																				
5.21	5.16	0.04	9.07E-01	9.74E-01	---	---	---	229866_at	---																				
3.64	3.61	0.03	9.07E-01	9.74E-01	SLC12A4	Solute carrier family 12 (potassium/chloride transporters), member 4	chr16q22.1	209400_at	NM_005072																				
2.80	2.79	0.02	9.07E-01	9.74E-01	---	---	---	37590_g_at	---																				
5.36	5.32	0.04	9.07E-01	9.74E-01	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	chr2p15-p13	209611_s_at	NM_003038																				
9.30	9.25	0.05	9.07E-01	9.74E-01	PAM	peptidylglycine alpha-amidating monooxygenase	chr5q14-q21	202336_s_at	NM_000919 /// NM_138766 /// NM_138821 /// NM_138822																				
6.25	6.20	0.06	9.07E-01	9.74E-01	---	---	---	235666_at	---																				
3.97	3.91	0.06	9.07E-01	9.74E-01	SFRP2	secreted frizzled-related protein 2	chr4q31.3	223121_s_at	NM_003013																				
7.23	7.13	0.09	9.07E-01	9.74E-01	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	chr5q22.3	220116_at	NM_021614 /// NM_170775																				
5.41	5.39	0.02	9.07E-01	9.74E-01	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	chr4q25	226393_at	NM_183075																				
6.12	6.08	0.04	9.07E-01	9.74E-01	---	---	---	235912_at	---																				
2.53	2.52	0.01	9.07E-01	9.74E-01	CEP97	centrosomal protein 97kDa	chr3q12.3	241836_x_at	NM_024548																				
6.95	6.91	0.04	9.07E-01	9.74E-01	MAN2A1	mannosidase, alpha, class 2A, member 1	chr5q21-q22	226538_at	NM_002372																				
3.17	3.15	0.03	9.07E-01	9.74E-01	LZTS1	leucine zipper, putative tumor suppressor 1	chr8p22	47550_at	NM_021020																				
2.57	2.55	0.02	9.07E-01	9.74E-01	---	---	---	237665_at	---																				
2.86	2.85	0.01	9.07E-01	9.74E-01	KCNIP3	Kv channel interacting protein 3, calsenilin	chr2q21.1	234198_at	NM_001034914 /// NM_013434																				
6.93	6.89	0.04	9.07E-01	9.74E-01	RUNDC3B	RUN domain containing 3B	chr7q21.12	241703_at	NM_001134405 /// NM_001134406 /// NM_138290																				
5.91	5.87	0.04	9.07E-01	9.74E-01	SPOPL	speckle-type POZ protein-like	chr2q22.1	225658_at	NM_001001664																				
2.37	2.36	0.02	9.07E-01	9.74E-01	EYA3	eyes absent homolog 3 (Drosophila)	chr1p36	1552314_a_at	NM_001990																				

3.10	3.08	0.02	9.07E-01	9.74E-01	---	---	---	1569624_at	---
2.32	2.31	0.01	9.07E-01	9.74E-01	SKAP2	Src kinase associated phosphoprotein 2	chr7p21-p15	241331_at	NM_003930
2.56	2.54	0.02	9.07E-01	9.74E-01	LOC400756	hypothetical gene supported by BC030752	chr1p31.3	1556255_a_at	XM_001130528 /// XM_001133106
3.91	3.89	0.02	9.07E-01	9.74E-01	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	chr20q11.22-q11.23	239101_at	NM_031483
2.07	2.06	0.01	9.07E-01	9.74E-01	---	---	---	242641_at	---
1.90	1.88	0.01	9.07E-01	9.75E-01	---	---	---	237520_x_at	---
2.84	2.82	0.02	9.08E-01	9.75E-01	LOC113230	hypothetical protein LOC113230	chr19p13.12	1558412_at	XM_001719438 /// XM_053966 /// XM_937316
2.57	2.55	0.02	9.08E-01	9.75E-01	---	---	---	1570061_at	---
2.10	2.09	0.01	9.08E-01	9.75E-01	---	---	---	243328_at	---
2.66	2.65	0.02	9.08E-01	9.75E-01	BCORL1	BCL6 co-repressor-like 1	chrXq25-q26.1	228752_at	NM_021946
2.26	2.25	0.02	9.08E-01	9.75E-01	ATF2	activating transcription factor 2	chr2q32	1555146_at	NM_001880
2.02	2.01	0.02	9.08E-01	9.75E-01	CA10	carbonic anhydrase X	chr17q21.33	220889_s_at	NM_001082533 /// NM_001082534 /// NM_020178
4.65	4.60	0.04	9.08E-01	9.75E-01	RASL11B	RAS-like, family 11, member B	chr4q12	219142_at	NM_023940
2.40	2.39	0.02	9.08E-01	9.75E-01	---	---	---	243360_at	---
5.09	5.04	0.05	9.08E-01	9.75E-01	---	---	---	222363_at	---
3.04	3.02	0.02	9.08E-01	9.75E-01	---	---	---	244426_at	---
5.83	5.80	0.03	9.08E-01	9.75E-01	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	227391_x_at	NM_004735
3.71	3.68	0.03	9.08E-01	9.75E-01	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	chr4q13.3	238438_at	NM_144571
4.15	4.13	0.02	9.08E-01	9.75E-01	ZNF818P	zinc finger protein 818 pseudogene	chr19q13.41	238148_s_at	XR_040818 /// XR_040819 /// XR_040820
6.15	6.12	0.03	9.08E-01	9.75E-01	GIGYF2	GRB10 interacting GYF protein 2	chr2q37.1	212260_at	NM_001103146 /// NM_001103147 /// NM_001103148 /// NM_015575
9.36	9.33	0.03	9.08E-01	9.75E-01	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	chr5p13	201279_s_at	NM_001343
2.50	2.48	0.02	9.08E-01	9.75E-01	FLJ33544	hypothetical protein LOC728283	chr20p12.3	1564157_at	XM_001130238 /// XM_001132687 /// XM_001725197
2.71	2.68	0.03	9.08E-01	9.75E-01	SLN	sarcolipin	chr11q22-q23	205374_at	NM_003063
3.13	3.11	0.02	9.08E-01	9.75E-01	PLAC4	placenta-specific 4	chr21q22.3	214750_at	NM_182832
3.66	3.64	0.02	9.08E-01	9.75E-01	ZNF434	zinc finger protein 434	chr16p13.3	220292_at	NM_017810
2.99	2.97	0.02	9.08E-01	9.75E-01	SMA4	glucuronidase, beta pseudogene	chr5q13	206565_x_at	---
6.02	5.98	0.04	9.08E-01	9.75E-01	UBA5	ubiquitin-like modifier activating enzyme 5	chr3q22.1	218289_s_at	NM_024818 /// NM_198329
7.48	7.44	0.04	9.08E-01	9.75E-01	SEC23B	Sec23 homolog B (S. cerevisiae)	chr20p11.23	201583_s_at	NM_006363 /// NM_032985 /// NM_032986
1.92	1.90	0.01	9.09E-01	9.75E-01	LOC340017	hypothetical protein LOC340017	chr4q32.1	1560823_at	---
1.90	1.89	0.01	9.09E-01	9.75E-01	---	---	---	237479_at	---
2.17	2.16	0.01	9.09E-01	9.75E-01	DLX2	distal-less homeobox 2	chr2q32	207147_at	NM_004405
5.88	5.84	0.05	9.09E-01	9.75E-01	RAB27A	RAB27A, member RAS oncogene family	chr15q15-q21.1	210951_x_at	NM_004580 /// NM_183234 /// NM_183235 /// NM_183236
11.44	11.41	0.03	9.09E-01	9.75E-01	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	chr12q13.1	200016_x_at	NM_002136 /// NM_031157
3.29	3.28	0.02	9.09E-01	9.75E-01	LOC151484	hypothetical protein LOC151484	chr2q37.1	1562689_at	---
2.19	2.17	0.02	9.09E-01	9.75E-01	---	---	---	1562870_at	---

3.19	3.16	0.02	9.09E-01	9.75E-01	LOC81691	exonuclease NEF-sp	chr16p12.2	215215_s_at	NM_030941
2.29	2.27	0.01	9.09E-01	9.75E-01	CEP27	centrosomal protein 27kDa	chr15q15.1	228744_at	NM_001130447 /// NM_018097
2.00	1.99	0.01	9.09E-01	9.75E-01	---	---	---	237474_at	---
2.81	2.79	0.02	9.09E-01	9.75E-01	NRP2	Neuropilin 2	chr2q33.3	230410_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279
2.82	2.80	0.02	9.09E-01	9.75E-01	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	chr19p13.3	206760_s_at	NM_002002
7.21	7.18	0.03	9.09E-01	9.75E-01	TMEM222	transmembrane protein 222	chr1p36.11	221512_at	NM_032125
1.90	1.89	0.01	9.09E-01	9.75E-01	TSPYL1	TSPY-like 1	chr6q22-q23	1560647_at	NM_003309
1.97	1.96	0.01	9.09E-01	9.75E-01	---	---	---	243888_at	---
9.26	9.23	0.02	9.09E-01	9.75E-01	FIS1	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	chr7q22.1	218034_at	NM_016068
2.07	2.05	0.01	9.09E-01	9.75E-01	KRT18P33	Keratin 18 pseudogene 33	chr2p14	1560628_at	XM_001719210 /// XR_017456 /// XR_019330
6.78	6.74	0.03	9.09E-01	9.75E-01	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	chr8q24.3	212090_at	NM_000837 /// NM_001009184
3.15	3.12	0.03	9.09E-01	9.75E-01	BBS7	Bardet-Biedl syndrome 7	chr4q27	235007_at	NM_018190 /// NM_176824
2.55	2.54	0.02	9.10E-01	9.75E-01	ZMYND8	zinc finger, MYND-type containing 8	chr20q13.12	207130_at	NM_012408 /// NM_183047 /// NM_183048
8.46	8.44	0.02	9.10E-01	9.75E-01	C11orf58	chromosome 11 open reading frame 58	chr11p15.1	200084_at	NM_014267
2.15	2.14	0.02	9.10E-01	9.75E-01	---	---	---	233714_at	---
6.73	6.68	0.04	9.10E-01	9.75E-01	TMEM9B	TMEM9 domain family, member B	chr11p15.3	222507_s_at	NM_020644
2.27	2.25	0.01	9.10E-01	9.75E-01	HYDIN	hydrocephalus inducing homolog (mouse)	chr16q22.1-q22.3	1554908_at	NM_017558 /// NM_032821
1.79	1.77	0.01	9.10E-01	9.75E-01	COL11A1	collagen, type XI, alpha 1	chr1p21	229271_x_at	NM_001854 /// NM_080629 /// NM_080630
2.52	2.51	0.01	9.10E-01	9.75E-01	---	---	---	229462_at	---
4.23	4.19	0.04	9.10E-01	9.75E-01	SPATA6	spermatogenesis associated 6	chr1p33	220298_s_at	NM_019073
7.03	6.99	0.03	9.10E-01	9.75E-01	LOC643988	hypothetical LOC643988	chr1p36.33	227185_at	XR_042002 /// XR_042003 /// XR_042004
4.82	4.80	0.02	9.10E-01	9.75E-01	TAL1	T-cell acute lymphocytic leukemia 1	chr1p32	1561651_s_at	NM_003189
12.28	12.27	0.02	9.10E-01	9.75E-01	RPL9	ribosomal protein L9	chr4p13	200032_s_at	NM_000661 /// NM_001024921
3.02	3.01	0.02	9.10E-01	9.75E-01	CD8B /// CD8BP /// LOC652565	CD8b molecule /// CD8b molecule pseudogene /// similar to T-cell surface glycoprotein CD8 beta chain precursor (Antigen CD8B)	chr2p12 /// chr2p12|2q12.1	1553562_at	NM_004931 /// NM_172099 /// NM_172101 /// NM_172102 /// NM_172213 /// XM_001715834 /// XM_942071
6.76	6.73	0.03	9.10E-01	9.75E-01	PLCD3	phospholipase C, delta 3	chr17q21.31	234971_x_at	NM_133373

2.54	2.51	0.02	9.10E-01	9.75E-01	HAPLN4	hyaluronan and proteoglycan link protein 4	chr19p13.1	235420_at	NM_023002
4.44	4.40	0.04	9.10E-01	9.75E-01	SMC6	structural maintenance of chromosomes 6	chr2p24.2	218781_at	NM_024624
2.91	2.89	0.02	9.10E-01	9.75E-01	USP2	ubiquitin specific peptidase 2	chr11q23.3	207211_at	NM_004205 /// NM_171997
3.89	3.85	0.04	9.10E-01	9.75E-01	---	---	---	239294_at	---
2.30	2.28	0.01	9.10E-01	9.75E-01	---	---	---	241248_at	---
2.15	2.14	0.01	9.10E-01	9.75E-01	---	---	---	1561424_at	---
2.49	2.47	0.02	9.10E-01	9.75E-01	---	---	---	1565073_at	---
6.19	6.16	0.03	9.10E-01	9.75E-01	PRDM4	PR domain containing 4	chr12q23-q24.1	218329_at	NM_012406
4.98	4.93	0.05	9.10E-01	9.75E-01	SUSD2	sushi domain containing 2	chr22q11-q12	227480_at	NM_019601
2.93	2.91	0.01	9.10E-01	9.75E-01	CCL13	chemokine (C-C motif) ligand 13	chr17q11.2	216714_at	NM_005408
2.42	2.41	0.01	9.10E-01	9.75E-01	---	---	---	242089_at	---
2.33	2.31	0.02	9.11E-01	9.75E-01	FAM83C	family with sequence similarity 83, member C	chr20q11.22	1556793_a_at	NM_178468
7.65	7.62	0.03	9.11E-01	9.75E-01	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	chr12q22	201523_x_at	NM_003348
4.72	4.66	0.07	9.11E-01	9.75E-01	ATRNL1	attractin-like 1	chr10q26	213744_at	NM_207303
4.43	4.41	0.02	9.11E-01	9.75E-01	LOC100133109	similar to histone	chr2q31.1	213826_s_at	XM_001716009 /// XM_001716442 /// XM_001718803
3.59	3.57	0.02	9.11E-01	9.75E-01	RDH8	retinol dehydrogenase 8 (all-trans)	chr19p13.2-p13.3	220683_at	NM_015725
2.08	2.07	0.01	9.11E-01	9.75E-01	---	---	---	1562898_at	---
4.55	4.53	0.02	9.11E-01	9.76E-01	GRM2	glutamate receptor, metabotropic 2	chr3p21.1	241802_x_at	NM_000839 /// NM_001130063
3.66	3.64	0.02	9.11E-01	9.76E-01	TIMELESS	timeless homolog (Drosophila)	chr12q12-q13	215455_at	NM_003920
6.83	6.79	0.03	9.11E-01	9.76E-01	SSFA2	sperm specific antigen 2	chr2q31.3	202506_at	NM_001130445 /// NM_006751
2.54	2.52	0.02	9.11E-01	9.76E-01	ZNF354B	zinc finger protein 354B	chr5q35.3	1553612_at	NM_058230
5.18	5.13	0.05	9.11E-01	9.76E-01	ATP8B2	ATPase, class I, type 8B, member 2	chr1q21.3	226771_at	NM_001005855 /// NM_020452
2.24	2.23	0.02	9.11E-01	9.76E-01	ANKRD10	ankyrin repeat domain 10	chr13q34	241414_at	NM_017664
3.06	3.04	0.02	9.11E-01	9.76E-01	---	---	---	217629_at	---
2.30	2.29	0.01	9.11E-01	9.76E-01	---	---	---	1567389_at	---
2.04	2.02	0.02	9.12E-01	9.76E-01	EZH1	enhancer of zeste homolog 1 (Drosophila)	chr17q21.1-q21.3	211310_at	NM_001991
2.63	2.62	0.02	9.12E-01	9.76E-01	GIP	gastric inhibitory polypeptide	chr17q21.3-q22	207899_at	NM_004123
3.47	3.45	0.02	9.12E-01	9.76E-01	ITGA11	integrin, alpha 11	chr15q23	1554819_a_at	NM_001004439
3.03	3.01	0.02	9.12E-01	9.76E-01	---	---	---	1570105_at	---
1.90	1.88	0.01	9.12E-01	9.76E-01	ANKRD30B	ankyrin repeat domain 30B	chr18p11.21	1562292_at	XM_001716904 /// XM_001717561 /// XM_001717810
3.12	3.10	0.02	9.12E-01	9.76E-01	TPM3	tropomyosin 3	chr1q21.2	224164_at	NM_001043351 /// NM_001043352 /// NM_001043353 /// NM_152263 /// NM_153649
4.43	4.37	0.06	9.12E-01	9.76E-01	TLR4	toll-like receptor 4	chr9q32-q33	1552798_a_at	NM_138554
2.31	2.29	0.01	9.12E-01	9.76E-01	LOC100132810 /// LOC441179	hypothetical protein LOC100132810 /// hypothetical gene supported by AK055887; AK125190	chr6q27	239665_at	XM_001723739 /// XR_017855 /// XR_040771 /// XR_040772
3.35	3.32	0.03	9.12E-01	9.76E-01	LOC441383	hypothetical gene supported by AF086559; BC065734	chr8q24.3	239753_at	---
2.36	2.34	0.02	9.12E-01	9.76E-01	---	---	---	243396_at	---
6.84	6.79	0.05	9.12E-01	9.76E-01	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	chr1q32.1	212136_at	NM_001001396 /// NM_001684
5.07	5.02	0.05	9.12E-01	9.76E-01	---	---	---	239451_at	---
2.25	2.23	0.02	9.12E-01	9.76E-01	HDGFRP3	Hepatoma-derived growth factor, related protein 3	chr15q25.2	209525_at	NM_016073
2.63	2.61	0.01	9.13E-01	9.76E-01	TTF2	transcription termination factor, RNA polymerase II	chr1p22	204407_at	NM_003594

7.23	7.20	0.03	9.13E-01	9.76E-01	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	chr16p12.3	1568619_s_at	NM_001034841																			
2.98	2.96	0.02	9.13E-01	9.76E-01	---	---	---	243272_at	---																			
6.31	6.28	0.03	9.13E-01	9.76E-01	NF1	neurofibromin 1	chr17q11.2	212676_at	NM_000267 /// NM_001042492 /// NM_001128147																			
4.50	4.46	0.04	9.13E-01	9.76E-01	PROK1	prokineticin 1	chr1p21	229124_at	NM_032414																			
2.28	2.25	0.02	9.13E-01	9.76E-01	USP49	ubiquitin specific peptidase 49	chr6p21	1564029_at	NM_018561																			
2.66	2.64	0.02	9.13E-01	9.76E-01	LOC100133916 /// MED18	hypothetical protein LOC100133916 /// mediator complex subunit 18	chr1p35.3	219730_at	NM_001127350 /// NM_017638 /// XM_001713715																			
6.00	5.98	0.02	9.13E-01	9.76E-01	FXR1	fragile X mental retardation, autosomal homolog 1	chr3q28	229519_at	NM_001013438 /// NM_001013439 /// NM_005087																			
3.73	3.66	0.06	9.13E-01	9.76E-01	RAB8B	RAB8B, member RAS oncogene family	chr15q22.2	222846_at	NM_016530																			
2.02	2.00	0.02	9.13E-01	9.76E-01	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	chr4q28-q32	217678_at	NM_014331																			
7.43	7.39	0.04	9.13E-01	9.77E-01	MARCKS	myristoylated alanine-rich protein kinase C substrate	chr6q22.2	201670_s_at	NM_002356																			
4.95	4.88	0.07	9.13E-01	9.77E-01	LGALS8	lectin, galactoside-binding, soluble, 8	chr1q42-q43	208934_s_at	NM_006499 /// NM_201543 /// NM_201544 /// NM_201545																			
2.42	2.40	0.01	9.13E-01	9.77E-01	---	---	---	1569005_at	---																			
5.25	5.22	0.03	9.13E-01	9.77E-01	STXBP3	syntaxin binding protein 3	chr1p13.3	203310_at	NM_007269																			
5.67	5.65	0.02	9.13E-01	9.77E-01	CREBBP	CREB binding protein	chr16p13.3	228177_at	NM_001079846 /// NM_004380																			
2.45	2.43	0.02	9.13E-01	9.77E-01	---	---	---	1562922_at	---																			
1.93	1.92	0.02	9.13E-01	9.77E-01	LOC100130725 /// PAGE2 /// PAGE2B	similar to PAGE-5 protein /// P antigen family, member 2 (prostate associated) /// P antigen family, member 2B	chrXp11.21	231307_at	NM_001015038 /// NM_207339 /// XM_001719226 /// XM_001720100 /// XM_001720978																			
2.73	2.71	0.01	9.14E-01	9.77E-01	---	---	---	217655_at	---																			
6.92	6.89	0.03	9.14E-01	9.77E-01	GLT25D1	glycosyltransferase 25 domain containing 1	chr19p13.11	218473_s_at	NM_024656																			
2.96	2.94	0.02	9.14E-01	9.77E-01	C6orf125	Chromosome 6 open reading frame 125	chr6p21.31	228192_at	NM_032340																			
2.76	2.74	0.02	9.14E-01	9.77E-01	MMP16	matrix metallopeptidase 16 (membrane-inserted)	chr8q21	208167_s_at	NM_005941 /// NM_022564																			
2.83	2.81	0.02	9.14E-01	9.77E-01	C20orf79	chromosome 20 open reading frame 79	chr20p11.23	231134_at	NM_178483																			
2.22	2.21	0.01	9.14E-01	9.77E-01	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	chr1q25	243066_at	NM_030769																			
3.48	3.46	0.02	9.14E-01	9.77E-01	MPP5	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	chr14q23.3	235864_at	NM_022474																			
2.40	2.39	0.02	9.14E-01	9.77E-01	TYMP	thymidine phosphorylase	chr22q13|22q13.33	217497_at	NM_001113755 /// NM_001113756 /// NM_001953																			
3.14	3.12	0.02	9.14E-01	9.77E-01	SH3BP2	SH3-domain binding protein 2	chr4p16.3	217253_at	NM_001122681 /// NM_003023																			
2.50	2.49	0.02	9.14E-01	9.77E-01	FETUB	Fetuin B	chr3q27	214417_s_at	NM_014375																			
2.27	2.25	0.02	9.14E-01	9.77E-01	FIGLA	folliculogenesis specific basic helix-loop-helix	chr2p13.3	1570337_at	NM_001004311																			

3.12	3.11	0.02	9.14E-01	9.77E-01	LOC100130328 /// LOC650686 /// NXF2 /// NXF2B	similar to hCG2045904 /// similar to nuclear RNA export factor 2 /// nuclear RNA export factor 2 /// nuclear RNA export factor 2B	chrXq22.1	220981_x_at	NM_001099686 /// NM_017809 /// NM_022053 /// XM_001713916 /// XM_001713918 /// XM_001713996 /// XM_001714190																			
7.09	7.01	0.08	9.14E-01	9.77E-01	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	chrXq25	215294_s_at	NM_003069 /// NM_139035																			
2.26	2.25	0.02	9.14E-01	9.77E-01	C14orf83	chromosome 14 open reading frame 83	chr14q24.1	1558177_at	NM_182526																			
2.95	2.93	0.02	9.14E-01	9.77E-01	---	---	---	232459_at	---																			
2.11	2.10	0.01	9.14E-01	9.77E-01	---	---	---	216814_at	---																			
6.11	6.10	0.02	9.14E-01	9.77E-01	PCBP2	poly(rC) binding protein 2	chr12q13.12-q13.13	213264_at	NM_001098620 /// NM_001128911 /// NM_001128912 /// NM_001128913 /// NM_001128914 /// NM_005016 /// NM_031989																			
4.21	4.17	0.04	9.14E-01	9.77E-01	DAPK3	death-associated protein kinase 3	chr19p13.3	203890_s_at	NM_001348																			
3.53	3.51	0.02	9.14E-01	9.77E-01	PXN	paxillin	chr12q24.31	211823_s_at	NM_001080855 /// NM_002859 /// NM_025157																			
2.44	2.43	0.01	9.14E-01	9.77E-01	ACSM2A /// ACSM2B	acyl-CoA synthetase medium-chain family member 2A /// acyl-CoA synthetase medium-chain family member 2B	chr16p12.3	241914_s_at	NM_001010845 /// NM_001105069 /// NM_182617 /// XM_001724180 /// XM_001724186 /// XM_001724187																			
2.75	2.74	0.02	9.14E-01	9.77E-01	OSBPL3	oxysterol binding protein-like 3	chr7p15	209627_s_at	NM_015550 /// NM_145320 /// NM_145321 /// NM_145322																			
5.49	5.42	0.07	9.14E-01	9.77E-01	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	chr12p12.3	225946_at	NM_007211																			
2.69	2.67	0.02	9.15E-01	9.77E-01	RGS5	Regulator of G-protein signaling 5	chr1q23.1	1558785_a_at	NM_003617																			
2.40	2.39	0.01	9.15E-01	9.77E-01	USP29	ubiquitin specific peptidase 29	chr19q13.43	220895_at	NM_020903																			
2.82	2.79	0.03	9.15E-01	9.77E-01	TTBK1	tau tubulin kinase 1	chr6p21.1	240643_at	NM_032538																			
4.74	4.71	0.03	9.15E-01	9.77E-01	---	---	---	236625_at	---																			
2.35	2.33	0.01	9.15E-01	9.77E-01	---	---	---	215183_at	---																			
2.41	2.40	0.01	9.15E-01	9.77E-01	---	---	---	244643_at	---																			
2.25	2.24	0.01	9.15E-01	9.77E-01	---	---	---	237671_at	---																			
5.02	4.99	0.03	9.15E-01	9.77E-01	NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	chr4q26	230329_s_at	NM_007083 /// NM_198041																			
3.11	3.06	0.05	9.15E-01	9.77E-01	ANKRD13C	ankyrin repeat domain 13C	chr1p32.3-p31.3	223418_x_at	NM_030816																			
2.95	2.93	0.02	9.15E-01	9.77E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	227344_at	NM_006060																			
2.60	2.58	0.02	9.15E-01	9.77E-01	PITRM1	pitrilysin metallopeptidase 1	chr10p15.2	239378_at	NM_014889																			
2.49	2.47	0.02	9.15E-01	9.77E-01	NPW	neuropeptide W	chr16p13.3	243110_x_at	NM_001099456																			
1.96	1.95	0.01	9.15E-01	9.77E-01	---	---	---	244817_at	---																			

2.69	2.66	0.03	9.15E-01	9.77E-01	CC2D2A	coiled-coil and C2 domain containing 2A	chr4p15.33	1559409_a_at	NM_001080522 /// NM_020785 /// NR_024098																				
2.03	2.02	0.02	9.15E-01	9.77E-01	---	---	---	244621_x_at	---																				
2.38	2.37	0.01	9.15E-01	9.77E-01	GSX1	GS homeobox 1	chr13q12.2	1555676_s_at	NM_145657																				
3.60	3.56	0.05	9.15E-01	9.77E-01	C2orf3	chromosome 2 open reading frame 3	chr2p11.2-p11.1	216305_s_at	NM_003203																				
2.96	2.94	0.02	9.15E-01	9.77E-01	LOC100131581	hypothetical LOC100131581	chr8p23.1	1560001_at	XM_001721737 /// XM_001732868 /// XM_001732869																				
3.02	3.00	0.01	9.15E-01	9.77E-01	DKFZp761P0212	hypothetical protein DKFZp761P0212	chr17q25.3	234845_at	---																				
4.80	4.77	0.03	9.15E-01	9.77E-01	FECH	ferrochelatase (protoporphyria)	chr18q21.3	203115_at	NM_000140 /// NM_001012515																				
2.60	2.59	0.01	9.16E-01	9.77E-01	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	chrXp11.21	237777_at	NM_002625																				
1.91	1.90	0.01	9.16E-01	9.77E-01	---	---	---	1557018_a_at	---																				
2.30	2.29	0.02	9.16E-01	9.77E-01	PLCE1	Phospholipase C, epsilon 1	chr10q23	1566740_at	NM_016341																				
2.40	2.39	0.01	9.16E-01	9.77E-01	---	---	---	234760_at	---																				
6.34	6.32	0.02	9.16E-01	9.77E-01	KLF11	Kruppel-like factor 11	chr2p25	218486_at	NM_003597																				
8.44	8.43	0.02	9.16E-01	9.77E-01	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	chr3q25.31	222411_s_at	NM_007107																				
5.45	5.41	0.04	9.16E-01	9.77E-01	PTGFR	prostaglandin F receptor (FP)	chr1p31.1	207177_at	NM_000959 /// NM_001039585																				
2.99	2.97	0.02	9.16E-01	9.77E-01	---	---	---	236303_at	---																				
2.19	2.17	0.02	9.16E-01	9.77E-01	TTTY12	testis-specific transcript, Y-linked 12	chrYp11.2	224195_at	NR_001551																				
2.02	2.01	0.01	9.16E-01	9.77E-01	PMCHL1	pro-melanin-concentrating hormone-like 1	chr5p14.3	217123_x_at	NR_003921																				
6.41	6.37	0.04	9.16E-01	9.77E-01	---	---	---	227221_at	---																				
5.18	5.15	0.03	9.16E-01	9.77E-01	CCR1	chemokine (C-C motif) receptor 1	chr3p21	205099_s_at	NM_001295																				
2.04	2.02	0.02	9.16E-01	9.77E-01	---	---	---	237812_at	---																				
2.82	2.80	0.01	9.16E-01	9.78E-01	SLC4A1AP	Solute carrier family 4 (anion exchanger), member 1, adaptor protein	chr2p23.2	242030_at	NM_018158																				
3.69	3.67	0.02	9.16E-01	9.78E-01	FLJ25758	hypothetical locus FLJ25758	chr19p13.3	1554286_at	XR_040427 /// XR_040428 /// XR_040429																				
4.60	4.57	0.02	9.16E-01	9.78E-01	MTA1	metastasis associated 1	chr14q32.3	202247_s_at	NM_004689																				
2.84	2.82	0.02	9.16E-01	9.78E-01	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	chr12q13.12	242970_at	NM_173602																				
1.89	1.88	0.01	9.17E-01	9.78E-01	PKP2	plakophilin 2	chr12p11	207717_s_at	NM_001005242 /// NM_004572																				
3.82	3.79	0.02	9.17E-01	9.78E-01	C15orf29	chromosome 15 open reading frame 29	chr15q14	222745_s_at	NM_024713																				
2.61	2.59	0.02	9.17E-01	9.78E-01	CCL25	chemokine (C-C motif) ligand 25	chr19p13.2	206988_at	NM_005624																				
5.30	5.28	0.02	9.17E-01	9.78E-01	SBNO2	strawberry notch homolog 2 (Drosophila)	chr19p13.3	204166_at	NM_001100122 /// NM_014963																				
2.30	2.29	0.02	9.17E-01	9.78E-01	WDR21C	WD repeat domain 21C	chr8q21.3	1553199_at	NM_152418																				
5.60	5.55	0.04	9.17E-01	9.78E-01	SPIN1	spindlin 1	chr9q22.1-q22.3	217813_s_at	NM_006717																				
2.45	2.43	0.02	9.17E-01	9.78E-01	VASH2	vasohibin 2	chr1q32.3	1555092_at	NM_024749																				
2.02	2.01	0.01	9.17E-01	9.78E-01	C4orf35	chromosome 4 open reading frame 35	chr4q13.3	231612_at	NM_033122																				
7.08	7.06	0.02	9.17E-01	9.78E-01	MARK3	MAP/microtubule affinity-regulating kinase 3	chr14q32.3	202568_s_at	NM_001128918 /// NM_001128919 /// NM_001128920 /// NM_001128921 /// NM_002376																				
7.46	7.44	0.02	9.17E-01	9.78E-01	RPP21 /// TRIM39R	ribonuclease P/MRP 21kDa subunit /// TRIM39-like protein	chr6p21.33	218836_at	NM_024839																				
2.67	2.65	0.02	9.17E-01	9.78E-01	RET	ret proto-oncogene	chr10q11.2	211421_s_at	NM_020630 /// NM_020975																				
2.76	2.74	0.01	9.17E-01	9.78E-01	---	---	---	218054_s_at	---																				
2.46	2.44	0.01	9.17E-01	9.78E-01	---	---	---	234705_at	---																				
2.22	2.20	0.01	9.17E-01	9.78E-01	XG	Xg blood group	chrXp22.33	241931_at	NM_175569																				
2.23	2.21	0.02	9.17E-01	9.78E-01	---	---	---	232980_at	---																				
7.51	7.49	0.02	9.17E-01	9.78E-01	BECN1	beclin 1, autophagy related	chr17q21	208946_s_at	NM_003766																				

3.83	3.82	0.02	9.18E-01	9.78E-01	LOC283888	hypothetical protein LOC283888	chr16p12.2	1559443_s_at	---
3.42	3.40	0.02	9.18E-01	9.78E-01	C9orf3	Chromosome 9 open reading frame 3	chr9q22.32	232270_at	NM_032823
3.15	3.14	0.01	9.18E-01	9.78E-01	C17orf50	chromosome 17 open reading frame 50	chr17q12	237929_at	NM_145272
2.25	2.23	0.01	9.18E-01	9.78E-01	KIAA1466	KIAA1466 gene	chr7q33	222139_at	---
2.24	2.23	0.01	9.18E-01	9.78E-01	PSG2	pregnancy specific beta-1-glycoprotein 2	chr19q13.1-q13.2	208134_x_at	NM_031246
2.23	2.22	0.02	9.18E-01	9.78E-01	---	---	---	240403_at	---
6.45	6.44	0.02	9.18E-01	9.78E-01	ELP3	elongation protein 3 homolog (S. cerevisiae)	chr8p21.1	221094_s_at	NM_018091
7.74	7.72	0.03	9.18E-01	9.78E-01	RNF103	ring finger protein 103	chr2p11.2	202636_at	NM_005667
8.23	8.20	0.03	9.18E-01	9.78E-01	---	---	---	216565_x_at	---
7.02	7.00	0.02	9.18E-01	9.78E-01	CENTD2	centaurin, delta 2	chr11q13.4	212516_at	NM_001040118 /// NM_015242 /// NM_139181
1.78	1.77	0.01	9.18E-01	9.78E-01	---	---	---	241674_s_at	---
2.49	2.48	0.02	9.18E-01	9.78E-01	KCNJ1	potassium inwardly-rectifying channel, subfamily J, member 1	chr11q24	210402_at	NM_000220 /// NM_153764 /// NM_153765 /// NM_153766 /// NM_153767
3.34	3.29	0.05	9.18E-01	9.78E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	239439_at	NM_014423
2.86	2.84	0.01	9.18E-01	9.78E-01	NOS1	Nitric oxide synthase 1 (neuronal)	chr12q24.2-q24.31	240911_at	NM_000620
4.65	4.63	0.03	9.18E-01	9.78E-01	TIAM1	T-cell lymphoma invasion and metastasis 1	chr21q22.1|21q22.11	213135_at	NM_003253
2.15	2.14	0.01	9.18E-01	9.78E-01	---	---	---	1560850_at	---
4.12	4.09	0.03	9.18E-01	9.78E-01	OVGP1	oviductal glycoprotein 1, 120kDa	chr1p13	205432_at	NM_002557
1.97	1.96	0.01	9.18E-01	9.78E-01	---	---	---	1564656_at	---
7.79	7.76	0.03	9.18E-01	9.78E-01	DEXI	dexamethasone-induced transcript	chr16p13.13	203733_at	NM_014015
2.25	2.23	0.02	9.18E-01	9.78E-01	SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1	chr1p31.3	223672_at	NM_032291
3.49	3.46	0.03	9.19E-01	9.78E-01	KLF7	Kruppel-like factor 7 (ubiquitous)	chr2q32	1555420_a_at	NM_003709
2.59	2.58	0.02	9.19E-01	9.78E-01	C6orf89	Chromosome 6 open reading frame 89	chr6p21.2	1556359_at	NM_152734
3.61	3.60	0.02	9.19E-01	9.78E-01	RET	ret proto-oncogene	chr10q11.2	205879_x_at	NM_020630 /// NM_020975
2.57	2.56	0.01	9.19E-01	9.78E-01	TMEM151B	transmembrane protein 151B	chr6p21.1	213678_at	XM_001723534 /// XM_001723740 /// XM_001725716
1.83	1.82	0.01	9.19E-01	9.78E-01	C7orf57	chromosome 7 open reading frame 57	chr7p12.3	1557636_a_at	NM_001100159
4.09	4.07	0.01	9.19E-01	9.78E-01	GDF11	growth differentiation factor 11	chr12q13.2	216854_at	NM_005811
2.28	2.26	0.01	9.19E-01	9.78E-01	---	---	---	1564151_at	---
2.90	2.88	0.02	9.19E-01	9.78E-01	---	---	---	237710_at	---
3.01	2.99	0.01	9.19E-01	9.78E-01	---	---	---	1561440_at	---
3.22	3.21	0.01	9.19E-01	9.78E-01	TOB2	transducer of ERBB2, 2	chr22q13.2-q13.31	234720_s_at	NM_016272
2.64	2.62	0.02	9.19E-01	9.78E-01	---	---	---	233032_x_at	---
3.18	3.17	0.01	9.19E-01	9.78E-01	---	---	---	244843_x_at	---
3.04	3.03	0.02	9.19E-01	9.78E-01	C11orf42	chromosome 11 open reading frame 42	chr11p15.4	1553895_at	NM_173525
2.32	2.31	0.01	9.19E-01	9.78E-01	---	---	---	234124_at	---
2.30	2.29	0.01	9.19E-01	9.78E-01	---	---	---	241535_at	---
3.60	3.58	0.02	9.19E-01	9.78E-01	LOC441178 /// LOC730015	hypothetical LOC441178 /// similar to LOC441178 protein	chr6q27	1561685_a_at	XM_001132090 /// XR_040768 /// XR_040769 /// XR_040770
3.82	3.80	0.02	9.19E-01	9.78E-01	PAAF1	proteasomal ATPase-associated factor 1	chr11q13.4	1568702_a_at	NM_025155
2.35	2.34	0.01	9.19E-01	9.78E-01	LOC348817	hypothetical protein LOC348817	chr3p21.33	1557652_a_at	---
3.61	3.60	0.01	9.20E-01	9.78E-01	---	---	---	241632_x_at	---
2.85	2.83	0.01	9.20E-01	9.78E-01	---	---	---	243224_at	---
9.96	9.95	0.02	9.20E-01	9.78E-01	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	chr9q32	208737_at	NM_004888

4.92	4.89	0.03	9.20E-01	9.78E-01	PPA2	pyrophosphatase (inorganic) 2	chr4q25	1559496_at	NM_001034191 /// NM_006903 /// NM_176866 /// NM_176867 /// NM_176869
4.89	4.87	0.02	9.20E-01	9.78E-01	ZBTB17	zinc finger and BTB domain containing 17	chr1p36.2-p36.1	203601_s_at	NM_003443
2.97	2.96	0.01	9.20E-01	9.78E-01	CCBL1	cysteine conjugate-beta lyase, cytoplasmic	chr9q34.11	1570651_at	NM_001122671 /// NM_001122672 /// NM_004059
3.38	3.36	0.02	9.20E-01	9.78E-01	PLXNA3	plexin A3	chrXq28	203623_at	NM_017514
4.34	4.33	0.02	9.20E-01	9.78E-01	---	---	---	228548_at	---
3.78	3.76	0.02	9.20E-01	9.78E-01	NUDT17	nudix (nucleoside diphosphate linked moiety X)-type motif 17	chr1q21.1	229044_at	NM_001012758
7.02	6.99	0.03	9.20E-01	9.78E-01	HIAT1	hippocampus abundant transcript 1	chr1p21.2	225222_at	NM_033055
1.95	1.94	0.01	9.20E-01	9.78E-01	C12orf55	chromosome 12 open reading frame 55	chr12q23.1	1560426_at	XM_001131723 /// XM_001715090 /// XM_001717983
3.07	3.05	0.02	9.20E-01	9.78E-01	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	chr19p13.3	206759_at	NM_002002
3.73	3.72	0.02	9.20E-01	9.78E-01	KIAA0226	KIAA0226	chr3q29	1554613_a_at	NM_014687
2.26	2.24	0.01	9.20E-01	9.78E-01	LOC284669	hypothetical protein LOC284669	chr1q32.3	1560934_at	---
4.93	4.90	0.03	9.20E-01	9.78E-01	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	chr4q23-q25	217457_s_at	NM_001100426 /// NM_001100427 /// NM_001100428 /// NM_001100429 /// NM_001100430 /// NM_021159
3.43	3.41	0.02	9.20E-01	9.78E-01	DLEC1	deleted in lung and esophageal cancer 1	chr3p22-p21.3	215085_x_at	NM_007335 /// NM_007337
2.56	2.55	0.01	9.20E-01	9.78E-01	---	---	---	1556019_at	---
2.11	2.10	0.01	9.20E-01	9.78E-01	---	---	---	1561017_at	---
2.69	2.68	0.01	9.20E-01	9.78E-01	UROC1	urocanase domain containing 1	chr3q21.2-q21.3	1553341_at	NM_144639
1.97	1.96	0.01	9.20E-01	9.78E-01	---	---	---	244720_at	---
4.39	4.35	0.03	9.20E-01	9.79E-01	KLHL20	kelch-like 20 (Drosophila)	chr1q24.1-q24.3	210635_s_at	NM_014458
5.39	5.33	0.05	9.20E-01	9.79E-01	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	chr17q23.3	1559954_s_at	NM_007372 /// NM_203499
2.08	2.06	0.01	9.20E-01	9.79E-01	GPR98	G protein-coupled receptor 98	chr5q13	224275_at	NM_032119 /// NR_003149
3.03	3.01	0.02	9.20E-01	9.79E-01	---	---	---	1558937_s_at	---
2.15	2.13	0.01	9.20E-01	9.79E-01	FFAR1	Free fatty acid receptor 1	chr19q13.1	1561507_at	NM_005303
4.91	4.89	0.02	9.21E-01	9.79E-01	MTF2	metal response element binding transcription factor 2	chr1p22.1	209705_at	NM_007358
5.22	5.19	0.03	9.21E-01	9.79E-01	C22orf39	chromosome 22 open reading frame 39	chr22q11.21	1553974_at	NM_173793
5.78	5.75	0.02	9.21E-01	9.79E-01	CHD3	chromodomain helicase DNA binding protein 3	chr17p13.1	208806_at	NM_001005271 /// NM_001005273 /// NM_005852
1.93	1.92	0.01	9.21E-01	9.79E-01	---	---	---	242955_x_at	---
2.87	2.85	0.02	9.21E-01	9.79E-01	---	---	---	242147_at	---
2.71	2.70	0.01	9.21E-01	9.79E-01	---	---	---	239358_at	---
3.18	3.16	0.02	9.21E-01	9.79E-01	---	---	---	222345_at	---
3.10	3.09	0.02	9.21E-01	9.79E-01	TRIM72	tripartite motif-containing 72	chr16p11.2	1554803_s_at	NM_001008274
2.30	2.29	0.02	9.21E-01	9.79E-01	---	---	---	1561778_at	---
3.85	3.82	0.02	9.21E-01	9.79E-01	C8orf68	chromosome 8 open reading frame 68	chr8p23.3	1557679_at	XM_001719813 /// XM_001721201 /// XM_927505
2.64	2.63	0.01	9.21E-01	9.79E-01	---	---	---	1562274_at	---
5.54	5.52	0.02	9.21E-01	9.79E-01	---	---	---	229493_at	---

2.22	2.20	0.01	9.21E-01	9.79E-01	FFAR2	free fatty acid receptor 2	chr19q13.1	221345_at	NM_005306
2.01	1.99	0.01	9.21E-01	9.79E-01	LOC730432 /// STYX	similar to serine/threonine/tyrosine interacting protein /// serine/threonine/tyrosine interacting protein	---	235180_at	NM_001130701 /// NM_145251 /// XM_001125680
3.50	3.48	0.02	9.21E-01	9.79E-01	NAV1	neuron navigator 1	chr1q32.3	224770_s_at	NM_020443
2.70	2.68	0.02	9.21E-01	9.79E-01	---	---	---	234773_x_at	---
2.60	2.58	0.02	9.21E-01	9.79E-01	TRIP11	thyroid hormone receptor interactor 11	chr14q31-q32	210760_x_at	NM_004239
7.20	7.12	0.07	9.21E-01	9.79E-01	LRRN3	leucine rich repeat neuronal 3	chr7q31.1	209840_s_at	NM_001099658 /// NM_001099660 /// NM_018334
2.69	2.67	0.02	9.21E-01	9.79E-01	---	---	---	215474_at	---
3.67	3.66	0.01	9.21E-01	9.79E-01	---	---	---	1566110_at	---
4.16	4.14	0.02	9.21E-01	9.79E-01	MICAL3	Microtubule associated monoxygenase, calponin and LIM domain containing 3	chr22q11.21	231553_s_at	NM_001122731 /// NM_015241 /// XM_001721205 /// XM_001725408 /// XM_001726352
3.47	3.44	0.02	9.21E-01	9.79E-01	GPER	G protein-coupled estrogen receptor 1	chr7p22.3	211829_s_at	NM_001039966 /// NM_001098201 /// NM_001505
3.63	3.62	0.02	9.22E-01	9.79E-01	POU3F1	POU class 3 homeobox 1	chr1p34.1	210475_at	NM_002699
3.33	3.31	0.02	9.22E-01	9.79E-01	---	---	---	235685_at	---
3.02	3.01	0.02	9.22E-01	9.79E-01	TMEM106C	Transmembrane protein 106C	chr12q13.1	239831_at	NM_024056
2.68	2.66	0.02	9.22E-01	9.79E-01	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger), member 7	chrXp11.3-p11.23|Xp11.3	214860_at	NM_032591
2.21	2.20	0.01	9.22E-01	9.79E-01	---	---	---	1556677_at	---
2.16	2.15	0.01	9.22E-01	9.79E-01	CCDC88A	coiled-coil domain containing 88A	chr2p16.1	239233_at	NM_018084
6.56	6.54	0.02	9.22E-01	9.79E-01	WDFY1	WD repeat and FYVE domain containing 1	chr2q36.1	224800_at	NM_020830
2.11	2.10	0.01	9.22E-01	9.79E-01	---	---	---	244195_at	---
3.98	3.94	0.03	9.22E-01	9.79E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	232864_s_at	NM_014423
3.64	3.60	0.03	9.22E-01	9.79E-01	PELO	Pelota homolog (Drosophila)	chr5q11.2	1560359_at	NM_015946
2.91	2.89	0.02	9.22E-01	9.79E-01	---	---	---	244299_at	---
5.38	5.35	0.03	9.22E-01	9.79E-01	TRIM73 /// TRIM74	tripartite motif-containing 73 /// tripartite motif-containing 74	chr7q11.23	1554183_s_at	NM_198853 /// NM_198924
2.52	2.51	0.01	9.22E-01	9.79E-01	MED24	mediator complex subunit 24	chr17q21.1	215337_at	NM_001079518 /// NM_014815
2.17	2.16	0.01	9.22E-01	9.79E-01	FAM82B	Family with sequence similarity 82, member B	chr8q21.3	229843_at	NM_016033
2.07	2.06	0.01	9.22E-01	9.79E-01	KIF23	kinesin family member 23	chr15q23	204709_s_at	NM_004856 /// NM_138555
9.03	9.01	0.02	9.22E-01	9.79E-01	MUTED /// TXNDC5	muted homolog (mouse) /// thioredoxin domain containing 5	chr6p24.3 /// chr6p25.1-p24.3	221253_s_at	NM_022085 /// NM_030810 /// NM_201280
3.77	3.75	0.02	9.22E-01	9.79E-01	ZFP90	zinc finger protein 90 homolog (mouse)	chr16q22.1	242400_at	NM_133458
1.85	1.84	0.01	9.22E-01	9.79E-01	LOC653479	Similar to mitochondrial ribosomal protein L45	chr17q21.32	237182_at	XR_017538 /// XR_040085
2.82	2.81	0.01	9.22E-01	9.79E-01	KRT19	Keratin 19	chr17q21.2	228491_at	NM_002276
3.37	3.35	0.02	9.22E-01	9.79E-01	---	---	---	243469_at	---
2.26	2.24	0.01	9.22E-01	9.79E-01	---	---	---	1561889_at	---
5.38	5.35	0.03	9.22E-01	9.79E-01	LYPLA3	lysophospholipase 3 (lysosomal phospholipase A2)	chr16q22.1	204458_at	NM_012320
7.47	7.46	0.01	9.22E-01	9.79E-01	C16orf62	chromosome 16 open reading frame 62	chr16p12.3	203173_s_at	NM_020314
6.71	6.69	0.02	9.22E-01	9.79E-01	HS1BP3	HCLS1 binding protein 3	chr2p24.1	219020_at	NM_022460
3.20	3.18	0.01	9.22E-01	9.79E-01	LOC100128003	Hypothetical protein LOC100128003	chr1p36.33	1558544_at	XM_001715367 /// XM_001718749 /// XM_001724970
2.11	2.10	0.01	9.22E-01	9.79E-01	IL2	interleukin 2	chr4q26-q27	207849_at	NM_000586
8.79	8.77	0.03	9.22E-01	9.79E-01	C9orf16	chromosome 9 open reading frame 16	chr9q34.1	222165_x_at	NM_024112

3.11	3.10	0.01	9.23E-01	9.79E-01	---	---	---	233677_at	---																				
3.72	3.70	0.02	9.23E-01	9.79E-01	---	---	---	1566425_at	---																				
2.28	2.27	0.01	9.23E-01	9.79E-01	---	---	---	240338_at	---																				
2.26	2.24	0.01	9.23E-01	9.79E-01	ZSCAN23	zinc finger and SCAN domain containing 23	chr6p22.1	1564039_at	NM_001012455 /// XM_001715453 /// XM_001715639 /// XM_001717784																				
2.30	2.29	0.01	9.23E-01	9.79E-01	TBX5	T-box 5	chr12q24.1	1563018_at	NM_000192 /// NM_080717 /// NM_080718 /// NM_181486																				
3.99	3.96	0.04	9.23E-01	9.79E-01	SP6	Sp6 transcription factor	chr17q21.32	228975_at	NM_199262																				
2.14	2.13	0.01	9.23E-01	9.79E-01	---	---	---	1562693_at	---																				
4.79	4.75	0.04	9.23E-01	9.79E-01	---	---	---	236836_at	---																				
7.37	7.34	0.03	9.23E-01	9.79E-01	GFM1	G elongation factor, mitochondrial 1	chr3q25.1-q26.2	225153_at	NM_024996																				
2.51	2.48	0.03	9.23E-01	9.79E-01	LOC283501	hypothetical protein LOC283501	chr13q34	1556854_at	---																				
3.44	3.42	0.02	9.23E-01	9.79E-01	MATR3	matrin 3	chr5q31.2	228012_at	NM_018834 /// NM_199189																				
1.96	1.95	0.01	9.23E-01	9.79E-01	USH2A	Usher syndrome 2A (autosomal recessive, mild)	chr1q41	207706_at	NM_007123 /// NM_206933																				
2.75	2.74	0.01	9.23E-01	9.79E-01	---	---	---	241645_at	---																				
2.46	2.44	0.02	9.23E-01	9.79E-01	---	---	---	1560896_a_at	---																				
3.26	3.25	0.02	9.23E-01	9.79E-01	GNAT1	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1	chr3p21	214286_at	NM_000172 /// NM_144499																				
5.31	5.29	0.02	9.23E-01	9.79E-01	ZNF419	zinc finger protein 419	chr19q13.43	58367_s_at	NM_001098491 /// NM_001098492 /// NM_001098493 /// NM_001098494 /// NM_001098495 /// NM_001098496 /// NM_024691																				
4.28	4.24	0.05	9.23E-01	9.79E-01	OSMR	oncostatin M receptor	chr5p13.1	205729_at	NM_003999																				
6.09	6.07	0.02	9.23E-01	9.79E-01	TBC1D22B	TBC1 domain family, member 22B	chr6p21.2	223375_at	NM_017772																				
4.21	4.18	0.04	9.23E-01	9.79E-01	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	chr14q11.2-q21	203552_at	NM_006575 /// NM_198794																				
2.41	2.39	0.02	9.23E-01	9.79E-01	TSC22D2	TSC22 domain family, member 2	chr3q25.1	210954_s_at	NM_014779																				
5.68	5.64	0.04	9.23E-01	9.79E-01	LOC92482	UPF0604 protein	chr10q25.2	213224_s_at	XM_001716109 /// XM_001725802 /// XM_001725803 /// XM_001725804 /// XM_001726022 /// XM_001726023 /// XM_001726024																				
2.35	2.34	0.01	9.23E-01	9.79E-01	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	chr13q12.11-q12.3	223827_at	NM_018647 /// NM_148957																				
6.63	6.61	0.02	9.23E-01	9.79E-01	---	---	---	226375_at	---																				
2.19	2.18	0.01	9.23E-01	9.79E-01	DEFB119	defensin, beta 119	chr20q11.1	1553093_a_at	NM_153289 /// NM_153323 /// NM_173460																				

3.54	3.51	0.03	9.23E-01	9.79E-01	CXorf36	chromosome X open reading frame 36	chrXp11.3	241381_at	NM_024689 /// NM_176819																				
2.09	2.08	0.01	9.23E-01	9.79E-01	MTMR7	myotubularin related protein 7	chr8p22	215793_at	NM_004686																				
3.15	3.14	0.01	9.23E-01	9.79E-01	CEACAM4	carcinoembryonic antigen-related cell adhesion molecule 4	chr19q13.2	207205_at	NM_001817																				
3.13	3.11	0.02	9.23E-01	9.79E-01	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	chr16q22.1	215092_s_at	NM_001113178 /// NM_006599 /// NM_138713 /// NM_138714 /// NM_173214																				
2.44	2.43	0.01	9.23E-01	9.79E-01	---	---	---	1557873_at	---																				
2.04	2.03	0.01	9.24E-01	9.79E-01	MAGEB18	melanoma antigen family B, 18	chrXp21.3	1552913_at	NM_173699																				
2.50	2.48	0.01	9.24E-01	9.79E-01	---	---	---	244102_at	---																				
9.38	9.36	0.02	9.24E-01	9.79E-01	SEC14L1	SEC14-like 1 (S. cerevisiae)	chr17q25.1-q25.2	202084_s_at	NM_001039573 /// NM_003003																				
1.99	1.98	0.01	9.24E-01	9.79E-01	---	---	---	233115_at	---																				
3.08	3.06	0.01	9.24E-01	9.79E-01	NEURL	neuralized homolog (Drosophila)	chr10q25.1	204888_s_at	NM_004210																				
5.40	5.37	0.03	9.24E-01	9.79E-01	RICTOR	rapamycin-insensitive companion of mTOR	chr5p13.1	226312_at	NM_152756																				
2.23	2.21	0.02	9.24E-01	9.79E-01	---	---	---	241542_at	---																				
2.81	2.74	0.07	9.24E-01	9.79E-01	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	chrYq11.222	204410_at	NM_004681																				
2.50	2.48	0.01	9.24E-01	9.79E-01	LOC145845	hypothetical protein LOC145845	chr15q14	233311_at	XR_040653 /// XR_040654 /// XR_040655																				
5.60	5.57	0.02	9.24E-01	9.79E-01	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	chrXq13.3	226199_at	NM_145052																				
2.61	2.59	0.02	9.24E-01	9.79E-01	---	---	---	217554_at	---																				
4.57	4.53	0.04	9.24E-01	9.79E-01	PTCD3	Pentatricopeptide repeat domain 3	chr2p11.2	228512_at	NM_017952																				
8.51	8.49	0.03	9.24E-01	9.79E-01	CSNK1A1	casein kinase 1, alpha 1	chr5q32	208865_at	NM_001025105 /// NM_001892																				
2.63	2.62	0.01	9.24E-01	9.79E-01	C10orf4	chromosome 10 open reading frame 4	chr10q23.33	238596_at	NM_145246																				
2.38	2.36	0.01	9.24E-01	9.79E-01	MGC39900 /// TMSL8	thymosin beta15b /// thymosin-like 8	chrXq21.33-q22.3 /// chrXq22.2	205347_s_at	NM_021992 /// NM_194324 /// XR_042096 /// XR_042097 /// XR_042098																				
1.91	1.90	0.01	9.24E-01	9.79E-01	---	---	---	1561437_at	---																				
2.67	2.66	0.01	9.24E-01	9.79E-01	NRXN3	neurexin 3	chr14q31	215020_at	NM_001105250 /// NM_004796 /// NM_138970																				
3.03	3.01	0.02	9.24E-01	9.79E-01	PHF8	PHD finger protein 8	chrXp11.22	238837_at	NM_015107																				
8.44	8.42	0.02	9.24E-01	9.79E-01	ARHGAP1	Rho GTPase activating protein 1	chr11p12-q12	202117_at	NM_004308																				
5.27	5.25	0.02	9.24E-01	9.79E-01	---	---	---	239084_at	---																				
3.29	3.27	0.02	9.24E-01	9.79E-01	ZNF536	zinc finger protein 536	chr19q12	206403_at	NM_014717																				
2.99	2.97	0.02	9.24E-01	9.79E-01	---	---	---	232788_at	---																				
4.02	4.01	0.01	9.24E-01	9.79E-01	RHO	rhodopsin	chr3q21-q24	206455_s_at	NM_000539																				
1.84	1.83	0.01	9.24E-01	9.79E-01	---	---	---	1566970_at	---																				
2.99	2.96	0.04	9.24E-01	9.79E-01	---	---	---	237860_at	---																				
6.32	6.30	0.03	9.24E-01	9.79E-01	WWC3	WWC family member 3	chrXp22.32	219520_s_at	NM_015691																				
7.32	7.28	0.04	9.24E-01	9.79E-01	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	chr6q14-q15	217832_at	NM_006372																				
2.58	2.57	0.01	9.24E-01	9.79E-01	---	---	---	241454_at	---																				
2.15	2.14	0.01	9.25E-01	9.79E-01	---	---	---	234064_at	---																				
7.12	7.10	0.02	9.25E-01	9.79E-01	ASCC2	activating signal cointegrator 1 complex subunit 2	chr22q12.1	215684_s_at	NM_032204																				
2.08	2.07	0.01	9.25E-01	9.79E-01	C11orf40	chromosome 11 open reading frame 40	chr11p15.5	1553086_at	NM_144663																				
2.51	2.50	0.01	9.25E-01	9.79E-01	---	---	---	1566807_a_at	---																				
2.18	2.17	0.01	9.25E-01	9.79E-01	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	chr19q13.2	206199_at	NM_006890																				
2.78	2.76	0.01	9.25E-01	9.79E-01	LOC339929	hypothetical protein LOC339929	chr3q28	1556827_at	---																				
2.22	2.21	0.01	9.25E-01	9.79E-01	---	---	---	1562847_at	---																				
2.02	2.01	0.01	9.25E-01	9.79E-01	---	---	---	1560051_at	---																				
9.83	9.79	0.03	9.25E-01	9.79E-01	IFITM2	interferon induced transmembrane protein 2 (1-8D)	chr11p15.5	201315_x_at	NM_006435																				
5.60	5.58	0.02	9.25E-01	9.79E-01	ZHX3	zinc fingers and homeoboxes 3	chr20q12	217367_s_at	NM_015035																				

7.65	7.62	0.02	9.25E-01	9.79E-01	LSP1	lymphocyte-specific protein 1	chr11p15.5	203523_at	NM_001013253 /// NM_001013254 /// NM_001013255 /// NM_002339																				
3.06	3.04	0.02	9.25E-01	9.79E-01	MPP2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	chr17q12-q21	207984_s_at	NM_005374																				
3.90	3.88	0.02	9.25E-01	9.79E-01	ANKDD1A	ankyrin repeat and death domain containing 1A	chr15q22.31	237316_at	NM_182703																				
5.54	5.51	0.03	9.25E-01	9.79E-01	TRIM38	tripartite motif-containing 38	chr6p21.3	203567_s_at	NM_006355																				
2.23	2.22	0.01	9.25E-01	9.79E-01	ZNF568	zinc finger protein 568	chr19q13.12	1564356_at	NM_198539																				
3.07	3.04	0.02	9.25E-01	9.79E-01	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	chr20q11.23	41577_at	NM_015568																				
2.52	2.51	0.01	9.25E-01	9.79E-01	BMP10	bone morphogenetic protein 10	chr2p14	208292_at	NM_014482																				
2.36	2.34	0.01	9.26E-01	9.79E-01	PABPC1	Poly(A) binding protein, cytoplasmic 1	chr8q22.2-q23	1560770_at	NM_002568																				
4.45	4.44	0.02	9.26E-01	9.79E-01	SLC19A1	solute carrier family 19 (folate transporter), member 1	chr21q22.3	209777_s_at	NM_194255																				
3.28	3.26	0.01	9.26E-01	9.79E-01	DYNC1H1	Dynein, cytoplasmic 1, heavy chain 1	chr14q32.3-qter|14q32	1556831_at	NM_001376																				
3.23	3.21	0.02	9.26E-01	9.79E-01	---	---	---	239440_at	---																				
1.96	1.95	0.01	9.26E-01	9.79E-01	---	---	---	1564294_at	---																				
2.94	2.93	0.01	9.26E-01	9.79E-01	CILP2	cartilage intermediate layer protein 2	chr19p13.11	1552289_a_at	NM_153221																				
4.11	4.10	0.01	9.26E-01	9.79E-01	ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	chr4q21-q24|4q22	223781_x_at	NM_000670																				
5.01	4.98	0.03	9.26E-01	9.79E-01	FBXO33	F-box protein 33	chr14q21.1	226970_at	NM_203301																				
1.99	1.98	0.01	9.26E-01	9.79E-01	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	chr11p13-p12	1558009_at	NM_004171																				
4.53	4.52	0.02	9.26E-01	9.79E-01	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	chr6p21.3	208490_x_at	NM_003518 /// NM_003522 /// NM_003523 /// NM_003525 /// NM_003526																				
2.61	2.60	0.02	9.26E-01	9.80E-01	LOC441046	glucuronidase, beta pseudogene	chr4q31.21	240063_at	NR_003675																				
4.08	4.06	0.02	9.26E-01	9.80E-01	C14orf172	chromosome 14 open reading frame 172	chr14q32.33	1554317_s_at	NM_152307																				
2.22	2.21	0.01	9.26E-01	9.80E-01	SESN3	sestrin 3	chr11q21	1553869_at	NM_144665																				
2.53	2.51	0.02	9.26E-01	9.80E-01	C12orf51	chromosome 12 open reading frame 51	chr12q24.13	1557529_at	NM_001109662																				
3.16	3.14	0.02	9.26E-01	9.80E-01	PNCK	pregnancy up-regulated non-ubiquitously expressed CaM kinase	chrXq28	229411_at	NM_001039582																				
2.39	2.38	0.01	9.26E-01	9.80E-01	---	---	---	1555176_at	---																				
2.57	2.56	0.01	9.26E-01	9.80E-01	---	---	---	239195_at	---																				
2.68	2.66	0.02	9.26E-01	9.80E-01	---	---	---	222344_at	---																				
2.26	2.25	0.01	9.26E-01	9.80E-01	ZNF781	zinc finger protein 781	chr19q13.12	1559789_a_at	NM_152605																				
5.76	5.73	0.04	9.26E-01	9.80E-01	MINPP1	multiple inositol polyphosphate histidine phosphatase, 1	chr10q23	209585_s_at	NM_004897																				
3.88	3.84	0.04	9.26E-01	9.80E-01	ACBD5	acyl-Coenzyme A binding domain containing 5	chr10p12.1	1568877_a_at	NM_001042473 /// NM_145698																				
2.07	2.06	0.01	9.26E-01	9.80E-01	PER3	period homolog 3 (Drosophila)	chr1p36.23	1555130_at	NM_016831																				
2.79	2.78	0.02	9.26E-01	9.80E-01	TERT	telomerase reverse transcriptase	chr5p15.33	1555271_a_at	NM_198253 /// NM_198255																				
2.08	2.07	0.01	9.26E-01	9.80E-01	---	---	---	233805_at	---																				
2.34	2.33	0.01	9.27E-01	9.80E-01	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	chr1q41	219391_at	NM_006085																				
3.79	3.77	0.02	9.27E-01	9.80E-01	PEX13	peroxisomal biogenesis factor 13	chr2p14-p16	205246_at	NM_002618																				
2.85	2.84	0.01	9.27E-01	9.80E-01	TEF	thyrotrophic embryonic factor	chr22q13|22q13.2	210167_s_at	NM_003216																				
4.24	4.22	0.02	9.27E-01	9.80E-01	---	---	---	227571_at	---																				
4.93	4.91	0.02	9.27E-01	9.80E-01	PACS2	phosphofurin acidic cluster sorting protein 2	chr14q32.33	1555824_a_at	NM_001100913 /// NM_015197																				
2.46	2.45	0.01	9.27E-01	9.80E-01	NFRKB	nuclear factor related to kappaB binding protein	chr11q24-q25	237210_at	NM_006165																				
3.84	3.83	0.01	9.27E-01	9.80E-01	---	---	---	1568191_at	---																				
8.18	8.16	0.02	9.27E-01	9.80E-01	HM13	histocompatibility (minor) 13	chr20q11.21	224615_x_at	NM_030789 /// NM_178580 /// NM_178581 /// NM_178582																				
2.52	2.51	0.02	9.27E-01	9.80E-01	WDR59	WD repeat domain 59	chr16q23.1	228295_at	NM_030581																				
2.24	2.23	0.01	9.27E-01	9.80E-01	MTHFD1	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	chr14q24	239846_at	NM_005956																				

2.54	2.53	0.01	9.27E-01	9.80E-01	KRTAP7-1	keratin associated protein 7-1	chr21q22.1	1564960_at	XM_001724754 /// XM_927228 /// XM_941037																				
2.53	2.52	0.01	9.27E-01	9.80E-01	DBC1	deleted in bladder cancer 1	chr9q32-q33	205818_at	NM_014618																				
2.15	2.14	0.01	9.27E-01	9.80E-01	---	---	---	1556927_at	---																				
7.62	7.61	0.01	9.27E-01	9.80E-01	PARL	presenilin associated, rhomboid-like	chr3q27.1	218271_s_at	NM_001037639 /// NM_018622																				
2.02	2.01	0.01	9.27E-01	9.80E-01	---	---	---	1563162_at	---																				
3.82	3.80	0.02	9.27E-01	9.80E-01	CX3CL1	chemokine (C-X3-C motif) ligand 1	chr16q13	823_at	NM_002996																				
2.50	2.50	0.01	9.27E-01	9.80E-01	LOC645468	similar to putative RNA binding protein KOC	chr6q27	216494_at	XR_017635 /// XR_038251 /// XR_039797																				
3.15	3.13	0.02	9.28E-01	9.80E-01	ANK1	ankyrin 1, erythrocytic	chr8p11.1	205390_s_at	NM_000037 /// NM_020475 /// NM_020476 /// NM_020477 /// NM_020478 /// NM_020480																				
3.86	3.83	0.03	9.28E-01	9.80E-01	CASR	calcium-sensing receptor	chr3q13	210577_at	NM_000388																				
3.93	3.90	0.03	9.28E-01	9.80E-01	FZD2	frizzled homolog 2 (Drosophila)	chr17q21.1	210220_at	NM_001466																				
4.85	4.74	0.11	9.28E-01	9.80E-01	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	chr6p21.3	203290_at	NM_002122 /// XM_001722240 /// XM_001723439																				
2.31	2.30	0.01	9.28E-01	9.80E-01	FBXO11	F-box protein 11	chr2p16.3	232364_at	NM_012167 /// NM_018693 /// NM_025133																				
2.11	2.10	0.01	9.28E-01	9.80E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	1561042_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376																				
3.01	3.00	0.01	9.28E-01	9.80E-01	AIM1L	absent in melanoma 1-like	chr1p36.11	220289_s_at	NM_001039775 /// NM_017977																				
6.06	6.04	0.02	9.28E-01	9.80E-01	UBTD2	ubiquitin domain containing 2	chr5q35.1	224827_at	NM_152277																				
3.70	3.68	0.02	9.28E-01	9.80E-01	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	chr11q23.3	214447_at	NM_005238																				
2.67	2.66	0.02	9.28E-01	9.80E-01	---	---	---	1561214_at	---																				
2.04	2.03	0.01	9.28E-01	9.80E-01	---	---	---	1563386_at	---																				
6.63	6.62	0.01	9.28E-01	9.81E-01	LOC91548	hypothetical protein LOC91548	chr1q32.3	234341_x_at	---																				
2.04	2.03	0.01	9.28E-01	9.81E-01	---	---	---	1556417_a_at	---																				
2.03	2.02	0.01	9.28E-01	9.81E-01	SOX11	SRY (sex determining region Y)-box 11	chr2p25	204913_s_at	NM_003108																				
4.74	4.71	0.04	9.28E-01	9.81E-01	MINA	MYC induced nuclear antigen	chr3q11.2	213189_at	NM_001042533 /// NM_032778 /// NM_153182																				
3.06	3.04	0.01	9.28E-01	9.81E-01	TMPRSS11D	transmembrane protease, serine 11D	chr4q13.2	207602_at	NM_004262																				
2.63	2.62	0.01	9.28E-01	9.81E-01	CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21	chr19q13.2	216605_s_at	NM_001098506 /// NM_033543																				
2.25	2.24	0.01	9.28E-01	9.81E-01	ZNF407	zinc finger protein 407	chr18q23	220835_s_at	NM_017757																				
4.10	4.08	0.02	9.28E-01	9.81E-01	AKIRIN2	akirin 2	chr6q15	223143_s_at	NM_018064																				

4.62	4.58	0.04	9.29E-01	9.81E-01	SPTBN1	spectrin, beta, non-erythrocytic 1	chr2p21	215918_s_at	NM_003128 /// NM_178313
2.95	2.92	0.02	9.29E-01	9.81E-01	---	---	---	242289_at	---
4.56	4.53	0.03	9.29E-01	9.81E-01	PHACTR4	phosphatase and actin regulator 4	chr1p35.3	219235_s_at	NM_001048183 /// NM_023923
3.76	3.74	0.02	9.29E-01	9.81E-01	ESD	esterase D/formylglutathione hydrolase	chr13q14.1-q14.2	228162_at	NM_001984
2.07	2.06	0.01	9.29E-01	9.81E-01	GOSR1	golgi SNAP receptor complex member 1	chr17q11	1555199_at	NM_001007024 /// NM_001007025 /// NM_004871
2.39	2.37	0.01	9.29E-01	9.81E-01	ZDHHC21	Zinc finger, DHHC-type containing 21	chr9p22.3	229240_at	NM_178566
2.07	2.05	0.01	9.29E-01	9.81E-01	ZNF294	zinc finger protein 294	chr21q22.11	233818_at	NM_015565
2.89	2.87	0.02	9.29E-01	9.81E-01	LOC340357	hypothetical LOC340357	chr8p23.1-p22	1562924_at	NR_015383
2.64	2.62	0.02	9.29E-01	9.81E-01	INHBA	inhibin, beta A	chr7p15-p13	204926_at	NM_002192
2.28	2.27	0.02	9.29E-01	9.81E-01	LGALS14	lectin, galactoside-binding, soluble, 14	chr19q13.2	220158_at	NM_020129 /// NM_203471
1.92	1.90	0.01	9.29E-01	9.81E-01	PDE3B	Phosphodiesterase 3B, cGMP-inhibited	chr11p15.1	222317_at	NM_000922
3.14	3.12	0.02	9.29E-01	9.81E-01	---	---	---	239401_at	---
5.10	5.08	0.02	9.29E-01	9.81E-01	NCOA3	nuclear receptor coactivator 3	chr20q12	207700_s_at	NM_006534 /// NM_181659
6.06	6.02	0.04	9.29E-01	9.81E-01	ZFHX4	zinc finger homeobox 4	chr8q21.11	219779_at	NM_024721
3.40	3.38	0.02	9.29E-01	9.81E-01	SETMAR	SET domain and mariner transposase fusion gene	chr3p26.2	1554059_at	NM_006515 /// NR_024022
2.86	2.84	0.02	9.29E-01	9.81E-01	C1orf52	chromosome 1 open reading frame 52	chr1p22.3	239038_at	NM_198077 /// NR_024113
2.14	2.13	0.01	9.29E-01	9.81E-01	---	---	---	244314_at	---
6.34	6.32	0.03	9.29E-01	9.81E-01	tcag7.1228	hypothetical protein FLJ25778	chr7q34	225445_at	NM_173569
3.80	3.78	0.02	9.29E-01	9.81E-01	PRICKLE3	prickle homolog 3 (Drosophila)	chrXp11.23-p11.22	217349_s_at	NM_006150
2.00	1.99	0.01	9.29E-01	9.81E-01	FGFR1OP2	FGFR1 oncogene partner 2	chr12p11.23	1556282_at	NM_015633
2.46	2.45	0.01	9.30E-01	9.81E-01	PCDHGA12 /// PCDHGC5	protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily C, 5	chr5q31	224536_s_at	NM_003735 /// NM_018929 /// NM_032094 /// NM_032407
2.53	2.52	0.01	9.30E-01	9.81E-01	CSPP1	centrosome and spindle pole associated protein 1	chr8q13.2	1554873_at	NM_001077204 /// NM_024790
9.40	9.38	0.02	9.30E-01	9.81E-01	FLOT1	flotillin 1	chr6p21.3	208749_x_at	NM_005803
2.43	2.42	0.02	9.30E-01	9.81E-01	LOC100130856	hypothetical protein LOC100130856	chr19p13.3	1564240_at	XM_001723600 /// XM_001726292 /// XM_001726438
3.43	3.41	0.02	9.30E-01	9.81E-01	LOC641467	hypothetical LOC641467	---	229990_at	---
2.45	2.43	0.02	9.30E-01	9.81E-01	MAN1A2	mannosidase, alpha, class 1A, member 2	chr1p13	1552481_s_at	NM_006699
4.83	4.82	0.01	9.30E-01	9.81E-01	C1QTNF6	C1q and tumor necrosis factor related protein 6	chr22q13.1	223571_at	NM_031910 /// NM_182486
4.79	4.74	0.04	9.30E-01	9.81E-01	ZMAT3	zinc finger, matrin type 3	chr3q26.3-q27	1555609_a_at	NM_022470 /// NM_152240
4.48	4.45	0.03	9.30E-01	9.81E-01	---	---	---	242494_at	---
5.51	5.49	0.03	9.30E-01	9.81E-01	FANCF	Fanconi anemia, complementation group F	chr11p15	218689_at	NM_022725
2.58	2.57	0.01	9.30E-01	9.81E-01	LOC400684	hypothetical gene supported by BC000922	chr19q13.11	232965_at	---
2.41	2.40	0.01	9.30E-01	9.81E-01	---	---	---	1562630_at	---
2.61	2.59	0.02	9.30E-01	9.81E-01	EIF2C3 /// EIF2C4	eukaryotic translation initiation factor 2C, 3 /// eukaryotic translation initiation factor 2C, 4	chr1p34.3	219190_s_at	NM_017629 /// NM_024852 /// NM_177422
2.89	2.88	0.01	9.30E-01	9.81E-01	AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	chr8p11.21	236743_at	NM_178819
1.92	1.91	0.01	9.30E-01	9.81E-01	CAGE1	cancer antigen 1	chr6p24.3	1563787_a_at	NM_205864
4.63	4.61	0.02	9.30E-01	9.81E-01	FAM152A	family with sequence similarity 152, member A	chr1q44	1558914_at	NM_016076
4.54	4.53	0.02	9.30E-01	9.81E-01	DYNLRB1	Dynein, light chain, roadblock-type 1	chr20q11.21	1565611_at	NM_014183

6.40	6.38	0.02	9.30E-01	9.81E-01	PKN1	protein kinase N1	chr19p13.1-p12	202161_at	NM_002741 /// NM_213560
5.21	5.20	0.02	9.30E-01	9.81E-01	LPHN1	latrophilin 1	chr19p13.2	203488_at	NM_001008701 /// NM_014921
3.95	3.93	0.02	9.31E-01	9.81E-01	---	---	---	1556296_at	---
1.94	1.93	0.01	9.31E-01	9.81E-01	LOC642636	similar to Double-strand-break repair protein rad21 homolog (Pokeweed agglutinin-binding protein 29) (PW29) (SCC1 homolog)	chr20p13	234662_at	XM_001717761
2.60	2.59	0.01	9.31E-01	9.81E-01	TM4SF1	transmembrane 4 L six family member 1	chr3q21-q25	238168_at	NM_014220
2.23	2.22	0.01	9.31E-01	9.81E-01	CHRNB4	cholinergic receptor, nicotinic, beta 4	chr15q24	207516_at	NM_000750
2.24	2.23	0.01	9.31E-01	9.81E-01	JMJD2C	Jumonji domain containing 2C	chr9p24.1	244385_at	NM_015061
2.45	2.44	0.01	9.31E-01	9.81E-01	CREB3L3	cAMP responsive element binding protein 3-like 3	chr19p13.3	234361_at	NM_032607
3.66	3.64	0.02	9.31E-01	9.81E-01	TBX18	T-box 18	chr6q14-q15	233889_at	NM_001080508
2.12	2.11	0.01	9.31E-01	9.81E-01	POU2AF1	POU class 2 associating factor 1	chr11q23.1	1569675_at	NM_006235
2.54	2.52	0.01	9.31E-01	9.81E-01	PNPLA7	patatin-like phospholipase domain containing 7	chr9q34.3	236135_at	NM_001098537 /// NM_152286
2.60	2.59	0.01	9.31E-01	9.81E-01	C16orf46	chromosome 16 open reading frame 46	chr16q23.2	1553303_at	NM_001100873 /// NM_152337
2.20	2.19	0.01	9.31E-01	9.81E-01	HTR1F	5-hydroxytryptamine (serotonin) receptor 1F	chr3p12	221458_at	NM_000866
2.13	2.11	0.01	9.31E-01	9.81E-01	---	---	---	1569756_at	---
2.08	2.07	0.01	9.31E-01	9.81E-01	SLC26A3	solute carrier family 26, member 3	chr7q31	206143_at	NM_000111
2.68	2.67	0.01	9.31E-01	9.82E-01	---	---	---	215423_at	---
3.21	3.19	0.02	9.31E-01	9.82E-01	ZNF286A	zinc finger protein 286A	chr17p11.2	239898_x_at	NM_001130842 /// NM_020652
2.64	2.63	0.01	9.31E-01	9.82E-01	RFPL2	ret finger protein-like 2	chr22q12.3	207227_x_at	NM_001098527 /// NM_006605
5.27	5.22	0.05	9.31E-01	9.82E-01	C4orf41	chromosome 4 open reading frame 41	chr4q35.1	233558_s_at	NM_021942 /// NM_199053
2.12	2.11	0.01	9.31E-01	9.82E-01	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	chr6p21.32	1554862_at	NR_002174
3.96	3.94	0.02	9.31E-01	9.82E-01	PGS1	phosphatidylglycerophosphate synthase 1	chr17q25.3	226266_at	NM_024419
8.70	8.69	0.01	9.31E-01	9.82E-01	RBX1	ring-box 1	chr22q13.2	218117_at	NM_014248
3.16	3.14	0.02	9.31E-01	9.82E-01	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	chr5q31	209223_at	NM_002488
4.46	4.45	0.02	9.31E-01	9.82E-01	---	---	---	243710_at	---
3.93	3.91	0.02	9.31E-01	9.82E-01	ADORA2A	adenosine A2a receptor	chr22q11.23	205013_s_at	NM_000675
4.78	4.75	0.02	9.31E-01	9.82E-01	SLC25A10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	chr17q25.3	218275_at	NM_012140
2.73	2.71	0.02	9.31E-01	9.82E-01	LOC145786	hypothetical protein LOC145786	chr15q21.1	229178_at	---
5.89	5.87	0.02	9.32E-01	9.82E-01	PCNT	pericentrin	chr21q22.3	203660_s_at	NM_006031
5.35	5.30	0.06	9.32E-01	9.82E-01	MLF1	myeloid leukemia factor 1	chr3q25.1	204784_s_at	NM_001130156 /// NM_001130157 /// NM_022443
2.42	2.40	0.01	9.32E-01	9.82E-01	SORT1	sortilin 1	chr1p21.3-p13.1|1p21.3-p13.1	212797_at	NM_002959
3.03	3.01	0.02	9.32E-01	9.82E-01	PIK3R6	phosphoinositide-3-kinase, regulatory subunit 6	chr17p13.1	1558770_a_at	NM_001010855
3.65	3.63	0.02	9.32E-01	9.82E-01	MIP	major intrinsic protein of lens fiber	chr12q13	220863_at	NM_012064
8.50	8.46	0.03	9.32E-01	9.82E-01	NCOA7	nuclear receptor coactivator 7	chr6q22.31-q22.32	225344_at	NM_001122842 /// NM_181782
6.65	6.63	0.02	9.32E-01	9.82E-01	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	chr14q22.1	206992_s_at	NM_001003803 /// NM_001003805 /// NM_015684
2.60	2.58	0.01	9.32E-01	9.82E-01	BMP5	bone morphogenetic protein 5	chr6p12.1	205431_s_at	NM_021073
2.24	2.23	0.01	9.32E-01	9.82E-01	FNDC3B	fibronectin type III domain containing 3B	chr3q26.31	1569490_at	NM_022763
4.33	4.32	0.02	9.32E-01	9.82E-01	SCARNA17	small Cajal body-specific RNA 17	chr18q21.1	240830_at	NR_003003
1.96	1.95	0.01	9.32E-01	9.82E-01	---	---	---	1561415_at	---
2.83	2.81	0.01	9.32E-01	9.82E-01	---	---	---	239332_at	---
2.86	2.84	0.02	9.32E-01	9.82E-01	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	216624_s_at	NM_005933
3.57	3.55	0.02	9.32E-01	9.82E-01	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	chr17p13	242242_at	NM_004505

2.21	2.20	0.01	9.32E-01	9.82E-01	SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter family), member 2	chr13q33	207095_at	NM_000452																				
2.60	2.59	0.01	9.32E-01	9.82E-01	CENTD1	Centaurin, delta 1	chr4p14	1561407_at	NM_015230 /// NM_139182																				
3.17	3.15	0.02	9.32E-01	9.82E-01	OSBPL10	oxysterol binding protein-like 10	chr3p22.3	231656_x_at	NM_017784																				
4.94	4.90	0.04	9.32E-01	9.82E-01	HPS5	Hermansky-Pudlak syndrome 5	chr11p14	204544_at	NM_007216 /// NM_181507 /// NM_181508																				
3.87	3.84	0.03	9.32E-01	9.82E-01	FRY	furry homolog (Drosophila)	chr13q13.1	204072_s_at	NM_023037																				
2.11	2.09	0.01	9.32E-01	9.82E-01	MAP9	microtubule-associated protein 9	chr4q32.1	235550_at	NM_001039580																				
3.53	3.51	0.02	9.33E-01	9.82E-01	---	---	---	1566454_at	---																				
2.59	2.58	0.02	9.33E-01	9.82E-01	MIER2	mesoderm induction early response 1, family member 2	chr19p13.3	221862_at	NM_017550																				
5.30	5.29	0.01	9.33E-01	9.82E-01	MTMR14	Myotubularin related protein 14	chr3p26	232342_at	NM_001077525 /// NM_001077526 /// NM_022485																				
6.55	6.51	0.04	9.33E-01	9.82E-01	SFRS3	splicing factor, arginine/serine-rich 3	chr6p21	208673_s_at	NM_003017																				
2.96	2.94	0.02	9.33E-01	9.82E-01	FAM84A	family with sequence similarity 84, member A	chr2p24.3	228459_at	NM_145175																				
2.38	2.36	0.01	9.33E-01	9.82E-01	PCLO	piccolo (presynaptic cytomatrix protein)	chr7q11.23-q21.3	217096_at	NM_014510 /// NM_033026																				
3.05	3.03	0.02	9.33E-01	9.82E-01	---	---	---	1565150_at	---																				
7.28	7.27	0.01	9.33E-01	9.82E-01	---	---	---	243147_x_at	---																				
4.34	4.32	0.02	9.33E-01	9.82E-01	ZMYND8	zinc finger, MYND-type containing 8	chr20q13.12	214795_at	NM_012408 /// NM_183047 /// NM_183048																				
4.10	4.08	0.02	9.33E-01	9.82E-01	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	chr5q35.2	214149_s_at	NM_003945																				
4.37	4.34	0.03	9.33E-01	9.82E-01	GIT2	G protein-coupled receptor kinase interactor 2	chr12q24.1	209876_at	NM_014776 /// NM_057169 /// NM_057170 /// NM_139201																				
2.11	2.10	0.01	9.33E-01	9.82E-01	---	---	---	1569931_at	---																				
3.05	2.97	0.07	9.33E-01	9.82E-01	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	chrYq11.222	204409_s_at	NM_004681																				
7.75	7.73	0.02	9.33E-01	9.82E-01	DCTN1	dynactin 1 (p150, glued homolog, Drosophila)	chr2p13	211780_x_at	NM_004082 /// NM_023019																				
2.97	2.96	0.01	9.33E-01	9.82E-01	LOC145678	hypothetical protein LOC145678	chr15q24.3	216106_at	---																				
6.01	5.99	0.01	9.33E-01	9.82E-01	HUS1	HUS1 checkpoint homolog (S. pombe)	chr7p13-p12	204883_s_at	NM_004507																				
2.23	2.22	0.01	9.33E-01	9.82E-01	---	---	---	239625_at	---																				
6.32	6.30	0.02	9.33E-01	9.82E-01	NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	chr10q23.33	218889_at	NM_022451																				
2.15	2.14	0.01	9.33E-01	9.82E-01	FAM66C	family with sequence similarity 66, member C	chr12p13.31	1570397_x_at	XR_040642 /// XR_040643																				
2.74	2.73	0.01	9.33E-01	9.82E-01	FAM83E	family with sequence similarity 83, member E	chr19q13.32-q13.33	220312_at	NM_017708																				
2.46	2.45	0.01	9.33E-01	9.82E-01	BTLA	B and T lymphocyte associated	chr3q13.2	236226_at	NM_001085357 /// NM_181780																				
2.23	2.22	0.01	9.33E-01	9.82E-01	LOC400958	hypothetical gene supported by BC037562	chr2p14	1570006_at	XR_041695 /// XR_041696 /// XR_041697																				
6.10	6.08	0.02	9.34E-01	9.82E-01	ORAI2	ORAI calcium release-activated calcium modulator 2	chr7q22.1	1558426_x_at	NM_001126340 /// NM_032831																				
2.82	2.81	0.01	9.34E-01	9.82E-01	---	---	---	230632_at	---																				
5.70	5.67	0.04	9.34E-01	9.82E-01	PTPN12	protein tyrosine phosphatase, non-receptor type 12	chr7q11.23	202006_at	NM_001131008 /// NM_001131009 /// NM_002835																				
1.84	1.83	0.01	9.34E-01	9.82E-01	---	---	---	234489_at	---																				
5.47	5.43	0.04	9.34E-01	9.82E-01	PTGER4	prostaglandin E receptor 4 (subtype EP4)	chr5p13.1	204897_at	NM_000958																				

2.18	2.17	0.01	9.34E-01	9.82E-01	TREML3 /// TREML4	triggering receptor expressed on myeloid cells-like 3 /// triggering receptor expressed on myeloid cells-like 4	chr6p21.1	1567559_s_at	NM_198153 /// XM_001717580 /// XM_929970 /// XM_941488																				
3.14	3.11	0.03	9.34E-01	9.82E-01	TMEM30B	transmembrane protein 30B	chr14q23.1	213285_at	NM_001017970																				
3.20	3.17	0.03	9.34E-01	9.82E-01	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	1569022_a_at	NM_002645																				
5.12	5.10	0.02	9.34E-01	9.82E-01	UTS2R	urotensin 2 receptor	chr17q25.3	1553262_a_at	NM_018949																				
2.62	2.61	0.01	9.34E-01	9.82E-01	TTC33	tetratricopeptide repeat domain 33	chr5p15.2-p12	231479_at	NM_012382																				
2.24	2.23	0.01	9.34E-01	9.82E-01	LOC100133724	similar to Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	---	217139_at	XR_038734																				
2.52	2.51	0.01	9.34E-01	9.82E-01	---	---	---	243103_at	---																				
2.49	2.48	0.01	9.34E-01	9.82E-01	---	---	---	1570587_at	---																				
2.76	2.75	0.01	9.34E-01	9.82E-01	SCNN1D	sodium channel, nonvoltage-gated 1, delta	chr1p36.3-p36.2	208458_at	NM_001130413 /// NM_002978																				
2.58	2.56	0.02	9.34E-01	9.82E-01	---	---	---	231673_at	---																				
4.69	4.68	0.01	9.34E-01	9.82E-01	AIRE	autoimmune regulator	chr21q22.3	208090_s_at	NM_000383 /// NM_000658																				
2.62	2.61	0.01	9.34E-01	9.82E-01	ALKBH6 /// C19orf46	alkB, alkylation repair homolog 6 (E. coli) /// chromosome 19 open reading frame 46	chr19q13.12	235515_at	NM_001039876 /// NM_032878 /// NM_198867																				
2.89	2.88	0.01	9.34E-01	9.82E-01	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	chr1p22.3	203015_s_at	NM_014021																				
2.92	2.90	0.01	9.34E-01	9.82E-01	---	---	---	244292_at	---																				
2.08	2.07	0.01	9.34E-01	9.82E-01	SCRN3	secernin 3	chr2q31.1	232108_at	NM_024583																				
5.74	5.71	0.04	9.34E-01	9.82E-01	LOC100129513	similar to PRO0756	---	210596_at	XM_001720954 /// XM_001721572 /// XM_001722247																				
3.04	3.03	0.01	9.34E-01	9.82E-01	---	---	---	236400_at	---																				
5.73	5.69	0.04	9.35E-01	9.82E-01	UFM1	ubiquitin-fold modifier 1	chr13q13.3	222502_s_at	NM_016617																				
3.93	3.91	0.02	9.35E-01	9.82E-01	C19orf23	chromosome 19 open reading frame 23	chr19p13.3	1552868_at	NM_152480																				
2.17	2.16	0.01	9.35E-01	9.82E-01	DLEU2 /// DLEU2L	deleted in lymphocytic leukemia 2 (non-protein coding) /// deleted in lymphocytic leukemia 2-like	chr13q14.3 /// chr1p31-p22	215629_s_at	NR_002612 /// NR_002771																				
6.81	6.79	0.02	9.35E-01	9.82E-01	ABHD10	abhydrolase domain containing 10	chr3q13.2	218633_x_at	NM_018394																				
2.18	2.17	0.01	9.35E-01	9.82E-01	C5orf42	chromosome 5 open reading frame 42	chr5p13.2	219381_at	NM_023073																				
3.01	2.99	0.02	9.35E-01	9.82E-01	FAM62A	Family with sequence similarity 62 (C2 domain containing), member A	chr12q13.2	244234_at	NM_015292																				
2.22	2.21	0.01	9.35E-01	9.82E-01	---	---	---	1570122_at	---																				
3.37	3.35	0.02	9.35E-01	9.82E-01	---	---	---	243730_at	---																				
2.07	2.06	0.01	9.35E-01	9.82E-01	C12orf56	chromosome 12 open reading frame 56	chr12q14.2	236840_at	NM_001099676																				
5.54	5.51	0.02	9.35E-01	9.82E-01	LOC149832	Hypothetical protein LOC149832	chr20p13	230502_s_at	---																				
2.19	2.18	0.01	9.35E-01	9.82E-01	LOC100130268	Similar to hCG1648866	chr12q21.1	1558336_at	XM_001722869 /// XM_001724504 /// XM_001726615																				
2.03	2.01	0.01	9.35E-01	9.82E-01	---	---	---	1561741_at	---																				
2.23	2.22	0.01	9.35E-01	9.82E-01	STX8	syntaxin 8	chr17p12	1570357_at	NM_004853																				
8.20	8.17	0.03	9.35E-01	9.82E-01	HSBP1	heat shock factor binding protein 1	chr16q23.3	200941_at	NM_001537																				
2.18	2.17	0.01	9.35E-01	9.82E-01	---	---	---	242285_at	---																				
2.45	2.44	0.01	9.35E-01	9.82E-01	---	---	---	1556931_at	---																				
4.70	4.68	0.02	9.35E-01	9.82E-01	SH2D3C	SH2 domain containing 3C	chr9q34.11	226673_at	NM_005489 /// NM_170600																				
2.55	2.54	0.01	9.35E-01	9.82E-01	---	---	---	1556111_s_at	---																				
4.03	4.01	0.02	9.35E-01	9.82E-01	SEC23IP	SEC23 interacting protein	chr10q25-q26	209176_at	NM_007190																				
6.58	6.56	0.02	9.35E-01	9.82E-01	MXD4	MAX dimerization protein 4	chr4p16.3	212346_s_at	NM_006454																				
3.32	3.31	0.01	9.35E-01	9.82E-01	AFF1	AF4/FMR2 family, member 1	chr4q21	211826_s_at	NM_005935																				
3.59	3.57	0.01	9.35E-01	9.82E-01	---	---	---	233593_at	---																				

6.07	6.04	0.03	9.35E-01	9.82E-01	DPH5	DPH5 homolog (S. cerevisiae)	chr1p21.2	224060_s_at	NM_001077394 /// NM_001077395 /// NM_015958																				
3.63	3.61	0.01	9.35E-01	9.82E-01	CD177	CD177 molecule	chr19q13.2	219669_at	NM_020406																				
2.41	2.39	0.01	9.35E-01	9.82E-01	C3orf35	Chromosome 3 open reading frame 35	chr3p22.2	237368_at	NM_178339 /// NM_178342																				
3.29	3.28	0.01	9.35E-01	9.82E-01	---	---	---	1556976_s_at	---																				
3.18	3.16	0.02	9.35E-01	9.83E-01	C1orf55	chromosome 1 open reading frame 55	chr1q42.12	1553338_at	NM_152608																				
1.86	1.85	0.01	9.35E-01	9.83E-01	GSPT1	G1 to S phase transition 1	chr16p13.1	217595_at	NM_001130006 /// NM_001130007 /// NM_002094																				
3.18	3.17	0.01	9.36E-01	9.83E-01	---	---	---	243983_at	---																				
6.52	6.51	0.02	9.36E-01	9.83E-01	GPR172A	G protein-coupled receptor 172A	chr8q24.3	218151_x_at	NM_024531																				
2.22	2.21	0.01	9.36E-01	9.83E-01	---	---	---	215494_at	---																				
3.84	3.82	0.01	9.36E-01	9.83E-01	MELK	maternal embryonic leucine zipper kinase	chr9p13.2	204825_at	NM_014791																				
2.68	2.67	0.01	9.36E-01	9.83E-01	---	---	---	1564004_at	---																				
3.51	3.49	0.02	9.36E-01	9.83E-01	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	chr2p16.1	1559078_at	NM_018014 /// NM_022893 /// NM_138559																				
4.24	4.22	0.01	9.36E-01	9.83E-01	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	chr12q12-q13	1563034_at	NM_005276																				
2.63	2.62	0.01	9.36E-01	9.83E-01	OTUD7B	OTU domain containing 7B	chr1q21.2	220031_at	NM_020205																				
4.72	4.68	0.04	9.36E-01	9.83E-01	---	---	---	1556007_s_at	---																				
2.40	2.39	0.01	9.36E-01	9.83E-01	TLL2	tolloid-like 2	chr10q23-q24	208027_s_at	NM_012465																				
4.95	4.94	0.01	9.36E-01	9.83E-01	EBF4	early B-cell factor 4	chr20p13	233850_s_at	NM_001110514 /// XM_001713721 /// XM_001713722 /// XM_001717843																				
3.07	3.05	0.02	9.36E-01	9.83E-01	C10orf53	chromosome 10 open reading frame 53	chr10q11.23	1555051_at	NM_001042427 /// NM_182554																				
2.29	2.27	0.02	9.36E-01	9.83E-01	HERC2P3	hect domain and RLD 2 pseudogene 3	chr15q11.2	215847_at	NM_001024682																				
2.84	2.83	0.01	9.36E-01	9.83E-01	---	---	---	243094_at	---																				
2.57	2.56	0.01	9.36E-01	9.83E-01	---	---	---	237223_at	---																				
2.89	2.86	0.03	9.36E-01	9.83E-01	PSME4	proteasome (prosome, macropain) activator subunit 4	chr2p16.2	212220_at	NM_014614																				
3.96	3.94	0.02	9.36E-01	9.83E-01	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	chr2q36-q37	216898_s_at	NM_000091 /// NM_031362 /// NM_031365 /// NM_031366																				
2.47	2.45	0.01	9.36E-01	9.83E-01	CTNS	cystinosis, nephropathic	chr17p13	215459_at	NM_001031681 /// NM_004937																				
2.35	2.34	0.01	9.36E-01	9.83E-01	---	---	---	243154_at	---																				
2.37	2.36	0.01	9.37E-01	9.83E-01	---	---	---	234624_at	---																				
2.72	2.71	0.01	9.37E-01	9.83E-01	---	---	---	1562915_at	---																				
2.43	2.41	0.01	9.37E-01	9.83E-01	SPEF2	sperm flagellar 2	chr5p13.2	232745_x_at	NM_024867 /// NM_144722																				
2.94	2.87	0.07	9.37E-01	9.83E-01	LOC100130216 /// USP9Y	hypothetical protein LOC100130216 /// ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	chrYq11.2	228492_at	NM_004654 /// XM_001713696																				
2.20	2.19	0.01	9.37E-01	9.83E-01	DNAH9	dynein, axonemal, heavy chain 9	chr17p12	240857_at	NM_001372 /// NM_004662																				
2.54	2.53	0.01	9.37E-01	9.83E-01	---	---	---	1561726_s_at	---																				
2.22	2.21	0.01	9.37E-01	9.83E-01	LOC100129510	hypothetical protein LOC100129510	chr17q25.3	1560163_at	XM_001720757 /// XM_001725209 /// XM_001726691																				

2.42	2.41	0.01	9.37E-01	9.83E-01	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	chr17p13.1	217420_s_at	NM_000937																				
3.17	3.15	0.02	9.37E-01	9.83E-01	---	---	---	238920_at	---																				
6.26	6.23	0.03	9.37E-01	9.83E-01	GPR89A /// GPR89B /// GPR89C	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	chr1q21.1	223531_x_at	NM_001097612 /// NM_001097613 /// NM_001097616 /// NM_016334																				
5.58	5.56	0.02	9.37E-01	9.83E-01	PXMP3	peroxisomal membrane protein 3, 35kDa	chr8q21.1	228225_at	NM_000318 /// NM_001079867																				
2.21	2.20	0.01	9.37E-01	9.83E-01	---	---	---	1556776_a_at	---																				
3.22	3.20	0.01	9.37E-01	9.83E-01	ZDHHC3	Hypothetical LOC57245	chr3p21.31	236507_at	NM_016598																				
2.63	2.61	0.02	9.37E-01	9.83E-01	---	---	---	236495_at	---																				
5.21	5.20	0.01	9.37E-01	9.83E-01	---	---	---	217446_x_at	---																				
2.17	2.16	0.01	9.37E-01	9.83E-01	RBM39	RNA binding motif protein 39	chr20q11.22	238357_at	NM_004902 /// NM_184234																				
2.13	2.12	0.01	9.37E-01	9.83E-01	LOC149351	hypothetical protein LOC149351	chr1p22.2	232450_at	XR_041994 /// XR_041995 /// XR_041996																				
2.32	2.31	0.01	9.37E-01	9.83E-01	---	---	---	1563568_at	---																				
2.08	2.07	0.01	9.37E-01	9.83E-01	SNRPN	small nuclear ribonucleoprotein polypeptide N	chr15q11.2	240204_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																				

3.21	3.20	0.01	9.37E-01	9.83E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	228540_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855
6.58	6.56	0.02	9.37E-01	9.83E-01	SNX21	sorting nexin family member 21	chr20q13.12	226595_at	NM_001042632 /// NM_001042633 /// NM_033421 /// NM_152897
5.06	5.03	0.04	9.37E-01	9.83E-01	CDH5	cadherin 5, type 2 (vascular endothelium)	chr16q22.1	204677_at	NM_001795
3.34	3.33	0.01	9.37E-01	9.83E-01	---	---	---	220875_at	---
8.67	8.64	0.03	9.37E-01	9.83E-01	NEK7	NIMA (never in mitosis gene a)-related kinase 7	chr1q31.3	212530_at	NM_133494
2.43	2.42	0.01	9.38E-01	9.83E-01	GPR50	G protein-coupled receptor 50	chrXq28	208311_at	NM_004224
8.62	8.59	0.02	9.38E-01	9.83E-01	CNN3	calponin 3, acidic	chr1p22-p21	201445_at	NM_001839
2.21	2.20	0.01	9.38E-01	9.83E-01	IL1RN	interleukin 1 receptor antagonist	chr2q14.2	216245_at	NM_000577 /// NM_173841 /// NM_173842 /// NM_173843
12.46	12.45	0.01	9.38E-01	9.83E-01	RPS23	ribosomal protein S23	chr5q14.2	200926_at	NM_001025
3.75	3.72	0.02	9.38E-01	9.83E-01	ERO1L	ERO1-like (S. cerevisiae)	chr14q22.1	222646_s_at	NM_014584
1.94	1.93	0.01	9.38E-01	9.83E-01	---	---	---	1562823_at	---
2.71	2.70	0.01	9.38E-01	9.83E-01	TXNRD2	thioredoxin reductase 2	chr22q11.21	210803_at	NM_006440
3.92	3.90	0.02	9.38E-01	9.83E-01	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	chr11p13-p12	208389_s_at	NM_004171
2.40	2.39	0.01	9.38E-01	9.83E-01	---	---	---	240904_at	---
3.45	3.43	0.02	9.38E-01	9.83E-01	DLG4	discs, large homolog 4 (Drosophila)	chr17p13.1	204592_at	NM_001128827 /// NM_001365
2.01	2.00	0.01	9.38E-01	9.83E-01	SOX2	SRY (sex determining region Y)-box 2	chr3q26.3-q27	228038_at	NM_003106
2.05	2.04	0.01	9.38E-01	9.83E-01	---	---	---	240880_at	---
5.58	5.56	0.02	9.38E-01	9.83E-01	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	chr7q22	204692_at	NM_002319
2.82	2.81	0.01	9.38E-01	9.83E-01	CACNA1E	calcium channel, voltage-dependent, R type, alpha 1E subunit	chr1q25-q31	208432_s_at	NM_000721
3.03	3.02	0.01	9.38E-01	9.83E-01	---	---	---	244376_at	---
5.85	5.83	0.01	9.38E-01	9.83E-01	C1orf56	chromosome 1 open reading frame 56	chr1q21.2	223459_s_at	NM_017860
2.69	2.68	0.01	9.38E-01	9.83E-01	TWIST2	twist homolog 2 (Drosophila)	chr2q37.3	1554163_at	NM_057179
3.25	3.24	0.01	9.38E-01	9.83E-01	---	---	---	1570295_at	---
6.58	6.57	0.02	9.38E-01	9.83E-01	R3HCC1	R3H domain and coiled-coil containing 1	chr8p21.3	212866_at	XM_001716421 /// XM_114618 /// XM_939319
6.70	6.68	0.01	9.38E-01	9.83E-01	GLI3	GLI-Kruppel family member GLI3	chr7p13	205201_at	NM_000168
4.49	4.48	0.01	9.38E-01	9.83E-01	---	---	---	1569091_at	---
2.39	2.38	0.01	9.39E-01	9.83E-01	FAM55A	family with sequence similarity 55, member A	chr11q23.2	1561387_a_at	NM_152315
5.65	5.63	0.02	9.39E-01	9.83E-01	PSD4	pleckstrin and Sec7 domain containing 4	chr2q13	203317_at	NM_012455
2.58	2.56	0.01	9.39E-01	9.83E-01	CCDC41	coiled-coil domain containing 41	chr12q22	219644_at	NM_001042399 /// NM_016122
5.41	5.38	0.02	9.39E-01	9.83E-01	---	---	---	217322_x_at	---
2.22	2.21	0.01	9.39E-01	9.83E-01	IL22RA2	interleukin 22 receptor, alpha 2	chr6q25.1	237493_at	NM_052962 /// NM_181309 /// NM_181310
3.02	3.00	0.02	9.39E-01	9.83E-01	FAM133A	family with sequence similarity 133, member A	chrXq21.32	239481_at	NM_173698
2.16	2.15	0.01	9.39E-01	9.83E-01	---	---	---	244211_at	---
2.20	2.19	0.01	9.39E-01	9.83E-01	HESRG	embryonic stem cell related protein	chr3p14.3	231381_at	---
2.94	2.93	0.01	9.39E-01	9.83E-01	LARP2	La ribonucleoprotein domain family, member 2	chr4q28.2	231011_at	NM_018078 /// NM_032239 /// NM_178043
2.44	2.43	0.01	9.39E-01	9.83E-01	FAM135B	family with sequence similarity 135, member B	chr8q24.23	236786_at	NM_015912
3.06	3.05	0.01	9.39E-01	9.83E-01	---	---	---	1570405_at	---
2.17	2.16	0.01	9.39E-01	9.83E-01	---	---	---	1564937_at	---
1.91	1.91	0.01	9.39E-01	9.83E-01	---	---	---	240222_at	---

5.12	5.10	0.01	9.39E-01	9.83E-01	MRM1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	chr17q12	219967_at	NM_024864
2.63	2.61	0.01	9.39E-01	9.83E-01	LOC145899	hypothetical protein LOC145899	chr15q24.2	214905_at	---
3.02	3.01	0.01	9.39E-01	9.83E-01	CAMK1G	calcium/calmodulin-dependent protein kinase IG	chr1q32-q41	215161_at	NM_020439
2.30	2.29	0.01	9.39E-01	9.83E-01	---	---	---	1560747_at	---
2.02	2.01	0.01	9.39E-01	9.83E-01	---	---	---	1560863_a_at	---
3.32	3.30	0.01	9.40E-01	9.83E-01	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	chr11q24.2	1552360_a_at	NM_001039661 /// NM_148910
5.97	5.95	0.02	9.40E-01	9.83E-01	HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	chr11p15.5	212983_at	NM_001130442 /// NM_005343 /// NM_176795
6.68	6.66	0.02	9.40E-01	9.83E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	200623_s_at	NM_001743 /// NM_005184 /// NM_006888
3.47	3.45	0.01	9.40E-01	9.83E-01	TSPAN9	Tetraspanin 9	chr12p13.33-p13.32	233435_at	NM_006675
8.40	8.37	0.03	9.40E-01	9.83E-01	MRPL3	mitochondrial ribosomal protein L3	chr3q21-q23	208787_at	NM_007208
2.54	2.53	0.01	9.40E-01	9.83E-01	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	chr3p25.3	234741_at	NM_001001331 /// NM_001683
2.33	2.32	0.01	9.40E-01	9.83E-01	C10orf67	chromosome 10 open reading frame 67	chr10p12.2	1553844_a_at	NM_153714
3.49	3.48	0.01	9.40E-01	9.83E-01	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	chr16q24.1	1555809_at	NM_031476
2.00	1.99	0.01	9.40E-01	9.83E-01	HAVCR1	hepatitis A virus cellular receptor 1	chr5q33.2	207052_at	NM_001099414 /// NM_012206
5.82	5.78	0.04	9.40E-01	9.83E-01	LY96	lymphocyte antigen 96	chr8q21.11	206584_at	NM_015364
2.71	2.70	0.01	9.40E-01	9.83E-01	LYRM2	LYR motif containing 2	chr6q14.2-q16.1	233763_at	NM_020466
6.77	6.76	0.01	9.40E-01	9.83E-01	TIMM9	translocase of inner mitochondrial membrane 9 homolog (yeast)	chr14q21	218316_at	NM_012460
1.81	1.81	0.01	9.40E-01	9.83E-01	---	---	---	1556625_a_at	---
2.65	2.63	0.01	9.40E-01	9.83E-01	---	---	---	241916_at	---
5.50	5.48	0.03	9.40E-01	9.83E-01	RSL1D1	ribosomal L1 domain containing 1	chr16p13.13	213750_at	NM_015659
3.25	3.24	0.02	9.40E-01	9.83E-01	ZMYND15	zinc finger, MYND-type containing 15	chr17p13.2	223683_at	NM_032265
3.46	3.44	0.02	9.40E-01	9.84E-01	---	---	---	238561_s_at	---
2.04	2.03	0.01	9.40E-01	9.84E-01	TRGV5	T cell receptor gamma variable 5	chr7p14	216298_at	---
1.87	1.86	0.01	9.40E-01	9.84E-01	---	---	---	244551_at	---
2.74	2.72	0.02	9.40E-01	9.84E-01	NUP160	nucleoporin 160kDa	chr11p11.2	214962_s_at	NM_015231
4.09	4.07	0.02	9.41E-01	9.84E-01	NEK11	NIMA (never in mitosis gene a)- related kinase 11	chr3q22.1	219542_at	NM_024800 /// NM_145910
2.15	2.14	0.01	9.41E-01	9.84E-01	C13orf36	chromosome 13 open reading frame 36	chr13q13.3	241672_at	NM_203451
1.94	1.93	0.01	9.41E-01	9.84E-01	---	---	---	243563_at	---
9.01	8.99	0.02	9.41E-01	9.84E-01	DHRS7	dehydrogenase/reductase (SDR family) member 7	chr14q23.1	210788_s_at	NM_016029
2.76	2.75	0.01	9.41E-01	9.84E-01	KCNA6	potassium voltage-gated channel, shaker-related subfamily, member 6	chr12p13	1553347_s_at	NM_002235
2.39	2.38	0.01	9.41E-01	9.84E-01	HHLA3	HERV-H LTR-associating 3	chr1p31.1	234703_at	NM_001031693 /// NM_001036645 /// NM_001036646 /// NM_007071
2.38	2.37	0.01	9.41E-01	9.84E-01	---	---	---	237743_at	---
4.77	4.74	0.02	9.41E-01	9.84E-01	SLCO2B1	solute carrier organic anion transporter family, member 2B1	chr11q13	203472_s_at	NM_007256
2.97	2.96	0.01	9.41E-01	9.84E-01	FAM38B2	family with sequence similarity 38, member B2	chr18p11.22	1562488_at	XM_001130754
3.97	3.96	0.01	9.41E-01	9.84E-01	---	---	---	1559753_at	---
4.07	4.05	0.02	9.41E-01	9.84E-01	LOC400099	hypothetical gene supported by BC024195	chr13q12.11	230136_at	XR_040794 /// XR_040795 /// XR_040796
4.95	4.93	0.02	9.41E-01	9.84E-01	CXorf56	chromosome X open reading frame 56	chrXq23	219805_at	NM_022101
3.26	3.25	0.01	9.41E-01	9.84E-01	ACOT11	acyl-CoA thioesterase 11	chr1p32.3	1555321_at	NM_015547 /// NM_147161
3.49	3.48	0.02	9.41E-01	9.84E-01	---	---	---	229297_at	---
8.95	8.91	0.04	9.41E-01	9.84E-01	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	chr9q21.13	212224_at	NM_000689
2.16	2.15	0.01	9.41E-01	9.84E-01	C4orf19	chromosome 4 open reading frame 19	chr4p14	235350_at	NM_001104629 /// NM_018302

1.98	1.97	0.01	9.41E-01	9.84E-01	---	---	---	237874_at	---
2.19	2.18	0.01	9.41E-01	9.84E-01	TDRD5	tudor domain containing 5	chr1q25.2	231104_at	NM_173533
1.98	1.97	0.01	9.41E-01	9.84E-01	CLLU1	chronic lymphocytic leukemia up-regulated 1	chr12q22	1558185_at	NM_001025233
4.07	4.06	0.01	9.41E-01	9.84E-01	LOC100132357 /// LOC100132784	similar to hCG1656091 /// similar to hCG1795400	chr9p11.2 /// chr9q12	239702_x_at	XM_001714380 /// XM_001720461
3.72	3.69	0.04	9.42E-01	9.84E-01	LOC100132181 /// LOC389831	hypothetical protein LOC100132181 /// hypothetical gene supported by AL713796	---	225062_at	XM_001722051
2.08	2.07	0.01	9.42E-01	9.84E-01	LRRC40	Leucine rich repeat containing 40	chr1p31.1	1566449_at	NM_017768
3.54	3.50	0.04	9.42E-01	9.84E-01	---	---	---	232600_at	---
2.92	2.91	0.01	9.42E-01	9.84E-01	SSR3	Signal sequence receptor, gamma (translocon-associated protein gamma)	chr3q25.31	237817_at	NM_007107
1.97	1.97	0.01	9.42E-01	9.84E-01	---	---	---	AFFX-TrpnX-3_at	---
2.30	2.29	0.01	9.42E-01	9.84E-01	ZFHX4	zinc finger homeobox 4	chr8q21.11	1559270_at	NM_024721
2.06	2.05	0.01	9.42E-01	9.84E-01	---	---	---	215290_at	---
2.08	2.07	0.01	9.42E-01	9.84E-01	NAG18	NAG18 mRNA	chr19q13.4	210496_at	NR_002568
6.81	6.80	0.02	9.42E-01	9.84E-01	NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)	chr8q24.13	226536_at	NM_173685
6.56	6.54	0.02	9.42E-01	9.84E-01	SRP54	signal recognition particle 54kDa	chr14q13.2	203605_at	NM_003136
3.66	3.64	0.01	9.42E-01	9.84E-01	---	---	---	242533_at	---
4.15	4.13	0.02	9.42E-01	9.84E-01	FOXP4	forkhead box P4	chr6p21.1	227120_at	NM_001012426 /// NM_001012427 /// NM_138457
2.30	2.30	0.01	9.42E-01	9.84E-01	---	---	---	241132_at	---
6.70	6.68	0.02	9.42E-01	9.84E-01	CNOT2	CCR4-NOT transcription complex, subunit 2	chr12q15	217798_at	NM_014515
5.73	5.71	0.02	9.42E-01	9.84E-01	PDK2	pyruvate dehydrogenase kinase, isozyme 2	chr17q21.33	213724_s_at	NM_002611
4.71	4.69	0.02	9.42E-01	9.84E-01	USH1G	Usher syndrome 1G (autosomal recessive)	chr17q25.1	1553263_at	NM_173477
2.46	2.45	0.02	9.42E-01	9.84E-01	ZNF273	zinc finger protein 273	chr7q11.21	243661_at	NM_021148 /// NR_003099
2.42	2.41	0.01	9.42E-01	9.84E-01	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	chr20q13.2	205287_s_at	NM_003222
3.31	3.30	0.01	9.42E-01	9.84E-01	HNF4A	hepatocyte nuclear factor 4, alpha	chr20q12-q13.1	214851_at	NM_000457 /// NM_001030003 /// NM_001030004 /// NM_175914 /// NM_178849 /// NM_178850
2.68	2.67	0.01	9.42E-01	9.84E-01	ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18	chr16q23	1553234_at	NM_199355
2.58	2.57	0.01	9.42E-01	9.84E-01	---	---	---	1558666_at	---
6.97	6.95	0.02	9.42E-01	9.84E-01	TSPAN17	tetraspanin 17	chr5q35.3	225235_at	NM_001006616 /// NM_012171 /// NM_130465
2.33	2.32	0.01	9.42E-01	9.84E-01	---	---	---	220881_at	---
2.21	2.19	0.01	9.43E-01	9.84E-01	---	---	---	244690_at	---
2.69	2.68	0.01	9.43E-01	9.84E-01	ESD	Esterase D/formylglutathione hydrolase	chr13q14.1-q14.2	215095_at	NM_001984
4.80	4.79	0.01	9.43E-01	9.84E-01	C12orf65	chromosome 12 open reading frame 65	chr12q24.31	223476_s_at	NM_152269
4.12	4.09	0.02	9.43E-01	9.84E-01	NKG7	natural killer cell group 7 sequence	chr19q13.33	213915_at	NM_005601
5.63	5.61	0.02	9.43E-01	9.84E-01	---	---	---	228638_at	---
2.28	2.27	0.01	9.43E-01	9.84E-01	TXNL1	Thioredoxin-like 1	chr18q21.31	243664_at	NM_004786
5.52	5.48	0.04	9.43E-01	9.84E-01	ANKRD28	ankyrin repeat domain 28	chr3p24.3	226025_at	NM_015199
3.20	3.17	0.02	9.43E-01	9.84E-01	SRGN	serglycin	chr10q22.1	1554676_at	NM_002727
6.72	6.70	0.02	9.43E-01	9.84E-01	KIAA1033	KIAA1033	chr12q24.11	212795_at	NM_015275
1.74	1.73	0.01	9.43E-01	9.84E-01	---	---	---	1559612_at	---
2.77	2.76	0.01	9.43E-01	9.84E-01	SLC28A3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	chr9q22.2	220475_at	NM_022127
2.63	2.61	0.02	9.43E-01	9.84E-01	GUF1	GUF1 GTPase homolog (S. cerevisiae)	chr4p13	218884_s_at	NM_021927
2.25	2.24	0.01	9.43E-01	9.84E-01	---	---	---	244258_at	---
2.16	2.15	0.01	9.43E-01	9.84E-01	RNMT	RNA (guanine-7-) methyltransferase	chr18p11.22-p11.23	202684_s_at	NM_003799
3.23	3.21	0.02	9.43E-01	9.84E-01	MLF1IP	MLF1 interacting protein	chr4q35.1	218883_s_at	NM_024629

6.30	6.27	0.02	9.43E-01	9.84E-01	SMTN	smoothelin	chr22q12.2	209427_at	NM_006932 /// NM_134269 /// NM_134270																				
3.08	3.07	0.01	9.43E-01	9.84E-01	THBD	thrombomodulin	chr20p11.2	237252_at	NM_000361																				
2.33	2.32	0.01	9.44E-01	9.84E-01	DNAH11	dynein, axonemal, heavy chain 11	chr7p21	1560416_at	NM_003777																				
8.02	8.01	0.01	9.44E-01	9.84E-01	FUCA2	fucosidase, alpha-L- 2, plasma	chr6q24	223120_at	NM_032020																				
2.83	2.81	0.02	9.44E-01	9.84E-01	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	chr14q32.2	219164_s_at	NM_018036																				
2.61	2.58	0.03	9.44E-01	9.84E-01	HOXB8	homeobox B8	chr17q21.3	229667_s_at	NM_024016																				
2.34	2.33	0.01	9.44E-01	9.84E-01	FBXL22	F-box and leucine-rich repeat protein 22	chr15q22.31	241350_at	NM_203373																				
2.88	2.87	0.01	9.44E-01	9.84E-01	THRSP	thyroid hormone responsive (SPOT14 homolog, rat)	chr11q13.5	1553583_a_at	NM_003251																				
5.04	5.03	0.01	9.44E-01	9.84E-01	ZW10	ZW10, kinetochore associated, homolog (Drosophila)	chr11q23.2	204812_at	NM_004724																				
2.58	2.56	0.01	9.44E-01	9.84E-01	LOC146053 /// LOC400652 /// LOC439992 /// LOC643932 /// LOC646527 /// RPS3A	similar to 40S ribosomal protein S3a /// similar to ribosomal protein S3A /// similar to v-fos transformation effector protein /// similar to ribosomal protein S3A /// similar to ribosomal protein S3A /// ribosomal protein S3A	chr10q23.1 /// chr13q12.13 /// chr15q15.2 /// chr18q21.32 /// chr4q31.2-q31.3 /// chr5q14.1	216823_at	NM_001006 /// XM_001723347 /// XM_001723350 /// XM_495839 /// XM_926528 /// XM_937069 /// XM_943171 /// XR_016632 /// XR_017187 /// XR_017289 /// XR_018891 /// XR_019418 /// XR_019637 /// XR_038216 /// XR_038320 /// XR_038326 /// XR_038859 /// XR_038913																				
2.41	2.40	0.01	9.44E-01	9.84E-01	MOBP	myelin-associated oligodendrocyte basic protein	chr3p22.1	242765_at	NM_182935 /// NR_003090																				
4.35	4.34	0.01	9.44E-01	9.85E-01	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	chr20pter-q12	208725_at	NM_003908																				
3.81	3.80	0.01	9.44E-01	9.85E-01	LENG9	leukocyte receptor cluster (LRC) member 9	chr19q13.4	1554589_at	NM_198988																				
2.19	2.19	0.01	9.44E-01	9.85E-01	---	---	---	AFFX-DapX-M_at	---																				
7.86	7.84	0.01	9.44E-01	9.85E-01	SND1	staphylococcal nuclease and tudor domain containing 1	chr7q31.3	201622_at	NM_014390																				
2.47	2.46	0.01	9.44E-01	9.85E-01	---	---	---	234667_at	---																				
6.12	6.11	0.02	9.44E-01	9.85E-01	DLG1	discs, large homolog 1 (Drosophila)	chr3q29	202515_at	NM_001098424 /// NM_004087																				
5.60	5.58	0.02	9.44E-01	9.85E-01	---	---	---	235767_x_at	---																				

2.09	2.08	0.01	9.44E-01	9.85E-01	NRG1	neuregulin 1	chr8p12	208231_at	NM_004495 /// NM_013956 /// NM_013957 /// NM_013958 /// NM_013959 /// NM_013960 /// NM_013961 /// NM_013962 /// NM_013964																				
4.35	4.34	0.02	9.44E-01	9.85E-01	CDH15	cadherin 15, M-cadherin (myotubule)	chr16q24.3	206327_s_at	NM_004933																				
5.38	5.36	0.03	9.44E-01	9.85E-01	---	---	---	1560327_at	---																				
8.54	8.53	0.01	9.44E-01	9.85E-01	GANAB	glucosidase, alpha; neutral AB	chr11q12.3	214626_s_at	NM_198334 /// NM_198335																				
2.37	2.36	0.01	9.44E-01	9.85E-01	---	---	---	241444_at	---																				
2.27	2.27	0.01	9.44E-01	9.85E-01	GRM8	glutamate receptor, metabotropic 8	chr7q31.3-q32.1	216255_s_at	NM_000845 /// NM_001127323 /// NM_001127326																				
2.94	2.93	0.01	9.45E-01	9.85E-01	DNAH10	dynein, axonemal, heavy chain 10	chr12q24.31	1562462_at	NM_001083900 /// NM_207437																				
9.27	9.25	0.01	9.45E-01	9.85E-01	HLA-G	major histocompatibility complex, class I, G	chr6p21.3	211528_x_at	NM_002127																				
2.17	2.16	0.01	9.45E-01	9.85E-01	---	---	---	1561083_at	---																				
3.35	3.34	0.01	9.45E-01	9.85E-01	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	chr12q21.31	206973_at	NM_003625																				
3.26	3.25	0.01	9.45E-01	9.85E-01	STK19	serine/threonine kinase 19	chr6p21.3	243719_at	NM_004197 /// NM_032454																				
1.93	1.92	0.01	9.45E-01	9.85E-01	---	---	---	1556592_at	---																				
8.69	8.66	0.03	9.45E-01	9.85E-01	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	chr3p24.3	201810_s_at	NM_001018009 /// NM_004844																				
2.36	2.35	0.01	9.45E-01	9.85E-01	SFRP4	secreted frizzled-related protein 4	chr7p14.1	204052_s_at	NM_003014																				
2.93	2.92	0.01	9.45E-01	9.85E-01	C22orf36	Chromosome 22 open reading frame 36	chr22q11.23	217668_at	NM_207644																				
5.40	5.38	0.02	9.45E-01	9.85E-01	FGFR1	fibroblast growth factor receptor 1	chr8p11.2-p11.1	211535_s_at	NM_015850 /// NM_023105 /// NM_023106 /// NM_023107 /// NM_023108 /// NM_023110 /// NM_023111																				
4.64	4.63	0.02	9.45E-01	9.85E-01	RTEL1	regulator of telomere elongation helicase 1	chr20q13.3	216325_x_at	NM_016434 /// NM_032957																				
3.94	3.93	0.01	9.45E-01	9.85E-01	LOC728723	hypothetical LOC728723	chr5q14.1	241423_at	XR_042120 /// XR_042121 /// XR_042122																				
5.87	5.84	0.02	9.45E-01	9.85E-01	RBMS1	RNA binding motif, single stranded interacting protein 1	chr2q24.2	225265_at	NM_002897 /// NM_016836 /// NM_016839																				
2.82	2.81	0.01	9.45E-01	9.85E-01	---	---	---	229188_s_at	---																				
4.25	4.22	0.03	9.45E-01	9.85E-01	AIM1	absent in melanoma 1	chr6q21	212543_at	NM_001624																				
2.19	2.18	0.01	9.45E-01	9.85E-01	ZNF440	Zinc finger protein 440	chr19p13.2	215892_at	NM_152357																				
3.32	3.31	0.01	9.45E-01	9.85E-01	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	chr13q34	1563407_x_at	NM_000705																				
1.96	1.96	0.01	9.45E-01	9.85E-01	C15orf33	chromosome 15 open reading frame 33	chr15q21.1-q21.2	1553799_at	NM_152647																				

2.39	2.37	0.01	9.45E-01	9.85E-01	MORN1	MORN repeat containing 1	chr1p36.33-p36.32	1554268_at	NM_024848
3.80	3.79	0.01	9.45E-01	9.85E-01	FAM123B	family with sequence similarity 123B	chrXq11.1	1552882_a_at	NM_152424
2.99	2.98	0.01	9.45E-01	9.85E-01	CG012	hypothetical gene CG012	chr13q12-q13	215318_at	---
2.25	2.24	0.01	9.45E-01	9.85E-01	---	---	---	1569307_s_at	---
2.93	2.91	0.01	9.45E-01	9.85E-01	FLJ33534	hypothetical LOC285150	chr2p25.1	1564233_at	XR_040331 /// XR_040332 /// XR_040333
2.90	2.89	0.01	9.45E-01	9.85E-01	TFF1	trefoil factor 1	chr21q22.3	205009_at	NM_003225
3.03	3.01	0.01	9.45E-01	9.85E-01	C18orf25	chromosome 18 open reading frame 25	chr18q21.1	1553686_at	NM_001008239 /// NM_145055
3.77	3.75	0.01	9.46E-01	9.85E-01	FLJ36031	hypothetical protein FLJ36031	chr7q22.3	227883_at	NM_175884
2.41	2.40	0.01	9.46E-01	9.85E-01	EMILIN2	Elastin microfibril interfacer 2	chr18p11.3	221980_at	NM_032048
7.95	7.93	0.01	9.46E-01	9.85E-01	URM1	ubiquitin related modifier 1 homolog (S. cerevisiae)	chr9q34.11	208101_s_at	NM_030914
4.59	4.58	0.01	9.46E-01	9.85E-01	---	---	---	1556468_at	---
5.79	5.77	0.02	9.46E-01	9.85E-01	CHCHD6	coiled-coil-helix-coiled-coil-helix domain containing 6	chr3q21.3	224462_s_at	NM_032343
4.82	4.80	0.01	9.46E-01	9.85E-01	tcag7.907	hypothetical LOC402483	chr7q32.1	238678_at	XR_040932 /// XR_040933 /// XR_040934 /// XR_040935
3.18	3.18	0.01	9.46E-01	9.85E-01	---	---	---	216423_at	---
2.16	2.15	0.01	9.46E-01	9.85E-01	CHRM3	cholinergic receptor, muscarinic 3	chr1q43	1559634_at	NM_000740
2.01	2.00	0.01	9.46E-01	9.85E-01	---	---	---	1563033_x_at	---
4.78	4.76	0.02	9.46E-01	9.85E-01	TMEM38B	transmembrane protein 38B	chr9q31.2	218772_x_at	NM_018112
3.95	3.93	0.02	9.46E-01	9.85E-01	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	chr20q11.23	212750_at	NM_015568
2.68	2.67	0.01	9.46E-01	9.85E-01	---	---	---	1557495_at	---
1.87	1.86	0.01	9.46E-01	9.85E-01	---	---	---	242107_x_at	---
2.75	2.74	0.01	9.46E-01	9.85E-01	MGC39821	hypothetical protein MGC39821	chr19p13.11	1569318_at	XR_041448 /// XR_041449 /// XR_041450
4.45	4.42	0.02	9.46E-01	9.85E-01	NDFIP2	Nedd4 family interacting protein 2	chr13q31.1	224801_at	NM_019080
2.71	2.70	0.01	9.46E-01	9.85E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	214541_s_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855
3.56	3.55	0.01	9.46E-01	9.85E-01	PROP1	PROP paired-like homeobox 1	chr5q35.3	211223_at	NM_006261
3.60	3.58	0.03	9.46E-01	9.85E-01	CUL4B	cullin 4B	chrXq23	215997_s_at	NM_001079872 /// NM_003588
3.90	3.89	0.01	9.46E-01	9.85E-01	PTPN3	protein tyrosine phosphatase, non-receptor type 3	chr9q31	227944_at	NM_002829
2.31	2.30	0.01	9.46E-01	9.85E-01	---	---	---	239465_at	---
3.70	3.69	0.02	9.46E-01	9.85E-01	RAB11B	RAB11B, member RAS oncogene family	chr19p13.2	34478_at	NM_004218
2.10	2.09	0.01	9.46E-01	9.85E-01	XRN1	5'-3' exoribonuclease 1	chr3q23	1570394_at	NM_001042604 /// NM_019001
3.62	3.61	0.01	9.47E-01	9.85E-01	FAM132A	family with sequence similarity 132, member A	chr1p36.33	243292_at	NM_001014980
2.03	2.02	0.01	9.47E-01	9.85E-01	BCAS1	Breast carcinoma amplified sequence 1	chr20q13.2	234221_at	NM_003657
3.88	3.87	0.01	9.47E-01	9.85E-01	E2F2	E2F transcription factor 2	chr1p36	228361_at	NM_004091
2.16	2.15	0.01	9.47E-01	9.85E-01	FLJ42709	hypothetical gene supported by AK124699	chr5q15	1556695_a_at	NR_015369 /// NR_021490 /// NR_021491 /// XM_499008 /// XM_943794
2.34	2.33	0.01	9.47E-01	9.85E-01	---	---	---	240470_at	---
3.09	3.08	0.01	9.47E-01	9.85E-01	GSC	goosecoid homeobox	chr14q32.1	1552338_at	NM_173849
4.95	4.91	0.03	9.47E-01	9.85E-01	CAPN7	calpain 7	chr3p24	203356_at	NM_014296
2.38	2.37	0.01	9.47E-01	9.85E-01	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	chr6q24-q25.1	1570425_s_at	NM_004690

2.92	2.91	0.01	9.47E-01	9.85E-01	KLHL29	kelch-like 29 (Drosophila)	chr2p24.1	1554262_s_at	XM_001717454 /// XM_001717533 /// XM_940375																				
1.97	1.96	0.01	9.47E-01	9.85E-01	---	---	---	1562949_at	---																				
3.79	3.77	0.02	9.47E-01	9.85E-01	THAP10	THAP domain containing 10	chr15q23	219596_at	NM_020147																				
2.05	2.04	0.01	9.47E-01	9.86E-01	C18orf54	chromosome 18 open reading frame 54	chr18q21.2	1553651_at	NM_173529																				
3.77	3.76	0.01	9.47E-01	9.86E-01	KIAA0146	KIAA0146	chr8q11.21	212523_s_at	NM_001080394																				
2.68	2.68	0.01	9.47E-01	9.86E-01	PUS10	pseudouridylate synthase 10	chr2p16.1	1553280_at	NM_144709																				
2.29	2.29	0.01	9.47E-01	9.86E-01	CAST	Calpastatin	chr5q15	1564010_at	NM_001042440 /// NM_001042441 /// NM_001042442 /// NM_001042443 /// NM_001042444 /// NM_001042445 /// NM_001042446 /// NM_001750 /// NM_173060 /// NM_173061 /// NM_173063																				
4.83	4.81	0.01	9.47E-01	9.86E-01	TINAGL1	tubulointerstitial nephritis antigen-like 1	chr1p35.2	219058_x_at	NM_022164																				
6.92	6.89	0.03	9.48E-01	9.86E-01	SLCO2A1	solute carrier organic anion transporter family, member 2A1	chr3q21	204368_at	NM_005630																				
2.72	2.71	0.01	9.48E-01	9.86E-01	---	---	---	236000_s_at	---																				
2.67	2.66	0.01	9.48E-01	9.86E-01	GPX2	glutathione peroxidase 2 (gastrointestinal)	chr14q24.1	239595_at	NM_002083																				
5.08	5.05	0.03	9.48E-01	9.86E-01	CHN2	chimerin (chimaerin) 2	chr7p15.3	213385_at	NM_001039936 /// NM_004067																				
2.10	2.09	0.01	9.48E-01	9.86E-01	---	---	---	240852_at	---																				
2.35	2.34	0.01	9.48E-01	9.86E-01	---	---	---	240237_at	---																				
2.10	2.09	0.01	9.48E-01	9.86E-01	IQCA1	IQ motif containing with AAA domain 1	chr2q37.2-q37.3	238584_at	NM_024726																				
2.20	2.19	0.01	9.48E-01	9.86E-01	RASSF6	Ras association (RalGDS/AF-6) domain family member 6	chr4q13.3	233463_at	NM_177532 /// NM_201431																				
2.13	2.12	0.01	9.48E-01	9.86E-01	---	---	---	243920_x_at	---																				
2.51	2.50	0.01	9.48E-01	9.86E-01	RAB39	RAB39, member RAS oncogene family	---	1554800_at	NM_017516																				
2.25	2.24	0.01	9.48E-01	9.86E-01	HMGA2	high mobility group AT-hook 2	chr12q15	208025_s_at	NM_003483 /// NM_003484																				
7.17	7.15	0.02	9.48E-01	9.86E-01	CORO1C	coronin, actin binding protein, 1C	chr12q24.1	221676_s_at	NM_014325																				
6.09	6.05	0.03	9.48E-01	9.86E-01	---	---	---	1569540_at	---																				
4.94	4.92	0.02	9.48E-01	9.86E-01	ARHGAP5	Rho GTPase activating protein 5	chr14q12	233849_s_at	NM_001030055 /// NM_001173																				
2.74	2.73	0.01	9.48E-01	9.86E-01	RIMS1	regulating synaptic membrane exocytosis 1	chr6q12-q13	216184_s_at	NM_014989																				
2.49	2.47	0.01	9.48E-01	9.86E-01	---	---	---	1561738_at	---																				
2.33	2.32	0.01	9.48E-01	9.86E-01	MEP1B	meprin A, beta	chr18q12.2-q12.3	207251_at	NM_005925																				
2.46	2.45	0.01	9.48E-01	9.86E-01	DPP6	dipeptidyl-peptidase 6	chr7q36.2	1554796_at	NM_001039350 /// NM_001936 /// NM_130797																				
2.65	2.63	0.02	9.48E-01	9.86E-01	HEPACAM	hepatocyte cell adhesion molecule	chr11q24.2	238003_at	NM_152722																				
2.18	2.17	0.01	9.49E-01	9.86E-01	---	---	---	1556469_s_at	---																				

5.27	5.24	0.03	9.49E-01	9.86E-01	DTNA	dystrobrevin, alpha	chr18q12	227084_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981																				
5.96	5.94	0.02	9.49E-01	9.86E-01	ZNF618	zinc finger protein 618	chr9q32	226592_at	NM_133374																				
2.20	2.19	0.01	9.49E-01	9.86E-01	FABP6	fatty acid binding protein 6, ileal	chr5q33.3-q34	1566124_a_at	NM_001040442 /// NM_001130958 /// NM_001445																				
5.27	5.24	0.03	9.49E-01	9.86E-01	KATNA1	katanin p60 (ATPase-containing) subunit A 1	chr6q25.1	205526_s_at	NM_007044																				
5.75	5.74	0.02	9.49E-01	9.86E-01	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	chr1q43	203774_at	NM_000254																				
7.15	7.13	0.02	9.49E-01	9.86E-01	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	chr20p13	207713_s_at	NM_006462 /// NM_031229																				
2.87	2.86	0.01	9.49E-01	9.86E-01	---	---	---	240290_at	---																				
3.09	3.08	0.01	9.49E-01	9.86E-01	---	---	---	214423_x_at	---																				
2.48	2.47	0.01	9.49E-01	9.86E-01	LOC389906	Hypothetical protein LOC441528	chrXp22.33	1564639_at	XM_001713861 /// XM_928240 /// XM_942518																				
4.25	4.23	0.02	9.49E-01	9.86E-01	ABLIM2	actin binding LIM protein family, member 2	chr4p16-p15	228132_at	NM_001130083 /// NM_001130084 /// NM_001130085 /// NM_001130086 /// NM_001130087 /// NM_001130088 /// NM_032432																				
5.46	5.44	0.02	9.49E-01	9.86E-01	LYRM4	LYR motif containing 4	chr6p25.1	222672_at	NM_020408																				
2.47	2.46	0.01	9.49E-01	9.86E-01	SPIRE2	spire homolog 2 (Drosophila)	chr16q24	1569723_a_at	NM_032451																				
2.27	2.26	0.01	9.49E-01	9.86E-01	NAV2	neuron navigator 2	chr11p15.1	1567357_at	NM_001111018 /// NM_001111019 /// NM_145117 /// NM_182964																				
4.89	4.87	0.02	9.49E-01	9.86E-01	ZNF84	zinc finger protein 84	chr12q24.33	204453_at	NM_001127372 /// NM_003428																				
2.29	2.28	0.01	9.49E-01	9.86E-01	SLC26A4	solute carrier family 26, member 4	chr7q31	206529_x_at	NM_000441																				
2.93	2.92	0.01	9.49E-01	9.86E-01	---	---	---	240219_at	---																				
1.94	1.93	0.01	9.49E-01	9.86E-01	---	---	---	243478_at	---																				
2.23	2.22	0.01	9.49E-01	9.86E-01	ZNF595	Zinc finger protein 595	chr4p16.3	1570038_at	NM_182524																				
2.52	2.51	0.01	9.49E-01	9.86E-01	SLC25A2	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2	chr5q31	224166_at	NM_031947																				
1.87	1.86	0.01	9.49E-01	9.86E-01	SOBP	Sine oculis binding protein homolog (Drosophila)	chr6q21	233766_at	NM_018013																				
2.69	2.69	0.01	9.49E-01	9.86E-01	LOC285857	hypothetical protein LOC285857	chr6p21.1	1564125_at	---																				
2.38	2.37	0.01	9.49E-01	9.86E-01	GLYAT	glycine-N-acyltransferase	chr11q12.1	206930_at	NM_005838 /// NM_201648																				
6.31	6.29	0.02	9.50E-01	9.86E-01	LUC7L2	LUC7-like 2 (S. cerevisiae)	chr7q34	226758_at	NM_016019																				
2.73	2.72	0.01	9.50E-01	9.86E-01	KCNA1	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	chr12p13.32	208479_at	NM_000217																				
3.73	3.72	0.01	9.50E-01	9.86E-01	---	---	---	234565_x_at	---																				
2.07	2.06	0.01	9.50E-01	9.86E-01	SH3GL3	SH3-domain GRB2-like 3	chr15q24	211565_at	NM_003027																				
3.25	3.24	0.01	9.50E-01	9.86E-01	---	---	---	244605_at	---																				

2.10	2.09	0.01	9.50E-01	9.86E-01	RBM35A	RNA binding motif protein 35A	chr8q22.1	225846_at	NM_001034915 /// NM_001122825 /// NM_001122826 /// NM_001122827 /// NM_017697																			
6.03	6.01	0.02	9.50E-01	9.86E-01	C9orf69	chromosome 9 open reading frame 69	chr9q34.3	224962_at	NM_152833																			
6.61	6.59	0.02	9.50E-01	9.86E-01	GAMT	guanidinoacetate N-methyltransferase	chr19p13.3	205354_at	NM_000156 /// NM_138924																			
9.35	9.33	0.02	9.50E-01	9.86E-01	UBXN6	UBX domain protein 6	chr19p13	223012_at	NM_025241																			
5.92	5.91	0.02	9.50E-01	9.86E-01	GIYD1 /// GIYD2 /// SULT1A3 /// SULT1A4	GIY-YIG domain containing 1 /// GIY-YIG domain containing 2 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	chr16p11.2	233334_x_at	NM_001014999 /// NM_001015000 /// NM_001017387 /// NM_001017389 /// NM_001017390 /// NM_001017391 /// NM_003166 /// NM_024044 /// NM_177552 /// NM_178044																			
3.55	3.54	0.01	9.50E-01	9.86E-01	---	---	---	243305_at	---																			
2.37	2.36	0.01	9.50E-01	9.86E-01	LOC728099	hypothetical protein LOC728099	chr13q12.11	1561221_x_at	XR_015256																			
3.94	3.93	0.01	9.50E-01	9.86E-01	---	---	---	227959_at	---																			
4.18	4.17	0.01	9.51E-01	9.86E-01	CDC23	cell division cycle 23 homolog (S. cerevisiae)	chr5q31	202892_at	NM_004661																			
2.59	2.58	0.01	9.51E-01	9.86E-01	---	---	---	1561006_at	---																			
2.74	2.73	0.01	9.51E-01	9.86E-01	---	---	---	1559692_at	---																			
2.58	2.57	0.01	9.51E-01	9.86E-01	LOC285463	hypothetical protein LOC285463	chr4p16.3	1563571_at	---																			
4.76	4.74	0.02	9.51E-01	9.86E-01	TRAM2	translocation associated membrane protein 2	chr6p21.1-p12	202368_s_at	NM_012288																			
2.38	2.37	0.01	9.51E-01	9.86E-01	---	---	---	1559108_at	---																			
8.95	8.93	0.03	9.51E-01	9.86E-01	TPD52L1	tumor protein D52-like 1	chr6q22-q23	210372_s_at	NM_001003395 /// NM_001003396 /// NM_001003397 /// NM_003287																			
3.23	3.22	0.01	9.51E-01	9.86E-01	EXOSC2	exosome component 2	chr9q34	216117_at	NM_014285																			
3.19	3.18	0.01	9.51E-01	9.87E-01	ZNF697	zinc finger protein 697	chr1p12	1553702_at	NM_001080470																			

2.98	2.96	0.01	9.51E-01	9.87E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	206951_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054																			
3.29	3.27	0.01	9.51E-01	9.87E-01	---	---	---	240831_at	---																				
4.11	4.10	0.02	9.51E-01	9.87E-01	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	chr19q13.1-q13.4	214219_x_at	NM_001042600 /// NM_007181																				
2.20	2.19	0.01	9.51E-01	9.87E-01	LOC388907 /// LOC647436 /// RPL5	similar to MSTP030 /// similar to ribosomal protein L5 /// ribosomal protein L5	chr1p22.1 /// chr22q13.2	210034_s_at	NM_000969 /// XM_001722636 /// XM_001722638 /// XM_001724883 /// XM_937113 /// XR_017615 /// XR_037140 /// XR_039555																				
4.35	4.34	0.01	9.51E-01	9.87E-01	FBXL20	F-box and leucine-rich repeat protein 20	chr17q12	239223_s_at	NM_032875																				
2.08	2.07	0.01	9.51E-01	9.87E-01	OR12D3 /// OR5V1	olfactory receptor, family 12, subfamily D, member 3 /// olfactory receptor, family 5, subfamily V, member 1	chr6p22.1	208098_at	NM_030876 /// NM_030959																				
2.51	2.49	0.01	9.51E-01	9.87E-01	OPA3	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	chr19q13.32	238630_at	NM_001017989 /// NM_025136																				
2.30	2.29	0.01	9.51E-01	9.87E-01	LOC91431	Prematurely terminated mRNA decay factor-like	chr4q25	1565934_at	NM_001099776																				
7.75	7.73	0.02	9.51E-01	9.87E-01	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	chr13q11-q12	223380_s_at	NM_014572																				
2.13	2.13	0.01	9.51E-01	9.87E-01	IL17A	interleukin 17A	chr6p12	216876_s_at	NM_002190																				
2.18	2.17	0.01	9.51E-01	9.87E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	1566511_at	NM_012347 /// NM_033480 /// NM_033481																				
2.60	2.58	0.01	9.51E-01	9.87E-01	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	chr1q42.3	1562391_at	NM_152490																				
4.13	4.12	0.01	9.51E-01	9.87E-01	---	---	---	1569416_at	---																				
7.95	7.94	0.01	9.51E-01	9.87E-01	SYF2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	chr1p36.11	202553_s_at	NM_015484 /// NM_207170																				
2.30	2.30	0.01	9.51E-01	9.87E-01	LOC144766	hypothetical LOC144766	chr13q21.31	243986_at	---																				
5.90	5.84	0.06	9.51E-01	9.87E-01	WDR63	WD repeat domain 63	chr1p22.3	243087_at	NM_145172																				

2.45	2.44	0.01	9.51E-01	9.87E-01	HNF4A	hepatocyte nuclear factor 4, alpha	chr20q12-q13.1	230914_at	NM_000457 /// NM_001030003 /// NM_001030004 /// NM_175914 /// NM_178849 /// NM_178850																					
2.15	2.15	0.01	9.51E-01	9.87E-01	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	chr5q22.2	220120_s_at	NM_022140																					
3.21	3.20	0.01	9.51E-01	9.87E-01	C7orf20	Chromosome 7 open reading frame 20	chr7p22.3	224816_at	NM_015949																					
2.29	2.28	0.01	9.51E-01	9.87E-01	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	chr1p34.2	231323_at	NM_002794																					
3.00	2.98	0.01	9.51E-01	9.87E-01	---	---	---	235954_at	---																					
3.96	3.95	0.02	9.52E-01	9.87E-01	ZNF174	zinc finger protein 174	chr16p13.3	205252_at	NM_001032292 /// NM_003450																					
3.34	3.33	0.01	9.52E-01	9.87E-01	---	---	---	236695_at	---																					
2.39	2.38	0.01	9.52E-01	9.87E-01	ASIP	agouti signaling protein, nonagouti homolog (mouse)	chr20q11.2-q12	214498_at	NM_001672																					
3.63	3.62	0.01	9.52E-01	9.87E-01	---	---	---	237412_at	---																					
2.78	2.77	0.01	9.52E-01	9.87E-01	ARHGAP8 /// LOC553158 /// PRR5	Rho GTPase activating protein 8 /// PRR5-ARHGAP8 fusion /// proline rich 5 (renal)	chr22q13 /// chr22q13.31	37117_at	NM_001017526 /// NM_001017528 /// NM_001017529 /// NM_001017530 /// NM_015366 /// NM_181333 /// NM_181334 /// NM_181335																					
5.60	5.58	0.02	9.52E-01	9.87E-01	PRPS1	phosphoribosyl pyrophosphate synthetase 1	chrXq21.32-q24	208447_s_at	NM_002764																					
2.94	2.93	0.01	9.52E-01	9.87E-01	LOC400752	hypothetical gene supported by BC006119	chr1p34.1	1564697_a_at	XM_001133020 /// XM_001133824																					
2.56	2.56	0.01	9.52E-01	9.87E-01	SOX8	SRY (sex determining region Y)-box 8	chr16p13.3	226913_s_at	NM_014587																					
3.66	3.64	0.01	9.52E-01	9.87E-01	---	---	---	235959_at	---																					
5.62	5.61	0.01	9.52E-01	9.87E-01	LAMA5	laminin, alpha 5	chr20q13.2-q13.3	210150_s_at	NM_005560																					
2.24	2.23	0.01	9.52E-01	9.87E-01	hCG_2015435 /// LOC100128554	hypothetical LOC144678 /// hypothetical protein LOC100128554	chr12q24.32	1561294_a_at	XM_001719470 /// XM_001721494 /// XM_001726744 /// XM_378390 /// XM_945548																					
2.01	2.00	0.01	9.52E-01	9.87E-01	EGF	epidermal growth factor (beta-urogastrone)	chr4q25	206254_at	NM_001963																					
2.83	2.82	0.01	9.52E-01	9.87E-01	FMN1	formin 1	chr15q13.3	1570156_s_at	NM_001103184																					
3.05	3.04	0.01	9.52E-01	9.87E-01	RHBDL1	rhomboid, veinlet-like 1 (Drosophila)	chr16p13.3	207383_s_at	NM_003961																					
2.76	2.75	0.01	9.52E-01	9.87E-01	---	---	---	237655_at	---																					
2.38	2.36	0.02	9.52E-01	9.87E-01	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	chrXq25	203873_at	NM_003069 /// NM_139035																					
4.71	4.69	0.02	9.52E-01	9.87E-01	UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	chr12q23	209725_at	NM_014503																					
4.38	4.37	0.01	9.52E-01	9.87E-01	---	---	---	225137_at	---																					
2.49	2.47	0.01	9.52E-01	9.87E-01	---	---	---	1565976_at	---																					
2.97	2.96	0.01	9.52E-01	9.87E-01	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	chr12p12.3	207754_at	NM_007211																					
2.27	2.27	0.01	9.52E-01	9.87E-01	HMMR	hyaluronan-mediated motility receptor (RHAMM)	chr5q33.2-qter	209709_s_at	NM_012484 /// NM_012485																					
2.47	2.46	0.01	9.52E-01	9.87E-01	DBF4B	DBF4 homolog B (S. cerevisiae)	chr17q21.31|17q21	206661_at	NM_025104 /// NM_145663																					
2.07	2.06	0.01	9.52E-01	9.87E-01	GC	group-specific component (vitamin D binding protein)	chr4q12-q13	204965_at	NM_000583																					

5.28	5.27	0.01	9.52E-01	9.87E-01	LDB1	LIM domain binding 1	chr10q24-q25	35160_at	NM_001113407 /// NM_003893																				
7.05	7.03	0.03	9.52E-01	9.87E-01	MAPRE1	microtubule-associated protein, RP/EB family, member 1	chr20q11.1-q11.23	200712_s_at	NM_012325																				
1.95	1.95	0.01	9.53E-01	9.87E-01	---	---	---	242948_x_at	---																				
2.81	2.80	0.01	9.53E-01	9.87E-01	ZNF765	zinc finger protein 765	chr19q13.41	223897_at	NM_001040185																				
2.74	2.72	0.01	9.53E-01	9.87E-01	---	---	---	240150_at	---																				
5.50	5.48	0.02	9.53E-01	9.87E-01	WDFY3	WD repeat and FYVE domain containing 3	chr4q21.23	212602_at	NM_014991 /// NM_178583 /// NM_178585																				
2.29	2.28	0.01	9.53E-01	9.87E-01	---	---	---	241487_at	---																				
1.98	1.97	0.01	9.53E-01	9.87E-01	ITGB6	integrin, beta 6	chr2q24.2	208083_s_at	NM_000888																				
2.43	2.42	0.01	9.53E-01	9.87E-01	---	---	---	1564749_at	---																				
2.11	2.10	0.01	9.53E-01	9.87E-01	---	---	---	233739_at	---																				
2.62	2.61	0.01	9.53E-01	9.87E-01	C21orf113	chromosome 21 open reading frame 113	chr21q22.3	1559254_at	NR_024089																				
2.30	2.29	0.01	9.53E-01	9.87E-01	ZC3H12B	zinc finger CCCH-type containing 12B	chrXq11.1	229234_at	NM_001010888																				
2.14	2.13	0.01	9.53E-01	9.87E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	208169_s_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719																				
5.36	5.35	0.01	9.53E-01	9.87E-01	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	chr1p36.21	1563639_a_at	NM_052929 /// XM_001714211 /// XM_934889 /// XM_946265																				
4.41	4.40	0.01	9.53E-01	9.87E-01	SLC5A8	solute carrier family 5 (iodide transporter), member 8	chr12q23.2	237503_at	NM_145913																				
5.02	5.01	0.01	9.53E-01	9.87E-01	ADAD2	adenosine deaminase domain containing 2	chr16q24.1	236463_at	NM_139174																				
2.63	2.62	0.01	9.54E-01	9.87E-01	FXR2	Fragile X mental retardation, autosomal homolog 2	chr17p13.1	222050_at	NM_004860																				
10.15	10.14	0.01	9.54E-01	9.87E-01	C14orf2	chromosome 14 open reading frame 2	chr14q32.33	210532_s_at	NM_001127393 /// NM_004894																				
2.94	2.92	0.02	9.54E-01	9.87E-01	CEP120	centrosomal protein 120kDa	chr5q23.2	1554606_at	NM_153223																				
2.94	2.93	0.01	9.54E-01	9.87E-01	---	---	---	237699_at	---																				
5.54	5.52	0.02	9.54E-01	9.87E-01	XRN1	5'-3' exoribonuclease 1	chr3q23	233632_s_at	NM_001042604 /// NM_019001																				
2.22	2.21	0.01	9.54E-01	9.87E-01	---	---	---	1570284_x_at	---																				
2.12	2.11	0.01	9.54E-01	9.87E-01	---	---	---	234656_x_at	---																				
2.01	2.01	0.01	9.54E-01	9.87E-01	---	---	---	236451_at	---																				
4.87	4.86	0.02	9.54E-01	9.87E-01	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)	chr6q21-q22	222939_s_at	NM_018593																				
7.08	7.07	0.01	9.54E-01	9.87E-01	C1orf57	chromosome 1 open reading frame 57	chr1q42.2	226813_at	NM_032324																				
2.98	2.97	0.01	9.54E-01	9.87E-01	IL1RN	interleukin 1 receptor antagonist	chr2q14.2	212657_s_at	NM_000577 /// NM_173841 /// NM_173842 /// NM_173843																				
5.22	5.21	0.01	9.54E-01	9.87E-01	CRIPT	cysteine-rich PDZ-binding protein	chr2p21	218643_s_at	NM_014171																				
2.20	2.19	0.01	9.54E-01	9.87E-01	---	---	---	207737_at	---																				
2.04	2.03	0.01	9.54E-01	9.87E-01	LOC100132661	PRO0419	chr3q24	224103_at	XM_001725567																				

6.28	6.27	0.01	9.54E-01	9.87E-01	OCIAD1	OCIA domain containing 1	chr4p11	232644_x_at	NM_001079839 /// NM_001079840 /// NM_001079841 /// NM_001079842 /// NM_017830																			
2.33	2.32	0.01	9.54E-01	9.87E-01	FLJ23519 /// RNH1	hypothetical protein FLJ23519 /// ribonuclease/angiogenin inhibitor 1	chr11p15.5	216798_at	NM_002939 /// NM_203383 /// NM_203384 /// NM_203385 /// NM_203386 /// NM_203387 /// NM_203388 /// NM_203389																			
3.33	3.32	0.01	9.54E-01	9.87E-01	PTCHD2	patched domain containing 2	chr1p36.22	234355_s_at	NM_020780																			
3.26	3.25	0.01	9.54E-01	9.87E-01	C1orf61	Chromosome 1 open reading frame 61	chr1q22	222301_at	NM_006365																			
2.65	2.64	0.01	9.54E-01	9.87E-01	---	---	---	233037_at	---																			
2.15	2.14	0.01	9.54E-01	9.87E-01	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	chr5q12	210836_x_at	NM_001104631 /// NM_006203																			
4.72	4.70	0.02	9.54E-01	9.87E-01	C1orf53	chromosome 1 open reading frame 53	chr1q31.3	1558507_at	NM_001024594																			
2.32	2.32	0.01	9.54E-01	9.87E-01	---	---	---	230429_at	---																			
2.13	2.12	0.01	9.54E-01	9.88E-01	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	chr15q22.31	1555591_at	NM_025049																			
7.88	7.87	0.02	9.55E-01	9.88E-01	PUM1	pumilio homolog 1 (Drosophila)	chr1p35.2	201164_s_at	NM_001020658 /// NM_014676																			
3.20	3.19	0.01	9.55E-01	9.88E-01	C1orf86	Hypothetical protein LOC100129828	chr1p36.33	230649_at	NM_182533 /// XM_001718861																			
2.83	2.82	0.01	9.55E-01	9.88E-01	RARG	retinoic acid receptor, gamma	chr12q13	217178_at	NM_000966 /// NM_001042728																			
5.78	5.77	0.01	9.55E-01	9.88E-01	SGPL1	sphingosine-1-phosphate lyase 1	chr10q21	212322_at	NM_003901																			
2.44	2.43	0.01	9.55E-01	9.88E-01	ZIC4	Zic family member 4	chr3q24	236711_at	NM_032153																			
4.37	4.35	0.02	9.55E-01	9.88E-01	ZNF655	zinc finger protein 655	chr7q22.1	223302_s_at	NM_001009958 /// NM_001009960 /// NM_001083956 /// NM_001085366 /// NM_001085367 /// NM_001085368 /// NM_024061 /// NM_138494																			
9.20	9.19	0.01	9.55E-01	9.88E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	200774_at	NM_014612																			
2.77	2.76	0.01	9.55E-01	9.88E-01	TCEB1P3	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C) pseudogene 3	chr10p14	216426_at	XM_001717201 /// XM_927664 /// XM_938718																			
2.49	2.49	0.01	9.55E-01	9.88E-01	---	---	---	1561104_at	---																			
3.93	3.92	0.01	9.55E-01	9.88E-01	PRR7	proline rich 7 (synaptic)	chr5q35.3	219742_at	NM_030567																			
2.59	2.58	0.01	9.55E-01	9.88E-01	PLCD4	phospholipase C, delta 4	chr2q35	224505_s_at	NM_032726																			
1.98	1.97	0.01	9.55E-01	9.88E-01	NR5A2	nuclear receptor subfamily 5, group A, member 2	chr1q32.1	1560469_at	NM_003822 /// NM_205860																			
6.61	6.59	0.01	9.55E-01	9.88E-01	SRRM2	serine/arginine repetitive matrix 2	chr16p13.3	208610_s_at	NM_016333																			

3.30	3.29	0.01	9.55E-01	9.88E-01	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	chr2q31.3	213416_at	NM_000885
7.24	7.22	0.03	9.55E-01	9.88E-01	SOAT1	sterol O-acyltransferase 1	chr1q25	221561_at	NM_003101
6.78	6.75	0.02	9.55E-01	9.88E-01	USP1	ubiquitin specific peptidase 1	chr1p31.3	202413_s_at	NM_001017415 /// NM_001017416 /// NM_003368
2.45	2.45	0.01	9.55E-01	9.88E-01	NEK6	NIMA (never in mitosis gene a)-related kinase 6	chr9q33.3-q34.11	237406_at	NM_014397
5.11	5.10	0.02	9.56E-01	9.88E-01	---	---	---	229541_at	---
1.95	1.94	0.01	9.56E-01	9.88E-01	---	---	---	231239_at	---
2.54	2.53	0.01	9.56E-01	9.88E-01	AAA1	asthma-associated alternatively spliced gene 1	chr7p14.3	1561490_at	NM_207283 /// NM_207284 /// NM_207285 /// NM_207286 /// NM_207287 /// NM_207288 /// NM_207289 /// NM_207290 /// NR_015356
2.11	2.11	0.01	9.56E-01	9.88E-01	FAM81B	family with sequence similarity 81, member B	chr5q15	240065_at	NM_152548
9.36	9.35	0.01	9.56E-01	9.88E-01	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	chr22q13.2-q13.33	201651_s_at	NM_007229
4.49	4.47	0.02	9.56E-01	9.88E-01	MYO6	myosin VI	chr6q13	210480_s_at	NM_004999
2.13	2.13	0.01	9.56E-01	9.88E-01	NTNG1	netrin G1	chr1p13.3	206713_at	NM_001113226 /// NM_001113228 /// NM_014917
3.00	2.99	0.01	9.56E-01	9.88E-01	PTPN9	Protein tyrosine phosphatase, non-receptor type 9	chr15q24.2	233226_at	NM_002833
2.26	2.25	0.01	9.56E-01	9.88E-01	AQP2	aquaporin 2 (collecting duct)	chr12q12-q13	240285_at	NM_000486
2.25	2.24	0.01	9.56E-01	9.88E-01	ANLN	anillin, actin binding protein	chr7p15-p14	1552619_a_at	NM_018685
4.23	4.20	0.02	9.56E-01	9.88E-01	GNG12	guanine nucleotide binding protein (G protein), gamma 12	chr1p31.3	1555240_s_at	NM_018841
3.35	3.34	0.01	9.56E-01	9.88E-01	---	---	---	239645_at	---
2.50	2.49	0.01	9.56E-01	9.88E-01	CLCN4	chloride channel 4	chrXp22.3	217556_at	NM_001830
3.14	3.13	0.01	9.56E-01	9.88E-01	GPR126	G protein-coupled receptor 126	chr6q24.1	213094_at	NM_001032394 /// NM_001032395 /// NM_020455 /// NM_198569
4.49	4.48	0.01	9.56E-01	9.88E-01	LPAR5	lysophosphatidic acid receptor 5	chr12p13.31	231788_at	NM_020400
2.73	2.72	0.01	9.56E-01	9.88E-01	---	---	---	1557052_at	---
2.54	2.53	0.01	9.56E-01	9.88E-01	LOC255167	hypothetical LOC255167	chr5p15.31	1559033_at	XR_041376 /// XR_041377 /// XR_041378
4.00	3.99	0.01	9.56E-01	9.88E-01	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	chr11q13	1553540_a_at	NM_001532
2.01	2.00	0.01	9.56E-01	9.88E-01	---	---	---	1561016_at	---
2.62	2.60	0.01	9.57E-01	9.88E-01	CYTIP	cytohesin 1 interacting protein	chr2q11.2	209606_at	NM_004288
2.64	2.62	0.01	9.57E-01	9.88E-01	---	---	---	1561595_x_at	---
3.53	3.52	0.01	9.57E-01	9.88E-01	---	---	---	230607_at	---
12.39	12.38	0.02	9.57E-01	9.88E-01	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	chr1p13.1	206294_at	NM_000198
2.71	2.70	0.01	9.57E-01	9.88E-01	---	---	---	1566835_at	---
2.45	2.45	0.01	9.57E-01	9.88E-01	OR4F16 /// OR4F21 /// OR4F29 /// OR4F3	olfactory receptor, family 4, subfamily F, member 16 /// olfactory receptor, family 4, subfamily F, member 21 /// olfactory receptor, family 4, subfamily F, member 29 /// olfactory receptor, family 4, subfamily F, member 3	chr1p36.33 /// chr5q35.3 /// chr8p23.3	234369_at	NM_001005221 /// NM_001005224 /// NM_001005277 /// NM_001005504
2.88	2.87	0.01	9.57E-01	9.88E-01	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	chr4q27	1554768_a_at	NM_002358
2.51	2.51	0.01	9.57E-01	9.88E-01	---	---	---	238292_at	---

2.88	2.87	0.01	9.57E-01	9.88E-01	ATF7	Activating transcription factor 7	chr12q13	235160_at	NM_001130059 /// NM_001130060 /// NM_006856
3.69	3.68	0.01	9.57E-01	9.88E-01	---	---	---	237739_at	---
2.34	2.33	0.01	9.57E-01	9.88E-01	---	---	---	1570181_a_at	---
3.92	3.90	0.01	9.57E-01	9.88E-01	---	---	---	230761_at	---
3.03	3.02	0.01	9.57E-01	9.89E-01	RHCE /// RHD	Rh blood group, CcEe antigens /// Rh blood group, D antigen	chr1p36.11	210430_x_at	NM_001127691 /// NM_016124 /// NM_020485 /// NM_138616 /// NM_138617 /// NM_138618
2.79	2.78	0.01	9.57E-01	9.89E-01	TBL1Y	transducin (beta)-like 1Y-linked	chrYp11.2	211462_s_at	NM_033284 /// NM_134258 /// NM_134259
3.46	3.45	0.01	9.57E-01	9.89E-01	LOC389634	hypothetical LOC389634	chr12p13.31	1560119_at	XR_041469 /// XR_041470 /// XR_041471
2.20	2.19	0.01	9.58E-01	9.89E-01	VSIG1	V-set and immunoglobulin domain containing 1	chrXq22.3	243764_at	NM_182607
2.55	2.54	0.01	9.58E-01	9.89E-01	JPH3	junctophilin 3	chr16q24.3	220188_at	NM_020655
3.91	3.90	0.01	9.58E-01	9.89E-01	SDCCAG8	serologically defined colon cancer antigen 8	chr1q43-q44	227785_at	NM_006642
2.36	2.35	0.01	9.58E-01	9.89E-01	---	---	---	241242_at	---
2.89	2.88	0.01	9.58E-01	9.89E-01	---	---	---	1565595_at	---
2.32	2.31	0.01	9.58E-01	9.89E-01	---	---	---	240574_at	---
2.47	2.46	0.01	9.58E-01	9.89E-01	C20orf187	chromosome 20 open reading frame 187	chr20p12.2	233598_at	XM_001131465
3.31	3.30	0.01	9.58E-01	9.89E-01	CCDC90B	Coiled-coil domain containing 90B	chr11q14.1	222577_at	NM_021825
6.90	6.89	0.02	9.58E-01	9.89E-01	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1	chr6q15	203306_s_at	NM_006416
2.49	2.48	0.01	9.58E-01	9.89E-01	UHRF1BP1L	UHRF1 binding protein 1-like	chr12q23.1	1554292_a_at	NM_001006947 /// NM_015054
6.40	6.39	0.02	9.58E-01	9.89E-01	RPRD2	regulation of nuclear pre-mRNA domain containing 2	chr1q21.2	212553_at	NM_015203
6.17	6.15	0.01	9.58E-01	9.89E-01	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	chr2q11.2	219039_at	NM_017789
7.29	7.27	0.01	9.58E-01	9.89E-01	EFR3A	EFR3 homolog A (S. cerevisiae)	chr8q24.22	212149_at	NM_015137
2.85	2.84	0.01	9.58E-01	9.89E-01	LOC100128484	Hypothetical protein LOC100128484	chr21q22.13	239308_at	XM_001715473 /// XM_001718924
2.64	2.63	0.01	9.58E-01	9.89E-01	USP37	ubiquitin specific peptidase 37	chr2q35	232033_at	NM_020935
2.07	2.07	0.01	9.58E-01	9.89E-01	LOC283697	hypothetical protein LOC283697	chr15q13.1	1557405_at	---
3.21	3.20	0.01	9.58E-01	9.89E-01	GPR114	G protein-coupled receptor 114	chr16q13	229971_at	NM_153837
2.31	2.31	0.01	9.58E-01	9.89E-01	WBSCR16	Williams-Beuren syndrome chromosome region 16	chr7q11.23	1554409_at	NM_030798
4.83	4.82	0.01	9.58E-01	9.89E-01	FOXN3	forkhead box N3	chr14q31.3	205021_s_at	NM_001085471 /// NM_005197
5.60	5.56	0.04	9.58E-01	9.89E-01	CXCL14	chemokine (C-X-C motif) ligand 14	chr5q31	222484_s_at	NM_004887
6.38	6.36	0.02	9.58E-01	9.89E-01	PODXL	podocalyxin-like	chr7q32-q33	201578_at	NM_001018111 /// NM_005397
3.21	3.20	0.01	9.58E-01	9.89E-01	SAMHD1	SAM domain and HD domain 1	chr20pter-q12	1559882_at	NM_015474
2.19	2.18	0.01	9.58E-01	9.89E-01	---	---	---	1560859_at	---
10.89	10.88	0.01	9.58E-01	9.89E-01	ACTB	actin, beta	chr7p15-p12	AFFX-HSAC07/X00351_5_at	NM_001101
2.36	2.36	0.01	9.58E-01	9.89E-01	---	---	---	215976_at	---
3.22	3.21	0.01	9.59E-01	9.89E-01	REG3A	regenerating islet-derived 3 alpha	chr2p12	205815_at	NM_002580 /// NM_138937 /// NM_138938
2.30	2.29	0.01	9.59E-01	9.89E-01	LOC339298	hypothetical protein LOC339298	chr18q23	1561277_at	---
3.34	3.33	0.01	9.59E-01	9.89E-01	SIGLEC9	sialic acid binding Ig-like lectin 9	chr19q13.41	210569_s_at	NM_014441

6.64	6.63	0.01	9.59E-01	9.89E-01	PFKL	phosphofructokinase, liver	chr21q22.3	211065_x_at	NM_001002021 /// NM_002626 /// NR_024108																				
2.54	2.53	0.01	9.59E-01	9.89E-01	EPHA7	EPH receptor A7	chr6q16.1	1554629_at	NM_004440																				
3.23	3.22	0.01	9.59E-01	9.89E-01	CNTNAP1	contactin associated protein 1	chr17q21	219400_at	NM_003632																				
4.34	4.33	0.01	9.59E-01	9.89E-01	C1orf95	chromosome 1 open reading frame 95	chr1q42.12	232104_at	NM_001003665																				
3.51	3.50	0.01	9.59E-01	9.89E-01	---	---	---	216578_at	---																				
2.27	2.27	0.01	9.59E-01	9.89E-01	---	---	---	239766_at	---																				
2.30	2.29	0.01	9.59E-01	9.89E-01	KIAA0020	KIAA0020	chr9p24.2	1570529_at	NM_014878																				
5.11	5.10	0.01	9.59E-01	9.89E-01	GFER	growth factor, augmenter of liver regeneration	chr16p13.3-p13.12	204659_s_at	NM_005262																				
3.81	3.80	0.01	9.59E-01	9.89E-01	MIER3	mesoderm induction early response 1, family member 3	chr5q11.2	228961_at	NM_152622																				
2.88	2.87	0.01	9.59E-01	9.89E-01	FGF22	Fibroblast growth factor 22	chr19p13.3	1566814_at	NM_020637																				
1.94	1.93	0.01	9.59E-01	9.89E-01	---	---	---	243390_at	---																				
2.31	2.30	0.01	9.59E-01	9.89E-01	---	---	---	243032_at	---																				
3.97	3.97	0.01	9.59E-01	9.89E-01	CALCA	calcitonin-related polypeptide alpha	chr11p15.2-p15.1	210728_s_at	NM_001033952 /// NM_001033953 /// NM_001741																				
5.48	5.47	0.01	9.59E-01	9.89E-01	C9orf7	chromosome 9 open reading frame 7	chr9q34	219223_at	NM_017586																				
2.12	2.11	0.01	9.59E-01	9.89E-01	---	---	---	237923_at	---																				
2.48	2.47	0.01	9.60E-01	9.89E-01	---	---	---	1566656_a_at	---																				
5.84	5.83	0.02	9.60E-01	9.89E-01	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	chr10q26.13	226030_at	NM_001609																				
5.40	5.38	0.02	9.60E-01	9.89E-01	NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma	chr18p11.22	225448_at	NM_003826																				
2.27	2.27	0.01	9.60E-01	9.89E-01	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	chr13q14-q21	207135_at	NM_000621																				
2.19	2.19	0.01	9.60E-01	9.89E-01	STBD1	Starch binding domain 1	chr4q24-q25	1570398_at	NM_003943																				
13.05	13.05	0.01	9.60E-01	9.89E-01	TPT1	tumor protein, translationally-controlled 1	chr13q12-q14	212869_x_at	NM_003295																				
2.78	2.78	0.01	9.60E-01	9.89E-01	S100A7A	S100 calcium binding protein A7A	chr1q21.3	232170_at	NM_176823																				
2.48	2.47	0.01	9.60E-01	9.89E-01	DPPA5	developmental pluripotency associated 5	chr6q13	241550_at	NM_001025290																				
2.92	2.91	0.01	9.60E-01	9.89E-01	PPA2	pyrophosphatase (inorganic) 2	chr4q25	1554499_s_at	NM_001034191 /// NM_006903 /// NM_176866 /// NM_176867 /// NM_176869																				
2.96	2.95	0.01	9.60E-01	9.89E-01	---	---	---	1570087_at	---																				
3.74	3.73	0.01	9.60E-01	9.89E-01	---	---	---	234128_at	---																				
2.29	2.28	0.01	9.60E-01	9.89E-01	FLJ11292	hypothetical protein FLJ11292	chr5q14.3	217335_at	NM_018382																				
5.69	5.68	0.01	9.60E-01	9.89E-01	LOC100129502	hypothetical protein LOC100129502	chr15q26.1	228791_at	XM_001720085 /// XM_001721688 /// XM_001721701																				
2.71	2.70	0.01	9.60E-01	9.89E-01	---	---	---	237023_at	---																				
5.47	5.44	0.02	9.60E-01	9.89E-01	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	chr13q12.3	207956_x_at	NM_015032																				
3.21	3.21	0.01	9.60E-01	9.89E-01	MUS81	MUS81 endonuclease homolog (S. cerevisiae)	chr11q13	230870_at	NM_025128																				
2.09	2.08	0.01	9.60E-01	9.89E-01	C21orf131	chromosome 21 open reading frame 131	---	1564392_at	NR_024090																				
5.27	5.26	0.01	9.60E-01	9.89E-01	FBXL18	F-box and leucine-rich repeat protein 18	chr7p22.2	1553359_at	NM_024963																				
2.61	2.60	0.01	9.61E-01	9.89E-01	COL14A1	collagen, type XIV, alpha 1	chr8q23	216866_s_at	NM_021110																				
5.14	5.14	0.01	9.61E-01	9.89E-01	---	---	---	238092_at	---																				
1.96	1.95	0.01	9.61E-01	9.89E-01	BCL2L14	BCL2-like 14 (apoptosis facilitator)	chr12p13-p12	233464_at	NM_030766 /// NM_138722 /// NM_138723 /// NM_138724																				

2.68	2.67	0.01	9.61E-01	9.89E-01	UGT1A1 /// UGT1A10 /// UGT1A3 /// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 family, polypeptide A3 /// UDP glucuronosyltransferase 1 family, polypeptide A4 /// UDP glucuronosyltransferase 1 family, polypeptide A5 /// UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A7 /// UDP glucuronosyltransferase 1 family, polypeptide A8 /// UDP glucuronosyltransferase 1 family, polypeptide A9	chr2q37	208596_s_at	NM_000463 /// NM_001072 /// NM_007120 /// NM_019075 /// NM_019076 /// NM_019077 /// NM_019078 /// NM_019093 /// NM_021027 /// NM_205862																			
3.44	3.43	0.01	9.61E-01	9.89E-01	GFM2	G elongation factor, mitochondrial 2	chr5q13	231917_at	NM_032380 /// NM_170681 /// NM_170691																				
6.15	6.14	0.01	9.61E-01	9.89E-01	ZNF286A	zinc finger protein 286A	chr17p11.2	227077_at	NM_001130842 /// NM_020652																				
2.11	2.10	0.01	9.61E-01	9.89E-01	---	---	---	1569794_at	---																				
2.10	2.09	0.01	9.61E-01	9.89E-01	C6orf170	chromosome 6 open reading frame 170	chr6q22.31	1553726_s_at	NM_152730																				
2.48	2.47	0.01	9.61E-01	9.89E-01	SLC30A1	solute carrier family 30 (zinc transporter), member 1	chr1q32-q41	242716_at	NM_021194																				
2.52	2.51	0.01	9.61E-01	9.89E-01	---	---	---	232627_at	---																				
2.80	2.79	0.01	9.61E-01	9.89E-01	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	chr1p22.3	203018_s_at	NM_014021																				
2.84	2.83	0.01	9.61E-01	9.89E-01	REG1A	regenerating islet-derived 1 alpha	chr2p12	209752_at	NM_002909																				
2.02	2.02	0.01	9.61E-01	9.89E-01	MTHFSD	Methenyltetrahydrofolate synthetase domain containing	chr16q24.1	244734_at	NM_022764																				
2.20	2.19	0.01	9.61E-01	9.89E-01	---	---	---	234556_at	---																				
2.59	2.59	0.01	9.61E-01	9.89E-01	---	---	---	242787_at	---																				
2.37	2.36	0.01	9.61E-01	9.89E-01	ANP32C	acidic (leucine-rich) nuclear phosphoprotein 32 family, member C	chr4q32.3	208538_at	NM_012403																				
3.31	3.29	0.02	9.61E-01	9.90E-01	---	---	---	244485_at	---																				
2.29	2.28	0.01	9.61E-01	9.90E-01	FLJ35816	FLJ35816 protein	chr4p16.3	1564152_at	XR_017847 /// XR_039811 /// XR_039812																				
2.28	2.28	0.01	9.62E-01	9.90E-01	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	chr16p13.1	206641_at	NM_001192																				
3.00	2.99	0.01	9.62E-01	9.90E-01	LOC100128398	Hypothetical protein LOC100128398	chr19q13.43	1556724_at	XM_001725704 /// XM_001725733 /// XM_001726270																				
2.34	2.33	0.01	9.62E-01	9.90E-01	ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	chr6p24.2	220029_at	NM_017770																				
3.60	3.59	0.01	9.62E-01	9.90E-01	FAM168B	family with sequence similarity 168, member B	chr2q21.1	229946_at	NM_001009993																				
2.37	2.36	0.01	9.62E-01	9.90E-01	PCP4L1	Purkinje cell protein 4 like 1	chr1q23.3	241382_at	NM_001102566																				
2.99	2.98	0.01	9.62E-01	9.90E-01	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	chr15q22-q24	205749_at	NM_000499																				
2.84	2.83	0.01	9.62E-01	9.90E-01	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	chr22q11.21	204126_s_at	NM_003504																				
2.58	2.57	0.01	9.62E-01	9.90E-01	TEAD2	TEA domain family member 2	chr19q13.3	238321_at	NM_003598																				
2.64	2.63	0.01	9.62E-01	9.90E-01	---	---	---	231624_s_at	---																				
3.09	3.09	0.01	9.62E-01	9.90E-01	FAM124A	Family with sequence similarity 124A	chr13q14.3	230067_at	NM_145019																				
2.81	2.80	0.01	9.62E-01	9.90E-01	---	---	---	1564854_at	---																				
2.47	2.46	0.01	9.62E-01	9.90E-01	---	---	---	1569338_at	---																				
2.26	2.25	0.01	9.62E-01	9.90E-01	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	chr3p21.3	219614_s_at	NM_020208 /// NM_022405																				
3.79	3.78	0.01	9.62E-01	9.90E-01	---	---	---	244534_at	---																				
5.93	5.92	0.01	9.62E-01	9.90E-01	RAB40C	RAB40C, member RAS oncogene family	chr16p13.3	1569396_at	NM_021168																				
6.20	6.19	0.01	9.62E-01	9.90E-01	ZNF449	zinc finger protein 449	chrXq26.3	228968_at	NM_152695																				
6.23	6.23	0.01	9.62E-01	9.90E-01	WDTC1	WD and tetratricopeptide repeats 1	chr1p36.11	40829_at	NM_015023																				

2.54	2.53	0.01	9.62E-01	9.90E-01	DMD	dystrophin	chrXp21.2	207660_at	NM_000109 /// NM_004006 /// NM_004007 /// NM_004009 /// NM_004010 /// NM_004011 /// NM_004012 /// NM_004013 /// NM_004014 /// NM_004015 /// NM_004016 /// NM_004017 /// NM_004018 /// NM_004019 /// NM_004020 /// NM_004021 /// NM_004022 /// NM_004023																			
2.21	2.20	0.01	9.62E-01	9.90E-01	ZIC2	Zic family member 2 (odd-paired homolog, Drosophila)	chr13q32	223642_at	NM_007129																				
2.74	2.73	0.01	9.62E-01	9.90E-01	CDSN	corneodesmosin	chr6p21.3	206192_at	NM_001264																				
2.17	2.16	0.01	9.62E-01	9.90E-01	LOC728853	similar to RIKEN cDNA 4930432E11	chr19q13.13	1568690_a_at	XR_015396 /// XR_015633 /// XR_037738																				
2.51	2.50	0.01	9.62E-01	9.90E-01	GDA	guanine deaminase	chr9q21.13	1569555_at	NM_004293																				
4.13	4.13	0.01	9.62E-01	9.90E-01	ROR2	Receptor tyrosine kinase-like orphan receptor 2	chr9q22	231000_at	NM_004560																				
6.34	6.34	0.01	9.62E-01	9.90E-01	RNF126	ring finger protein 126	chr19p13.3	215031_x_at	NM_194460																				
2.04	2.03	0.00	9.62E-01	9.90E-01	---	---	---	240832_at	---																				
1.96	1.96	0.01	9.62E-01	9.90E-01	---	---	---	1569955_at	---																				
2.51	2.50	0.01	9.63E-01	9.90E-01	PEX14	peroxisomal biogenesis factor 14	chr1p36.22	1558915_a_at	NM_004565																				
1.88	1.87	0.01	9.63E-01	9.90E-01	C1orf114	chromosome 1 open reading frame 114	chr1q24	1555111_at	NM_021179																				
2.45	2.44	0.01	9.63E-01	9.90E-01	---	---	---	236196_at	---																				
4.71	4.70	0.01	9.63E-01	9.90E-01	ABCA7	ATP-binding cassette, sub-family A (ABC1), member 7	chr19p13.3	219577_s_at	NM_019112																				
6.12	6.07	0.05	9.63E-01	9.90E-01	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	chr22q13.1	208151_x_at	NM_001098504 /// NM_001098505 /// NM_006386 /// NM_030881																				
3.20	3.19	0.01	9.63E-01	9.90E-01	---	---	---	237444_at	---																				
4.17	4.16	0.01	9.63E-01	9.90E-01	NFX1	nuclear transcription factor, X-box binding 1	chr9p13.3	1553348_a_at	NM_002504 /// NM_147133 /// NM_147134																				
1.96	1.95	0.01	9.63E-01	9.90E-01	MTBP	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa	chr8q24.12	233436_at	NM_022045																				
3.11	3.11	0.01	9.63E-01	9.90E-01	MBOAT2	membrane bound O-acyltransferase domain containing 2	chr2p25.1	226726_at	NM_138799																				
2.16	2.15	0.01	9.63E-01	9.90E-01	---	---	---	1561353_at	---																				
2.63	2.62	0.01	9.63E-01	9.90E-01	---	---	---	1563023_at	---																				
2.20	2.19	0.01	9.63E-01	9.90E-01	---	---	---	1562828_at	---																				
2.30	2.29	0.01	9.63E-01	9.90E-01	C21orf29	chromosome 21 open reading frame 29	chr21q22.3	1555048_a_at	NM_144991																				
7.29	7.28	0.01	9.63E-01	9.90E-01	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	chr3p14.1	215772_x_at	NM_003848																				

2.91	2.91	0.01	9.63E-01	9.90E-01	FAHD2A /// FAHD2B /// LOC729234	fumarylacetoacetate hydrolase domain containing 2A /// fumarylacetoacetate hydrolase domain containing 2B /// fumarylacetoacetate hydrolase domain containing 2 pseudogene	chr2p24.3-p11.2 /// chr2q11.2	222055_at	NM_016044 /// NM_199336 /// NR_003698																				
1.79	1.79	0.01	9.63E-01	9.90E-01	---	---	---	222970_at	---																				
1.84	1.84	0.01	9.63E-01	9.90E-01	ZNF441	zinc finger protein 441	chr19p13.2	1553193_at	NM_152355																				
2.10	2.10	0.01	9.63E-01	9.90E-01	---	---	---	1568908_at	---																				
5.55	5.54	0.01	9.64E-01	9.90E-01	RIPK5	receptor interacting protein kinase 5	chr1q32.1	229017_s_at	NM_015375 /// NM_199462																				
2.69	2.69	0.01	9.64E-01	9.90E-01	---	---	---	1556675_s_at	---																				
2.11	2.11	0.01	9.64E-01	9.90E-01	---	---	---	1568722_at	---																				
2.18	2.17	0.01	9.64E-01	9.90E-01	NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	chr4q26	220429_at	NM_004784																				
3.01	3.01	0.01	9.64E-01	9.90E-01	LOC100129420	similar to hCG1990547	chr8p23.1	234049_at	XM_001720857 /// XM_001721359 /// XM_001721781																				
6.97	6.96	0.02	9.64E-01	9.90E-01	NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	chr4q22.1	218375_at	NM_024047 /// NM_198038																				
3.30	3.29	0.01	9.64E-01	9.90E-01	CST2 /// CST3	cystatin SA /// cystatin C	chr20p11.21	237623_at	NM_000099 /// NM_001322																				
6.30	6.29	0.01	9.64E-01	9.90E-01	NFKBIL1	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	chr6p21.3	209973_at	NM_005007																				
5.66	5.65	0.01	9.64E-01	9.90E-01	MTF1	metal-regulatory transcription factor 1	chr1p33	205322_s_at	NM_005955																				
2.25	2.25	0.01	9.64E-01	9.90E-01	---	---	---	239903_at	---																				
2.34	2.34	0.01	9.64E-01	9.90E-01	CEP70	centrosomal protein 70kDa	chr3q22-q23	1554488_at	NM_024491																				
4.27	4.25	0.02	9.64E-01	9.90E-01	FTSJD1	FtsJ methyltransferase domain containing 1	chr16q22.3	222811_at	NM_001099642 /// NM_018348																				
2.52	2.51	0.01	9.64E-01	9.90E-01	---	---	---	240212_at	---																				
2.01	2.00	0.01	9.64E-01	9.90E-01	---	---	---	240987_at	---																				
2.69	2.69	0.01	9.64E-01	9.90E-01	---	---	---	236401_at	---																				
3.88	3.87	0.01	9.64E-01	9.90E-01	TBC1D16	TBC1 domain family, member 16	chr17q25.3	1558066_s_at	NM_019020																				
3.17	3.16	0.01	9.64E-01	9.90E-01	BTN2A3	butyrophilin, subfamily 2, member A3	chr6p22.1	208585_at	NM_024018																				
2.74	2.73	0.01	9.64E-01	9.90E-01	PAIP2	poly(A) binding protein interacting protein 2	chr5q31.2	1560065_at	NM_001033112 /// NM_016480																				
2.53	2.52	0.01	9.64E-01	9.90E-01	CHCHD5	Coiled-coil-helix-coiled-coil-helix domain containing 5	chr2q13	1562892_at	NM_032309																				
8.06	8.05	0.01	9.64E-01	9.90E-01	GOLGA7	golgi autoantigen, golgin subfamily a, 7	chr8p11.21	217819_at	NM_001002296 /// NM_016099																				
2.81	2.80	0.01	9.64E-01	9.90E-01	INDO	indoleamine-pyrrole 2,3 dioxygenase	chr8p12-p11	210029_at	NM_002164																				
6.34	6.33	0.01	9.64E-01	9.90E-01	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	chr20p13	212862_at	NM_003818																				
6.00	5.99	0.01	9.65E-01	9.90E-01	CTNND1	catenin (cadherin-associated protein), delta 1	chr11q11	208407_s_at	NM_001085458 /// NM_001085459 /// NM_001085460 /// NM_001085461 /// NM_001085462 /// NM_001085463 /// NM_001085464 /// NM_001085465 /// NM_001085466 /// NM_001085467 /// NM_001085468 /// NM_001085469 /// NM_001331																				
2.50	2.49	0.01	9.65E-01	9.90E-01	LRRC16A	leucine rich repeat containing 16A	chr6p22.2	1562939_at	NM_017640																				

2.55	2.55	0.01	9.65E-01	9.90E-01	FBXO10	F-box protein 10	chr9p13.2	1558062_at	NM_012166
11.23	11.22	0.01	9.65E-01	9.90E-01	EIF3EIP	eukaryotic translation initiation factor 3, subunit E interacting protein	chr22q	217719_at	NM_016091
5.48	5.47	0.01	9.65E-01	9.90E-01	LOC652900 /// SEZ6L2	similar to seizure related 6 homolog (mouse)-like 2 isoform 1 /// seizure related 6 homolog (mouse)-like 2	chr16p11.2	223458_at	NM_001114099 /// NM_001114100 /// NM_012410 /// NM_201575 /// XM_001724912
7.65	7.64	0.01	9.65E-01	9.90E-01	CDC2L5	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	chr7p13	232266_x_at	NM_003718 /// NM_031267
2.55	2.54	0.01	9.65E-01	9.90E-01	FAM53B	family with sequence similarity 53, member B	chr10q26.13	1554165_at	NM_014661
2.78	2.77	0.01	9.65E-01	9.90E-01	PSG9	pregnancy specific beta-1-glycoprotein 9	chr19q13.2	209594_x_at	NM_002784
2.83	2.82	0.01	9.65E-01	9.90E-01	ZNF280B	zinc finger protein 280B	chr22q11.22	215048_at	NM_080764
3.02	3.01	0.02	9.65E-01	9.90E-01	DPYSL4	dihydropyrimidinase-like 4	chr10q26	205493_s_at	NM_006426
2.60	2.59	0.01	9.65E-01	9.90E-01	ACRV1	acrosomal vesicle protein 1	chr11q23-q24	207991_x_at	NM_001612 /// NM_020069 /// NM_020107 /// NM_020108 /// NM_020109 /// NM_020110 /// NM_020111 /// NM_020113 /// NM_020115
2.38	2.37	0.01	9.65E-01	9.90E-01	41609	deleted in esophageal cancer 1	chr9q32	220781_at	NM_017418
5.23	5.22	0.01	9.65E-01	9.90E-01	hCG_2007354	hCG2007354	---	1556959_at	XR_041592 /// XR_041593
2.14	2.13	0.01	9.66E-01	9.90E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	217083_at	---
3.43	3.43	0.01	9.66E-01	9.90E-01	DPY19L4	dpy-19-like 4 (C. elegans)	chr8q22.1	226721_at	NM_181787
2.41	2.40	0.01	9.66E-01	9.90E-01	TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2	chr2q32.3	224321_at	NM_016192
3.18	3.17	0.01	9.66E-01	9.90E-01	---	---	---	1560917_at	---
5.44	5.42	0.02	9.66E-01	9.90E-01	CDK6	cyclin-dependent kinase 6	chr7q21-q22	224848_at	NM_001259
2.48	2.47	0.01	9.66E-01	9.90E-01	SCN2A	sodium channel, voltage-gated, type II, alpha subunit	chr2q23-q24	206381_at	NM_001040142 /// NM_001040143 /// NM_021007
7.36	7.34	0.02	9.66E-01	9.90E-01	MORC4	MORC family CW-type zinc finger 4	chrXq22.3	219038_at	NM_001085354 /// NM_024657
6.66	6.64	0.02	9.66E-01	9.90E-01	FNDC3A	fibronectin type III domain containing 3A	chr13q14.2	202304_at	NM_001079673 /// NM_014923
2.36	2.35	0.01	9.66E-01	9.90E-01	---	---	---	224108_at	---
2.58	2.57	0.01	9.66E-01	9.90E-01	LOC100132279 /// WTAP	hypothetical protein LOC100132279 /// Wilms tumor 1 associated protein	chr6q25-q27 /// chr6q25.3	1560274_at	NM_004906 /// NM_152857 /// NM_152858 /// XM_001713953 /// XM_001714206 /// XM_001719888
4.05	4.03	0.01	9.66E-01	9.91E-01	FIGNL1	fidgetin-like 1	chr7p12.2	222843_at	NM_001042762 /// NM_022116
3.15	3.14	0.01	9.66E-01	9.91E-01	---	---	---	242159_at	---

4.60	4.59	0.01	9.66E-01	9.91E-01	APOBEC3F /// APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F /// apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	chr22q13.1 /// chr22q13.1-q13.2	214994_at	NM_001006666 /// NM_021822 /// NM_145298																				
3.01	3.00	0.01	9.66E-01	9.91E-01	SLC41A2	solute carrier family 41, member 2	chr12q23.3	243894_at	NM_032148																				
2.07	2.07	0.00	9.66E-01	9.91E-01	MSMB	microseminoprotein, beta-	chr10q11.2	207430_s_at	NM_002443 /// NM_138634																				
1.82	1.81	0.01	9.66E-01	9.91E-01	---	---	---	1562998_at	---																				
7.03	7.02	0.01	9.66E-01	9.91E-01	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	chr1q22-q24	207391_s_at	NM_003557																				
4.40	4.39	0.01	9.66E-01	9.91E-01	ARX	Aristaless related homeobox	chrXp21	231020_at	NM_139058																				
3.69	3.68	0.01	9.66E-01	9.91E-01	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	chr10q23.3	222563_s_at	NM_025235																				
2.23	2.22	0.00	9.66E-01	9.91E-01	---	---	---	1557882_at	---																				
5.53	5.53	0.01	9.67E-01	9.91E-01	MKRN2	makorin ring finger protein 2	chr3p25	218071_s_at	NM_014160																				
4.05	4.04	0.01	9.67E-01	9.91E-01	C10orf118	chromosome 10 open reading frame 118	chr10q25.3	227701_at	NM_018017																				
2.66	2.66	0.01	9.67E-01	9.91E-01	NUP153	nucleoporin 153kDa	chr6p22.3	1559064_at	NM_005124																				
1.96	1.95	0.00	9.67E-01	9.91E-01	IYD	iodotyrosine deiodinase	chr6q25.1	231070_at	NM_203395																				
2.25	2.25	0.01	9.67E-01	9.91E-01	ZNF326	zinc finger protein 326	chr1p22.2	234093_at	NM_182975 /// NM_182976																				
2.06	2.06	0.00	9.67E-01	9.91E-01	IL31RA	interleukin 31 receptor A	chr5q11.2	243541_at	NM_139017																				
4.11	4.11	0.01	9.67E-01	9.91E-01	TNS4	tensin 4	chr17q21.2	230398_at	NM_032865																				
2.28	2.27	0.01	9.67E-01	9.91E-01	LOC729083	hypothetical protein LOC729083	chr3p22.1	1563053_at	XM_001133289																				
2.41	2.40	0.01	9.67E-01	9.91E-01	FKBP15	FK506 binding protein 15, 133kDa	chr9q32	242574_at	NM_015258																				
2.20	2.19	0.01	9.67E-01	9.91E-01	FAM135A	family with sequence similarity 135, member A	chr6q12-q13	233730_at	NM_001105531 /// NM_020819																				
3.17	3.16	0.01	9.67E-01	9.91E-01	---	---	---	1565811_at	---																				
5.76	5.75	0.02	9.67E-01	9.91E-01	IGFBP5	insulin-like growth factor binding protein 5	chr2q33-q36	203425_s_at	NM_000599																				
4.53	4.53	0.01	9.67E-01	9.91E-01	GLI4	GLI-Kruppel family member GLI4	chr8q24.3	243076_x_at	NM_138465																				
2.03	2.02	0.01	9.67E-01	9.91E-01	---	---	---	239806_at	---																				
3.93	3.92	0.01	9.67E-01	9.91E-01	ERAP1	endoplasmic reticulum aminopeptidase 1	chr5q15	210385_s_at	NM_001040458 /// NM_016442																				
2.27	2.27	0.01	9.67E-01	9.91E-01	DKFZp434F142	hypothetical protein DKFZp434F142	chr7q11.21	224123_at	---																				
3.61	3.60	0.01	9.67E-01	9.91E-01	SLC16A3	Solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	chr17q25	217685_at	NM_001042422 /// NM_001042423 /// NM_004207																				
4.68	4.67	0.01	9.67E-01	9.91E-01	KIAA1432	KIAA1432	chr9p24.1	226222_at	NM_020829																				
2.30	2.29	0.01	9.67E-01	9.91E-01	---	---	---	235156_at	---																				
3.18	3.17	0.01	9.67E-01	9.91E-01	CYTL1	cytokine-like 1	chr4p16-p15	219837_s_at	NM_018659																				
4.83	4.80	0.03	9.67E-01	9.91E-01	PRPS2	phosphoribosyl pyrophosphate synthetase 2	chrXp22.3-p22.2	203401_at	NM_001039091 /// NM_002765																				
2.82	2.81	0.01	9.67E-01	9.91E-01	---	---	---	230208_at	---																				
2.25	2.25	0.00	9.67E-01	9.91E-01	TACC1	Transforming, acidic coiled-coil containing protein 1	chr8p11	1557305_at	NM_001122824 /// NM_006283																				
5.13	5.12	0.01	9.67E-01	9.91E-01	WDR22	WD repeat domain 22	chr14q23-q24.1	224696_s_at	NM_003861																				
5.01	5.00	0.01	9.68E-01	9.91E-01	ZNF720	zinc finger protein 720	chr16p11.2	238510_at	NM_001004300 /// NM_001130913																				
2.50	2.50	0.01	9.68E-01	9.91E-01	GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	chr9q31.1	233220_at	NM_133445																				
2.63	2.62	0.01	9.68E-01	9.91E-01	---	---	---	222961_at	---																				
4.68	4.66	0.02	9.68E-01	9.91E-01	NUPL1	nucleoporin like 1	chr13q12.13	204435_at	NM_001008564 /// NM_001008565 /// NM_014089																				
4.14	4.13	0.01	9.68E-01	9.91E-01	ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	chr7q36	229539_at	NM_007188																				
2.74	2.73	0.01	9.68E-01	9.91E-01	SVOP	SV2 related protein homolog (rat)	chr12q24.11	229818_at	NM_018711																				
7.43	7.42	0.01	9.68E-01	9.91E-01	---	---	---	225221_at	---																				
9.44	9.43	0.01	9.68E-01	9.91E-01	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	chr8q23.1	200640_at	NM_003406 /// NM_145690																				
2.34	2.34	0.00	9.68E-01	9.91E-01	---	---	---	1560810_at	---																				
2.71	2.70	0.01	9.68E-01	9.91E-01	FAM90A1 /// FAM90A7	family with sequence similarity 90, member A1 /// family with sequence similarity 90, member A7	chr12p13.31 /// chr8p23.1	233643_at	NM_018088 /// XM_496948																				

2.31	2.29	0.02	9.68E-01	9.91E-01	LOC100130224 /// UTY	hypothetical protein LOC100130224 /// ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	chrYq11	211149_at	NM_007125 /// NM_182659 /// NM_182660 /// XM_001713700 /// XM_001713765 /// XM_001713766																				
1.84	1.83	0.00	9.68E-01	9.91E-01	DNAH6 /// DNHL1 /// LOC200383	dynein, axonemal, heavy chain 6 /// dynein heavy chain-like 1 /// similar to Dynein heavy chain at 16F	chr2p11.2	1553362_at	NM_001370 /// NM_173645																				
2.89	2.88	0.01	9.68E-01	9.91E-01	ACSF3	acyl-CoA synthetase family member 3	chr16q24.3	1556552_a_at	NM_001127214 /// NM_174917 /// NR_023316																				
3.09	3.09	0.00	9.68E-01	9.91E-01	LOC100130850 /// LOC339240 /// LOC729704	hypothetical protein LOC100130850 /// keratin pseudogene /// hypothetical LOC729704	chr17p11.2 /// chr17q11.2	237576_x_at	NR_001443 /// XM_001133899 /// XM_001719067 /// XM_001721195 /// XM_001723496 /// XM_001725990 /// XR_042158																				
2.70	2.70	0.01	9.68E-01	9.91E-01	OR51I2	olfactory receptor, family 51, subfamily I, member 2	chr11p15.4	234521_at	NM_001004754																				
2.20	2.19	0.00	9.68E-01	9.91E-01	---	---	---	224026_at	---																				
2.25	2.25	0.00	9.68E-01	9.91E-01	MLF1	myeloid leukemia factor 1	chr3q25.1	204782_at	NM_001130156 /// NM_001130157 /// NM_022443																				
2.64	2.63	0.01	9.68E-01	9.91E-01	ITPK1 /// LOC100130685	inositol 1,3,4-triphosphate 5/6 kinase /// hypothetical protein LOC100130685	chr14q31 /// chr14q32.12	210197_at	NM_014216 /// XM_001719559 /// XM_001724253 /// XM_001726235																				
3.01	3.00	0.01	9.68E-01	9.91E-01	---	---	---	232877_at	---																				
2.00	2.00	0.00	9.68E-01	9.91E-01	FLJ42418	FLJ42418 protein	chr2p25.2	231455_at	XR_041683 /// XR_041684 /// XR_041685																				
2.62	2.61	0.01	9.68E-01	9.91E-01	RHAG	Rh-associated glycoprotein	chr6p21.1-p11	211254_x_at	NM_000324																				
4.90	4.89	0.01	9.68E-01	9.91E-01	DHX37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	chr12q24.31	223365_at	NM_032656																				
2.60	2.59	0.01	9.68E-01	9.91E-01	---	---	---	217429_at	---																				
2.24	2.23	0.01	9.69E-01	9.91E-01	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	chr11p11.2	1554121_at	NM_016142																				
2.19	2.19	0.01	9.69E-01	9.91E-01	PTK7	PTK7 protein tyrosine kinase 7	chr6p21.1-p12.2	1555324_at	NM_002821 /// NM_152880 /// NM_152881 /// NM_152882																				
2.25	2.24	0.01	9.69E-01	9.91E-01	GPR125	G protein-coupled receptor 125	chr4p15.31	1555122_at	NM_145290																				
3.28	3.27	0.01	9.69E-01	9.91E-01	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	chr1p36.3	217070_at	NM_005957																				
11.23	11.22	0.01	9.69E-01	9.91E-01	MXRA7	matrix-remodelling associated 7	chr17q25.1-q25.2	212509_s_at	NM_001008528 /// NM_001008529 /// NM_198530																				
2.43	2.43	0.00	9.69E-01	9.91E-01	DGKE	diacylglycerol kinase, epsilon 64kDa	chr17q22	1554621_at	NM_003647																				

6.10	6.09	0.01	9.69E-01	9.91E-01	C9orf86	chromosome 9 open reading frame 86	chr9q34.3	223166_x_at	NM_017995 /// NM_024718																				
2.86	2.85	0.01	9.69E-01	9.91E-01	METTL5	methyltransferase like 5	chr2q31.1	220839_at	NM_014168																				
3.48	3.47	0.01	9.69E-01	9.91E-01	LOC201175	Hypothetical protein LOC201175	chr17q21.31	243536_x_at	NM_174919																				
2.41	2.40	0.01	9.69E-01	9.91E-01	HDAC9	histone deacetylase 9	chr7p21.1	234393_at	NM_014707 /// NM_058176 /// NM_058177 /// NM_178423 /// NM_178425																				
3.21	3.20	0.01	9.69E-01	9.91E-01	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	chr9p13	211631_x_at	NM_001497																				
4.13	4.11	0.02	9.69E-01	9.91E-01	SLFN5	schlafen family member 5	chr17q12	1557078_at	NM_144975																				
2.46	2.45	0.01	9.69E-01	9.91E-01	---	---	---	239752_at	---																				
3.77	3.77	0.01	9.69E-01	9.91E-01	CMKLR1	chemokine-like receptor 1	chr12q24.1	210659_at	NM_004072																				
2.42	2.42	0.00	9.69E-01	9.91E-01	NODAL	nodal homolog (mouse)	chr10q22.1	237896_at	NM_018055																				
3.18	3.17	0.01	9.69E-01	9.91E-01	FNDC7	fibronectin type III domain containing 7	chr1p13.3	240837_at	NM_173532																				
2.43	2.43	0.00	9.69E-01	9.91E-01	---	---	---	235027_at	---																				
11.24	11.22	0.02	9.69E-01	9.91E-01	EGR1	Early growth response 1	chr5q31.1	227404_s_at	NM_001964																				
2.01	2.00	0.01	9.69E-01	9.91E-01	INVS	inversin	chr9q31	211054_at	NM_014425 /// NM_183245																				
4.05	4.04	0.01	9.69E-01	9.91E-01	ISY1	ISY1 splicing factor homolog (S. cerevisiae)	chr3q21.3	232142_at	NM_020701																				
3.00	3.00	0.01	9.69E-01	9.91E-01	GSDMB	gasdermin B	chr17q12	240701_at	NM_001042471 /// NM_018530																				
4.25	4.24	0.01	9.70E-01	9.91E-01	PROX1	prospero homeobox 1	chr1q32.2-q32.3	229376_at	NM_002763																				
5.72	5.71	0.02	9.70E-01	9.91E-01	HEATR5B	HEAT repeat containing 5B	chr2p22.2	233642_s_at	NM_019024																				
1.98	1.98	0.01	9.70E-01	9.91E-01	---	---	---	1563012_x_at	---																				
2.75	2.74	0.01	9.70E-01	9.91E-01	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	chr12q13	215638_at	NM_001005915 /// NM_001982																				
2.52	2.52	0.00	9.70E-01	9.91E-01	---	---	---	234272_at	---																				
2.23	2.22	0.01	9.70E-01	9.91E-01	KLF12	Kruppel-like factor 12	chr13q22	239019_at	NM_007249																				
2.78	2.77	0.01	9.70E-01	9.92E-01	RBM5	RNA binding motif protein 5	chr3p21.3	209936_at	NM_005778																				
5.69	5.68	0.01	9.70E-01	9.92E-01	HMGB1	high-mobility group box 1	chr13q12	224734_at	NM_002128																				
4.48	4.47	0.01	9.70E-01	9.92E-01	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	chr15q25.1	1554334_a_at	NM_001130182 /// NM_001130183 /// NM_018602																				
2.23	2.23	0.01	9.70E-01	9.92E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	233969_at	---																				
3.51	3.51	0.01	9.70E-01	9.92E-01	KIAA0368	KIAA0368	chr9q31.3	236368_at	NM_001080398																				
6.82	6.81	0.01	9.70E-01	9.92E-01	GLTPD1 /// LOC727825	glycolipid transfer protein domain containing 1 /// hypothetical LOC727825	chr1p36.33	220734_s_at	NM_001029885 /// XR_015127																				
3.75	3.74	0.01	9.70E-01	9.92E-01	TRIM3	tripartite motif-containing 3	chr11p15.5	204911_s_at	NM_006458 /// NM_033278																				
3.01	3.01	0.00	9.70E-01	9.92E-01	DKFZp761E198	DKFZp761E198 protein	chr11q13.1	231858_x_at	NM_138368																				
2.41	2.41	0.01	9.70E-01	9.92E-01	---	---	---	236522_at	---																				
3.19	3.19	0.01	9.70E-01	9.92E-01	C1orf133	chromosome 1 open reading frame 133	chr1q32.2	230121_at	XM_001134414 /// XM_001134415 /// XM_001134416 /// XM_001134417 /// XM_001720763																				
2.39	2.38	0.01	9.70E-01	9.92E-01	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	chr4q25	1554853_at	NM_183075																				
2.70	2.70	0.00	9.71E-01	9.92E-01	FSTL4	follistatin-like 4	chr5q31.1	214859_at	NM_015082																				
4.11	4.11	0.00	9.71E-01	9.92E-01	MTERFD2	MTERF domain containing 2	chr2q37.3	214364_at	NM_182501																				
2.57	2.57	0.01	9.71E-01	9.92E-01	NKAIN4	Na+/K+ transporting ATPase interacting 4	chr20q13.33	230771_at	NM_152864																				
2.09	2.08	0.00	9.71E-01	9.92E-01	C14orf145	chromosome 14 open reading frame 145	chr14q31.1	1557756_a_at	NM_152446																				

3.10	3.09	0.01	9.71E-01	9.92E-01	CSH1 /// CSH2 /// CSHL1 /// GH1 /// GH2	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// chorionic somatomammotropin hormone-like 1 /// growth hormone 1 /// growth hormone 2	chr17q24.2	208068_x_at	NM_000515 /// NM_001317 /// NM_001318 /// NM_002059 /// NM_020991 /// NM_022556 /// NM_022557 /// NM_022558 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022579 /// NM_022580 /// NM_022581 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645																			
7.31	7.29	0.02	9.71E-01	9.92E-01	NAP1L1	nucleosome assembly protein 1-like 1	chr12q21.2	208753_s_at	NM_004537 /// NM_139207																				
2.72	2.71	0.01	9.71E-01	9.92E-01	HKDC1	hexokinase domain containing 1	chr10q21.3	237323_at	NM_025130																				
2.04	2.03	0.00	9.71E-01	9.92E-01	CFHR3	Complement factor H-related 3	chr1q32	1570228_at	NM_021023																				
2.37	2.36	0.01	9.71E-01	9.92E-01	C20orf152	chromosome 20 open reading frame 152	chr20q11.23	1552687_a_at	NM_080834																				
4.39	4.38	0.01	9.71E-01	9.92E-01	HBS1L	HBS1-like (S. cerevisiae)	chr6q23-q24	209314_s_at	NM_006620																				
4.25	4.24	0.01	9.71E-01	9.92E-01	TNFAIP8L2	tumor necrosis factor, alpha-induced protein 8-like 2	chr1q21.2	223583_at	NM_024575																				
3.63	3.62	0.01	9.71E-01	9.92E-01	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	chr1q32.1	1556202_at	NM_001042758 /// NM_015326																				
3.83	3.82	0.01	9.71E-01	9.92E-01	CD276	CD276 molecule	chr15q23-q24	1552914_a_at	NM_001024736 /// NM_025240																				
2.29	2.29	0.00	9.71E-01	9.92E-01	---	---	---	232956_at	---																				
2.58	2.58	0.01	9.71E-01	9.92E-01	---	---	---	244172_at	---																				
8.00	7.99	0.01	9.71E-01	9.92E-01	BRD3	bromodomain containing 3	chr9q34	203825_at	NM_007371																				
5.67	5.66	0.01	9.72E-01	9.92E-01	EZH1	enhancer of zeste homolog 1 (Drosophila)	chr17q21.1-q21.3	203249_at	NM_001991																				
2.27	2.27	0.00	9.72E-01	9.92E-01	TNC	Tenascin C	chr9q33	216005_at	NM_002160																				
1.89	1.89	0.00	9.72E-01	9.92E-01	NRXN1	neurexin 1	chr2p16.3	228547_at	NM_004801 /// NM_138735																				
2.71	2.71	0.00	9.72E-01	9.92E-01	---	---	---	240005_at	---																				
2.20	2.19	0.01	9.72E-01	9.92E-01	GUSBL2	glucuronidase, beta-like 2	chr6p11.2	243909_x_at	NR_003660 /// XR_042150 /// XR_042151																				
1.98	1.98	0.00	9.72E-01	9.92E-01	---	---	---	239467_at	---																				
7.62	7.61	0.01	9.72E-01	9.92E-01	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	chr5q23.1	225660_at	NM_020796																				
2.79	2.79	0.01	9.72E-01	9.92E-01	---	---	---	241339_at	---																				
5.44	5.44	0.01	9.72E-01	9.92E-01	ADAM17	ADAM metallopeptidase domain 17	chr2p25	205745_x_at	NM_003183																				
5.90	5.89	0.01	9.72E-01	9.92E-01	MFAP3	Microfibrillar-associated protein 3	chr5q32-q33.2	213123_at	NM_005927																				
3.31	3.31	0.00	9.72E-01	9.92E-01	KIRREL3	kin of IRRE like 3 (Drosophila)	chr11q24	240402_at	NM_032531																				

3.19	3.18	0.01	9.72E-01	9.92E-01	LOC440456 /// MGC40489	similar to pleckstrin homology domain containing, family M (with RUN domain) member 1; adapter protein 162 /// hypothetical protein MGC40489	chr17q24 /// chr17q24.1	228779_at	XM_001724417 /// XM_935188 /// XM_940040 /// XR_016048 /// XR_041390 /// XR_041391																				
2.10	2.10	0.01	9.72E-01	9.92E-01	C12orf67	chromosome 12 open reading frame 67	chr12p12.1	1553484_at	NM_144667																				
3.11	3.10	0.01	9.72E-01	9.93E-01	LOC400831	hypothetical LOC400831	chr20p13	1556266_a_at	NM_001009612 /// XM_001724704 /// XM_930959 /// XM_943808																				
1.96	1.96	0.00	9.72E-01	9.93E-01	---	---	---	1560516_at	---																				
2.39	2.38	0.00	9.72E-01	9.93E-01	TROVE2	TROVE domain family, member 2	chr1q31	207520_at	NM_001042369 /// NM_001042370 /// NM_004600																				
5.05	5.04	0.01	9.72E-01	9.93E-01	---	---	---	239225_at	---																				
2.93	2.92	0.01	9.72E-01	9.93E-01	FLJ25328	hypothetical LOC148231	chr19p13.12	1562914_a_at	NM_152483																				
6.95	6.94	0.01	9.72E-01	9.93E-01	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	chr6p21.1	222500_at	NM_016059																				
4.53	4.52	0.01	9.72E-01	9.93E-01	NEK6	NIMA (never in mitosis gene a)-related kinase 6	chr9q33.3-q34.11	223158_s_at	NM_014397																				
2.28	2.28	0.00	9.73E-01	9.93E-01	---	---	---	241466_at	---																				
2.44	2.44	0.00	9.73E-01	9.93E-01	---	---	---	1569263_at	---																				
2.08	2.08	0.00	9.73E-01	9.93E-01	---	---	---	241186_at	---																				
2.71	2.71	0.00	9.73E-01	9.93E-01	TCF20	Transcription factor 20 (AR1)	chr22q13.3|22q13.3	238667_at	NM_005650 /// NM_181492																				
2.03	2.02	0.00	9.73E-01	9.93E-01	DCTN1	dynactin 1 (p150, glued homolog, Drosophila)	chr2p13	204296_at	NM_004082 /// NM_023019																				
2.63	2.62	0.01	9.73E-01	9.93E-01	---	---	---	1563325_at	---																				
3.00	2.99	0.01	9.73E-01	9.93E-01	KIR3DL1 /// KIR3DS1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, three domains, short cytoplasmic tail, 1	chr19q13.4	211389_x_at	NM_001083539 /// NM_013289																				
5.14	5.13	0.01	9.73E-01	9.93E-01	---	---	---	241303_x_at	---																				
6.90	6.89	0.01	9.73E-01	9.93E-01	TSNAX	translin-associated factor X	chr1q42.1	203983_at	NM_005999																				
2.65	2.65	0.00	9.73E-01	9.93E-01	DCBLD2	discoidin, CUB and LCCL domain containing 2	chr3q12.1|3	213873_at	NM_080927																				
7.80	7.80	0.01	9.73E-01	9.93E-01	PTPN11	protein tyrosine phosphatase, non-receptor type 11	chr12q24	212610_at	NM_002834																				
1.93	1.92	0.00	9.73E-01	9.93E-01	---	---	---	231560_at	---																				
2.70	2.70	0.01	9.73E-01	9.93E-01	---	---	---	244249_at	---																				
2.13	2.13	0.00	9.73E-01	9.93E-01	---	---	---	1557560_at	---																				
3.21	3.20	0.01	9.73E-01	9.93E-01	SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	chr4q13.3	207601_at	NM_014465																				
2.19	2.18	0.00	9.73E-01	9.93E-01	---	---	---	216002_at	---																				
4.91	4.90	0.01	9.73E-01	9.93E-01	PRR12	proline rich 12	chr19q13.33	226716_at	NM_020719																				
2.40	2.39	0.01	9.74E-01	9.93E-01	---	---	---	216871_at	---																				
5.86	5.85	0.01	9.74E-01	9.93E-01	FLJ20489	hypothetical protein FLJ20489	chr12q13.11	218417_s_at	NM_017842																				
2.35	2.35	0.00	9.74E-01	9.93E-01	---	---	---	1566248_at	---																				
3.48	3.47	0.01	9.74E-01	9.93E-01	C2orf16	chromosome 2 open reading frame 16	chr2p23.3	224000_at	NM_032266																				
2.08	2.08	0.00	9.74E-01	9.93E-01	LOC100130134	similar to STAU2 variant protein	chrXq21.31	216087_at	XR_037580 /// XR_037810																				
2.30	2.30	0.00	9.74E-01	9.93E-01	ADAM29	ADAM metallopeptidase domain 29	chr4q34	221337_s_at	NM_001130703 /// NM_001130704 /// NM_001130705 /// NM_014269																				
5.92	5.92	0.01	9.74E-01	9.93E-01	CHMP6	chromatin modifying protein 6	chr17q25.3	218743_at	NM_024591																				
2.92	2.92	0.01	9.74E-01	9.93E-01	LOC285928	hypothetical protein LOC285928	chr7p22.1	1562541_at	---																				
2.15	2.15	0.01	9.74E-01	9.93E-01	---	---	---	222168_at	---																				
4.90	4.89	0.01	9.74E-01	9.93E-01	MAPK14	mitogen-activated protein kinase 14	chr6p21.3-p21.2	210449_x_at	NM_001315 /// NM_139012 /// NM_139013 /// NM_139014																				

2.06	2.06	0.00	9.74E-01	9.93E-01	---	---	---	1560728_at	---																			
2.50	2.49	0.00	9.74E-01	9.93E-01	GATAD2A	GATA zinc finger domain containing 2A	chr19p13.11	229166_s_at	NM_017660																			
3.15	3.15	0.00	9.75E-01	9.93E-01	EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)	chr16p12.1	1555437_at	NM_001083614 /// NR_003501																			
6.59	6.58	0.01	9.75E-01	9.93E-01	NOL11	nucleolar protein 11	chr17q24.2	221970_s_at	NM_015462																			
3.06	3.05	0.01	9.75E-01	9.93E-01	CAPRIN1	cell cycle associated protein 1	chr11p13	226289_at	NM_005898 /// NM_203364																			
2.05	2.04	0.00	9.75E-01	9.93E-01	LOC100132218 /// LOC728555	hypothetical protein LOC100132218 /// hypothetical LOC728555	chr5q13.2	242491_at	XM_001127758 /// XM_001715393																			
2.65	2.65	0.01	9.75E-01	9.93E-01	---	---	---	1564012_at	---																			
6.08	6.07	0.01	9.75E-01	9.93E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	243318_at	NM_015726																			
1.98	1.98	0.00	9.75E-01	9.93E-01	---	---	---	241142_at	---																			
2.21	2.20	0.01	9.75E-01	9.93E-01	---	---	---	1563427_at	---																			
5.52	5.50	0.02	9.75E-01	9.93E-01	FCGR3A /// FCGR3B	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) /// Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	chr1q23	204006_s_at	NM_000569 /// NM_000570 /// NM_001127592 /// NM_001127593 /// NM_001127595 /// NM_001127596																			
3.39	3.39	0.01	9.75E-01	9.93E-01	CDK2	cyclin-dependent kinase 2	chr12q13	211803_at	NM_001798 /// NM_052827																			
2.23	2.23	0.00	9.75E-01	9.93E-01	C9orf68	chromosome 9 open reading frame 68	chr9p24.2-p24.1	220218_at	NM_001039395																			
6.70	6.69	0.01	9.75E-01	9.93E-01	HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	chr19q13.33	224497_x_at	NM_016246																			
1.93	1.93	0.00	9.75E-01	9.93E-01	---	---	---	1560557_at	---																			
2.31	2.31	0.01	9.75E-01	9.93E-01	---	---	---	1558494_at	---																			
2.45	2.44	0.00	9.75E-01	9.93E-01	---	---	---	230020_at	---																			
2.47	2.47	0.00	9.75E-01	9.93E-01	LOC147004	hypothetical protein LOC147004	chr17q12	1564203_at	---																			
2.12	2.12	0.00	9.75E-01	9.93E-01	ANK2	Ankyrin 2, neuronal	chr4q25-q27	232606_at	NM_001127493 /// NM_001148 /// NM_020977																			
2.49	2.49	0.01	9.75E-01	9.93E-01	NUP210	Nucleoporin 210kDa	chr3p25.1	213945_s_at	NM_024923																			
5.97	5.95	0.01	9.75E-01	9.93E-01	C20orf117	chromosome 20 open reading frame 117	chr20q11.23	225473_at	NM_199181																			
3.74	3.73	0.01	9.75E-01	9.93E-01	TPPP3	tubulin polymerization-promoting protein family member 3	chr16q22.1	218876_at	NM_015964 /// NM_016140																			
3.15	3.14	0.01	9.75E-01	9.93E-01	CCDC64	coiled-coil domain containing 64	chr12q24.23	215015_at	NM_207311																			
2.99	2.99	0.00	9.75E-01	9.93E-01	LOC730202	hypothetical protein LOC730202	chr14q32.2	1558128_at	XR_041804 /// XR_041805 /// XR_041806																			
9.24	9.24	0.01	9.75E-01	9.93E-01	TMEM147	transmembrane protein 147	chr19q13.1	202475_at	NM_032635																			
6.84	6.83	0.01	9.75E-01	9.93E-01	ETV1	ets variant gene 1	chr7p21.3	221911_at	NM_004956																			
2.81	2.80	0.00	9.75E-01	9.94E-01	ZBED5	Zinc finger, BED-type containing 5	chr11p15.3	240381_at	XR_041298 /// XR_041299 /// XR_041300																			
3.27	3.27	0.01	9.75E-01	9.94E-01	WDR87	WD repeat domain 87	chr19q13.13	224135_at	XM_001717392 /// XM_371164 /// XM_940478																			
4.96	4.95	0.01	9.75E-01	9.94E-01	SS18	synovial sarcoma translocation, chromosome 18	chr18q11.2	216684_s_at	NM_001007559 /// NM_005637																			
2.51	2.51	0.00	9.76E-01	9.94E-01	HS3ST4	heparan sulfate (glucosamine) 3-O-sulfotransferase 4	chr16p11.2	228206_at	NM_006040																			
2.11	2.10	0.00	9.76E-01	9.94E-01	---	---	---	1565834_a_at	---																			
1.94	1.94	0.00	9.76E-01	9.94E-01	PHLPP	PH domain and leucine rich repeat protein phosphatase	chr18q21.33	210919_at	NM_194449																			
2.75	2.74	0.00	9.76E-01	9.94E-01	---	---	---	215610_at	---																			
2.27	2.26	0.00	9.76E-01	9.94E-01	TGDS	TDP-glucose 4,6-dehydratase	chr13q32.1	237346_at	NM_014305																			

2.42	2.41	0.01	9.76E-01	9.94E-01	AZGP1P1	alpha-2-glycoprotein 1, zinc-binding pseudogene 1	chr7q22.1	217013_at	XR_017216 /// XR_037935 /// XR_039311 /// XR_039317																				
1.94	1.93	0.00	9.76E-01	9.94E-01	PDCL2	phosducin-like 2	chr4q12	237477_at	NM_152401																				
3.10	3.10	0.00	9.76E-01	9.94E-01	LOC731789	similar to amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	chr10p12.1	243971_x_at	XM_001130818 /// XM_001721652 /// XM_001722670																				
4.16	4.15	0.01	9.76E-01	9.94E-01	SLC25A30	solute carrier family 25, member 30	chr13q14.12	226782_at	NM_001010875																				
2.06	2.06	0.00	9.76E-01	9.94E-01	---	---	---	235947_at	---																				
2.09	2.09	0.00	9.76E-01	9.94E-01	NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	chr5q21.2	1562775_at	NM_031438																				
4.87	4.87	0.00	9.76E-01	9.94E-01	TCTN1	tectonic family member 1	chr12q24.11	1556864_at	NM_001082537 /// NM_001082538 /// NM_024549																				
2.03	2.03	0.00	9.76E-01	9.94E-01	---	---	---	1562850_at	---																				
2.94	2.94	0.00	9.76E-01	9.94E-01	---	---	---	240357_at	---																				
4.53	4.52	0.01	9.76E-01	9.94E-01	CHDH	Choline dehydrogenase	chr3p21.1	230484_at	NM_018397																				
3.19	3.19	0.01	9.76E-01	9.94E-01	MYL4	myosin, light chain 4, alkali; atrial, embryonic	chr17q21-qter	210088_x_at	NM_001002841 /// NM_002476																				
2.56	2.56	0.00	9.76E-01	9.94E-01	EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	chr3q26.3-q28	205222_at	NM_001966																				
9.18	9.18	0.01	9.76E-01	9.94E-01	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	chr22pter-q11.2|22q11.1	208678_at	NM_001039366 /// NM_001039367 /// NM_001696																				
3.91	3.91	0.00	9.76E-01	9.94E-01	LOC100128977	similar to hCG1654542	chr17q21.31	237331_s_at	XM_001715841 /// XM_001717446 /// XM_001719146																				
1.96	1.96	0.00	9.76E-01	9.94E-01	---	---	---	1553356_at	---																				
2.62	2.62	0.00	9.77E-01	9.94E-01	---	---	---	241314_at	---																				
4.21	4.20	0.01	9.77E-01	9.94E-01	ENOX2	ecto-NOX disulfide-thiol exchanger 2	chrXq25-q26.2	32042_at	NM_006375 /// NM_182314																				
3.01	3.01	0.01	9.77E-01	9.94E-01	ZNF251	zinc finger protein 251	chr8q24.3	226754_at	NM_138367																				
2.92	2.92	0.00	9.77E-01	9.94E-01	---	---	---	1559629_at	---																				
6.12	6.11	0.01	9.77E-01	9.94E-01	DIRC2	disrupted in renal carcinoma 2	chr3q21.1	226026_at	NM_032839																				
4.53	4.53	0.00	9.77E-01	9.94E-01	---	---	---	1562577_at	---																				
8.55	8.54	0.01	9.77E-01	9.94E-01	YPEL5	yippee-like 5 (Drosophila)	chr2p23.1	217783_s_at	NM_001127399 /// NM_001127400 /// NM_001127401 /// NM_016061																				
2.38	2.38	0.00	9.77E-01	9.94E-01	MGC10981	hypothetical protein MGC10981	chr4p16.1	1558216_at	XR_040178 /// XR_040179 /// XR_040180																				
4.19	4.18	0.01	9.77E-01	9.94E-01	SAPS3	SAPS domain family, member 3	chr11q13	232312_at	NM_018312																				
1.93	1.92	0.00	9.77E-01	9.94E-01	C2orf65	chromosome 2 open reading frame 65	chr2p13.1	1552849_at	NM_138804																				
5.81	5.80	0.01	9.77E-01	9.94E-01	PQLC2	PQ loop repeat containing 2	chr1p36.13	1555783_x_at	NM_001040125 /// NM_001040126 /// NM_017765																				
2.15	2.15	0.00	9.77E-01	9.94E-01	---	---	---	1567179_at	---																				
2.22	2.22	0.00	9.77E-01	9.94E-01	LY6K	lymphocyte antigen 6 complex, locus K	chr8q24.3	223688_s_at	NM_017527																				
3.88	3.88	0.00	9.77E-01	9.94E-01	FGF22	Fibroblast growth factor 22	chr19p13.3	1566816_at	NM_020637																				
2.18	2.17	0.00	9.77E-01	9.94E-01	---	---	---	242805_at	---																				
3.72	3.72	0.01	9.77E-01	9.94E-01	---	---	---	239269_at	---																				
1.81	1.81	0.00	9.78E-01	9.94E-01	---	---	---	1561069_at	---																				

2.45	2.45	0.00	9.78E-01	9.94E-01	LOC389457	hypothetical protein LOC389457	chr7p22.2	1563324_at	XM_374200 /// XM_374711 /// XM_941424																				
2.27	2.26	0.00	9.78E-01	9.94E-01	KIR3DX1	killer cell immunoglobulin-like receptor, three domains, X1	chr19q13.42	216428_x_at	NM_001047605																				
7.15	7.14	0.01	9.78E-01	9.94E-01	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	chr11q13.5	209323_at	NM_004705																				
5.83	5.82	0.00	9.78E-01	9.94E-01	---	---	---	217579_x_at	---																				
2.36	2.35	0.00	9.78E-01	9.94E-01	---	---	---	237575_at	---																				
7.54	7.53	0.01	9.78E-01	9.94E-01	BSCL2	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)	chr11q12-q13.5	208906_at	NM_001122955 /// NM_001130702 /// NM_032667																				
2.30	2.30	0.00	9.78E-01	9.94E-01	UBR2	Ubiquitin protein ligase E3 component n-recognin 2	chr6p21.1	215558_at	NM_015255																				
6.94	6.93	0.01	9.78E-01	9.94E-01	NCOA1	nuclear receptor coactivator 1	chr2p23	209106_at	NM_003743 /// NM_147223 /// NM_147233																				
2.05	2.05	0.00	9.78E-01	9.94E-01	CTAGE1	cutaneous T-cell lymphoma-associated antigen 1	chr18p11.2	220957_at	NM_172241																				
2.41	2.40	0.00	9.78E-01	9.94E-01	OTUD4	OTU domain containing 4	chr4q31.21	220669_at	NM_001102653 /// NM_017493 /// NM_199324																				
3.29	3.28	0.01	9.78E-01	9.94E-01	CDCA8	cell division cycle associated 8	chr1p34.3	221520_s_at	NM_018101																				
2.83	2.83	0.00	9.78E-01	9.94E-01	LOC283331	hypothetical protein LOC283331	chr12q13.13	1562457_at	NM_001037806																				
4.64	4.64	0.00	9.78E-01	9.94E-01	SPAG4L	sperm associated antigen 4-like	chr20q11.21	242668_x_at	NM_080675																				
3.67	3.66	0.01	9.78E-01	9.94E-01	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	chr11q23.3	243475_at	NM_005188																				
2.14	2.14	0.00	9.78E-01	9.94E-01	---	---	---	1564236_at	---																				
3.72	3.71	0.00	9.78E-01	9.94E-01	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	chr2q24.2	1555259_at	NM_016653 /// NM_133646																				
2.98	2.98	0.00	9.79E-01	9.94E-01	NCAM1	neural cell adhesion molecule 1	chr11q23.1	229799_s_at	NM_000615 /// NM_001076682 /// NM_181351																				
1.99	1.99	0.00	9.79E-01	9.94E-01	---	---	---	241086_at	---																				
7.27	7.26	0.01	9.79E-01	9.95E-01	FLJ20489	hypothetical protein FLJ20489	chr12q13.11	48106_at	NM_017842																				
2.18	2.17	0.00	9.79E-01	9.95E-01	---	---	---	1555755_at	---																				
6.64	6.64	0.01	9.79E-01	9.95E-01	GLRX3	glutaredoxin 3	chr10q26	214205_x_at	NM_006541																				
3.43	3.42	0.01	9.79E-01	9.95E-01	---	---	---	233810_x_at	---																				
1.94	1.94	0.00	9.79E-01	9.95E-01	---	---	---	1568902_at	---																				
5.89	5.88	0.01	9.79E-01	9.95E-01	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	chr3p21	223679_at	NM_001098209 /// NM_001098210 /// NM_001904																				
3.29	3.28	0.01	9.79E-01	9.95E-01	NODAL	nodal homolog (mouse)	chr10q22.1	230916_at	NM_018055																				
2.30	2.30	0.00	9.79E-01	9.95E-01	FAM71E2 /// LOC100133695	family with sequence similarity 71, member E2 /// similar to hCG2008618	chr19q13.42	1552990_at	XM_001718412 /// XM_001718633 /// XR_040337 /// XR_040338 /// XR_040339																				
3.67	3.66	0.01	9.79E-01	9.95E-01	C4orf16	chromosome 4 open reading frame 16	chr4q25	219023_at	NM_001128426 /// NM_018569																				
2.27	2.26	0.00	9.79E-01	9.95E-01	---	---	---	242666_at	---																				
4.13	4.12	0.00	9.79E-01	9.95E-01	WWOX	WW domain containing oxidoreductase	chr16q23.3-q24.1	223868_s_at	NM_016373 /// NM_130791 /// NM_130844																				
5.82	5.81	0.01	9.79E-01	9.95E-01	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	chr2q33.1	218343_s_at	NM_012086																				
6.52	6.51	0.01	9.79E-01	9.95E-01	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	chr13q14	218589_at	NM_005767																				
4.21	4.20	0.01	9.79E-01	9.95E-01	---	---	---	235534_at	---																				

3.31	3.30	0.00	9.79E-01	9.95E-01	ZFP112	zinc finger protein 112 homolog (mouse)	chr19q13.2	222237_s_at	NM_001083335 /// NM_013380
4.24	4.23	0.01	9.79E-01	9.95E-01	C14orf180	chromosome 14 open reading frame 180	chr14q32.33	1558421_a_at	NM_001008404
2.41	2.41	0.00	9.79E-01	9.95E-01	KLK10	kallikrein-related peptidase 10	chr19q13.3-q13.4	215808_at	NM_001077500 /// NM_002776 /// NM_145888
6.10	6.09	0.01	9.79E-01	9.95E-01	SLC2A4RG	SLC2A4 regulator	chr20q13.33	218494_s_at	NM_020062
3.76	3.75	0.01	9.79E-01	9.95E-01	TMF1	TATA element modulatory factor 1	chr3p21-p12	215855_s_at	NM_007114
3.05	3.05	0.00	9.79E-01	9.95E-01	---	---	---	244242_at	---
1.99	1.99	0.00	9.79E-01	9.95E-01	TTC9	tetratricopeptide repeat domain 9	chr14q24.2	213172_at	NM_015351
1.92	1.92	0.00	9.79E-01	9.95E-01	---	---	---	241274_at	---
5.44	5.44	0.01	9.79E-01	9.95E-01	MIPEP	mitochondrial intermediate peptidase	chr13q12	204305_at	NM_005932
2.06	2.06	0.00	9.80E-01	9.95E-01	---	---	---	236793_at	---
3.87	3.86	0.01	9.80E-01	9.95E-01	FEM1B	fem-1 homolog b (C. elegans)	chr15q22	212374_at	NM_015322
2.77	2.77	0.00	9.80E-01	9.95E-01	DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22	chr12q13.12	220441_at	NM_024902
2.43	2.43	0.00	9.80E-01	9.95E-01	---	---	---	234527_at	---
3.48	3.47	0.01	9.80E-01	9.95E-01	C1orf204 /// VSIG8	chromosome 1 open reading frame 204 /// V-set and immunoglobulin domain containing 8	chr1q23.1 /// chr1q23.2	1556633_at	NM_001013661 /// NM_001134233
2.45	2.44	0.00	9.80E-01	9.95E-01	SETMAR	SET domain and mariner transposase fusion gene	chr3p26.2	1554060_s_at	NM_006515 /// NR_024022
1.87	1.87	0.00	9.80E-01	9.95E-01	ALB	albumin	chr4q11-q13	1565228_s_at	NM_000477
2.98	2.98	0.00	9.80E-01	9.95E-01	---	---	---	236982_at	---
2.01	2.01	0.00	9.80E-01	9.95E-01	---	---	---	1565837_at	---
3.10	3.09	0.00	9.80E-01	9.95E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	210374_x_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719
2.10	2.09	0.00	9.80E-01	9.95E-01	---	---	---	1569853_at	---
2.76	2.75	0.00	9.80E-01	9.95E-01	TARS	Threonyl-tRNA synthetase	chr5p13.2	240206_at	NM_152295
6.54	6.53	0.01	9.80E-01	9.95E-01	TOM1L2	target of myb1-like 2 (chicken)	chr17p11.2	226198_at	NM_001033551 /// NM_001082968
4.28	4.27	0.00	9.80E-01	9.95E-01	SORBS3	sorbin and SH3 domain containing 3	chr8p21.3	207788_s_at	NM_001018003 /// NM_005775
5.09	5.08	0.00	9.80E-01	9.95E-01	PAOX	polyamine oxidase (exo-N4-amino)	chr10q26.3	221941_at	NM_152911 /// NM_207127 /// NM_207128
2.42	2.42	0.00	9.80E-01	9.95E-01	---	---	---	1561291_at	---
9.04	9.04	0.00	9.80E-01	9.95E-01	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	chr9q12	201347_x_at	NM_012203
2.83	2.83	0.00	9.81E-01	9.95E-01	SPEF2	sperm flagellar 2	chr5p13.2	233429_at	NM_024867 /// NM_144722
4.52	4.51	0.01	9.81E-01	9.95E-01	SERAC1	serine active site containing 1	chr6q25.3	232183_at	NM_032861
2.25	2.25	0.00	9.81E-01	9.95E-01	---	---	---	220767_at	---
2.37	2.37	0.00	9.81E-01	9.95E-01	FOXF2	forkhead box F2	chr6p25.3	206377_at	NM_001452
2.84	2.83	0.00	9.81E-01	9.95E-01	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	chr3p25-p24	211030_s_at	NM_001134367 /// NM_001134368 /// NM_003043
5.08	5.08	0.01	9.81E-01	9.95E-01	---	---	---	242467_at	---

4.61	4.60	0.01	9.81E-01	9.95E-01	CBFB	core-binding factor, beta subunit	chr16q22.1	206788_s_at	NM_001755 /// NM_022845
3.28	3.27	0.01	9.81E-01	9.95E-01	LOC100009676	Putative uncharacterized protein LOC100009676	chr3q12.3	232259_s_at	---
2.70	2.69	0.01	9.81E-01	9.95E-01	FLJ44451	hypothetical protein FLJ44451	chrXq28	1569315_s_at	XM_001714058
2.42	2.41	0.01	9.81E-01	9.95E-01	---	---	---	1557326_at	---
3.00	3.00	0.00	9.81E-01	9.95E-01	---	---	---	241517_at	---
5.35	5.34	0.01	9.81E-01	9.95E-01	MSI2	musashi homolog 2 (Drosophila)	chr17q22	225233_at	NM_138962 /// NM_170721
2.09	2.08	0.00	9.81E-01	9.95E-01	---	---	---	240414_at	---
2.43	2.43	0.00	9.81E-01	9.95E-01	WDR88	WD repeat domain 88	chr19q13.11	1552452_at	NM_173479
2.17	2.16	0.00	9.81E-01	9.95E-01	FAM45A	family with sequence similarity 45, member A	chr10q25	1563920_at	NM_207009
4.88	4.87	0.01	9.81E-01	9.95E-01	C2orf69	chromosome 2 open reading frame 69	chr2q33.1	227973_at	NM_153689
2.02	2.01	0.00	9.82E-01	9.95E-01	---	---	---	1556511_a_at	---
2.53	2.53	0.00	9.82E-01	9.95E-01	---	---	---	243235_at	---
2.76	2.75	0.00	9.82E-01	9.95E-01	---	---	---	234412_at	---
7.41	7.40	0.01	9.82E-01	9.95E-01	TMEM167A	transmembrane protein 167A	chr5q14.2	224702_at	NM_174909
6.32	6.32	0.00	9.82E-01	9.95E-01	LOC222070	hypothetical protein LOC222070	chr7p13	58900_at	---
1.96	1.96	0.00	9.82E-01	9.95E-01	TBX18	T-box 18	chr6q14-q15	1559839_at	NM_001080508
7.28	7.27	0.01	9.82E-01	9.95E-01	TMCO1	transmembrane and coiled-coil domains 1	chr1q22-q25	208715_at	NM_019026
4.74	4.73	0.01	9.82E-01	9.95E-01	LRRC43	leucine rich repeat containing 43	chr12q24.31	1553728_at	NM_001098519 /// NM_152759
2.30	2.29	0.00	9.82E-01	9.95E-01	CDH20	cadherin 20, type 2	chr18q22-q23	210913_at	NM_031891
2.05	2.05	0.00	9.82E-01	9.95E-01	HEMGN	hemogen	chr9q22.33	223669_at	NM_018437 /// NM_197978
2.11	2.10	0.00	9.82E-01	9.95E-01	---	---	---	244837_at	---
2.17	2.17	0.00	9.82E-01	9.95E-01	---	---	---	1567183_s_at	---
8.07	8.06	0.02	9.82E-01	9.95E-01	MOBKL3	MOB1, Mps One Binder kinase activator-like 3 (yeast)	chr2q33.1	202918_s_at	NM_001100819 /// NM_015387 /// NM_199482
2.07	2.06	0.00	9.82E-01	9.95E-01	LOC283514	similar to seven in absentia 2	chr13q14.12	1560676_at	NM_198849
2.30	2.30	0.00	9.82E-01	9.95E-01	RAD51AP1	RAD51 associated protein 1	chr12p13.2-p13.1	204146_at	NM_001130862 /// NM_006479
2.51	2.51	0.00	9.82E-01	9.95E-01	SENP5	SUMO1/sentrin specific peptidase 5	chr3q29	222110_at	NM_152699
3.28	3.27	0.01	9.82E-01	9.95E-01	---	---	---	242920_at	---
2.37	2.36	0.00	9.82E-01	9.95E-01	---	---	---	239649_at	---
1.77	1.76	0.00	9.82E-01	9.95E-01	SCEL	sciellin	chr13q22	1554920_at	NM_003843 /// NM_144777
4.28	4.27	0.01	9.82E-01	9.95E-01	CXYorf2	chromosome X and Y open reading frame 2	chrXp22.33; Yp11.3	241354_at	XR_040863 /// XR_040864
5.60	5.60	0.01	9.82E-01	9.95E-01	RIN3	Ras and Rab interactor 3	chr14q32.12	219457_s_at	NM_024832
2.82	2.82	0.00	9.82E-01	9.95E-01	CDRT1	CMT1A duplicated region transcript 1	chr17p12	208279_s_at	NM_006382
10.33	10.33	0.01	9.82E-01	9.95E-01	HLA-B	major histocompatibility complex, class I, B	chr6p21.3	208729_x_at	NM_005514
3.93	3.93	0.00	9.82E-01	9.95E-01	USP46	ubiquitin specific peptidase 46	chr4q12	203870_at	NM_001134223 /// NM_022832
6.12	6.12	0.01	9.82E-01	9.95E-01	C17orf63	chromosome 17 open reading frame 63	chr17q11.2	222641_s_at	NM_001077498 /// NM_018182
2.58	2.58	0.00	9.82E-01	9.95E-01	---	---	---	244750_at	---
3.00	3.00	0.00	9.82E-01	9.95E-01	TGFB2	transforming growth factor, beta 2	chr1q41	220406_at	NM_003238
3.13	3.13	0.00	9.83E-01	9.96E-01	---	---	---	240496_at	---
8.23	8.23	0.00	9.83E-01	9.96E-01	---	---	---	211976_at	---
7.74	7.74	0.01	9.83E-01	9.96E-01	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	chr10q21.3-q23.1	207543_s_at	NM_000917 /// NM_001017962
2.25	2.24	0.00	9.83E-01	9.96E-01	---	---	---	236842_at	---
7.47	7.47	0.00	9.83E-01	9.96E-01	KIAA0194	KIAA0194 protein	chr5q33.1	212431_at	XM_001714730 /// XM_001717202 /// XM_001717459
2.38	2.38	0.00	9.83E-01	9.96E-01	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	chr6q15	227173_s_at	NM_021813

4.07	4.07	0.01	9.83E-01	9.96E-01	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	chr12q21.3	215716_s_at	NM_001001323 /// NM_001682
5.54	5.53	0.00	9.83E-01	9.96E-01	GMDS	GDP-mannose 4,6-dehydratase	chr6p25	214106_s_at	NM_001500
2.09	2.08	0.00	9.83E-01	9.96E-01	---	---	---	1560745_at	---
8.09	8.08	0.01	9.83E-01	9.96E-01	CCL14 /// CCL15	chemokine (C-C motif) ligand 14 /// chemokine (C-C motif) ligand 15	chr17q11.2	205392_s_at	NM_004166 /// NM_004167 /// NM_032962 /// NM_032963 /// NM_032964 /// NM_032965
2.98	2.98	0.00	9.83E-01	9.96E-01	---	---	---	1559186_at	---
3.25	3.25	0.01	9.83E-01	9.96E-01	ABHD5	abhydrolase domain containing 5	chr3p21	213805_at	NM_016006
6.57	6.56	0.00	9.84E-01	9.96E-01	CYTH3	cytohesin 3	chr7p22.1	225147_at	NM_004227
3.65	3.65	0.00	9.84E-01	9.96E-01	C17orf52	chromosome 17 open reading frame 52	chr17q25.2	1556533_at	---
3.09	3.09	0.00	9.84E-01	9.96E-01	MAPK1	Mitogen-activated protein kinase 1	chr22q11.2|22q11.21	229847_at	NM_002745 /// NM_138957
2.32	2.32	0.00	9.84E-01	9.96E-01	ZNF549	zinc finger protein 549	chr19q13.43	215315_at	NM_153263
2.63	2.63	0.00	9.84E-01	9.96E-01	REG4	regenerating islet-derived family, member 4	chr1p13.1-p12	223447_at	NM_032044
2.32	2.32	0.00	9.84E-01	9.96E-01	---	---	---	1566842_at	---
3.54	3.53	0.00	9.84E-01	9.96E-01	---	---	---	243521_at	---
2.08	2.07	0.00	9.84E-01	9.96E-01	---	---	---	207779_at	---
3.68	3.67	0.01	9.84E-01	9.96E-01	---	---	---	229202_at	---
4.02	4.01	0.01	9.84E-01	9.96E-01	ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	chr9q34.1-q34.2	216929_x_at	NM_020469
1.97	1.97	0.00	9.84E-01	9.96E-01	LOC100132832 /// LOC392713 /// LOC441259 /// LOC730324 /// PMS2 /// PMS2L1 /// PMS2L2 /// PMS2L3 /// PMS2L5	similar to postmeiotic segregation increased 2-like 5 /// similar to hCG1989139 /// PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like /// similar to postmeiotic segregation increased 2-like 2 /// PMS2 postmeiotic segregation increased 2 (S. cerevisiae) /// postmeiotic segregation increased 2-like 1 pseudogene /// postmeiotic segregation increased 2-like 2 pseudogene /// postmeiotic segregation increased 2-like 3 /// postmeiotic segregation increased 2-like 5	chr7p22.2 /// chr7q11-q22 /// chr7q11.23 /// chr7q22.1	216039_at	NM_000535 /// NM_001003686 /// NM_001129851 /// NM_005395 /// NM_174930 /// NR_003085 /// NR_003613 /// NR_003614 /// XM_001713820 /// XM_001713964 /// XM_001714277 /// XM_001716315 /// XM_001718001 /// XM_001718158 /// XM_001722095 /// XM_001722503 /// XR_042144 /// XR_042161 /// XR_042167
3.32	3.31	0.00	9.84E-01	9.96E-01	---	---	---	228579_at	---
2.67	2.67	0.00	9.84E-01	9.96E-01	---	---	---	213817_at	---
2.67	2.67	0.00	9.84E-01	9.96E-01	---	---	---	233774_at	---
2.72	2.71	0.01	9.84E-01	9.96E-01	MAN1A2	mannosidase, alpha, class 1A, member 2	chr1p13	217921_at	NM_006699
3.31	3.31	0.00	9.84E-01	9.96E-01	---	---	---	1556636_at	---
2.07	2.07	0.00	9.84E-01	9.96E-01	---	---	---	239460_at	---
3.57	3.57	0.00	9.84E-01	9.96E-01	FANCC	Fanconi anemia, complementation group C	chr9q22.3	205189_s_at	NM_000136

2.47	2.47	0.00	9.84E-01	9.96E-01	OR2H1	olfactory receptor, family 2, subfamily H, member 1	chr6p21.3	216817_s_at	NM_030883
2.13	2.13	0.00	9.84E-01	9.96E-01	---	---	---	1561212_at	---
11.19	11.18	0.01	9.84E-01	9.96E-01	RPS7	ribosomal protein S7	chr2p25	213941_x_at	NM_001011
3.15	3.15	0.00	9.84E-01	9.96E-01	SFRP1	secreted frizzled-related protein 1	chr8p12-p11.1	202036_s_at	NM_003012
4.13	4.12	0.00	9.84E-01	9.96E-01	C9orf117	chromosome 9 open reading frame 117	chr9q34.11	1557867_s_at	NM_001012502
2.48	2.48	0.01	9.84E-01	9.96E-01	LCN12	lipocalin 12	chr9q34.3	230717_at	NM_178536
2.96	2.96	0.00	9.84E-01	9.96E-01	LOC728450	hypothetical LOC728450	chr20p12.2	232836_at	XM_001131473 /// XM_001133133
3.88	3.87	0.00	9.84E-01	9.96E-01	JMJD5	jumonji domain containing 5	chr16p12.1	241045_at	NM_024773
2.68	2.68	0.00	9.84E-01	9.96E-01	LOC100132891	Hypothetical protein LOC100132891	chr8q13.3	228438_at	XM_001715640 /// XM_001715754 /// XM_001715815
5.46	5.46	0.01	9.84E-01	9.96E-01	RANBP10	RAN binding protein 10	chr16q22.1	221809_at	NM_020850
2.53	2.53	0.00	9.84E-01	9.96E-01	NT5DC2	5'-nucleotidase domain containing 2	chr3p21.1	1556895_a_at	NM_001134231 /// NM_022908
4.10	4.09	0.01	9.85E-01	9.96E-01	EDN1	endothelin 1	chr6p24.1	222802_at	NM_001955
5.18	5.18	0.01	9.85E-01	9.96E-01	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	chr9p13.3	212817_at	NM_012266
2.06	2.06	0.00	9.85E-01	9.96E-01	---	---	---	240322_at	---
4.99	4.98	0.00	9.85E-01	9.96E-01	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	chr6q14-q15	223441_at	NM_012434
8.64	8.64	0.00	9.85E-01	9.96E-01	PPP2R1A	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	chr19q13.33	200695_at	NM_014225
2.73	2.73	0.00	9.85E-01	9.96E-01	---	---	---	230479_at	---
2.60	2.60	0.00	9.85E-01	9.96E-01	SLC14A2	solute carrier family 14 (urea transporter), member 2	chr18q12.1-q21.1	208409_at	NM_007163
1.97	1.97	0.00	9.85E-01	9.96E-01	---	---	---	242412_at	---
2.59	2.59	0.00	9.85E-01	9.96E-01	---	---	---	244113_at	---
5.60	5.59	0.01	9.85E-01	9.96E-01	COL5A1	collagen, type V, alpha 1	chr9q34.2-q34.3	203325_s_at	NM_000093
6.33	6.32	0.01	9.85E-01	9.96E-01	CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase	chr12p12.1	218111_s_at	NM_018686
2.23	2.23	0.00	9.85E-01	9.96E-01	PDE6D	Phosphodiesterase 6D, cGMP-specific, rod, delta	chr2q35-q36	231065_at	NM_002601
3.22	3.21	0.00	9.85E-01	9.96E-01	MED6	Mediator complex subunit 6	chr14q24.2	235473_at	NM_005466
6.29	6.29	0.01	9.85E-01	9.96E-01	ECD	ecdysoneless homolog (Drosophila)	chr10q22.1	203013_at	NM_007265
8.50	8.49	0.01	9.85E-01	9.96E-01	HECTD1	HECT domain containing 1	chr14q12	224481_s_at	NM_015382
2.18	2.18	0.00	9.85E-01	9.96E-01	LHX2	LIM homeobox 2	chr9q33-q34.1	206140_at	NM_004789
1.80	1.80	0.00	9.85E-01	9.96E-01	---	---	---	1557762_at	---
2.11	2.11	0.00	9.85E-01	9.96E-01	---	---	---	234546_at	---
1.98	1.97	0.00	9.85E-01	9.96E-01	---	---	---	1561264_at	---
6.02	6.01	0.01	9.85E-01	9.96E-01	GAS6 /// LOC100133684	growth arrest-specific 6 /// similar to growth arrest-specific 6	chr13q34	202177_at	NM_000820 /// XM_001716774
1.96	1.95	0.00	9.85E-01	9.96E-01	---	---	---	230127_at	---
3.06	3.06	0.00	9.85E-01	9.96E-01	PA2G4 /// PA2G4P4	proliferation-associated 2G4, 38kDa /// proliferation-associated 2G4 pseudogene 4	chr12q13.2 /// chr3q25.31	216422_at	NM_006191 /// NR_003284
2.84	2.83	0.00	9.85E-01	9.96E-01	LOC399959	Hypothetical gene supported by BX647608	chr11q24.1	236640_at	---
3.06	3.06	0.00	9.85E-01	9.96E-01	---	---	---	230537_at	---
2.49	2.49	0.00	9.85E-01	9.96E-01	FLJ40296 /// LOC729233 /// LOC729240 /// LOC729246 /// LOC729250	FLJ40296 protein /// FLJ40296 protein family member /// FLJ40296 protein family member /// FLJ40296 protein family member /// FLJ40296 protein family member	chr13q21.1	1562722_at	NM_001130404 /// NM_001130405 /// NM_001130406 /// NM_001130407 /// NM_198441 /// XM_001132952 /// XM_001132957 /// XM_001132961 /// XM_001132965
1.90	1.89	0.00	9.86E-01	9.96E-01	RHAG	Rh-associated glycoprotein	chr6p21.1-p11	206145_at	NM_000324
2.25	2.25	0.00	9.86E-01	9.96E-01	---	---	---	1562918_at	---
6.52	6.51	0.00	9.86E-01	9.96E-01	---	---	---	230350_at	---
2.69	2.68	0.00	9.86E-01	9.96E-01	ALG10B	asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	chr12q12	228941_at	NM_001013620

2.65	2.65	0.00	9.86E-01	9.96E-01	---	---	---	1560913_at	---
12.50	12.49	0.00	9.86E-01	9.96E-01	ACTB	actin, beta	chr7p15-p12	200801_x_at	NM_001101
2.72	2.72	0.00	9.86E-01	9.96E-01	---	---	---	1565613_at	---
1.99	1.99	0.00	9.86E-01	9.96E-01	SMCHD1	Structural maintenance of chromosomes flexible hinge domain containing 1	chr18p11.32	241621_at	NM_015295
2.60	2.60	0.00	9.86E-01	9.96E-01	HYAL4	hyaluronoglucosaminidase 4	chr7q31.3	220249_at	NM_012269
2.23	2.22	0.00	9.86E-01	9.96E-01	KIAA1984	KIAA1984	chr9q34.3	236518_at	NM_001039374
3.54	3.54	0.00	9.86E-01	9.96E-01	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	chr4p16.1	223574_x_at	NM_020416 /// NM_181876
7.57	7.56	0.00	9.86E-01	9.96E-01	GIT2	G protein-coupled receptor kinase interactor 2	chr12q24.1	225558_at	NM_014776 /// NM_057169 /// NM_057170 /// NM_139201
2.09	2.09	0.00	9.86E-01	9.96E-01	---	---	---	1570246_at	---
4.66	4.65	0.01	9.86E-01	9.96E-01	GPR172A	G protein-coupled receptor 172A	chr8q24.3	222155_s_at	NM_024531
2.09	2.09	0.00	9.86E-01	9.96E-01	---	---	---	1570290_at	---
4.99	4.99	0.00	9.86E-01	9.96E-01	CCDC106	coiled-coil domain containing 106	chr19q13.42	207006_s_at	NM_013301
2.00	2.00	0.00	9.86E-01	9.96E-01	---	---	---	1563333_at	---
1.92	1.92	0.00	9.86E-01	9.96E-01	FLJ37035	FLJ37035 protein	chr10q26.13	1565806_at	XR_000880 /// XR_000881 /// XR_001301 /// XR_001302
3.16	3.16	0.00	9.86E-01	9.96E-01	PPARGC1B	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	chr5q33.1	1553639_a_at	NM_133263
1.89	1.89	0.00	9.86E-01	9.96E-01	PBRM1	polybromo 1	chr3p21	223400_s_at	NM_018165 /// NM_018313 /// NM_181042
3.04	3.03	0.00	9.86E-01	9.96E-01	RAB26	RAB26, member RAS oncogene family	chr16p13.3	219562_at	NM_014353
3.47	3.47	0.00	9.86E-01	9.96E-01	SPPL2B	signal peptide peptidase-like 2B	chr19p13.3	215833_s_at	NM_001077238 /// NM_152988
2.36	2.36	0.00	9.86E-01	9.96E-01	KRTAP9-8	keratin associated protein 9-8	chr17q12-q21	234639_x_at	NM_031963
2.53	2.52	0.00	9.87E-01	9.96E-01	ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	chr2q33.1-q33.2	219834_at	NM_001104586 /// NM_024744
4.89	4.89	0.00	9.87E-01	9.96E-01	TMEM25	transmembrane protein 25	chr11q23.3	238514_at	NM_032780
7.29	7.29	0.00	9.87E-01	9.96E-01	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	chr20p13	201052_s_at	NM_006814 /// NM_178578
2.64	2.63	0.00	9.87E-01	9.96E-01	LOC100131112	similar to hCG2002332	chr8p23.1	230562_at	XM_001720176 /// XM_001720260 /// XM_001721654
3.05	3.05	0.00	9.87E-01	9.96E-01	FAM166A	family with sequence similarity 166, member A	chr9q34.3	233971_at	NM_001001710
2.63	2.62	0.00	9.87E-01	9.96E-01	---	---	---	240543_at	---
6.77	6.76	0.01	9.87E-01	9.96E-01	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	chr4q21.1	208841_s_at	NM_012297 /// NM_203504 /// NM_203505
3.51	3.51	0.00	9.87E-01	9.96E-01	UBR5	ubiquitin protein ligase E3 component n-recognin 5	chr8q22	208883_at	NM_015902
2.51	2.51	0.00	9.87E-01	9.96E-01	---	---	---	240108_at	---
2.98	2.98	0.00	9.87E-01	9.96E-01	C1orf116	chromosome 1 open reading frame 116	chr1q32.1	219856_at	NM_001083924 /// NM_023938
4.88	4.88	0.00	9.87E-01	9.96E-01	GFM1	G elongation factor, mitochondrial 1	chr3q25.1-q26.2	225158_at	NM_024996
6.23	6.23	0.00	9.87E-01	9.96E-01	METTL2A /// METTL2B	methyltransferase like 2A /// methyltransferase like 2B	chr17q23.2 /// chr7q32.1	225253_s_at	NM_001005372 /// NM_018396 /// NM_181725

2.04	2.04	0.00	9.87E-01	9.96E-01	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4 /// LOC732447	deleted in azoospermia 1 /// deleted in azoospermia 2 /// deleted in azoospermia 3 /// deleted in azoospermia 4 /// similar to deleted in azoospermia-like	chrYq11.223	207909_x_at	NM_001005375 /// NM_001005785 /// NM_001005786 /// NM_004081 /// NM_020363 /// NM_020364 /// NM_020420 /// XM_001718583 /// XM_001720105 /// XM_001722775																			
2.41	2.41	0.00	9.87E-01	9.96E-01	---	---	---	1561610_at	---																				
7.19	7.19	0.01	9.87E-01	9.96E-01	ADD3	adducin 3 (gamma)	chr10q24.2-q24.3	201034_at	NM_001121 /// NM_016824 /// NM_019903																				
2.18	2.18	0.00	9.87E-01	9.96E-01	FAM80A	family with sequence similarity 80, member A	chr1p34.2	241075_at	NM_173642																				
4.65	4.65	0.00	9.87E-01	9.96E-01	C17orf28	chromosome 17 open reading frame 28	chr17q25.1	225981_at	NM_030630																				
2.80	2.79	0.00	9.87E-01	9.96E-01	FGFBP3	fibroblast growth factor binding protein 3	chr10q23.32	238453_at	NM_152429																				
3.25	3.25	0.00	9.87E-01	9.96E-01	OR7E47P	olfactory receptor, family 7, subfamily E, member 47 pseudogene	chr12q13.13	222304_x_at	---																				
7.05	7.04	0.00	9.87E-01	9.96E-01	CLINT1	clathrin interactor 1	chr5q33.3	201769_at	NM_014666 /// XM_001715730 /// XM_001723151 /// XM_001725023																				
5.09	5.08	0.01	9.88E-01	9.97E-01	ARHGAP18	Rho GTPase activating protein 18	chr6q22.33	225166_at	NM_033515																				
5.82	5.81	0.01	9.88E-01	9.97E-01	RASAL1	RAS protein activator like 1 (GAP1 like)	chr12q23-q24	219752_at	NM_004658																				
2.21	2.21	0.00	9.88E-01	9.97E-01	---	---	---	240266_at	---																				
2.34	2.34	0.00	9.88E-01	9.97E-01	LOC100129858	hypothetical protein LOC100129858	chr4q31.1	235869_at	XM_001720192 /// XM_001720230 /// XM_001725468																				
2.04	2.04	0.00	9.88E-01	9.97E-01	PROM1	prominin 1	chr4p15.32	204304_s_at	NM_006017																				
2.30	2.30	0.00	9.88E-01	9.97E-01	---	---	---	233731_at	---																				
2.49	2.49	0.00	9.88E-01	9.97E-01	SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	chr16q22.1	232564_at	NM_004594																				
2.91	2.91	0.00	9.88E-01	9.97E-01	LOC646588	hypothetical protein LOC646588	chr7p15.2	236977_at	XM_001722042 /// XM_933738 /// XM_935989 /// XM_943454																				
3.46	3.46	0.00	9.88E-01	9.97E-01	IL1RL1	Interleukin 1 receptor-like 1	chr2q12	234066_at	NM_003856 /// NM_016232																				
2.89	2.89	0.00	9.88E-01	9.97E-01	---	---	---	1559916_a_at	---																				
3.11	3.11	0.00	9.88E-01	9.97E-01	ARHGAP20	Rho GTPase activating protein 20	chr11q22.3-q23.1	1555020_a_at	NM_020809																				
5.56	5.56	0.00	9.88E-01	9.97E-01	C22orf39	chromosome 22 open reading frame 39	chr22q11.21	227086_at	NM_173793																				
2.01	2.01	0.00	9.88E-01	9.97E-01	MYLK4	myosin light chain kinase family, member 4	chr6p25.2	1561504_s_at	NM_001012418																				
2.37	2.37	0.00	9.88E-01	9.97E-01	FNBP1	formin binding protein 1	chr9q34	230086_at	NM_015033																				
3.08	3.08	0.00	9.88E-01	9.97E-01	TRAIP	TRAF interacting protein	chr3p21.31	205598_at	NM_005879																				
4.23	4.22	0.00	9.88E-01	9.97E-01	---	---	---	215553_x_at	---																				
6.63	6.63	0.00	9.88E-01	9.97E-01	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	chr10q24	202730_s_at	NM_014456 /// NM_145341																				

3.11	3.11	0.00	9.88E-01	9.97E-01	MRPS12	Mitochondrial ribosomal protein S12	chr19q13.1-q13.2	213840_s_at	NM_021107 /// NM_033362 /// NM_033363																				
3.15	3.15	0.00	9.88E-01	9.97E-01	SAP30	Sin3A-associated protein, 30kDa	chr4q34.1	213963_s_at	NM_003864																				
2.66	2.65	0.00	9.88E-01	9.97E-01	DPPA4	developmental pluripotency associated 4	chr3q13.13	241199_x_at	NM_018189																				
4.26	4.26	0.01	9.88E-01	9.97E-01	PDZD8	PDZ domain containing 8	chr10q25.3-q26.11	225829_at	NM_173791																				
2.19	2.19	0.00	9.89E-01	9.97E-01	LOC645188	hypothetical LOC645188	chrXq27.2	1560895_at	XR_040416 /// XR_040417																				
7.93	7.92	0.00	9.89E-01	9.97E-01	AP3S2	adaptor-related protein complex 3, sigma 2 subunit	chr15q26.1	202399_s_at	NM_005829 /// NR_023361																				
3.12	3.12	0.00	9.89E-01	9.97E-01	WDR36	WD repeat domain 36	chr5q22.1	238677_at	NM_139281																				
5.06	5.06	0.00	9.89E-01	9.97E-01	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	chr10p15.3	1565681_s_at	NM_014974																				
3.20	3.20	0.00	9.89E-01	9.97E-01	---	---	---	237156_at	---																				
6.03	6.01	0.01	9.89E-01	9.97E-01	CYB5A	cytochrome b5 type A (microsomal)	chr18q23	215726_s_at	NM_001914 /// NM_148923																				
3.57	3.56	0.01	9.89E-01	9.97E-01	GNA13	guanine nucleotide binding protein (G protein), alpha 13	chr17q24.3	206917_at	NM_006572																				
4.99	4.99	0.01	9.89E-01	9.97E-01	C16orf63	chromosome 16 open reading frame 63	chr16p13.11	225088_at	NM_144600																				
2.04	2.04	0.00	9.89E-01	9.97E-01	---	---	---	1562710_at	---																				
8.83	8.83	0.00	9.89E-01	9.97E-01	SELT	selenoprotein T	chr3q25.1	217811_at	NM_016275																				
6.32	6.32	0.00	9.89E-01	9.97E-01	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	chr2p15	222870_s_at	NM_006577																				
2.39	2.39	0.00	9.89E-01	9.97E-01	ZNF572	zinc finger protein 572	chr8q24.13	1553229_at	NM_152412																				
2.34	2.33	0.00	9.89E-01	9.97E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	216901_s_at	NM_006060																				
5.19	5.18	0.00	9.89E-01	9.97E-01	RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	chr2cen-q13	202101_s_at	NM_002881																				
7.64	7.64	0.00	9.89E-01	9.97E-01	UBE2L3	ubiquitin-conjugating enzyme E2L 3	chr22q11.21	200683_s_at	NM_003347 /// NM_198157																				
5.93	5.92	0.00	9.89E-01	9.97E-01	HSPB11	heat shock protein family B (small), member 11	chr1p32.1-p33	203960_s_at	NM_016126																				
3.34	3.34	0.00	9.89E-01	9.97E-01	KIAA1217	KIAA1217	chr10p12.2-p12.1	237167_at	NM_001098500 /// NM_001098501 /// NM_019590																				
2.54	2.54	0.00	9.89E-01	9.97E-01	---	---	---	241504_at	---																				
6.58	6.57	0.00	9.89E-01	9.97E-01	HPS1	Hermansky-Pudlak syndrome 1	chr10q23.1-q23.3	203308_x_at	NM_000195 /// NM_182639																				
4.01	4.00	0.00	9.89E-01	9.97E-01	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	chr5p15.2	229068_at	NM_012073																				
6.79	6.79	0.00	9.89E-01	9.97E-01	METRN	meteorin, glial cell differentiation regulator	chr16p13.3	232269_x_at	NM_024042																				
2.42	2.42	0.00	9.89E-01	9.97E-01	---	---	---	241118_at	---																				
3.70	3.70	0.00	9.89E-01	9.97E-01	CENTD3	centaurin, delta 3	chr5q31.3	235806_at	NM_022481																				
2.44	2.44	0.00	9.89E-01	9.97E-01	IFNA4	interferon, alpha 4	chr9p22	207964_x_at	NM_021068																				
4.00	4.00	0.00	9.89E-01	9.97E-01	---	---	---	244862_at	---																				
2.34	2.34	0.00	9.90E-01	9.97E-01	---	---	---	234146_at	---																				
2.92	2.91	0.00	9.90E-01	9.97E-01	FARSB	phenylalanyl-tRNA synthetase, beta subunit	chr2q36.1	232063_x_at	NM_005687																				
2.27	2.26	0.00	9.90E-01	9.97E-01	FCRL2	Fc receptor-like 2	chr1q21	1563674_at	NM_030764 /// NM_138738																				
5.74	5.73	0.01	9.90E-01	9.97E-01	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	chr11q12.2	244627_at	NM_015533																				
3.29	3.29	0.00	9.90E-01	9.97E-01	---	---	---	243574_at	---																				
2.95	2.94	0.00	9.90E-01	9.97E-01	CCNB3	cyclin B3	chrXp11	231481_at	NM_033031 /// NM_033670																				
5.30	5.30	0.00	9.90E-01	9.97E-01	NSUN4	NOL1/NOP2/Sun domain family, member 4	chr1p34	236247_at	NM_199044																				
3.87	3.87	0.00	9.90E-01	9.97E-01	TBC1D10C	TBC1 domain family, member 10C	chr11q13.1	228258_at	NM_198517																				
5.48	5.48	0.01	9.90E-01	9.97E-01	STAMBPL1	STAM binding protein-like 1	chr10q23.31	227606_s_at	NM_020799																				
5.60	5.59	0.01	9.90E-01	9.97E-01	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	chr7q36.3	208810_at	NM_005494 /// NM_058246																				
2.77	2.77	0.00	9.90E-01	9.97E-01	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	1558144_at	NR_002766 /// NR_003530 /// NR_003531																				
2.30	2.30	0.00	9.90E-01	9.97E-01	PCA3	Prostate cancer antigen 3 (non-protein coding)	chr9q21-q22	232572_at	NR_015342																				
2.29	2.29	0.00	9.90E-01	9.97E-01	---	---	---	230594_at	---																				

1.93	1.92	0.00	9.90E-01	9.97E-01	ARL17 /// ARL17P1	ADP-ribosylation factor-like 17 /// ADP-ribosylation factor-like 17 pseudogene 1	chr17q21.31 /// chr17q21.32	1555794_at	NM_001039083 /// NM_001103154 /// NM_001113738 /// NM_016632
2.06	2.05	0.00	9.90E-01	9.97E-01	PDLIM3	PDZ and LIM domain 3	chr4q35	238592_at	NM_001114107 /// NM_014476
2.86	2.86	0.00	9.90E-01	9.97E-01	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	chr16p13.11	1560014_s_at	NM_015027
2.51	2.51	0.00	9.90E-01	9.97E-01	GPRC6A	G protein-coupled receptor, family C, group 6, member A	chr6q22.2	1552775_at	NM_148963
5.67	5.66	0.00	9.90E-01	9.97E-01	GEMIN5	gem (nuclear organelle) associated protein 5	chr5q33.2	225712_at	NM_015465
4.52	4.52	0.00	9.90E-01	9.97E-01	FAM107A	family with sequence similarity 107, member A	chr3p21.1	207547_s_at	NM_001076778 /// NM_007177
2.50	2.50	0.00	9.90E-01	9.97E-01	IPO11	importin 11	chr5q12.1	1557770_at	NM_016338
1.89	1.89	0.00	9.90E-01	9.97E-01	---	---	---	1552974_at	---
2.49	2.49	0.00	9.91E-01	9.97E-01	---	---	---	1563171_at	---
3.28	3.28	0.00	9.91E-01	9.97E-01	HIF3A	hypoxia inducible factor 3, alpha subunit	chr19q13.32	222123_s_at	NM_022462 /// NM_152794 /// NM_152795
2.33	2.33	0.00	9.91E-01	9.97E-01	RSPH10B /// RSPH10B2	radial spoke head 10 homolog B (Chlamydomonas) /// radial spoke head 10 homolog B2 (Chlamydomonas)	chr7p22.1	1557417_s_at	NM_001099697 /// NM_173565
9.82	9.82	0.00	9.91E-01	9.97E-01	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	chr21q22.1-q22.2|21q22.11	200818_at	NM_001697
5.18	5.18	0.00	9.91E-01	9.97E-01	ACVR1B	activin A receptor, type IB	chr12q13	205209_at	NM_004302 /// NM_020327 /// NM_020328
6.43	6.42	0.00	9.91E-01	9.97E-01	TMEM132A	transmembrane protein 132A	chr11q12.2	218834_s_at	NM_017870 /// NM_178031
3.35	3.34	0.00	9.91E-01	9.97E-01	MMP11	matrix metallopeptidase 11 (stromelysin 3)	chr22q11.2|22q11.23	203877_at	NM_005940
1.88	1.88	0.00	9.91E-01	9.97E-01	ZNF479	zinc finger protein 479	chr7p11.2	1555367_at	NM_033273 /// XM_001714591 /// XM_001719979
9.38	9.37	0.00	9.91E-01	9.97E-01	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	chr5p13	210757_x_at	NM_001343
3.39	3.39	0.00	9.91E-01	9.97E-01	ZNF81	Zinc finger protein 81	chrXp11.23	240079_at	NM_007137
6.35	6.34	0.00	9.91E-01	9.97E-01	CRIPT	cysteine-rich PDZ-binding protein	chr2p21	227942_s_at	NM_014171
3.09	3.09	0.00	9.91E-01	9.97E-01	FGD2	FYVE, RhoGEF and PH domain containing 2	chr6p21.2	215602_at	NM_173558
6.92	6.91	0.00	9.91E-01	9.97E-01	EXTL2	exostoses (multiple)-like 2	chr1p21	209537_at	NM_001033025 /// NM_001439
2.07	2.07	0.00	9.91E-01	9.97E-01	---	---	---	1557921_s_at	---
2.89	2.89	0.00	9.91E-01	9.97E-01	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	chr3q29	228119_at	NM_032773
3.13	3.13	0.00	9.91E-01	9.97E-01	HBQ1	hemoglobin, theta 1	chr16p13.3	220807_at	NM_005331
3.02	3.02	0.00	9.91E-01	9.97E-01	FAM179A	family with sequence similarity 179, member A	chr2p23.2	236717_at	NM_199280
3.06	3.06	0.00	9.91E-01	9.97E-01	RHD	Rh blood group, D antigen	chr1p36.11	210586_x_at	NM_001127691 /// NM_016124
7.84	7.84	0.00	9.91E-01	9.97E-01	EHD2	EH-domain containing 2	chr19q13.3	221870_at	NM_014601
2.15	2.15	0.00	9.91E-01	9.97E-01	KLF12	Kruppel-like factor 12	chr13q22	238940_at	NM_007249
2.11	2.11	0.00	9.92E-01	9.97E-01	---	---	---	207331_at	---
2.42	2.42	0.00	9.92E-01	9.97E-01	---	---	---	1570644_at	---
2.80	2.80	0.00	9.92E-01	9.97E-01	---	---	---	244236_at	---
4.46	4.46	0.00	9.92E-01	9.97E-01	ZNF219	Zinc finger protein 219	chr14q11	228511_s_at	NM_001101672 /// NM_001102454 /// NM_016423
3.92	3.92	0.00	9.92E-01	9.97E-01	OPRL1	opiate receptor-like 1	chr20q13.33	206564_at	NM_000913 /// NM_182647
2.92	2.92	0.00	9.92E-01	9.97E-01	KRTAP13-1	keratin associated protein 13-1	chr21q22.1	1564921_at	NM_181599
1.99	1.99	0.00	9.92E-01	9.97E-01	CLTC	Clathrin, heavy chain (Hc)	chr17q11-qter	239871_at	NM_004859
3.05	3.05	0.00	9.92E-01	9.97E-01	MGC20647	hypothetical protein MGC20647	chr22q12.1	1554305_at	---

2.19	2.18	0.00	9.92E-01	9.97E-01	---	---	---	233222_at	---
2.57	2.57	0.00	9.92E-01	9.97E-01	---	---	---	1559683_at	---
4.79	4.79	0.00	9.92E-01	9.97E-01	RAB11B	RAB11B, member RAS oncogene family	chr19p13.2	217793_at	NM_004218
2.33	2.32	0.00	9.92E-01	9.97E-01	FBXO32	F-box protein 32	chr8q24.13	241763_s_at	NM_058229 /// NM_148177
2.26	2.26	0.00	9.92E-01	9.97E-01	TTLL2	tubulin tyrosine ligase-like family, member 2	chr6q27	223998_at	NM_031949
2.12	2.12	0.00	9.92E-01	9.97E-01	RNASE11	ribonuclease, RNase A family, 11 (non-active)	chr14q11.2	231603_at	NM_145250
4.50	4.50	0.00	9.92E-01	9.97E-01	---	---	---	234438_at	---
4.30	4.30	0.00	9.92E-01	9.97E-01	TCF7L2	Transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10q25.3	236094_at	NM_030756
3.11	3.11	0.00	9.92E-01	9.97E-01	FPR2	formyl peptide receptor 2	chr19q13.3-q13.4	210773_s_at	NM_001005738 /// NM_001462
2.65	2.65	0.00	9.92E-01	9.97E-01	WNK1	WNK lysine deficient protein kinase 1	chr12p13.3	39313_at	NM_018979
1.95	1.95	0.00	9.92E-01	9.97E-01	---	---	---	244228_at	---
1.88	1.88	0.00	9.92E-01	9.97E-01	---	---	---	241863_x_at	---
4.14	4.13	0.01	9.92E-01	9.97E-01	SULF1	sulfatase 1	chr8q13.2-q13.3	212354_at	NM_001128204 /// NM_001128205 /// NM_001128206 /// NM_015170
3.45	3.45	0.00	9.92E-01	9.97E-01	FLJ46321	FLJ46321 protein	chr9q21.32	237378_at	NM_001001670
2.61	2.61	0.00	9.92E-01	9.97E-01	---	---	---	1566217_at	---
4.98	4.98	0.00	9.92E-01	9.97E-01	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	chrXq24	211855_s_at	NM_003951 /// NM_022810
5.16	5.16	0.00	9.92E-01	9.97E-01	CABP4	calcium binding protein 4	chr11q13.1	1554201_at	NM_145200
2.26	2.26	0.00	9.93E-01	9.98E-01	ZBTB44	zinc finger and BTB domain containing 44	chr11q24.3	1554469_at	NM_014155
2.00	2.00	0.00	9.93E-01	9.98E-01	---	---	---	233419_at	---
3.34	3.34	0.00	9.93E-01	9.98E-01	---	---	---	238782_at	---
2.16	2.16	0.00	9.93E-01	9.98E-01	PCDHGC5	protocadherin gamma subfamily C, 5	chr5q31	224537_at	NM_018929 /// NM_032407
1.95	1.95	0.00	9.93E-01	9.98E-01	---	---	---	1570423_at	---
8.53	8.53	0.00	9.93E-01	9.98E-01	PPP6C	protein phosphatase 6, catalytic subunit	chr9q33.3	203529_at	NM_001123355 /// NM_001123369 /// NM_002721
2.25	2.25	0.00	9.93E-01	9.98E-01	---	---	---	241900_at	---
3.03	3.02	0.00	9.93E-01	9.98E-01	TMPO	thymopoietin	chr12q22	209753_s_at	NM_001032283 /// NM_001032284 /// NM_003276
7.35	7.34	0.00	9.93E-01	9.98E-01	INSR	insulin receptor	chr19p13.3-p13.2	226450_at	NM_000208 /// NM_001079817
5.08	5.08	0.00	9.93E-01	9.98E-01	C11orf53	chromosome 11 open reading frame 53	chr11q23.1	1554188_at	NM_198498
2.77	2.77	0.00	9.93E-01	9.98E-01	---	---	---	1562962_at	---
2.30	2.30	0.00	9.93E-01	9.98E-01	LOC285847	hypothetical protein LOC285847	chr6p21.31	1570131_at	XM_934928 /// XM_934929 /// XM_945988 /// XM_945990
2.00	2.00	0.00	9.93E-01	9.98E-01	HDAC9	histone deacetylase 9	chr7p21.1	1552760_at	NM_014707 /// NM_058176 /// NM_058177 /// NM_178423 /// NM_178425
2.46	2.46	0.00	9.93E-01	9.98E-01	---	---	---	1560024_at	---
4.18	4.18	0.00	9.93E-01	9.98E-01	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	chr2q31	1567013_at	NM_006164

3.23	3.23	0.00	9.93E-01	9.98E-01	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6	chr15q13-q15	220740_s_at	NM_001042494 /// NM_001042495 /// NM_001042496 /// NM_001042497 /// NM_005135 /// NM_133647																				
2.71	2.71	0.00	9.93E-01	9.98E-01	TCL1A	T-cell leukemia/lymphoma 1A	chr14q32.1	209995_s_at	NM_001098725 /// NM_021966																				
8.54	8.54	0.00	9.94E-01	9.98E-01	EGR1	early growth response 1	chr5q31.1	201694_s_at	NM_001964																				
2.35	2.35	0.00	9.94E-01	9.98E-01	PRKY	protein kinase, Y-linked	chrYp11.2	206279_at	NM_002760																				
5.66	5.66	0.00	9.94E-01	9.98E-01	PLAC9	placenta-specific 9	chr10q22.3	227419_x_at	NM_001012973																				
4.90	4.90	0.01	9.94E-01	9.98E-01	CD36	CD36 molecule (thrombospondin receptor)	chr7q11.2	206488_s_at	NM_000072 /// NM_001001547 /// NM_001001548 /// NM_001127443 /// NM_001127444																				
4.70	4.69	0.00	9.94E-01	9.98E-01	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	chr10q22.2	213092_x_at	NM_015190																				
2.10	2.10	0.00	9.94E-01	9.98E-01	---	---	---	240738_at	---																				
5.56	5.56	0.00	9.94E-01	9.98E-01	CUEDC1	CUE domain containing 1	chr17q23.2	1555786_s_at	NM_017949																				
1.93	1.93	0.00	9.94E-01	9.98E-01	---	---	---	1563503_at	---																				
4.60	4.59	0.00	9.94E-01	9.98E-01	CCDC13	coiled-coil domain containing 13	chr3p22.1	1553397_at	NM_144719																				
1.86	1.85	0.00	9.94E-01	9.98E-01	FAM84A	Family with sequence similarity 84, member A	chr2p24.3	234335_s_at	NM_145175																				
1.92	1.92	0.00	9.94E-01	9.98E-01	UNC13C	unc-13 homolog C (C. elegans)	chr15q21.3	1556095_at	NM_001080534																				
1.95	1.95	0.00	9.94E-01	9.98E-01	---	---	---	1565633_at	---																				
6.96	6.96	0.00	9.94E-01	9.98E-01	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	chr7p22	1567458_s_at	NM_006908 /// NM_018890 /// NM_198829																				
2.76	2.76	0.00	9.94E-01	9.98E-01	CACNG8	calcium channel, voltage-dependent, gamma subunit 8	chr19q13.4	234750_at	NM_031895																				
3.57	3.56	0.00	9.94E-01	9.98E-01	FKBP1B	FK506 binding protein 1B, 12.6 kDa	chr2p23.3	206857_s_at	NM_004116 /// NM_054033																				
2.55	2.55	0.00	9.94E-01	9.98E-01	JUB	jub, ajuba homolog (Xenopus laevis)	chr14q11.2	225807_at	NM_032876 /// NM_198086																				
6.86	6.86	0.00	9.94E-01	9.98E-01	DENR	density-regulated protein	chr12q24.31	221509_at	NM_003677																				
2.06	2.06	0.00	9.95E-01	9.98E-01	LOC730051	similar to hCG2044798	chr19q13.43	241912_at	XM_001725674 /// XM_001725708 /// XM_001726286																				
6.03	6.03	0.00	9.95E-01	9.98E-01	C1orf50	chromosome 1 open reading frame 50	chr1p34.2	219406_at	NM_024097																				
2.14	2.14	0.00	9.95E-01	9.98E-01	LOC51152	melanoma antigen	---	220771_at	XR_041657																				
4.69	4.69	0.00	9.95E-01	9.99E-01	PIK3R2	Phosphoinositide-3-kinase, regulatory subunit 2 (beta)	chr19q13.2-q13.4	229392_s_at	NM_005027																				
4.99	4.99	0.00	9.95E-01	9.99E-01	TPBG	trophoblast glycoprotein	chr6q14-q15	203476_at	NM_006670																				
6.16	6.15	0.00	9.95E-01	9.99E-01	RGNEF	Rho-guanine nucleotide exchange factor	chr5q13.2	232994_s_at	NM_001080479																				
2.43	2.43	0.00	9.95E-01	9.99E-01	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	chr4q13.3	1553267_a_at	NM_144571																				
4.11	4.10	0.00	9.95E-01	9.99E-01	---	---	---	240203_at	---																				
10.41	10.41	0.00	9.95E-01	9.99E-01	RPS27L	ribosomal protein S27-like	chr15q22.2	218007_s_at	NM_015920																				
7.89	7.89	0.00	9.95E-01	9.99E-01	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	chr11q12.1	223922_x_at	NM_022349 /// NM_152851 /// NM_152852																				
2.42	2.42	0.00	9.95E-01	9.99E-01	---	---	---	240319_at	---																				
2.90	2.90	0.00	9.95E-01	9.99E-01	---	---	---	234113_at	---																				
4.72	4.72	0.00	9.95E-01	9.99E-01	FBF1	Fas (TNFRSF6) binding factor 1	chr17q25.1	1555288_s_at	NM_001080542																				

2.81	2.81	0.00	9.95E-01	9.99E-01	NR1I2	nuclear receptor subfamily 1, group I, member 2	chr3q12-q13.3	207202_s_at	NM_003889 /// NM_022002 /// NM_033013
2.45	2.45	0.00	9.95E-01	9.99E-01	---	---	---	1559544_s_at	---
2.28	2.28	0.00	9.95E-01	9.99E-01	---	---	---	1569659_at	---
1.88	1.87	0.00	9.95E-01	9.99E-01	---	---	---	1570452_at	---
2.47	2.47	0.00	9.95E-01	9.99E-01	TMCO5A	transmembrane and coiled-coil domains 5A	chr15q14	1553637_s_at	NM_152453
2.25	2.25	0.00	9.95E-01	9.99E-01	PTPN2	Protein tyrosine phosphatase, non-receptor type 2	chr18p11.3-p11.2	241622_at	NM_002828 /// NM_080422 /// NM_080423
3.00	3.00	0.00	9.96E-01	9.99E-01	---	---	---	244161_at	---
2.46	2.46	0.00	9.96E-01	9.99E-01	TRAV8-3	T cell receptor alpha variable 8-3	chr14q11	215797_at	---
2.24	2.24	0.00	9.96E-01	9.99E-01	PRDM9	PR domain containing 9	chr5p14	221151_at	NM_020227
6.68	6.67	0.00	9.96E-01	9.99E-01	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	chr11q23.3	225234_at	NM_005188
3.74	3.74	0.00	9.96E-01	9.99E-01	RUNDC3A	RUN domain containing 3A	chr17q21.31	206196_s_at	NM_006695
7.06	7.06	0.00	9.96E-01	9.99E-01	PPME1	protein phosphatase methylesterase 1	chr11q13.4	49077_at	NM_016147
4.93	4.93	0.00	9.96E-01	9.99E-01	SELENBP1	selenium binding protein 1	chr1q21-q22	214433_s_at	NM_003944
2.57	2.57	0.00	9.96E-01	9.99E-01	LOC285431	hypothetical protein LOC285431	chr4q35.1	243688_at	---
2.00	2.00	0.00	9.96E-01	9.99E-01	---	---	---	241352_at	---
2.67	2.67	0.00	9.96E-01	9.99E-01	---	---	---	243553_x_at	---
2.29	2.28	0.00	9.96E-01	9.99E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	1570471_at	NM_015313
5.42	5.41	0.00	9.96E-01	9.99E-01	CKAP2	cytoskeleton associated protein 2	chr13q14	218252_at	NM_001098525 /// NM_018204
2.05	2.05	0.00	9.96E-01	9.99E-01	---	---	---	240707_at	---
4.86	4.86	0.00	9.96E-01	9.99E-01	MSH6	MutS homolog 6 (E. coli)	chr2p16	240148_at	NM_000179
5.50	5.50	0.00	9.96E-01	9.99E-01	TGFBR1	transforming growth factor, beta receptor 1	chr9q22	224793_s_at	NM_001130916 /// NM_004612
2.07	2.07	0.00	9.96E-01	9.99E-01	---	---	---	AFFX-r2-Bs-lys-5_at	---
2.99	2.99	0.00	9.96E-01	9.99E-01	HMG20B	High-mobility group 20B	chr19p13.3	213966_at	NM_006339
3.01	3.01	0.00	9.96E-01	9.99E-01	---	---	---	236901_at	---
2.46	2.46	0.00	9.97E-01	9.99E-01	GKN2	gastrokine 2	chr2p14	238222_at	NM_182536
2.30	2.30	0.00	9.97E-01	9.99E-01	DKFZP434P211	POM121-like protein	chr22q11.22	206819_at	NR_003714
3.22	3.22	0.00	9.97E-01	9.99E-01	---	---	---	244221_at	---
4.99	4.99	0.00	9.97E-01	9.99E-01	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	chrXq23	219015_s_at	NM_018466 /// XM_001713667 /// XM_001713668
2.84	2.84	0.00	9.97E-01	9.99E-01	---	---	---	240623_at	---
2.52	2.52	0.00	9.97E-01	9.99E-01	---	---	---	244140_at	---
2.82	2.82	0.00	9.97E-01	9.99E-01	---	---	---	239869_at	---
6.79	6.79	0.00	9.97E-01	9.99E-01	BAT2	HLA-B associated transcript 2	chr6p21.3	212081_x_at	NM_080686
2.33	2.33	0.00	9.97E-01	9.99E-01	---	---	---	237341_at	---
2.16	2.16	0.00	9.97E-01	9.99E-01	---	---	---	1566279_at	---
3.44	3.44	0.00	9.97E-01	9.99E-01	---	---	---	1564584_at	---
5.84	5.83	0.00	9.97E-01	9.99E-01	TUBB6	tubulin, beta 6	chr18p11.21	209191_at	NM_032525
2.22	2.22	0.00	9.97E-01	9.99E-01	---	---	---	1557796_at	---
2.23	2.23	0.00	9.97E-01	9.99E-01	---	---	---	241129_at	---
8.21	8.21	0.00	9.97E-01	9.99E-01	PDZD11	PDZ domain containing 11	chrXq13.1	223037_at	NM_016484
4.06	4.06	0.00	9.97E-01	9.99E-01	---	---	---	229318_at	---
2.25	2.25	0.00	9.97E-01	9.99E-01	WDHD1	WD repeat and HMG-box DNA binding protein 1	chr14q22.3	216228_s_at	NM_001008396 /// NM_007086
5.73	5.73	0.00	9.97E-01	9.99E-01	MED6	mediator complex subunit 6	chr14q24.2	210104_at	NM_005466
7.22	7.22	0.00	9.97E-01	9.99E-01	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)	chr19q13.11	212131_at	NM_001114093 /// NM_015578
2.42	2.42	0.00	9.98E-01	9.99E-01	---	---	---	241254_at	---
2.47	2.46	0.00	9.98E-01	9.99E-01	---	---	---	236419_at	---
1.98	1.98	0.00	9.98E-01	9.99E-01	---	---	---	241569_at	---
3.03	3.03	0.00	9.98E-01	9.99E-01	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	227513_s_at	NM_004735
6.79	6.79	0.00	9.98E-01	9.99E-01	IHPK1	inositol hexaphosphate kinase 1	chr3p21.31	212439_at	NM_001006115 /// NM_153273
2.39	2.39	0.00	9.98E-01	9.99E-01	---	---	---	215314_at	---
2.31	2.31	0.00	9.98E-01	9.99E-01	AGTR2	angiotensin II receptor, type 2	chrXq22-q23	207293_s_at	NM_000686

4.52	4.52	0.00	9.98E-01	9.99E-01	ARRB1	arrestin, beta 1	chr11q13	222756_s_at	NM_004041 /// NM_020251																				
2.66	2.66	0.00	9.98E-01	9.99E-01	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	chr22q12.2	211393_at	NM_014323 /// NM_032050 /// NM_032051 /// NM_032052																				
4.83	4.83	0.00	9.98E-01	9.99E-01	NBEA	neurobeachin	chr13q13	221207_s_at	NM_015678																				
4.10	4.10	0.00	9.98E-01	9.99E-01	ACPT	acid phosphatase, testicular	chr19q13.4	241715_x_at	NM_033068																				
2.21	2.21	0.00	9.98E-01	9.99E-01	---	---	---	1560988_a_at	---																				
3.34	3.34	0.00	9.98E-01	9.99E-01	LRRC27	leucine rich repeat containing 27	chr10q26.3	1558483_at	NM_030626																				
2.56	2.56	0.00	9.98E-01	9.99E-01	---	---	---	1558181_at	---																				
2.27	2.27	0.00	9.98E-01	9.99E-01	---	---	---	1556980_at	---																				
3.96	3.96	0.00	9.98E-01	9.99E-01	PRDM6	PR domain containing 6	chr5q23.2	230311_s_at	XM_001723255 /// XM_927647 /// XM_937753																				
5.14	5.14	0.00	9.98E-01	9.99E-01	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	chr6q23-q24	212641_at	NM_006734																				
2.36	2.36	0.00	9.98E-01	9.99E-01	POU4F3	POU class 4 homeobox 3	chr5q31	208554_at	NM_002700																				
2.20	2.20	0.00	9.98E-01	9.99E-01	ADAD1	Adenosine deaminase domain containing 1 (testis-specific)	chr4q27	240299_at	NM_139243																				
2.50	2.50	0.00	9.98E-01	9.99E-01	---	---	---	1559646_a_at	---																				
3.58	3.58	0.00	9.99E-01	1.00E+00	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	chr13q14	205136_s_at	NM_012345																				
2.23	2.23	0.00	9.99E-01	1.00E+00	FSTL4	follistatin-like 4	chr5q31.1	1565910_at	NM_015082																				
3.18	3.18	0.00	9.99E-01	1.00E+00	GP2	glycoprotein 2 (zymogen granule membrane)	chr16p12	206681_x_at	NM_001007240 /// NM_001007241 /// NM_001007242 /// NM_001502																				
4.63	4.63	0.00	9.99E-01	1.00E+00	PMEPA1	prostate transmembrane protein, androgen induced 1	chr20q13.31|20q13.31-q13.33	217875_s_at	NM_020182 /// NM_199169 /// NM_199170 /// NM_199171																				
2.10	2.10	0.00	9.99E-01	1.00E+00	---	---	---	234522_at	---																				
10.30	10.30	0.00	9.99E-01	1.00E+00	RPL14 /// RPL14L	ribosomal protein L14 /// ribosomal protein L14-like	chr12q14.2 /// chr3p22-p21.2	200074_s_at	NM_001034996 /// NM_003973 /// XR_017790 /// XR_041286 /// XR_041287																				
3.61	3.61	0.00	9.99E-01	1.00E+00	---	---	---	1557673_at	---																				
2.93	2.93	0.00	9.99E-01	1.00E+00	CASP8	caspase 8, apoptosis-related cysteine peptidase	chr2q33-q34	1553306_at	NM_001080124 /// NM_001080125 /// NM_001228 /// NM_033355 /// NM_033356 /// NM_033358																				
5.86	5.86	0.00	9.99E-01	1.00E+00	C10orf4	chromosome 10 open reading frame 4	chr10q23.33	226398_s_at	NM_145246																				
2.08	2.08	0.00	9.99E-01	1.00E+00	NARG2	NMDA receptor regulated 2	chr15q22.2	242639_at	NM_001018089 /// NM_024611																				
7.13	7.13	0.00	9.99E-01	1.00E+00	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	chr9q34	208874_x_at	NM_021131 /// NM_178000 /// NM_178001 /// NM_178003																				

2.57	2.57	0.00	9.99E-01	1.00E+00	RELL1	RELT-like 1	chr4p14	1554714_at	NM_001085399 /// NM_001085400																				
2.77	2.77	0.00	9.99E-01	1.00E+00	TRIM11	Tripartite motif-containing 11	chr1q42.13	228267_at	NM_145214																				
2.56	2.56	0.00	9.99E-01	1.00E+00	---	---	---	237941_at	---																				
4.09	4.09	0.00	9.99E-01	1.00E+00	---	---	---	227508_at	---																				
4.03	4.03	0.00	9.99E-01	1.00E+00	BRF1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	chr14q	215677_s_at	NM_001519 /// NM_145685																				
8.32	8.32	0.00	9.99E-01	1.00E+00	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	chr3p21	205417_s_at	NM_004393																				
2.48	2.48	0.00	9.99E-01	1.00E+00	---	---	---	1569885_at	---																				
6.21	6.21	0.00	9.99E-01	1.00E+00	JAG1	jagged 1 (Alagille syndrome)	chr20p12.1-p11.23	209099_x_at	NM_000214																				
2.28	2.28	0.00	9.99E-01	1.00E+00	---	---	---	231620_at	---																				
3.44	3.44	0.00	9.99E-01	1.00E+00	ZNF518A	zinc finger protein 518A	chr10q23.33	215644_at	NM_014803																				
8.86	8.86	0.00	1.00E+00	1.00E+00	CAPZB	capping protein (actin filament) muscle Z-line, beta	chr1p36.1	201950_x_at	NM_004930																				
2.47	2.47	0.00	1.00E+00	1.00E+00	---	---	---	235971_at	---																				
4.96	4.96	0.00	1.00E+00	1.00E+00	ZC3H7A	zinc finger CCCH-type containing 7A	chr16p13-p12	226897_s_at	NM_014153																				
5.97	5.97	0.00	1.00E+00	1.00E+00	---	---	---	241769_at	---																				
2.70	2.70	0.00	1.00E+00	1.00E+00	LOC389662	similar to hCG1984745	chr8q12.1	240937_at	XR_016813 /// XR_018408 /// XR_038132																				
4.41	4.41	0.00	1.00E+00	1.00E+00	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	234884_x_at	---																				
2.28	2.28	0.00	1.00E+00	1.00E+00	KRT18P33	Keratin 18 pseudogene 33	chr2p14	1559939_at	XM_001719210 /// XR_017456 /// XR_019330																				
2.79	2.79	0.00	1.00E+00	1.00E+00	---	---	---	1557565_a_at	---																				
3.46	3.46	0.00	1.00E+00	1.00E+00	CDT1	Chromatin licensing and DNA replication factor 1	chr16q24.3	228868_x_at	NM_030928																				
3.92	3.92	0.00	1.00E+00	1.00E+00	---	---	---	243219_x_at	---																				

Table S11: List of Genes with a LOW Expression in *ARMC5*-Mutated Compared with *ARMC5* Wild-Type ACTH-Independent Macronodular Adrenal Hyperplasia

[1.] p-values were generated with Limma, and adjusted for multiple testing using the Benjamini- Hochberg correction

[2]. GO stands for Gene Ontology. The significantly enriched Gene Ontologies (GO.1 to GO.20) within the differentially expressed genes are presented, with their annotations and the p-value of their enrichment (generated by DAVID). Whether any of these GO annotations applies to a gene or not, is mentioned for all the genes ("Yes" or "No").

To access the content of the table, please double-clic on the table

Mean.Mutated	Mean.NonMutated	logFoldChange	P.Value[1]	adj.P.Val[1]	Gene.Symbol	Gene.Title	Chromosomal.Location	Probe.Set.ID	Representative.Public.ID	GO.1[2]	GO.2[2]	GO.3[2]	GO.4[2]	GO.5[2]	GO.6[2]	GO.7[2]	GO.8[2]	GO.9[2]	GO.10[2]	GO.11[2]	GO.12[2]	GO.13[2]	GO.14[2]	GO.15[2]	GO.16[2]	GO.17[2]	GO.18[2]	GO.19[2]	GO.20[2]
										GO:0006396	GO:0008380	GO:0006397	GO:0016071	GO:0000375	GO:0000398	GO:0000377	GO:0003723	GO:0031981	GO:0070013	GO:0031974	GO:0043233	GO:0030529	GO:0003729	GO:0005730	GO:0005654	GO:0005681	GO:0030530	GO:0044451	GO:0016607
										RNA processing	RNA splicing	mRNA processing	mRNA metabolic process	RNA splicing, via transesterification reactions	nuclear mRNA splicing, via spliceosome	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RNA binding	nuclear lumen	intracellular organelle lumen	membrane-enclosed lumen	organelle lumen	ribonucleoprotein complex	mRNA binding	nucleolus	nucleoplasm	spliceosome	heterogeneous nuclear ribonucleoprotein complex	nucleoplasm part	nuclear speck
										Biological process	Biological process	Biological process	Biological process	Biological process	Biological process	Biological process	Molecular function	Cellular component	Cellular component	Cellular component	Cellular component	Cellular component	Molecular function	Cellular component	Cellular component	Cellular component	Cellular component	Cellular component	Cellular component
										P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 0	P.adj 6e-04	P.adj 0.0068	P.adj 0.0021	P.adj 0.0024	P.adj 0.0022	P.adj 0.0085	P.adj 0.0144	P.adj 0.027
3.79	5.93	-2.14	2.55E-06	7.45E-03	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)	chr4q35.1	219523_s_at	NM_018104	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.54	8.60	-3.06	8.13E-06	1.32E-02	---	---	---	235108_at	BG105700	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.84	10.43	-1.58	1.69E-05	1.77E-02	SNHG5	small nucleolar RNA host gene 5 (non-protein coding)	chr6q14.3	225155_at	BG339050	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.48	5.03	-1.55	2.47E-05	2.17E-02	C22:CTA-250D10.9	transmembrane protein 46-like	chr22q13.2	244467_at	AW136354	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.71	4.35	-0.65	3.39E-05	2.47E-02	APC	adenomatous polyposis coli	chr5q21-q22	203527_s_at	NM_000038	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.97	4.25	-1.29	3.32E-05	2.47E-02	---	---	---	229308_at	AW273796	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.17	7.07	-0.91	7.36E-05	3.46E-02	BACE1	beta-site APP-cleaving enzyme 1	chr11q23.2-q23.3	217904_s_at	NM_012104	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.85	3.79	-0.94	7.40E-05	3.46E-02	---	---	---	236586_at	R37396	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.12	5.04	-0.92	8.59E-05	3.78E-02	---	---	---	233055_at	AI755057	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.04	7.53	-2.49	9.86E-05	3.96E-02	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	chr1p33-p32	205738_s_at	NM_004102	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.70	3.97	-1.28	1.11E-04	4.13E-02	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	chr10p12	213714_at	AI040163	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.21	3.99	-0.78	1.12E-04	4.13E-02	---	---	---	236764_at	H49911	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.23	7.36	-1.13	1.31E-04	4.32E-02	---	---	---	237313_at	BE856800	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.95	6.68	-1.72	1.39E-04	4.32E-02	LOC100132288 /// LOC389833 /// LOC728312	hypothetical protein LOC100132288 /// similar to hypothetical protein MGC27019 /// similar to tektin 4	---	229748_x_at	AI380156	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.54	4.39	-0.85	1.46E-04	4.41E-02	SCAPER	S phase cyclin A-associated protein in the ER	chr15q24	215848_at	AW139369	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.10	2.69	-0.58	1.61E-04	4.56E-02	XK	X-linked Kx blood group (McLeod syndrome)	chrXp21.1	206698_at	NM_021083	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.04	5.02	-0.98	1.58E-04	4.56E-02	FBXO45	F-box protein 45	chr3q29	225100_at	BF590021	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

6.98	7.94	-0.96	1.76E-04	4.85E-02	ACO1	aconitase 1, soluble	chr9p22-q32|9p21.1	207071_s_at	NM_002197	No	No	No	No	No	No	No	Yes	No	No	No	No	No	Yes	No	No	No	No	No	No
2.25	4.71	-2.46	2.07E-04	5.19E-02	STMN2	stathmin-like 2	chr8q21.13	203000_at	BF967657	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.09	4.77	-0.69	2.12E-04	5.23E-02	C6orf35 /// LOC730074	chromosome 6 open reading frame 35 /// hypothetical	chr6q25.3	218453_s_at	NM_018452	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.58	4.47	-0.88	2.21E-04	5.32E-02	---	---	---	232544_at	AU144916	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.24	5.22	-0.98	2.28E-04	5.32E-02	DBT	dihydrolipoamide branched chain transacylase E2	chr1p31	244687_at	AI632010	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No	No
3.46	5.62	-2.16	2.26E-04	5.32E-02	---	---	---	228108_at	AW274846	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.86	7.01	-1.15	2.51E-04	5.44E-02	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	chr10q26.13	218523_at	NM_022126	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.43	4.19	-0.76	2.67E-04	5.62E-02	TMEM209	transmembrane protein 209	chr7q32.2	222267_at	BE619220	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.30	4.04	-0.74	2.79E-04	5.73E-02	MACROD1	MACRO domain containing 1	chr11q11	219188_s_at	NM_014067	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.74	3.40	-0.66	2.88E-04	5.80E-02	---	---	---	1569063_at	BC018945	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.41	4.01	-1.59	3.01E-04	5.91E-02	---	---	---	1563414_at	AF087981	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.11	6.18	-1.07	3.23E-04	5.96E-02	ACOT7	acyl-CoA thioesterase 7	chr1p36.31-p36.11	208002_s_at	NM_007274	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.40	2.92	-0.52	3.27E-04	5.97E-02	WDR78	WD repeat domain 78	chr1p31.3	1559576_at	BI088045	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.32	6.32	-1.01	3.41E-04	6.09E-02	FLJ39051	Hypothetical gene supported by AK096370	chr11q24.2	230999_at	AI743903	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.65	5.01	-1.36	3.50E-04	6.16E-02	---	---	---	228661_s_at	AI768374	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.72	4.86	-1.14	3.64E-04	6.28E-02	NEXN	nexilin (F actin binding protein)	chr1p31.1	1552309_a_at	NM_144573	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.57	5.97	-2.40	3.75E-04	6.32E-02	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	chr1p33-p32	214285_at	AI041520	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.14	3.26	-1.12	4.11E-04	6.45E-02	---	---	---	1563963_at	AL117570	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.72	4.40	-0.69	4.18E-04	6.50E-02	LOC730091	hypothetical protein LOC730091	chr3q25.31	230780_at	AI911972	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.73	5.76	-1.03	4.28E-04	6.54E-02	C2orf43	chromosome 2 open reading frame 43	chr2p24.1	222192_s_at	AK021672	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.32	5.42	-1.10	4.30E-04	6.54E-02	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	chr4q31.21	212956_at	AI348094	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.98	4.74	-1.77	4.32E-04	6.56E-02	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	chr4q31.22	242750_at	AA678047	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.67	4.71	-1.04	4.54E-04	6.72E-02	---	---	---	226480_at	N21475	Yes	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
3.21	4.43	-1.22	4.73E-04	6.79E-02	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	chr12p12.1-p11.2	210073_at	L32867	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.46	5.81	-1.34	4.78E-04	6.79E-02	ANKRD29	ankyrin repeat domain 29	chr18q11.2	238332_at	AI307802	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.31	4.84	-2.53	4.71E-04	6.79E-02	STMN2	stathmin-like 2	chr8q21.13	203001_s_at	NM_007029	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.12	3.88	-0.76	4.97E-04	6.88E-02	PAPOLA	poly(A) polymerase alpha	chr14q32.31	215374_at	AK024849	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
2.50	3.13	-0.63	5.29E-04	6.99E-02	---	---	---	239987_at	AV700714	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.61	4.30	-0.69	5.27E-04	6.99E-02	LYST	lysosomal trafficking regulator	chr1q42.1-q42.2	210943_s_at	U84744	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.08	5.03	-0.94	5.29E-04	6.99E-02	TMTC1	transmembrane and tetratricopeptide repeat containing 1	chr12p11.22	224397_s_at	AF319520	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.65	4.62	-0.97	5.31E-04	6.99E-02	---	---	---	222372_at	AW971248	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.73	7.44	-1.71	5.44E-04	7.00E-02	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	chr10q24.31	223839_s_at	AF132203	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.57	9.40	-0.83	5.48E-04	7.01E-02	IL23A	Enhancer of polycomb homolog 1 (Drosophila)	chr12q13.2	1568513_x_at	AJ296370	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.77	4.75	-0.98	5.51E-04	7.04E-02	GTDC1	glycosyltransferase-like domain containing 1	chr2q22.2-q22.3	239390_at	BE327650	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.64	3.26	-0.62	5.69E-04	7.15E-02	TMED5	transmembrane emp24 protein transport domain containing 5	chr1pter-q31.3	239283_at	AA259174	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.16	4.48	-1.32	5.68E-04	7.15E-02	---	---	---	227498_at	AI480314	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.45	4.06	-0.61	5.98E-04	7.27E-02	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	chr9q32	224543_at	AF308289	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.93	3.62	-0.70	5.98E-04	7.27E-02	---	---	---	241743_at	AI939527	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.91	4.70	-0.79	5.93E-04	7.27E-02	ALDOB	aldolase B, fructose-bisphosphate	chr9q21.3-q22.2	204705_x_at	NM_000035	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.44	7.15	-0.71	6.19E-04	7.37E-02	RHBDD1	rhomboid domain containing 1	chr2q36.3	233164_x_at	AK026955	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.73	3.28	-0.55	6.61E-04	7.44E-02	KGFLP2	keratinocyte growth factor-like protein 2	chr9p12	231031_at	AI761573	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.47	3.10	-0.63	6.54E-04	7.44E-02	---	---	---	235811_at	AW590853	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No
2.85	3.50	-0.64	6.62E-04	7.44E-02	MPHOSPH9	M-phase phosphoprotein 9	chr12q24.31	221965_at	AI990326	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.65	6.84	-1.19	6.44E-04	7.44E-02	PDLIM5	PDZ and LIM domain 5	chr4q22	203243_s_at	NM_006457	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.88	5.59	-1.71	6.37E-04	7.44E-02	CYB561	cytochrome b-561	chr17q11-qter	209164_s_at	BC002976	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
7.65	9.47	-1.82	6.60E-04	7.44E-02	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	chr10q24.31	200832_s_at	AB032261	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.71	5.69	-1.98	6.57E-04	7.44E-02	---	---	---	1555989_at	AA890373	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.97	5.95	-1.98	6.40E-04	7.44E-02	NEBL	nebulette	chr10p12	203961_at	AL157398	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.78	3.33	-0.55	6.71E-04	7.47E-02	SPTLC3	serine palmitoyltransferase, long chain base subunit 3	chr20p12.1	227752_at	AA005105	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.97	4.80	-0.83	6.72E-04	7.47E-02	hCG_2003663	hCG2003663	chr9q22.32	233599_at	AK025151	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.24	5.11	-0.87	6.83E-04	7.48E-02	DSC2	desmocollin 2	chr18q12.1	226817_at	AU154691	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.72	4.47	-0.74	6.90E-04	7.52E-02	EPS8L1	EPS8-like 1	chr19q13.42	221655_x_at	AF282167	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.84	7.01	-1.17	6.96E-04	7.53E-02	RGL1	ral guanine nucleotide dissociation stimulator-like 1	chr1q25.3	209568_s_at	AF186779	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.05	3.82	-0.77	7.05E-04	7.54E-02	GCLM	glutamate-cysteine ligase, modifier subunit	chr1p22.1	236140_at	AI753488	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.50	5.53	-1.02	7.12E-04	7.54E-02	---	---	---	1560492_at	BC014174	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.90	5.99	-1.09	7.06E-04	7.54E-02	CEP350	centrosomal protein 350kDa	chr1p36.13-q41	213956_at	AW299294	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.02	6.63	-1.61	7.11E-04	7.54E-02	RASAL2	RAS protein activator like 2	chr1q24	222810_s_at	BF435513	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.05	5.55	-1.49	7.21E-04	7.57E-02	---	---	---	243039_at	AI042377	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.03	4.64	-0.61	7.42E-04	7.65E-02	---	---	---	230842_at	AI807481	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.48	4.17	-0.69	7.51E-04	7.65E-02	---	---	---	230415_at	AU148090	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No	No
3.71	4.52	-0.80	7.52E-04	7.65E-02	TMTC3	transmembrane and tetratricopeptide repeat containing 3	chr12q21.32	226604_at	AA418403	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.55	4.99	-1.44	7.51E-04	7.65E-02	NEBL	nebulette	chr10p12	203962_s_at	NM_006393	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.17	5.13	-0.96	7.61E-04	7.70E-02	NEDD4	neural precursor cell expressed, developmentally down-regulated 4	chr15q	213012_at	D42055	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.27	4.13	-0.86	7.79E-04	7.78E-02	HS6ST3	heparan sulfate 6-O-sulfotransferase 3	chr13q32.1	229714_at	AF339796	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.92	3.49	-0.57	7.90E-04	7.84E-02	---	---	---	242423_x_at	AA179510	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

5.11	5.87	-0.76	8.05E-04	7.84E-02	ACOT7	acyl-CoA thioesterase 7	chr1p36.31-p36.11	215728_s_at	AL031848	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.61	3.16	-0.54	8.21E-04	7.86E-02	CNNM1	cyclin M1	chr10q24.2	220166_at	NM_020348	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.29	3.84	-0.55	8.13E-04	7.86E-02	TACSTD2	tumor-associated calcium signal transducer 2	chr1p32-p31	202285_s_at	AI627697	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.34	5.90	-0.56	8.33E-04	7.90E-02	TGOLN2	trans-golgi network protein 2	chr2p11.2	203833_s_at	BF061845	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
2.08	2.67	-0.60	8.41E-04	7.91E-02	---	---	---	1562612_at	BC020933	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No
3.64	4.30	-0.66	8.44E-04	7.91E-02	CEMP1	cementum protein 1	chr16p13.3	222009_at	AI829081	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.58	5.67	-1.08	8.43E-04	7.91E-02	---	---	---	233626_at	AK024580	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.48	3.08	-0.60	8.53E-04	7.95E-02	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	chr8p23.1	216695_s_at	AF082559	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.21	5.05	-0.83	8.68E-04	8.00E-02	CLMN	calmin (calponin-like, transmembrane)	chr14q32.13	225757_s_at	AU147564	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.73	11.79	-1.06	8.75E-04	8.00E-02	PTPRO	protein tyrosine phosphatase, receptor type, O	chr12p13.3-p13.2|12p13-p12	211600_at	U20489	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.89	3.52	-0.63	8.86E-04	8.00E-02	---	---	---	231057_at	AU144266	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.62	6.35	-0.73	8.77E-04	8.00E-02	LOC283875	hypothetical protein LOC283875	chr16p13.3	230525_at	AI762077	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.69	4.44	-0.75	8.88E-04	8.00E-02	HES5	hairy and enhancer of split 5 (Drosophila)	chr1p36.32	239230_at	AW079166	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
6.19	7.87	-1.68	8.90E-04	8.00E-02	---	---	---	241879_at	AW511222	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.47	5.51	-1.04	8.97E-04	8.03E-02	TMCC1	transmembrane and coiled-coil domain family 1	chr3q21.3	213351_s_at	AB018322	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.19	6.80	-1.61	9.30E-04	8.21E-02	ALPL	alkaline phosphatase, liver/bone/kidney	chr1p36.12	215783_s_at	X14174	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.01	5.91	-0.90	9.59E-04	8.34E-02	ZNF148	zinc finger protein 148	chr3q21	230821_at	AW594167	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
3.29	3.91	-0.62	9.69E-04	8.39E-02	---	---	---	236751_at	AI660254	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.74	5.63	-0.89	9.73E-04	8.40E-02	CYLD	cylindromatosis (turban tumor syndrome)	chr16q12.1	221905_at	BF516433	No	No	No	No	No	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No
3.51	5.06	-1.54	9.83E-04	8.46E-02	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	chr3q27.2	218847_at	NM_006548	No	No	No	No	No	No	Yes	No	No	No	No	No	Yes	No	No	No	No	No	No
11.00	11.45	-0.46	9.85E-04	8.47E-02	SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	chr12q23	200030_s_at	NM_002635	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.68	5.32	-0.64	9.86E-04	8.47E-02	KLK4	kallikrein-related peptidase 4	chr19q13.41	231782_s_at	AF259969	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.02	5.63	-1.61	9.97E-04	8.53E-02	COLEC12	collectin sub-family member 12	chr18pter-p11.3	221019_s_at	NM_030781	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.67	3.31	-0.64	1.02E-03	8.60E-02	CD53	CD53 molecule	chr1p13	242946_at	AW293276	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
8.96	9.76	-0.81	1.02E-03	8.60E-02	FOLR1	folate receptor 1 (adult)	chr11q13.3-q14.1	211074_at	AF000381	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.70	4.84	-1.14	1.01E-03	8.60E-02	KIF17	kinesin family member 17	chr1p36.12	222144_at	AA909345	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.19	6.64	-1.45	1.01E-03	8.60E-02	DMN	desmuslin	chr15q26.3	212730_at	AK026420	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.48	5.18	-0.70	1.06E-03	8.75E-02	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	chr2q24.2	238613_at	AI475164	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.69	3.23	-0.54	1.07E-03	8.80E-02	CERCAM	Cerebral endothelial cell adhesion molecule	chr9q34.11	227381_at	AI400646	No	No	No	No	No	No	No	No	No	Yes	Yes	Yes	No	No	No	No	No	No	No
6.75	8.01	-1.26	1.07E-03	8.80E-02	FAM107B	family with sequence similarity 107, member B	chr10p13	223059_s_at	BC004872	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
7.80	8.49	-0.69	1.11E-03	8.87E-02	FUCA1	fucosidase, alpha-L- 1, tissue	chr1p34	202838_at	NM_000147	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.51	4.26	-0.75	1.12E-03	8.89E-02	PNLIPRP1	pancreatic lipase-related protein 1	chr10q25.3	206694_at	NM_006229	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.95	5.12	-2.17	1.12E-03	8.89E-02	---	---	---	242476_at	AI436356	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.58	3.08	-0.50	1.16E-03	9.00E-02	KIAA1731	KIAA1731	chr11q21	215018_at	AB051518	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.74	6.84	-1.10	1.16E-03	9.00E-02	MAPK13	mitogen-activated protein kinase 13	chr6p21.31	210058_at	BC000433	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.05	3.97	-0.93	1.17E-03	9.02E-02	SLC25A34	solute carrier family 25, member 34	chr1p36.21	232245_at	AU151211	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.60	4.27	-0.67	1.18E-03	9.09E-02	RFTN2	raftlin family member 2	chr2q33.1	238955_at	BG535419	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.44	2.95	-0.51	1.20E-03	9.11E-02	OSBPL11	Oxysterol binding protein-like 11	chr3q21	229527_s_at	AA074624	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.44	5.95	-1.51	1.20E-03	9.11E-02	PPM1E	protein phosphatase 1E (PP2C domain containing)	chr17q22	236302_at	R40892	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
4.07	5.90	-1.83	1.21E-03	9.15E-02	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)	chr9p21.2	226844_at	AI375115	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
1.94	2.56	-0.62	1.22E-03	9.18E-02	---	---	---	242488_at	R55784	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.30	6.24	-0.94	1.23E-03	9.23E-02	FBXL17	F-box and leucine-rich repeat protein 17	chr5q21.3	227203_at	AA115629	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.27	5.90	-0.63	1.23E-03	9.23E-02	RNF207	Ring finger protein 207	chr1p36.31	244591_x_at	W92483	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.08	4.83	-0.75	1.24E-03	9.26E-02	LOC692247	hypothetical locus LOC692247	chr11p15.5	1569452_at	BG772667	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.29	5.01	-0.71	1.25E-03	9.29E-02	COL6A1	collagen, type VI, alpha 1	chr21q22.3	212937_s_at	M20776	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.81	4.58	-0.78	1.26E-03	9.29E-02	ZNF542	zinc finger protein 542	chr19q13.43	239250_at	BE966038	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.69	6.64	-1.95	1.26E-03	9.29E-02	CYB561	cytochrome b-561	chr17q11-qter	209163_at	AL514271	No	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	No	No	Yes	No	No	No	No
9.65	11.72	-2.07	1.26E-03	9.29E-02	GSTA1	glutathione S-transferase A1	chr6p12.1	203924_at	NM_000846	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.22	4.78	-0.56	1.29E-03	9.34E-02	RNASEL	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	chr1q25	221287_at	NM_021133	Yes	No	Yes	Yes	No	No	No	Yes	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No
3.33	3.95	-0.62	1.30E-03	9.34E-02	ZNF362	zinc finger protein 362	chr1p35.1	228957_at	AI224880	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.31	4.07	-0.76	1.30E-03	9.34E-02	HS6ST3	heparan sulfate 6-O-sulfotransferase 3	chr13q32.1	232276_at	AF339824	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.31	4.14	-0.83	1.28E-03	9.34E-02	---	---	---	236922_at	AA772352	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.76	3.35	-0.59	1.31E-03	9.36E-02	GPR150	G protein-coupled receptor 150	chr5q15	231349_at	AA845448	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.25	2.82	-0.57	1.31E-03	9.36E-02	---	---	---	1566426_at	AL833305	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.26	4.93	-0.67	1.31E-03	9.36E-02	---	---	---	217341_at	L07810	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.09	5.02	-0.93	1.34E-03	9.49E-02	BGN	biglycan	chrXq28	201262_s_at	NM_001711	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.88	4.51	-0.63	1.37E-03	9.60E-02	SLC30A7	solute carrier family 30 (zinc transporter), member 7	chr1p21.2	239596_at	AA521381	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.11	6.01	-0.90	1.38E-03	9.61E-02	ZNF671	zinc finger protein 671	chr19q13.43	219849_at	NM_024833	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.25	4.19	-0.94	1.39E-03	9.66E-02	ZNF117	zinc finger protein 117	chr7q11.21	235408_x_at	AW058673	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
10.05	10.86	-0.82	1.40E-03	9.70E-02	RTN4	reticulon 4	chr2p16.3	211509_s_at	AB015639	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.73	5.51	-0.77	1.42E-03	9.74E-02	---	---	---	243715_at	AW975013	Yes	Yes	Yes	Yes	No	No	No	No	Yes	Yes	Yes	Yes	Yes	No	Yes	No	Yes	No	No
9.73	10.41	-0.68	1.43E-03	9.76E-02	RTN4	reticulon 4	chr2p16.3	214629_x_at	AF320999	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.51	6.75	-3.24	1.45E-03	9.77E-02	SQLE	squalene epoxidase	chr8q24.1	209218_at	AF098865	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.20	4.99	-0.79	1.47E-03	9.83E-02	---	---	---	1569234_at	AI362687	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.50	6.52	-1.03	1.48E-03	9.87E-02	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	chr3q24	227791_at	BE222668	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
5.22	5.62	-0.40	1.52E-03	9.93E-02	---	---	---	240897_at	AW779654	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.42	2.92	-0.51	1.53E-03	9.93E-02	---	---	---	240001_at	AI078317	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.71	5.27	-0.57	1.52E-03	9.93E-02	---	---	---	242506_at	AI138785	No	No	No	No	No	No	No	No	No	No	No	No	Yes	No	No	No	No	No	No
3.35	4.16	-0.81	1.52E-03	9.93E-02	RNFT2	ring finger protein, transmembrane 2	chr12q24.22	221908_at	AL120375	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
3.00	3.98	-0.98	1.52E-03	9.93E-02	AZI2	5-azacytidine induced 2	chr3p24.1	223846_at	BC001139	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No

7.01	8.81	-1.80	1.51E-03	9.93E-02	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	chr10q24.31	200831_s_at	AA678241	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
4.61	5.25	-0.64	1.54E-03	9.94E-02	NAAA	N-acylethanolamine acid amidase	chr4q21.1	214765_s_at	AK024677	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No	No
2.45	3.02	0.56	1.59E-03	1.01E-01	---	---	---	242819_at	---																				
4.69	5.57	0.88	1.60E-03	1.01E-01	CALD1	caldesmon 1	chr7q33	215198_s_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157																				
3.21	4.09	0.88	1.61E-03	1.01E-01	---	---	---	229244_at	---																				
2.93	3.53	0.60	1.61E-03	1.01E-01	ZNF610	zinc finger protein 610	chr19q13.33	235953_at	NM_173530																				
2.58	3.36	0.78	1.67E-03	1.03E-01	RASAL2	RAS protein activator like 2	chr1q24	1557432_at	NM_004841 /// NM_170692																				
3.37	3.88	0.51	1.67E-03	1.03E-01	KRT4	Keratin 4	chr12q12-q13	214399_s_at	NM_002272																				
5.13	6.58	1.45	1.68E-03	1.03E-01	IGF1	insulin-like growth factor 1 (somatomedin C)	chr12q22-q23	209542_x_at	NM_000618 /// NM_001111283 /// NM_001111284 /// NM_001111285																				
3.07	4.21	1.14	1.68E-03	1.03E-01	---	---	---	233112_at	---																				
3.55	5.20	1.64	1.69E-03	1.04E-01	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	chr1p13.3	213832_at	NM_004980 /// NM_172198																				
4.16	5.86	1.70	1.71E-03	1.04E-01	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	chrXq22.3	204976_s_at	NM_001025580 /// NM_015365																				
3.25	3.86	0.60	1.71E-03	1.05E-01	ZNF335	zinc finger protein 335	chr20q11.21-q13.12	222059_at	NM_022095																				
4.30	5.72	1.41	1.72E-03	1.05E-01	PTPRF	protein tyrosine phosphatase, receptor type, F	chr1p34	200636_s_at	NM_002840 /// NM_130440																				
2.56	3.09	0.53	1.75E-03	1.06E-01	---	---	---	1557527_at	---																				
1.94	2.47	0.52	1.76E-03	1.06E-01	---	---	---	214078_at	---																				
9.39	10.16	0.76	1.77E-03	1.06E-01	RTN4	reticulon 4	chr2p16.3	210968_s_at	NM_007008 /// NM_020532 /// NM_153828 /// NM_207520 /// NM_207521																				
8.20	8.72	0.53	1.78E-03	1.06E-01	C1orf151	chromosome 1 open reading frame 151	chr1p36.13	224867_at	NM_001032363																				
3.19	3.81	0.62	1.80E-03	1.06E-01	GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	chr22q11.2	223563_at	NM_053004																				
3.47	4.44	0.97	1.82E-03	1.07E-01	TMCC1	transmembrane and coiled-coil domain family 1	chr3q21.3	213352_at	NM_001017395 /// NM_001128224 /// NM_015008																				
3.93	4.66	0.73	1.83E-03	1.07E-01	SH3KBP1	SH3-domain kinase binding protein 1	chrXp22.1-p21.3	235692_at	NM_001024666 /// NM_031892																				
4.47	5.32	0.85	1.87E-03	1.08E-01	CHD7	chromodomain helicase DNA binding protein 7	chr8q12.2	226123_at	NM_017780																				
5.22	6.04	0.83	1.87E-03	1.08E-01	LOC728264	hypothetical protein LOC728264	chr5q33.1	231987_at	XR_041006 /// XR_041007 /// XR_041008																				
3.05	3.63	0.58	1.88E-03	1.08E-01	---	---	---	234630_at	---																				
2.07	2.59	0.52	1.88E-03	1.08E-01	PPP1R12B	Protein phosphatase 1, regulatory (inhibitor) subunit 12B	chr1q32.1	1557553_at	NM_002481 /// NM_032103 /// NM_032104 /// NM_032105																				
2.69	3.15	0.46	1.88E-03	1.08E-01	C9orf40	chromosome 9 open reading frame 40	chr9q21.13	218904_s_at	NM_017998																				
4.44	5.34	0.89	1.88E-03	1.08E-01	IQCK	IQ motif containing K	chr16p12.3	213392_at	NM_153208																				
1.83	2.40	0.57	1.89E-03	1.08E-01	MRPL19	Mitochondrial ribosomal protein L19	chr2q11.1-q11.2	232071_at	NM_014763																				
3.07	3.82	0.75	1.90E-03	1.09E-01	NF-E4	transcription factor NF-E4	chr7q22.1	1560527_at	NM_001085386																				
4.50	5.15	0.66	1.91E-03	1.09E-01	FAM105A	family with sequence similarity 105, member A	chr5p15.2	219694_at	NM_019018																				
3.72	4.72	1.00	1.94E-03	1.09E-01	ARL17	ADP-ribosylation factor-like 17	chr17q21.31	232991_at	NM_001039083 /// NM_001103154																				
6.26	7.21	0.96	1.93E-03	1.09E-01	ACACA	acetyl-Coenzyme A carboxylase alpha	chr17q21	212186_at	NM_198834 /// NM_198836 /// NM_198837 /// NM_198838 /// NM_198839																				
2.46	3.35	0.89	1.92E-03	1.09E-01	---	---	---	233073_at	---																				
5.44	6.16	0.73	1.94E-03	1.09E-01	---	---	---	242300_at	---																				
3.88	4.49	0.61	1.96E-03	1.09E-01	---	---	---	1556192_x_at	---																				
3.80	4.30	0.50	1.97E-03	1.09E-01	SPEG	SPEG complex locus	chr2q35	205265_s_at	NM_005876																				
4.85	5.96	1.11	1.99E-03	1.10E-01	C16orf72	chromosome 16 open reading frame 72	chr16p13.2	228373_at	NM_014117																				

5.51	7.28	1.77	2.00E-03	1.10E-01	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	chr10p15-p14	209160_at	NM_003739
3.94	5.11	1.16	2.01E-03	1.10E-01	FAM120C	family with sequence similarity 120C	chrXp11.22	229512_at	NM_017848
3.13	3.69	0.56	2.02E-03	1.10E-01	BSPRY	B-box and SPRY domain containing	chr9q32	218792_s_at	NM_017688
4.94	5.48	0.54	2.02E-03	1.10E-01	ING5	inhibitor of growth family, member 5	chr2q37.3	223871_x_at	NM_032329
3.76	4.49	0.73	2.02E-03	1.10E-01	BHLHB3	basic helix-loop-helix domain containing, class B, 3	chr12p11.23-p12.1	231242_at	NM_030762
8.59	9.85	1.26	2.04E-03	1.11E-01	FAM162A	family with sequence similarity 162, member A	chr3q21.1	224345_x_at	NM_014367
4.08	4.78	0.71	2.05E-03	1.11E-01	MGC31957 /// TNFRSF10C	hypothetical protein MGC31957 /// tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	chr8p21.2 /// chr8p22-p21	210484_s_at	NM_003841
3.67	4.82	1.15	2.05E-03	1.11E-01	SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6	chr9q34	220091_at	NM_017585
2.96	3.63	0.67	2.12E-03	1.12E-01	ANKRD20A1 /// ANKRD20A2 /// ANKRD20A3 /// ANKRD20A4 /// C21orf81 /// CCDC29 /// LOC100132733 /// LOC284232 /// LOC391267 /// LOC643187 /// LOC647595 /// LOC653436 /// LOC727770 /// LOC728783	ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family, member A2 /// ankyrin repeat domain 20 family, member A3 /// ankyrin repeat domain 20 family, member A4 /// chromosome 21 open reading frame 81 /// coiled-coil domain containing 29 /// hypothetical protein LOC100132733 /// similar to ankyrin repeat domain 20 family, member A2 /// similar to ankyrin repeat domain 20 family, member A2 /// hypothetical LOC643187 /// similar to ankyrin repeat domain 20A /// hypothetical LOC653436 /// similar to ankyrin repeat domain 20 family, member A1 /// similar to FLJ00310 protein	chr13q11 /// chr1q12 /// chr21q11.2 /// chr9p11.2 /// chr9p12-p11.2 /// chr9q12	1569607_s_at	NM_001012419 /// NM_001012421 /// NM_001098805 /// NM_001098806 /// NM_032250 /// XM_001715342 /// XM_001716758 /// XR_018156 /// XR_018826 /// XR_037011 /// XR_037095 /// XR_037208 /// XR_037226 /// XR_037379 /// XR_040134 /// XR_040135 /// XR_042306 /// XR_042478
4.25	5.19	0.94	2.13E-03	1.13E-01	MRAS	muscle RAS oncogene homolog	chr3q22.3	206538_at	NM_001085049 /// NM_012219
4.93	5.68	0.75	2.14E-03	1.13E-01	LDB3	LIM domain binding 3	chr10q22.3-q23.2	234130_at	NM_001080114 /// NM_001080115 /// NM_001080116 /// NM_007078
5.64	6.29	0.66	2.14E-03	1.13E-01	MAPK13	mitogen-activated protein kinase 13	chr6p21.31	210059_s_at	NM_002754
3.87	4.45	0.57	2.15E-03	1.13E-01	LOC100134560	similar to hCG1821214	---	231402_at	XM_001718995
4.68	5.91	1.23	2.16E-03	1.14E-01	---	---	---	228731_at	---
4.04	5.87	1.83	2.17E-03	1.14E-01	ATP4A	ATPase, H+/K+ exchanging, alpha polypeptide	chr19q13.1	207139_at	NM_000704
3.54	4.42	0.88	2.17E-03	1.14E-01	SAMD9	sterile alpha motif domain containing 9	chr7q21.2	219691_at	NM_017654
5.06	6.41	1.35	2.21E-03	1.14E-01	LOC100132288 /// LOC389833 /// LOC728312	hypothetical protein LOC100132288 /// similar to hypothetical protein MGC27019 /// similar to tektin 4	---	227330_x_at	NM_001033515 /// XM_001713634 /// XR_042333 /// XR_042486
3.20	3.91	0.71	2.21E-03	1.14E-01	HFE	hemochromatosis	chr6p21.3	214647_s_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
3.05	3.53	0.48	2.23E-03	1.14E-01	CLCN4	chloride channel 4	chrXp22.3	214769_at	NM_001830
5.64	7.01	1.37	2.25E-03	1.14E-01	METTL9	methyltransferase like 9	chr16p13-p12	222447_at	NM_001077180 /// NM_016025
4.55	5.03	0.48	2.25E-03	1.14E-01	---	---	---	238144_s_at	---
6.01	6.60	0.59	2.26E-03	1.15E-01	CPNE7	copine VII	chr16q24.3	219707_at	NM_014427 /// NM_153636
6.78	7.38	0.60	2.29E-03	1.16E-01	PDXP /// SH3BP1	pyridoxal (pyridoxine, vitamin B6) phosphatase /// SH3-domain binding protein 1	chr22cen-q12.3 /// chr22q13.1	213633_at	NM_018957 /// NM_020315
5.69	6.69	1.01	2.31E-03	1.16E-01	RSF1	remodeling and spacing factor 1	chr11q14.1	222540_s_at	NM_016578
4.84	5.72	0.88	2.31E-03	1.16E-01	---	---	---	228070_at	---

3.19	3.66	0.47	2.34E-03	1.17E-01	FGF5	fibroblast growth factor 5	chr4q21	210310_s_at	NM_004464 /// NM_033143
5.91	6.65	0.74	2.37E-03	1.17E-01	MAP1B	microtubule-associated protein 1B	chr5q13	214577_at	NM_005909
4.08	4.60	0.52	2.37E-03	1.17E-01	SLC6A11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	chr3p25.3	207048_at	NM_014229
3.12	3.64	0.52	2.40E-03	1.18E-01	---	---	---	233306_at	---
3.31	4.16	0.85	2.42E-03	1.19E-01	FBXL18	F-box and leucine-rich repeat protein 18	chr7p22.2	215068_s_at	NM_024963
3.06	3.85	0.79	2.43E-03	1.19E-01	---	---	---	1562948_at	---
3.67	4.83	1.16	2.44E-03	1.19E-01	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	chr5q35	226997_at	NM_030955
11.53	12.19	0.66	2.45E-03	1.19E-01	FTH1	ferritin, heavy polypeptide 1	chr11q13	200748_s_at	NM_002032
2.52	3.11	0.59	2.44E-03	1.19E-01	---	---	---	234604_at	---
6.72	8.15	1.44	2.46E-03	1.19E-01	H19	H19, imprinted maternally expressed transcript (non-protein coding)	chr11p15.5	224997_x_at	NR_002196
4.25	4.96	0.71	2.47E-03	1.19E-01	FAM164A	family with sequence similarity 164, member A	chr8q21.12	205308_at	NM_016010
2.61	3.13	0.52	2.47E-03	1.19E-01	CNTLN	centlein, centrosomal protein	chr9p22.2	220095_at	NM_001114395 /// NM_017738
2.44	2.90	0.45	2.49E-03	1.20E-01	LOC100129961	hypothetical protein LOC100129961	chr2q21.3	236387_at	XM_001723477 /// XM_001724103 /// XM_001724423
2.73	3.76	1.04	2.49E-03	1.20E-01	ACTA2	Actin, alpha 2, smooth muscle, aorta	chr10q23.3	243140_at	NM_001613
4.48	5.15	0.67	2.50E-03	1.20E-01	HFE	hemochromatosis	chr6p21.3	206086_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
3.95	5.61	1.65	2.53E-03	1.20E-01	TMEM56	Transmembrane protein 56	chr1p21.3	234980_at	NM_152487
5.31	6.77	1.46	2.53E-03	1.20E-01	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	chr5p13.1	239270_at	NM_001005473
4.40	4.92	0.52	2.52E-03	1.20E-01	GFRA2	GDNF family receptor alpha 2	chr8p21.3	205721_at	NM_001495
3.95	5.25	1.30	2.55E-03	1.21E-01	GPC4	glypican 4	chrXq26.1	204984_at	NM_001448
2.27	2.79	0.52	2.56E-03	1.21E-01	---	---	---	1562456_at	---
3.22	3.73	0.51	2.59E-03	1.22E-01	AHNAK	AHNAK nucleoprotein	chr11q12.2	1563560_at	NM_001620 /// NM_024060
8.80	9.95	1.14	2.62E-03	1.23E-01	FAM162A	family with sequence similarity 162, member A	chr3q21.1	220942_x_at	NM_014367
5.11	5.82	0.71	2.63E-03	1.23E-01	---	---	---	229489_at	---
3.43	4.11	0.67	2.65E-03	1.23E-01	SLC6A10P /// SLC6A8	Solute carrier family 6 (neurotransmitter transporter, creatine), member 10 (pseudogene) /// Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	chr16p11.2 /// chrXq28	226903_s_at	NM_005629 /// NR_003083 /// XR_042169
3.50	4.12	0.61	2.65E-03	1.23E-01	PFTK1	PFTAIRE protein kinase 1	chr7q21-q22	204604_at	NM_012395
4.54	5.05	0.51	2.66E-03	1.23E-01	RLTPR	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing	chr16q22.1	227218_at	NM_001013838
3.53	4.11	0.58	2.67E-03	1.23E-01	ATP2A3	ATPase, Ca++ transporting, ubiquitous	chr17p13.3	207522_s_at	NM_005173 /// NM_174953 /// NM_174954 /// NM_174955 /// NM_174956 /// NM_174957 /// NM_174958
3.89	4.93	1.04	2.68E-03	1.24E-01	JAKMIP2	janus kinase and microtubule interacting protein 2	chr5q32	205888_s_at	NM_014790
2.79	3.48	0.68	2.71E-03	1.24E-01	ZMYND12	zinc finger, MYND-type containing 12	chr1p34.2	223636_at	NM_032257
4.89	6.48	1.59	2.73E-03	1.25E-01	OPN3	opsin 3	chr1q43	219032_x_at	NM_014322
5.80	6.71	0.91	2.75E-03	1.25E-01	---	---	---	224261_at	---
1.90	2.41	0.51	2.74E-03	1.25E-01	---	---	---	237049_at	---
3.46	4.95	1.49	2.84E-03	1.25E-01	GPC4	glypican 4	chrXq26.1	204983_s_at	NM_001448
3.51	4.23	0.73	2.83E-03	1.25E-01	FGFRL1	fibroblast growth factor receptor-like 1	chr4p16	223648_s_at	NM_001004356 /// NM_001004358 /// NM_021923
4.14	4.79	0.64	2.83E-03	1.25E-01	MFSD4	major facilitator superfamily domain containing 4	chr1q32.1	239304_at	NM_181644
5.56	6.10	0.54	2.81E-03	1.25E-01	---	---	---	237561_x_at	---
6.76	7.28	0.52	2.80E-03	1.25E-01	---	---	---	213690_s_at	---
2.98	3.48	0.50	2.81E-03	1.25E-01	FRMD4A	FERM domain containing 4A	chr10p13	208475_at	NM_018027
4.73	5.22	0.49	2.83E-03	1.25E-01	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	chr8q24.12	216646_at	NM_024094
2.99	3.39	0.40	2.83E-03	1.25E-01	---	---	---	230735_at	---

2.67	3.05	0.38	2.79E-03	1.25E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	213388_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359
6.66	7.34	0.68	2.85E-03	1.25E-01	FAM111A	Family with sequence similarity 111, member A	chr11q12.1	239368_at	NM_022074 /// NM_198847
3.06	3.57	0.51	2.86E-03	1.26E-01	HUS1B	HUS1 checkpoint homolog b (S. pombe)	chr6p25.3	1553660_at	NM_148959
3.85	4.80	0.96	2.89E-03	1.26E-01	---	---	---	227497_at	---
4.13	4.86	0.72	2.88E-03	1.26E-01	RBM12B	RNA binding motif protein 12B	chr8q22.1	221929_at	NM_203390
1.70	2.13	0.43	2.90E-03	1.26E-01	ZNF547	zinc finger protein 547	chr19q13.43	1552794_a_at	NM_173631
1.96	2.48	0.52	2.92E-03	1.26E-01	---	---	---	1563166_at	---
3.80	4.71	0.91	2.93E-03	1.26E-01	LQK1	LQK1 hypothetical protein short isoform	chr1q32.3	235126_at	XR_041451 /// XR_041452 /// XR_041453
4.30	5.66	1.36	2.95E-03	1.27E-01	PIR	pirin (iron-binding nuclear protein)	chrXp22.2	207469_s_at	NM_001018109 /// NM_003662
5.72	6.65	0.93	2.97E-03	1.27E-01	MPEG1	macrophage expressed gene 1	chr11q12.1	226818_at	NM_001039396
8.65	9.86	1.20	3.00E-03	1.27E-01	FAM162A	family with sequence similarity 162, member A	chr3q21.1	223193_x_at	NM_014367
3.45	4.21	0.76	3.01E-03	1.27E-01	---	---	---	215056_at	---
2.42	3.05	0.63	3.01E-03	1.27E-01	SAMD9L	sterile alpha motif domain containing 9-like	chr7q21.2-q21.3	235643_at	NM_152703
4.36	5.18	0.83	3.04E-03	1.28E-01	---	---	---	1555753_x_at	---
4.21	4.82	0.61	3.04E-03	1.28E-01	LOC100129420	similar to hCG1990547	chr8p23.1	237630_s_at	XM_001720857 /// XM_001721359 /// XM_001721781
2.78	3.53	0.75	3.06E-03	1.28E-01	---	---	---	233406_at	---
5.37	6.11	0.74	3.07E-03	1.29E-01	HEG1	HEG homolog 1 (zebrafish)	chr3q21.2	212822_at	NM_020733
2.82	3.27	0.45	3.07E-03	1.29E-01	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	chr1p21	210440_s_at	NM_003672 /// NM_033312 /// NM_033313
5.49	6.06	0.57	3.09E-03	1.29E-01	41530	Septin 13	chr7p13	239076_at	XM_001126402 /// XM_001133108 /// XM_001717249 /// XM_001718865
2.85	3.52	0.67	3.12E-03	1.29E-01	PDK3	pyruvate dehydrogenase kinase, isozyme 3	chrXp22.11	206348_s_at	NM_005391
8.09	9.80	1.71	3.19E-03	1.31E-01	KCNK3	potassium channel, subfamily K, member 3	chr2p23	205952_at	NM_002246
5.37	6.11	0.74	3.20E-03	1.31E-01	---	---	---	242320_at	---
5.49	6.00	0.51	3.19E-03	1.31E-01	LOC650656	hypothetical LOC650656	chr9q22.32	240742_at	XM_001717913
3.91	4.38	0.47	3.20E-03	1.31E-01	---	---	---	227343_at	---
5.01	5.77	0.76	3.23E-03	1.31E-01	ITGA8	integrin, alpha 8	chr10p13	242071_x_at	NM_003638
3.61	4.37	0.76	3.27E-03	1.33E-01	---	---	---	235224_s_at	---
4.75	5.88	1.13	3.29E-03	1.33E-01	C2orf43	chromosome 2 open reading frame 43	chr2p24.1	219008_at	NM_021925
4.00	5.07	1.07	3.29E-03	1.33E-01	---	---	---	1557478_at	---
3.07	3.80	0.73	3.28E-03	1.33E-01	PLCE1	phospholipase C, epsilon 1	chr10q23	205111_s_at	NM_016341
4.95	5.58	0.63	3.31E-03	1.33E-01	---	---	---	227730_at	---
2.31	2.90	0.59	3.31E-03	1.33E-01	---	---	---	244312_at	---
2.94	4.69	1.75	3.33E-03	1.33E-01	---	---	---	243791_at	---
3.10	3.63	0.53	3.32E-03	1.33E-01	---	---	---	1563903_x_at	---
3.34	4.09	0.74	3.37E-03	1.34E-01	OPN3	opsin 3	chr1q43	224392_s_at	NM_014322
2.96	3.51	0.56	3.37E-03	1.34E-01	---	---	---	238059_at	---
7.57	8.11	0.54	3.37E-03	1.34E-01	TMEM50A	transmembrane protein 50A	chr1p36.11	217766_s_at	NM_014313
3.69	4.62	0.93	3.40E-03	1.34E-01	---	---	---	228214_at	---
2.48	2.89	0.41	3.43E-03	1.35E-01	TTMA	Two transmembrane domain family member A	chr18p11.31	238128_at	NM_001080209
3.54	4.10	0.56	3.45E-03	1.36E-01	---	---	---	236703_at	---
4.96	5.42	0.46	3.49E-03	1.36E-01	SREBF2	sterol regulatory element binding transcription factor 2	chr22q13	242748_at	NM_004599
2.80	3.38	0.59	3.50E-03	1.36E-01	LOC151878	hypothetical protein LOC151878	chr3p14.3	239965_at	---
4.34	5.90	1.57	3.51E-03	1.36E-01	ASPN	asporin	chr9q22	219087_at	NM_017680
2.89	3.80	0.91	3.52E-03	1.36E-01	---	---	---	233036_at	---
2.88	3.63	0.75	3.52E-03	1.36E-01	ZNF285A	zinc finger protein 285A	---	236328_at	NM_152354
4.57	5.21	0.63	3.51E-03	1.36E-01	EML2	Echinoderm microtubule associated protein like 2	chr19q13.32	234021_at	NM_012155
3.13	3.72	0.60	3.51E-03	1.36E-01	---	---	---	207799_x_at	---
6.75	7.33	0.57	3.50E-03	1.36E-01	---	---	---	238869_at	---
3.41	3.97	0.56	3.51E-03	1.36E-01	---	---	---	1561599_at	---
1.93	2.39	0.46	3.54E-03	1.37E-01	---	---	---	244441_at	---
5.38	6.03	0.65	3.57E-03	1.38E-01	ZDHHC11	zinc finger, DHHC-type containing 11	chr5p15.33	232417_x_at	NM_024786
2.52	3.02	0.49	3.58E-03	1.38E-01	---	---	---	231695_at	---

2.17	2.55	0.38	3.58E-03	1.38E-01	INF2	inverted formin, FH2 and WH2 domain containing	chr14q32.33	222535_at	NM_001031714 /// NM_022489 /// NM_032714
6.28	6.87	0.59	3.59E-03	1.38E-01	---	---	---	230714_s_at	---
2.34	2.90	0.56	3.60E-03	1.38E-01	---	---	---	238009_at	---
1.76	2.19	0.43	3.61E-03	1.38E-01	---	---	---	234204_at	---
3.67	4.62	0.95	3.61E-03	1.38E-01	---	---	---	242099_at	---
2.98	3.77	0.79	3.62E-03	1.38E-01	ASPA	aspartoacylase (Canavan disease)	chr17pter-p13	206030_at	NM_000049 /// NM_001128085
6.32	7.06	0.75	3.63E-03	1.39E-01	PEX3	peroxisomal biogenesis factor 3	chr6q24.2	203970_s_at	NM_003630
2.60	3.38	0.78	3.65E-03	1.39E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	213684_s_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257
6.27	6.79	0.52	3.64E-03	1.39E-01	ARMC6	armadillo repeat containing 6	chr19p13.11	221758_at	NM_033415
3.03	3.54	0.51	3.66E-03	1.39E-01	TSHR	Thyroid stimulating hormone receptor	chr14q31	237349_at	NM_000369 /// NM_001018036
4.03	5.44	1.42	3.70E-03	1.39E-01	ZIM2	zinc finger, imprinted 2	chr19q13.4	220653_at	NM_015363
2.77	3.79	1.02	3.73E-03	1.39E-01	CLCC1	Chloride channel CLIC-like 1	chr1p13.3	230002_at	NM_001048210 /// NM_015127
6.23	7.18	0.95	3.69E-03	1.39E-01	FAM13A1	family with sequence similarity 13, member A1	chr4q22.1	202972_s_at	NM_001015045 /// NM_014883
2.31	3.03	0.73	3.68E-03	1.39E-01	TAS2R10	taste receptor, type 2, member 10	chr12p13	221397_at	NM_023921
8.11	8.84	0.72	3.72E-03	1.39E-01	RTN3	reticulon 3	chr11q13	219549_s_at	NM_006054 /// NM_201428 /// NM_201429 /// NM_201430
4.03	4.59	0.56	3.72E-03	1.39E-01	TFR2	transferrin receptor 2	chr7q22	215863_at	NM_003227
5.52	6.05	0.52	3.67E-03	1.39E-01	C1orf163	chromosome 1 open reading frame 163	chr1p32.3	219420_s_at	NM_023077
2.42	2.95	0.52	3.69E-03	1.39E-01	SAMD3	sterile alpha motif domain containing 3	chr6q23.1	236782_at	NM_001017373 /// NM_152552
3.46	3.98	0.51	3.72E-03	1.39E-01	---	---	---	241584_at	---
4.64	5.15	0.51	3.70E-03	1.39E-01	ZNF252	Zinc finger protein 252	chr8q24.3	233399_x_at	NR_023392 /// XM_001714325 /// XM_001714728 /// XM_001714801
3.18	4.27	1.09	3.74E-03	1.39E-01	SYNC1	syncoilin, intermediate filament 1	chr1p34.3-p33	221276_s_at	NM_030786
4.12	4.56	0.44	3.76E-03	1.39E-01	ASB8	ankyrin repeat and SOCS box-containing 8	chr12q13.11	218841_at	NM_024095
5.54	7.72	2.18	3.77E-03	1.40E-01	ZNF91	zinc finger protein 91	chr19p13.1-p12	206059_at	NM_003430
3.02	3.84	0.82	3.77E-03	1.40E-01	ZNF585A	zinc finger protein 585A	chr19q13.12	243790_at	NM_152655 /// NM_199126
2.60	3.00	0.39	3.77E-03	1.40E-01	FBXO45	F-box protein 45	chr3q29	242294_at	NM_001105573
2.42	2.89	0.48	3.78E-03	1.40E-01	ALDOAP2	aldolase A, fructose-bisphosphate pseudogene 2	chr10q26.13	211617_at	---
3.73	4.30	0.56	3.80E-03	1.40E-01	FAM131C	family with sequence similarity 131, member C	chr1p36.13	235455_at	NM_182623
4.59	5.11	0.52	3.80E-03	1.40E-01	FBXO22	F-box protein 22	chr15q24.2	225737_s_at	NM_012170 /// NM_147188
5.93	6.46	0.53	3.81E-03	1.40E-01	---	---	---	232937_at	---
6.29	6.77	0.48	3.81E-03	1.40E-01	---	---	---	237013_at	---
2.63	3.21	0.58	3.84E-03	1.41E-01	BAI2	brain-specific angiogenesis inhibitor 2	chr1p35	204966_at	NM_001703
2.90	3.71	0.81	3.86E-03	1.41E-01	ZNF667	zinc finger protein 667	chr19q13.43	207120_at	NM_022103
3.48	3.92	0.44	3.86E-03	1.41E-01	SP8	Sp8 transcription factor	chr7p21.2	239743_at	NM_182700 /// NM_198956 /// NR_024112
7.54	8.08	0.54	3.89E-03	1.41E-01	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	chr5p15.2	227522_at	NM_138809
4.58	5.03	0.46	3.89E-03	1.41E-01	---	---	---	242995_at	---
3.87	4.55	0.69	3.91E-03	1.41E-01	---	---	---	227729_at	---
6.19	6.74	0.55	3.95E-03	1.42E-01	---	---	---	233354_at	---
2.96	4.49	1.53	3.96E-03	1.42E-01	FAM69A	family with sequence similarity 69, member A	chr1p22.1	213689_x_at	NM_001006605
5.22	5.69	0.47	4.01E-03	1.43E-01	SLC39A11	solute carrier family 39 (metal ion transporter), member 11	chr17q24.3-q25.1	227046_at	NM_139177
2.52	2.91	0.39	4.02E-03	1.43E-01	---	---	---	235323_at	---
4.52	5.46	0.94	4.03E-03	1.43E-01	MTFR1	mitochondrial fission regulator 1	chr8q13.1	203207_s_at	NM_014637
3.85	4.57	0.72	4.04E-03	1.44E-01	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	chr14q24	205757_at	NM_001249
6.26	6.89	0.63	4.05E-03	1.44E-01	CENTA1	centaurin, alpha 1	chr7p22.3	219150_s_at	NM_006869

5.16	5.93	0.77	4.08E-03	1.44E-01	FREQ	frequenin homolog (Drosophila)	chr9q34	238753_at	NM_001128826 /// NM_014286
4.57	5.60	1.03	4.10E-03	1.44E-01	SESTD1	SEC14 and spectrin domains 1	chr2q31.2	226763_at	NM_178123
8.22	9.03	0.81	4.11E-03	1.44E-01	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	chr2p24.3-p24.1	222437_s_at	NM_001005753 /// NM_016079
2.00	2.80	0.79	4.09E-03	1.44E-01	---	---	---	229506_at	---
4.74	5.18	0.45	4.09E-03	1.44E-01	LTBP4	Latent transforming growth factor beta binding protein 4	chr19q13.1-q13.2	227989_at	NM_001042544 /// NM_001042545 /// NM_003573
3.59	4.92	1.33	4.12E-03	1.45E-01	DIAPH2	diaphanous homolog 2 (Drosophila)	chrXq21.33	205603_s_at	NM_006729 /// NM_007309
3.81	4.88	1.07	4.13E-03	1.45E-01	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	chr9q31-q32	223427_s_at	NM_018424 /// NM_019114
5.32	5.95	0.63	4.15E-03	1.45E-01	BRD4	Bromodomain containing 4	chr19p13.1	239000_at	NM_014299 /// NM_058243
2.96	3.53	0.57	4.17E-03	1.46E-01	IMPAD1	inositol monophosphatase domain containing 1	chr8q12.1	222655_s_at	NM_017813
2.24	2.72	0.48	4.16E-03	1.46E-01	SORCS1	sortilin-related VPS10 domain containing receptor 1	chr10q23-q25	228194_s_at	NM_001013031 /// NM_052918
3.52	4.45	0.93	4.18E-03	1.46E-01	---	---	---	222111_at	---
3.92	4.66	0.74	4.19E-03	1.46E-01	UBASH3B	Ubiquitin associated and SH3 domain containing, B	chr11q24.1	240387_at	NM_032873
2.34	2.96	0.62	4.19E-03	1.46E-01	ZNF542	zinc finger protein 542	chr19q13.43	235121_at	NR_003127 /// NR_024055 /// NR_024056 /// NR_024057 /// XR_017885 /// XR_017984
2.65	3.08	0.42	4.20E-03	1.46E-01	LOC389124	hypothetical LOC389124	chr3p21.1	231525_at	XM_001723363 /// XM_371643 /// XM_942552
2.05	2.42	0.37	4.21E-03	1.46E-01	UGT2A1 /// UGT2A2	UDP glucuronosyltransferase 2 family, polypeptide A1 /// UDP glucuronosyltransferase 2 family, polypeptide A2	chr4q13 /// chr4q13.3	207958_at	NM_001105677 /// NM_006798
6.79	7.69	0.89	4.22E-03	1.46E-01	RHOQ	ras homolog gene family, member Q	chr2p21	212119_at	NM_012249
2.12	2.57	0.45	4.25E-03	1.47E-01	---	---	---	216155_at	---
2.21	2.70	0.49	4.27E-03	1.47E-01	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	chr7q36.1	1557158_s_at	NM_170606
2.88	3.33	0.45	4.27E-03	1.47E-01	---	---	---	236054_at	---
4.78	5.29	0.51	4.28E-03	1.47E-01	CGB /// CGB5 /// CGB7 /// CGB8	chorionic gonadotropin, beta polypeptide /// chorionic gonadotropin, beta polypeptide 5 /// chorionic gonadotropin, beta polypeptide 7 /// chorionic gonadotropin, beta polypeptide 8	chr19q13.32	205387_s_at	NM_000737 /// NM_033043 /// NM_033142 /// NM_033183
5.01	5.54	0.54	4.30E-03	1.47E-01	---	---	---	240737_at	---
5.09	6.48	1.39	4.32E-03	1.47E-01	IGF1	insulin-like growth factor 1 (somatomedin C)	chr12q22-q23	209541_at	NM_000618 /// NM_001111283 /// NM_001111284 /// NM_001111285
5.43	5.97	0.54	4.33E-03	1.47E-01	HMCN2	hemicentin 2	chr9q34.11	241650_x_at	XM_001715154 /// XM_001726942
3.42	3.82	0.40	4.34E-03	1.47E-01	PRKCA	protein kinase C, alpha	chr17q22-q23.2	215194_at	NM_002737
4.78	5.90	1.11	4.35E-03	1.48E-01	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	chr10p11.22-p11.21	221527_s_at	NM_019619
3.89	4.72	0.83	4.35E-03	1.48E-01	C1orf97	chromosome 1 open reading frame 97	chr1q32.3	224443_at	XR_040057 /// XR_040058 /// XR_040059
4.14	4.62	0.48	4.37E-03	1.48E-01	---	---	---	216571_at	---
12.85	13.27	0.42	4.38E-03	1.48E-01	ND2	NADH dehydrogenase, subunit 2 (complex I)	---	1553551_s_at	---
4.21	4.85	0.63	4.39E-03	1.48E-01	RNASEL	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	chr1q25	229285_at	NM_021133
3.10	3.64	0.55	4.39E-03	1.48E-01	TACC1	transforming, acidic coiled-coil containing protein 1	chr8p11	242290_at	NM_001122824 /// NM_006283
3.94	4.37	0.43	4.39E-03	1.48E-01	TBC1D16	TBC1 domain family, member 16	chr17q25.3	222648_at	NM_019020
3.09	3.97	0.88	4.43E-03	1.48E-01	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	chrXq13.1-q21.1	208859_s_at	NM_000489 /// NM_138270
4.38	4.91	0.53	4.40E-03	1.48E-01	---	---	---	244535_at	---
3.01	3.52	0.51	4.41E-03	1.48E-01	AP1M2	adaptor-related protein complex 1, mu 2 subunit	chr19p13.2	218261_at	NM_005498
2.16	2.58	0.41	4.43E-03	1.48E-01	C16orf87	Chromosome 16 open reading frame 87	chr16q11.2	242555_at	NM_001001436

4.52	5.27	0.75	4.45E-03	1.48E-01	LOC100132288 /// LOC389833	hypothetical protein LOC100132288 /// similar to hypothetical protein MGC27019	---	227715_at	NM_001033515 /// XM_001713634
3.58	4.17	0.58	4.45E-03	1.48E-01	ZNF583	zinc finger protein 583	chr19q13.43	1553221_at	NM_152478
2.86	3.31	0.45	4.46E-03	1.48E-01	TP53BP1	tumor protein p53 binding protein 1	chr15q15-q21	1569097_at	NM_005657
2.11	2.59	0.48	4.48E-03	1.48E-01	JAKMIP2	janus kinase and microtubule interacting protein 2	chr5q32	205889_s_at	NM_014790
2.07	2.47	0.40	4.48E-03	1.48E-01	---	---	---	240642_at	---
4.81	5.70	0.89	4.49E-03	1.49E-01	---	---	---	235017_s_at	---
4.71	5.33	0.62	4.51E-03	1.49E-01	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	chr3p14.1	225465_at	NM_001033057 /// NM_004742 /// NM_015520
3.93	4.49	0.56	4.50E-03	1.49E-01	---	---	---	238405_at	---
1.79	2.16	0.36	4.53E-03	1.49E-01	LOC285326	hypothetical protein LOC285326	chr3p24.2	1556529_a_at	---
2.57	3.19	0.62	4.54E-03	1.49E-01	C1orf192	chromosome 1 open reading frame 192	chr1q23.3	231077_at	NM_001013625
2.47	2.95	0.48	4.55E-03	1.49E-01	---	---	---	240471_at	---
6.40	6.97	0.57	4.57E-03	1.50E-01	SFXN4	Sideroflexin 4	chr10q26.11	231505_s_at	NM_213649
2.43	2.86	0.43	4.57E-03	1.50E-01	LOC100131283	hypothetical protein LOC100131283	chr6p12.3	241256_at	XM_001716948 /// XM_001717272 /// XM_001718599
5.96	6.42	0.46	4.58E-03	1.50E-01	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	chr2q31.1	228168_at	NM_001002258 /// NM_001689
4.61	5.75	1.15	4.61E-03	1.50E-01	---	---	---	233867_at	---
4.22	5.03	0.81	4.61E-03	1.50E-01	AHI1	Abelson helper integration site 1	chr6q23.3	244699_at	NM_017651
2.70	3.40	0.70	4.61E-03	1.50E-01	TMTC1	transmembrane and tetratricopeptide repeat containing 1	chr12p11.22	244506_at	NM_175861
3.08	3.68	0.60	4.61E-03	1.50E-01	CRIM2	cysteine rich BMP regulator 2 (chordin-like)	chr7q32.1	242855_at	XM_001128429 /// XM_001715223 /// XM_001715714
6.99	7.69	0.70	4.62E-03	1.50E-01	ZFPM1	Zinc finger protein, multitype 1	chr16q24.2	237463_at	NM_153813
2.84	3.46	0.62	4.65E-03	1.50E-01	---	---	---	237218_at	---
2.04	2.65	0.61	4.69E-03	1.51E-01	---	---	---	230064_at	---
2.11	2.48	0.37	4.69E-03	1.51E-01	---	---	---	233468_at	---
2.83	3.78	0.95	4.70E-03	1.51E-01	NBN	nibrin	chr8q21	217299_s_at	NM_001024688 /// NM_002485
4.40	5.00	0.60	4.73E-03	1.52E-01	KCNK10	potassium channel, subfamily K, member 10	chr14q31	220727_at	NM_021161 /// NM_138317 /// NM_138318
4.70	5.16	0.46	4.73E-03	1.52E-01	KRT83	keratin 83	chr12q13	207669_at	NM_002282 /// XM_001714070 /// XM_001719155
2.94	3.35	0.41	4.73E-03	1.52E-01	PALMD	palmdelphin	chr1p22-p21	232187_at	NM_017734
3.17	3.68	0.51	4.74E-03	1.52E-01	LOC144486	hypothetical protein LOC144486	chr12q22	237021_at	---
4.31	5.38	1.07	4.76E-03	1.52E-01	MID1	midline 1 (Opitz/BBB syndrome)	chrXp22	203637_s_at	NM_000381 /// NM_001098624 /// NM_033290
5.09	6.06	0.98	4.80E-03	1.53E-01	TMEM45A	transmembrane protein 45A	chr3q12.2	219410_at	NM_018004
3.71	4.53	0.82	4.84E-03	1.53E-01	FAM126B	family with sequence similarity 126, member B	chr2q33.1	231874_at	NM_173822
6.77	7.33	0.57	4.84E-03	1.53E-01	SNX18	sorting nexin 18	chr5q11.2	226683_at	NM_001102575 /// NM_052870
4.20	4.60	0.40	4.83E-03	1.53E-01	ZNF79	zinc finger protein 79	chr9q34	216486_x_at	NM_007135
5.20	6.02	0.82	4.85E-03	1.53E-01	CYB561	cytochrome b-561	chr17q11-qter	207986_x_at	NM_001017916 /// NM_001017917 /// NM_001915
3.72	4.30	0.58	4.87E-03	1.53E-01	---	---	---	239567_at	---
2.85	3.40	0.55	4.86E-03	1.53E-01	APOOL	apolipoprotein O-like	chrXq21.1	222269_at	NM_198450
4.65	5.20	0.54	4.87E-03	1.53E-01	---	---	---	241486_at	---
3.49	4.03	0.53	4.88E-03	1.53E-01	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	chr10p12	207776_s_at	NM_000724 /// NM_201570 /// NM_201571 /// NM_201572 /// NM_201590 /// NM_201593 /// NM_201596 /// NM_201597
2.72	3.19	0.47	4.88E-03	1.53E-01	---	---	---	243904_at	---

2.27	3.07	0.80	4.89E-03	1.53E-01	APC	adenomatous polyposis coli	chr5q21-q22	216933_x_at	NM_000038 /// NM_001127510 /// NM_001127511
1.94	2.32	0.38	4.92E-03	1.54E-01	---	---	---	1561087_at	---
6.66	7.34	0.67	4.95E-03	1.54E-01	---	---	---	241618_at	---
2.76	3.32	0.56	4.96E-03	1.54E-01	---	---	---	231372_at	---
2.52	3.33	0.81	4.97E-03	1.54E-01	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)	chr9p21.2	229568_at	NM_024761
5.01	5.76	0.75	4.99E-03	1.55E-01	MVD	mevalonate (diphospho) decarboxylase	chr16q24.3	203027_s_at	NM_002461
4.60	5.61	1.02	5.00E-03	1.55E-01	PTRF	polymerase I and transcript release factor	chr17q21.31	208790_s_at	NM_012232
5.81	6.37	0.56	5.04E-03	1.56E-01	CCDC154	Coiled-coil domain containing 154	chr16p13.3	244409_at	XR_040660 /// XR_040661 /// XR_040662
6.02	8.17	2.16	5.09E-03	1.57E-01	F13A1	coagulation factor XIII, A1 polypeptide	chr6p25.3-p24.3	203305_at	NM_000129
5.04	5.94	0.90	5.12E-03	1.57E-01	FGFRL1	fibroblast growth factor receptor-like 1	chr4p16	223321_s_at	NM_001004356 /// NM_001004358 /// NM_021923
2.12	2.66	0.54	5.15E-03	1.57E-01	---	---	---	215578_at	---
3.03	3.59	0.55	5.16E-03	1.57E-01	---	---	---	232412_at	---
2.61	3.28	0.67	5.17E-03	1.57E-01	---	---	---	236184_at	---
4.77	5.34	0.57	5.19E-03	1.57E-01	---	---	---	241718_x_at	---
4.48	5.07	0.59	5.22E-03	1.58E-01	RAX	retina and anterior neural fold homeobox	chr18q21.32	208242_at	NM_013435
3.53	4.58	1.05	5.24E-03	1.58E-01	GALNTL1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	chr14q24.1	230417_at	NM_020692
2.67	3.24	0.56	5.24E-03	1.58E-01	NNT	nicotinamide nucleotide transhydrogenase	chr5p13.1-cen	238530_at	NM_012343 /// NM_182977
3.12	3.59	0.47	5.24E-03	1.58E-01	---	---	---	216144_at	---
4.60	5.16	0.56	5.25E-03	1.58E-01	---	---	---	234015_at	---
6.70	7.29	0.59	5.29E-03	1.58E-01	RPL18	ribosomal protein L18	chr19q13	214335_at	NM_000979
2.30	2.89	0.59	5.27E-03	1.58E-01	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	chr2q33	1552482_at	NM_203365 /// NM_213589
2.94	3.51	0.57	5.27E-03	1.58E-01	RBM /// RBMY1A1 /// RBMY1B /// RBMY1D /// RBMY1E /// RBMY1F /// RBMY1H /// RBMY1J /// RBMY3AP	similar to RNA binding motif protein, Y chromosome, family 2 member B /// RNA binding motif protein, Y-linked, family 1, member A1 /// RNA binding motif protein, Y-linked, family 1, member B /// RNA binding motif protein, Y-linked, family 1, member D /// RNA binding motif protein, Y-linked, family 1, member E /// RNA binding motif protein, Y-linked, family 1, member F /// RNA binding motif protein, Y-linked, family 1, member H /// RNA binding motif protein, Y-linked, family 1, member J /// RNA binding motif protein, Y-linked, family 3, member A pseudogene	chrYp11.2 /// chrYq11.223 /// chrYq11.23	216842_x_at	NM_001006117 /// NM_001006118 /// NM_001006120 /// NM_001006121 /// NM_001007526 /// NM_005058 /// NM_152585 /// NR_001573 /// XR_042013
5.76	6.93	1.18	5.32E-03	1.59E-01	SNCG	synuclein, gamma (breast cancer-specific protein 1)	chr10q23.2-q23.3	209877_at	NM_003087
3.26	3.79	0.53	5.34E-03	1.59E-01	PHTF1	putative homeodomain transcription factor 1	chr1p13	210191_s_at	NM_006608
3.34	3.77	0.43	5.35E-03	1.59E-01	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	chr16p12-p13.1	206384_at	NM_006539
6.43	7.18	0.75	5.35E-03	1.59E-01	PHPT1	phosphohistidine phosphatase 1	chr9q34.3	236744_at	NM_014172
4.48	6.05	1.57	5.49E-03	1.60E-01	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	chr10q24.31	211162_x_at	NM_005063 /// XM_001723785 /// XM_001725202 /// XM_001725496
9.36	10.80	1.44	5.45E-03	1.60E-01	RAB31	RAB31, member RAS oncogene family	chr18p11.3	217763_s_at	NM_006868
4.28	5.44	1.16	5.44E-03	1.60E-01	---	---	---	232935_at	---
5.24	6.16	0.92	5.45E-03	1.60E-01	RABL3	RAB, member of RAS oncogene family-like 3	chr3q13.33	213970_at	NM_173825
3.90	4.57	0.67	5.49E-03	1.60E-01	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	chr3q29	204209_at	NM_005017
3.03	3.68	0.65	5.46E-03	1.60E-01	BAG2	BCL2-associated athanogene 2	chr6p12.3-p11.2	230879_at	NM_004282
6.78	7.41	0.63	5.42E-03	1.60E-01	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	chr16q12.2	216611_s_at	NM_001043
3.71	4.23	0.52	5.44E-03	1.60E-01	---	---	---	243881_at	---
3.09	3.63	0.54	5.50E-03	1.60E-01	C1orf151	chromosome 1 open reading frame 151	chr1p36.13	228096_at	NM_001032363
2.43	2.82	0.39	5.50E-03	1.60E-01	---	---	---	237683_s_at	---
3.75	5.01	1.26	5.52E-03	1.61E-01	LOC572558	hypothetical locus LOC572558	chr9q13	231024_at	XR_017794 /// XR_041305
1.83	2.24	0.41	5.55E-03	1.61E-01	---	---	---	233548_at	---
2.46	3.24	0.78	5.56E-03	1.61E-01	---	---	---	1556685_at	---

6.45	7.62	1.17	5.58E-03	1.62E-01	ZC3HAV1	zinc finger CCCH-type, antiviral 1	chr7q34	213051_at	NM_020119 /// NM_024625
2.54	3.01	0.47	5.57E-03	1.62E-01	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	chr3p24.3	239461_at	NM_054110
5.38	7.07	1.68	5.63E-03	1.62E-01	---	---	---	238106_at	---
5.59	6.16	0.58	5.66E-03	1.63E-01	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	chr22q13.1-q13.2	215579_at	NM_021822
5.54	6.02	0.47	5.67E-03	1.63E-01	DKFZp761P0212	hypothetical protein DKFZp761P0212	chr17q25.3	234846_at	---
4.01	4.54	0.54	5.68E-03	1.63E-01	WDR90	WD repeat domain 90	chr16p13.3	242211_x_at	NM_145294
2.62	3.18	0.56	5.72E-03	1.63E-01	LAMA1	laminin, alpha 1	chr18p11.31	222346_at	NM_005559
3.38	3.91	0.53	5.73E-03	1.63E-01	---	---	---	1570166_a_at	---
4.52	5.02	0.50	5.74E-03	1.64E-01	---	---	---	215488_at	---
4.83	5.66	0.83	5.75E-03	1.64E-01	---	---	---	231101_at	---
4.17	4.85	0.69	5.79E-03	1.64E-01	YME1L1	YME1-like 1 (S. cerevisiae)	chr10p14	232216_at	NM_014263 /// NM_139312
3.44	4.00	0.56	5.79E-03	1.64E-01	MRPS5	Mitochondrial ribosomal protein S5	chr2p11.2-q11.2	236779_at	NM_031902
5.27	5.80	0.53	5.79E-03	1.64E-01	STAC2	SH3 and cysteine rich domain 2	chr17q12	228888_at	NM_198993
7.19	8.51	1.32	5.85E-03	1.65E-01	MYLK	myosin light chain kinase	chr3q21	202555_s_at	NM_053025 /// NM_053026 /// NM_053027 /// NM_053028 /// NM_053031 /// NM_053032
5.54	6.20	0.66	5.89E-03	1.65E-01	FLJ11506	hypothetical protein FLJ11506	chr15q22.33-q23	202851_at	NM_024666
3.40	4.04	0.63	5.88E-03	1.65E-01	NAG	neuroblastoma-amplified protein	chr2p24	242049_s_at	NM_015909
3.71	4.22	0.50	5.90E-03	1.65E-01	CDC25A	cell division cycle 25 homolog A (S. pombe)	chr3p21	204696_s_at	NM_001789 /// NM_201567
2.76	3.26	0.50	5.89E-03	1.65E-01	PRKCA	protein kinase C, alpha	chr17q22-q23.2	206923_at	NM_002737
4.58	5.08	0.50	5.90E-03	1.65E-01	LOC345630	similar to hCG1641252	chr5q35.1	236318_x_at	XM_001722529 /// XM_001725347 /// XM_293903
6.58	8.10	1.51	5.93E-03	1.65E-01	WWP1	WW domain containing E3 ubiquitin protein ligase 1	chr8q21	212638_s_at	NM_007013
3.10	3.72	0.63	5.93E-03	1.65E-01	---	---	---	1557551_at	---
3.08	4.57	1.49	5.95E-03	1.66E-01	SLC38A1	solute carrier family 38, member 1	chr12q13.11	224579_at	NM_001077484 /// NM_030674
3.77	5.11	1.34	5.96E-03	1.66E-01	---	---	---	235079_at	---
4.42	4.88	0.46	5.96E-03	1.66E-01	LOC100128570	Hypothetical protein LOC100128570	chr15q25.1	215140_at	XM_001720242 /// XM_001720250 /// XM_001726884
5.15	5.74	0.59	5.97E-03	1.66E-01	TMPRSS13	transmembrane protease, serine 13	chr11q23	223956_at	NM_001077263
6.51	7.25	0.73	6.00E-03	1.66E-01	ANXA2P2	annexin A2 pseudogene 2	chr9p13	208816_x_at	NR_003573
3.86	4.48	0.62	5.98E-03	1.66E-01	RTN4RL1	reticulon 4 receptor-like 1	chr17p13.3	230700_at	NM_178568
2.36	2.96	0.60	5.99E-03	1.66E-01	MGC39900 /// TMSL8	thymosin beta15b /// thymosin-like 8	chrXq21.33-q22.3 /// chrXq22.2	214051_at	NM_021992 /// NM_194324 /// XR_042096 /// XR_042097 /// XR_042098
2.79	3.37	0.58	5.98E-03	1.66E-01	---	---	---	239091_at	---
4.75	5.09	0.34	6.00E-03	1.66E-01	HFE	hemochromatosis	chr6p21.3	211326_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
5.00	6.11	1.11	6.01E-03	1.66E-01	RSC1A1	regulatory solute carrier protein, family 1, member 1	chr1p36.1	238519_at	NM_006511
4.14	4.71	0.57	6.03E-03	1.66E-01	PARP10	poly (ADP-ribose) polymerase family, member 10	chr8q24.3	238083_at	NM_032789
4.16	4.76	0.60	6.05E-03	1.67E-01	SLC38A3	solute carrier family 38, member 3	chr3p21.3	205972_at	NM_006841
2.46	3.04	0.58	6.05E-03	1.67E-01	API5	apoptosis inhibitor 5	chr11p11.2	233078_at	NM_006595
2.10	2.51	0.41	6.05E-03	1.67E-01	---	---	---	1566161_at	---
4.40	5.26	0.85	6.07E-03	1.67E-01	---	---	---	236168_at	---
4.49	4.97	0.48	6.08E-03	1.67E-01	---	---	---	234158_at	---
3.82	4.34	0.52	6.09E-03	1.67E-01	RAB9B	RAB9B, member RAS oncogene family	chrXq22.1-q22.3	222918_at	NM_016370
3.90	4.89	0.99	6.11E-03	1.67E-01	NEK1	NIMA (never in mitosis gene a)-related kinase 1	chr4q33	213328_at	NM_012224

4.10	4.55	0.44	6.12E-03	1.67E-01	A2BP1	ataxin 2-binding protein 1	chr16p13.3	235070_at	NM_018723 /// NM_145891 /// NM_145892 /// NM_145893																				
4.23	4.95	0.72	6.14E-03	1.67E-01	ZNF20	zinc finger protein 20	chr19p13.3-p13.2	213916_at	NM_021143																				
4.67	5.08	0.41	6.14E-03	1.67E-01	FAM71E2	family with sequence similarity 71, member E2	chr19q13.42	1564319_at	XR_040337 /// XR_040338 /// XR_040339																				
12.88	13.25	0.37	6.14E-03	1.67E-01	HNRNPM /// IQWD1 /// ND4 /// UNC5B	heterogeneous nuclear ribonucleoprotein M /// IQ motif and WD repeats 1 /// NADH dehydrogenase, subunit 4 (complex I) /// unc-5 homolog B (C. elegans)	chr10q22.1 /// chr19p13.3-p13.2 /// chr1q24.2	224373_s_at	NM_001017977 /// NM_005968 /// NM_018442 /// NM_031203 /// NM_170744																				
2.55	2.93	0.38	6.15E-03	1.68E-01	---	---	---	1561202_at	---																				
3.25	3.96	0.72	6.17E-03	1.68E-01	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16q22-q23	205314_x_at	NM_006750																				
6.80	7.98	1.18	6.18E-03	1.68E-01	---	---	---	228127_at	---																				
6.49	7.18	0.69	6.20E-03	1.68E-01	---	---	---	243731_at	---																				
4.14	4.71	0.56	6.22E-03	1.68E-01	PAFAH1B2	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kDa	chr11q23	210160_at	NM_002572																				
4.90	5.72	0.82	6.24E-03	1.68E-01	SAV1	salvador homolog 1 (Drosophila)	chr14q13-q23	222573_s_at	NM_021818																				
4.43	4.95	0.52	6.26E-03	1.68E-01	---	---	---	232522_at	---																				
2.38	2.81	0.44	6.25E-03	1.68E-01	---	---	---	1565105_at	---																				
2.48	2.86	0.38	6.25E-03	1.68E-01	LOC441025	hypothetical gene supported by BC039667	chr4q21.1	1562983_at	---																				
1.99	2.90	0.91	6.26E-03	1.68E-01	CCDC102B	coiled-coil domain containing 102B	chr18q22.1	220301_at	NM_001093729 /// NM_024781																				
4.12	5.42	1.29	6.29E-03	1.69E-01	NBEAL1	neurobeachin-like 1	chr2q33.2	1554106_at	NM_001099273 /// NM_198945																				
3.23	4.12	0.89	6.29E-03	1.69E-01	---	---	---	233664_at	---																				
5.13	5.77	0.64	6.28E-03	1.69E-01	FAM83C	family with sequence similarity 83, member C	chr20q11.22	1563805_a_at	NM_178468																				
5.73	6.32	0.59	6.29E-03	1.69E-01	C14orf126	chromosome 14 open reading frame 126	chr14q12	227158_at	NM_080664																				
4.36	4.87	0.51	6.31E-03	1.69E-01	ARHGEF2	Rho/rac guanine nucleotide exchange factor (GEF) 2	chr1q21-q22	235595_at	NM_004723																				
4.16	5.33	1.17	6.32E-03	1.69E-01	KIAA0256	KIAA0256 gene product	chr15q21.1	212451_at	NM_014701																				
3.04	3.57	0.53	6.33E-03	1.69E-01	---	---	---	242027_at	---																				
4.88	5.44	0.56	6.37E-03	1.69E-01	---	---	---	229148_at	---																				
2.50	2.97	0.48	6.38E-03	1.69E-01	---	---	---	1568813_at	---																				
3.92	4.39	0.46	6.37E-03	1.69E-01	CRX	cone-rod homeobox	chr19q13.3	217510_at	NM_000554																				
3.09	3.82	0.73	6.39E-03	1.70E-01	EDIL3	EGF-like repeats and discoidin I-like domains 3	chr5q14	207379_at	NM_005711																				
5.92	6.51	0.60	6.40E-03	1.70E-01	FAM22F	family with sequence similarity 22, member F	chr9q22.32	234414_at	NM_017561																				
4.88	5.42	0.54	6.40E-03	1.70E-01	---	---	---	209697_at	---																				
3.43	3.90	0.47	6.40E-03	1.70E-01	SH3PXD2A	SH3 and PX domains 2A	chr10q24.33	213252_at	NM_014631																				
5.05	5.67	0.61	6.42E-03	1.70E-01	MT1P3	Metallothionein 1 pseudogene 3	chr20q11.2	228016_s_at	---																				
1.91	2.27	0.36	6.42E-03	1.70E-01	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	chr12q21.31	232073_at	NM_003625																				
5.81	6.36	0.55	6.44E-03	1.70E-01	FBXO22	F-box protein 22	chr15q24.2	225736_at	NM_012170 /// NM_147188																				
4.00	4.40	0.40	6.45E-03	1.70E-01	GYPB	glycophorin B (MNS blood group)	chr4q28-q31	216398_at	NM_002100																				
4.76	6.05	1.30	6.51E-03	1.71E-01	AMT	aminomethyltransferase	chr3p21.2-p21.1	204294_at	NM_000481																				
4.21	4.87	0.66	6.52E-03	1.71E-01	C10orf46	chromosome 10 open reading frame 46	chr10q26.11	227258_at	NM_153810																				
2.26	2.90	0.64	6.51E-03	1.71E-01	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	chr3p25.3	216120_s_at	NM_001001331 /// NM_001683																				
3.04	3.67	0.63	6.49E-03	1.71E-01	---	---	---	234079_at	---																				
7.39	7.95	0.56	6.51E-03	1.71E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	212412_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257																				
3.57	4.09	0.52	6.51E-03	1.71E-01	---	---	---	236931_at	---																				
2.79	3.27	0.49	6.49E-03	1.71E-01	NRP1	neuropilin 1	chr10p12	210615_at	NM_001024628 /// NM_001024629 /// NM_003873																				
4.45	4.91	0.46	6.53E-03	1.71E-01	HGC6.3	similar to HGC6.3	chr6q27	211111_at	NM_001129895 /// XM_001715171 /// XM_001720008 /// XM_001720159																				
2.68	3.03	0.35	6.54E-03	1.71E-01	---	---	---	243975_at	---																				

3.51	4.26	0.74	6.57E-03	1.71E-01	MGC24125	hypothetical protein MGC24125	chr4q35.1	1554732_at	XR_000543 /// XR_000648
5.03	5.55	0.52	6.56E-03	1.71E-01	LOC648987	hypothetical LOC648987	chr5p12	227901_at	XR_018477 /// XR_039980 /// XR_039981
5.16	5.57	0.41	6.57E-03	1.71E-01	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	chr2q13	220113_x_at	NM_019014
3.42	5.32	1.90	6.59E-03	1.71E-01	SLC38A1	solute carrier family 38, member 1	chr12q13.11	218237_s_at	NM_001077484 /// NM_030674
6.11	6.68	0.56	6.60E-03	1.71E-01	---	---	---	244182_at	---
2.90	3.31	0.41	6.61E-03	1.71E-01	KCNK17	potassium channel, subfamily K, member 17	chr6p21.1	224049_at	NM_031460
2.90	3.38	0.47	6.63E-03	1.72E-01	ING X	inhibitor of growth family, X-linked, pseudogene	chrXq12	224245_at	NR_002226
3.66	4.25	0.58	6.65E-03	1.72E-01	---	---	---	243889_at	---
2.48	2.88	0.40	6.65E-03	1.72E-01	PRSS1	protease, serine, 1 (trypsin 1)	chr7q32-qter|7q34	216470_x_at	NM_002769
4.30	6.41	2.12	6.68E-03	1.73E-01	FLJ32252	hypothetical protein FLJ32252	chr16p13.3	1557146_a_at	XR_040906 /// XR_040907 /// XR_040908
3.89	4.35	0.46	6.70E-03	1.73E-01	---	---	---	232210_at	---
2.50	3.11	0.61	6.70E-03	1.73E-01	FAM49B	Family with sequence similarity 49, member B	chr8q24.21	217535_at	NM_016623
4.65	5.23	0.58	6.71E-03	1.73E-01	ZNF502	zinc finger protein 502	chr3p21.31	232247_at	NM_001134440 /// NM_001134441 /// NM_001134442 /// NM_033210
2.60	3.31	0.71	6.73E-03	1.73E-01	---	---	---	240600_at	---
4.76	5.28	0.52	6.74E-03	1.73E-01	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	chr9q31-q32	223426_s_at	NM_018424 /// NM_019114
3.06	3.81	0.75	6.75E-03	1.73E-01	---	---	---	232396_at	---
2.57	3.22	0.65	6.76E-03	1.73E-01	---	---	---	240927_at	---
2.44	3.11	0.67	6.79E-03	1.73E-01	TSHZ2	Teashirt zinc finger homeobox 2	chr20q13.2	244521_at	NM_173485
3.83	4.28	0.45	6.79E-03	1.73E-01	---	---	---	237355_at	---
3.35	3.75	0.41	6.80E-03	1.74E-01	---	---	---	237027_at	---
5.26	6.39	1.13	6.81E-03	1.74E-01	UHMK1	U2AF homology motif (UHM) kinase 1	chr1q23.3	227740_at	NM_175866
2.75	3.15	0.40	6.82E-03	1.74E-01	SFTPB	surfactant protein B	chr2p12-p11.2	37004_at	NM_000542 /// NM_198843
6.50	7.04	0.54	6.83E-03	1.74E-01	EPN1	epsin 1	chr19q13.42	221141_x_at	NM_001130071 /// NM_001130072 /// NM_013333
5.02	6.23	1.21	6.86E-03	1.74E-01	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	chr2p21	202435_s_at	NM_000104
1.88	2.39	0.51	6.86E-03	1.74E-01	EIF4ENIF1	eukaryotic translation initiation factor 4E nuclear import factor 1	chr22q11.2	242291_at	NM_019843
3.75	4.53	0.78	6.92E-03	1.74E-01	LUC7L2	LUC7-like 2 (S. cerevisiae)	chr7q34	243852_at	NM_016019
3.94	4.63	0.69	6.89E-03	1.74E-01	---	---	---	240165_at	---
7.33	7.95	0.61	6.89E-03	1.74E-01	MYLC2PL	myosin light chain 2, precursor lymphocyte-specific	chr7q22.1	221660_at	NM_138403
6.77	7.35	0.57	6.93E-03	1.74E-01	PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	chr1p36.31	237646_x_at	NM_001042663 /// NM_001042664 /// NM_001042665 /// NM_020631 /// NM_198681
4.26	4.83	0.57	6.88E-03	1.74E-01	TCP1	t-complex 1	chr6q25.3-q26	222011_s_at	NM_001008897 /// NM_030752
2.34	2.90	0.57	6.88E-03	1.74E-01	---	---	---	1557252_at	---
2.21	2.67	0.46	6.94E-03	1.74E-01	ATF7IP	activating transcription factor 7 interacting protein	chr12p13.1	216198_at	NM_018179
3.12	3.56	0.43	6.93E-03	1.74E-01	PDIA2	protein disulfide isomerase family A, member 2	chr16p13.3	206691_s_at	NM_006849
4.08	4.51	0.43	6.92E-03	1.74E-01	KIAA1328	KIAA1328	chr18q12.2	232358_at	NM_020776
2.68	3.10	0.42	6.93E-03	1.74E-01	---	---	---	215421_at	---
3.61	3.95	0.34	6.90E-03	1.74E-01	ALDH3A1	aldehyde dehydrogenase 3 family, memberA1	chr17p11.2	205623_at	NM_000691
3.46	3.96	0.50	6.95E-03	1.74E-01	---	---	---	244127_at	---
5.30	5.91	0.61	6.97E-03	1.74E-01	---	---	---	233912_x_at	---
2.60	3.14	0.54	7.00E-03	1.75E-01	---	---	---	1557343_at	---
2.98	3.40	0.42	7.00E-03	1.75E-01	CALML5	calmodulin-like 5	chr10p15.1	220414_at	NM_017422
3.26	3.75	0.49	7.01E-03	1.75E-01	---	---	---	242981_at	---
3.58	4.06	0.48	7.05E-03	1.75E-01	---	---	---	231949_at	---
7.43	8.01	0.58	7.07E-03	1.75E-01	---	---	---	230046_at	---
3.98	4.34	0.36	7.08E-03	1.76E-01	BARHL1	BarH-like homeobox 1	chr9q34	224092_at	NM_020064
5.43	6.39	0.97	7.10E-03	1.76E-01	PTP4A2	protein tyrosine phosphatase type IVA, member 2	chr1p35	208615_s_at	NM_080391 /// NM_080392
4.14	4.74	0.61	7.09E-03	1.76E-01	---	---	---	239643_at	---

4.70	6.28	1.58	7.11E-03	1.76E-01	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	chr2p21	209286_at	NM_006449
5.64	6.70	1.05	7.12E-03	1.76E-01	GGTA1	glycoprotein, alpha-galactosyltransferase 1	chr9q33.2-q34.11	228376_at	NR_003191
1.96	2.46	0.50	7.13E-03	1.76E-01	---	---	---	1570272_at	---
5.13	5.72	0.59	7.16E-03	1.76E-01	---	---	---	238209_at	---
3.48	4.12	0.63	7.17E-03	1.76E-01	RNF207	ring finger protein 207	chr1p36.31	242882_at	NM_207396 /// XM_001716213 /// XM_001718203 /// XM_001719665
4.54	5.06	0.52	7.18E-03	1.76E-01	SYT7	synaptotagmin VII	chr11q12-q13.1	226167_at	NM_004200
2.51	2.89	0.38	7.19E-03	1.76E-01	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	chr14q32.3	1557963_at	NM_006035
3.89	4.32	0.43	7.21E-03	1.77E-01	LOC389332	hypothetical LOC389332	chr5q31.2	237450_at	XR_017755 /// XR_017768 /// XR_041306
3.67	4.58	0.91	7.23E-03	1.77E-01	---	---	---	1556173_a_at	---
5.92	6.54	0.62	7.24E-03	1.77E-01	ENOX2	ecto-NOX disulfide-thiol exchanger 2	chrXq25-q26.2	234003_at	NM_006375 /// NM_182314
3.69	4.08	0.39	7.24E-03	1.77E-01	CHRNA4	cholinergic receptor, nicotinic, alpha 4	chr20q13.2-q13.3	206735_at	NM_000744
3.70	4.40	0.70	7.26E-03	1.77E-01	IGHA1 /// IGHD /// IGHG1 /// IGHG3 /// IGHM /// IGHV4-31 /// IGHV@ /// LOC100126583	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable group /// hypothetical LOC100126583	chr14q32.33	211650_x_at	---
3.48	3.92	0.44	7.28E-03	1.77E-01	GJD4	gap junction protein, delta 4, 40.1kDa	chr10p11.21	234116_at	NM_153368
4.44	5.28	0.85	7.31E-03	1.77E-01	---	---	---	233449_at	---
4.59	5.09	0.50	7.31E-03	1.77E-01	C20orf54	chromosome 20 open reading frame 54	chr20p13	233451_at	NM_033409
4.18	4.64	0.45	7.30E-03	1.77E-01	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	chr1p36.2	211230_s_at	NM_005026
3.22	3.60	0.38	7.31E-03	1.77E-01	TECTA	tectorin alpha	chr11q22-q24	236904_x_at	NM_005422
5.05	5.68	0.63	7.32E-03	1.77E-01	HMX1	H6 family homeobox 1	chr4p16.1	207353_s_at	NM_018942
1.75	2.10	0.34	7.34E-03	1.77E-01	FLJ35409	FLJ35409 protein	chr1p21.3	1559506_x_at	XR_017838 /// XR_017942 /// XR_040284
6.14	7.54	1.40	7.35E-03	1.78E-01	NRIP1	nuclear receptor interacting protein 1	chr21q11.2	202600_s_at	NM_003489
6.29	7.03	0.74	7.37E-03	1.78E-01	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	chr8p11.2	222544_s_at	NM_017778 /// NM_023034
2.51	2.96	0.45	7.37E-03	1.78E-01	AQP10	aquaporin 10	chr1q21.3	1555338_s_at	NM_080429
5.35	5.79	0.44	7.38E-03	1.78E-01	FLJ40142	FLJ40142 protein	chr12q24.11	229679_at	NM_207435
6.65	7.23	0.58	7.39E-03	1.78E-01	TNRC4	trinucleotide repeat containing 4	chr1q21	206817_x_at	NM_007185
2.54	2.93	0.39	7.42E-03	1.78E-01	CARD8	caspase recruitment domain family, member 8	chr19q13.32	232969_at	NM_014959
3.33	3.85	0.53	7.45E-03	1.79E-01	SMG7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr1q25	236367_at	NM_173156 /// NM_201568 /// NM_201569
1.85	2.17	0.32	7.45E-03	1.79E-01	EBF1	Early B-cell factor 1	chr5q34	233261_at	NM_024007
3.57	4.45	0.88	7.46E-03	1.79E-01	CPXM1	carboxypeptidase X (M14 family), member 1	chr20p13-p12.3	227860_at	NM_019609
3.00	3.41	0.41	7.47E-03	1.79E-01	---	---	---	239366_at	---
5.20	5.71	0.51	7.48E-03	1.79E-01	S1PR4	sphingosine-1-phosphate receptor 4	chr19p13.3	206437_at	NM_003775
4.58	5.05	0.47	7.51E-03	1.79E-01	TPSAB1	tryptase alpha/beta 1	chr16p13.3	216485_s_at	NM_003294 /// XM_001720738 /// XM_001720740
2.95	3.38	0.43	7.52E-03	1.79E-01	---	---	---	1556779_s_at	---
5.34	6.18	0.84	7.53E-03	1.79E-01	CYB561	cytochrome b-561	chr17q11-qter	217200_x_at	NM_001017916 /// NM_001017917 /// NM_001915
7.71	8.61	0.90	7.57E-03	1.80E-01	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	chr6q12	204059_s_at	NM_002395
5.04	5.51	0.47	7.56E-03	1.80E-01	---	---	---	243568_at	---
2.59	3.14	0.55	7.58E-03	1.80E-01	---	---	---	1562600_at	---
4.62	5.61	1.00	7.58E-03	1.80E-01	PRKD3	protein kinase D3	chr2p21	222565_s_at	NM_005813
5.12	5.57	0.45	7.59E-03	1.80E-01	NOXA1	NADPH oxidase activator 1	chr9q34.3	232373_at	NM_006647
1.91	2.29	0.38	7.59E-03	1.80E-01	MMP8	matrix metallopeptidase 8 (neutrophil collagenase)	chr11q22.3	207329_at	NM_002424
5.88	6.89	1.01	7.62E-03	1.80E-01	---	---	---	228151_at	---
3.99	4.63	0.64	7.62E-03	1.80E-01	MOSC2	MOCO sulphurase C-terminal domain containing 2	chr1q41	227417_at	NM_017898
2.97	3.42	0.45	7.64E-03	1.80E-01	---	---	---	241050_at	---
4.71	5.10	0.39	7.67E-03	1.81E-01	RBM17	RNA binding motif protein 17	chr10p15.1	221309_at	NM_032905
6.81	7.47	0.66	7.69E-03	1.81E-01	---	---	---	225906_at	---
3.04	3.51	0.47	7.69E-03	1.81E-01	---	---	---	235924_at	---
2.93	3.40	0.46	7.69E-03	1.81E-01	---	---	---	232607_at	---
2.90	3.57	0.67	7.70E-03	1.81E-01	SLC38A9	solute carrier family 38, member 9	chr5q11.2	243709_at	NM_173514

8.62	9.72	1.10	7.77E-03	1.82E-01	PGRMC1	progesterone receptor membrane component 1	chrXq22-q24	201121_s_at	NM_006667
4.71	5.46	0.75	7.76E-03	1.82E-01	MVK	mevalonate kinase	chr12q24	215649_s_at	NM_000431 /// NM_001114185
3.40	3.88	0.49	7.75E-03	1.82E-01	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	chr4q11-q13	215305_at	NM_006206
3.28	3.72	0.44	7.75E-03	1.82E-01	C9orf45	chromosome 9 open reading frame 45	chr9q33.2	221422_s_at	XR_017862 /// XR_017965 /// XR_040211
2.97	3.40	0.42	7.77E-03	1.82E-01	CCDC63	coiled-coil domain containing 63	chr12q24.11	244833_at	NM_152591
6.69	7.55	0.86	7.79E-03	1.82E-01	SAP30L	SAP30-like	chr5q33.2	222831_at	NM_001131062 /// NM_001131063 /// NM_024632 /// NR_024084
2.25	2.77	0.52	7.81E-03	1.82E-01	---	---	---	242737_at	---
3.86	4.30	0.44	7.81E-03	1.82E-01	---	---	---	217137_x_at	---
2.64	3.13	0.49	7.83E-03	1.82E-01	---	---	---	230154_at	---
3.03	3.41	0.38	7.83E-03	1.82E-01	NHEDC1	Na+/H+ exchanger domain containing 1	chr4q24	1553633_s_at	NM_001100874 /// NM_139173
5.69	6.59	0.90	7.84E-03	1.82E-01	PURB	purine-rich element binding protein B	chr7p13	226762_at	NM_033224
2.54	3.33	0.79	7.86E-03	1.82E-01	---	---	---	239630_at	---
2.16	2.50	0.34	7.85E-03	1.82E-01	---	---	---	237934_at	---
2.98	3.35	0.37	7.89E-03	1.83E-01	AIG1	androgen-induced 1	chr6q24.2	230520_at	NM_016108
3.94	4.56	0.63	7.93E-03	1.84E-01	LOC161527 /// PML	hypothetical protein LOC161527 /// promyelocytic leukemia	chr15q22 /// chr15q25.2	211014_s_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250 /// XM_929030
4.90	5.47	0.57	7.94E-03	1.84E-01	---	---	---	244707_at	---
4.42	5.70	1.28	7.96E-03	1.84E-01	CD209	CD209 molecule	chr19p13	207277_at	NM_021155
4.82	5.29	0.47	7.96E-03	1.84E-01	---	---	---	227422_at	---
10.32	11.48	1.16	8.02E-03	1.84E-01	CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	chr15q23-q24	204309_at	NM_000781 /// NM_001099773
4.67	5.60	0.94	8.02E-03	1.84E-01	ZNF518B	zinc finger protein 518B	chr4p16.1	226909_at	NM_053042
2.95	3.77	0.83	8.02E-03	1.84E-01	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	chr15q21.2	205769_at	NM_003645
4.49	5.24	0.75	7.99E-03	1.84E-01	MOSC2	MOCO sulphurase C-terminal domain containing 2	chr1q41	219527_at	NM_017898
2.17	2.83	0.66	8.00E-03	1.84E-01	---	---	---	1569238_a_at	---
4.65	5.24	0.58	7.97E-03	1.84E-01	HFE	hemochromatosis	chr6p21.3	211330_s_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
5.40	5.96	0.57	7.99E-03	1.84E-01	PDLIM7	PDZ and LIM domain 7 (enigma)	chr5q35.3	214122_at	NM_005451 /// NM_203352 /// NM_213636
1.80	2.28	0.48	8.01E-03	1.84E-01	HS6ST3	heparan sulfate 6-O-sulfotransferase 3	chr13q32.1	232275_s_at	NM_153456
2.05	2.42	0.36	7.98E-03	1.84E-01	---	---	---	1561983_at	---
5.41	6.95	1.55	8.06E-03	1.84E-01	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	chr12q13	207057_at	NM_004731
2.91	3.92	1.01	8.07E-03	1.84E-01	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	chr4q25	204256_at	NM_001130721 /// NM_024090
4.77	5.36	0.58	8.07E-03	1.84E-01	SMOX	spermine oxidase	chr20p13	217074_at	NM_175839 /// NM_175840 /// NM_175841 /// NM_175842
2.42	2.94	0.51	8.08E-03	1.84E-01	---	---	---	1556333_at	---
4.56	5.45	0.89	8.10E-03	1.85E-01	---	---	---	228917_at	---

5.55	6.03	0.48	8.13E-03	1.85E-01	ARF1	ADP-ribosylation factor 1	chr1q42	244504_x_at	NM_001024226 /// NM_001024227 /// NM_001024228 /// NM_001658
5.42	6.08	0.65	8.15E-03	1.85E-01	---	---	---	235663_at	---
6.14	6.68	0.55	8.16E-03	1.85E-01	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	chr3p22.2	218364_at	NM_001134369 /// NM_006309 /// NM_017724
2.60	3.15	0.55	8.16E-03	1.85E-01	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	chr14q24.3	204289_at	NM_005589
4.07	4.54	0.47	8.16E-03	1.85E-01	ZNF35	zinc finger protein 35	chr3p22-p21	206096_at	NM_003420
4.13	5.09	0.97	8.17E-03	1.85E-01	PPIG	peptidylprolyl isomerase G (cyclophilin G)	chr2q31.1	208994_s_at	NM_004792
5.15	5.66	0.51	8.20E-03	1.86E-01	LL22NC03-75B3.6	KIAA1644 protein	---	221901_at	NM_001099294
5.92	6.96	1.04	8.21E-03	1.86E-01	FMO2	flavin containing monooxygenase 2 (non-functional)	chr1q23-q25	211726_s_at	NM_001460
4.63	5.56	0.93	8.23E-03	1.86E-01	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	chr22q13.1	204017_at	NM_006855 /// NM_016657
6.23	6.73	0.50	8.25E-03	1.86E-01	IL17C	interleukin 17C	chr16q24	224079_at	NM_013278
3.08	3.55	0.47	8.22E-03	1.86E-01	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	chr8q24.12	219000_s_at	NM_024094
4.56	5.02	0.46	8.21E-03	1.86E-01	LOC286161	hypothetical protein LOC286161	chr8p23.3	228615_at	---
3.08	3.51	0.43	8.23E-03	1.86E-01	---	---	---	1558592_at	---
3.72	4.28	0.56	8.30E-03	1.86E-01	NPAS4	Neuronal PAS domain protein 4	chr11q13	240794_at	NM_178864
6.75	7.26	0.51	8.26E-03	1.86E-01	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	chr19q13.33	229617_x_at	NM_014203 /// NM_130787
3.05	3.48	0.43	8.28E-03	1.86E-01	---	---	---	243703_x_at	---
2.86	3.27	0.41	8.31E-03	1.86E-01	TULP1	tubby like protein 1	chr6p21.3	206705_at	NM_003322
2.47	2.86	0.39	8.32E-03	1.86E-01	PTPN1	Protein tyrosine phosphatase, non-receptor type 1	chr20q13.1-q13.2	239526_x_at	NM_002827
2.05	2.62	0.57	8.34E-03	1.86E-01	---	---	---	244061_at	---
4.64	6.70	2.06	8.37E-03	1.86E-01	TMEM200A	transmembrane protein 200A	chr6q23.1	234994_at	NM_052913
3.53	3.98	0.45	8.38E-03	1.86E-01	---	---	---	237073_at	---
5.46	6.09	0.63	8.40E-03	1.86E-01	SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	chr19p13.3	224182_x_at	NM_032108
2.61	2.99	0.37	8.41E-03	1.87E-01	---	---	---	243064_at	---
5.74	6.20	0.46	8.42E-03	1.87E-01	TCF3	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	216647_at	NM_003200
3.41	4.77	1.36	8.44E-03	1.87E-01	---	---	---	242865_at	---
4.77	5.48	0.71	8.44E-03	1.87E-01	FERMT2	fermitin family homolog 2 (Drosophila)	chr14q22.2	214212_x_at	NM_006832
4.44	4.95	0.51	8.43E-03	1.87E-01	GNG7	guanine nucleotide binding protein (G protein), gamma 7	chr19p13.3	232043_at	NM_052847
2.90	3.41	0.50	8.47E-03	1.87E-01	GPR173	G protein-coupled receptor 173	chrXp11	1556038_at	NM_018969
2.97	3.43	0.47	8.46E-03	1.87E-01	---	---	---	241155_at	---
2.69	3.13	0.43	8.45E-03	1.87E-01	NT5DC3	5'-nucleotidase domain containing 3	chr12q22-q23.1	234737_at	NM_001031701 /// NM_016575
2.67	3.31	0.64	8.49E-03	1.87E-01	---	---	---	1559987_at	---
4.35	4.95	0.60	8.52E-03	1.87E-01	PRLH	prolactin releasing hormone	chr2q37.3	221443_x_at	NM_015893
7.27	7.83	0.56	8.51E-03	1.87E-01	FADS2	fatty acid desaturase 2	chr11q12-q13.1	202218_s_at	NM_004265
2.27	2.88	0.61	8.54E-03	1.87E-01	EIF5B	eukaryotic translation initiation factor 5B	chr2q11.2	214314_s_at	NM_015904
3.76	4.23	0.48	8.54E-03	1.87E-01	SMYD1	SET and MYND domain containing 1	chr2p11.2	243045_at	NM_198274
2.32	2.71	0.38	8.55E-03	1.88E-01	C22orf37	chromosome 22 open reading frame 37	chr22q11.21	1556072_at	XR_040827 /// XR_040828 /// XR_040829
4.07	5.29	1.22	8.59E-03	1.88E-01	SYNPO2	synaptopodin 2	chr4q26	227662_at	NM_001128933 /// NM_001128934 /// NM_133477
3.50	4.09	0.59	8.59E-03	1.88E-01	NR1D1 /// THRA	nuclear receptor subfamily 1, group D, member 1 /// thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	chr17q11.2	217476_at	NM_003250 /// NM_021724 /// NM_199334
3.99	4.58	0.58	8.60E-03	1.88E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	209359_x_at	NM_001001890 /// NM_001122607 /// NM_001754
3.46	4.11	0.65	8.61E-03	1.88E-01	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15q22.1	207015_s_at	NM_003888 /// NM_170696 /// NM_170697
3.25	3.73	0.48	8.61E-03	1.88E-01	NTNG2	netrin G2	chr9q34	233072_at	NM_032536
2.91	3.52	0.61	8.64E-03	1.88E-01	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	chr1p13.3	211301_at	NM_004980 /// NM_172198
5.08	5.66	0.57	8.64E-03	1.88E-01	ARHGEF15	Rho guanine nucleotide exchange factor (GEF) 15	chr17p13.1	217348_x_at	NM_173728
2.98	3.48	0.50	8.65E-03	1.88E-01	IFNAR1	interferon (alpha, beta and omega) receptor 1	chr21q22.1|21q22.11	204191_at	NM_000629

5.54	6.38	0.84	8.67E-03	1.88E-01	MPEG1	macrophage expressed gene 1	chr11q12.1	226841_at	NM_001039396
4.23	5.12	0.89	8.69E-03	1.89E-01	DGCR5	DiGeorge syndrome critical region gene 5 (non-protein coding)	chr22q11	228804_at	NR_002733
5.07	5.60	0.53	8.71E-03	1.89E-01	---	---	---	216163_at	---
2.92	3.57	0.65	8.72E-03	1.89E-01	C1orf103	chromosome 1 open reading frame 103	chr1p13.3	220235_s_at	NM_001006945 /// NM_018372
5.10	5.56	0.45	8.74E-03	1.89E-01	ARMC9	armadillo repeat containing 9	chr2q37.1	219636_s_at	NM_025139
2.91	3.32	0.41	8.74E-03	1.89E-01	DQX1	DEAQ box polypeptide 1 (RNA-dependent ATPase)	chr2p13.1	236055_at	NM_133637
2.56	2.96	0.40	8.74E-03	1.89E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	234129_at	NM_015313
3.21	3.58	0.38	8.76E-03	1.89E-01	FLJ23172 /// TMEM212	hypothetical LOC389177 /// transmembrane protein 212	chr3q26.31	217016_x_at	XM_001723238 /// XM_001726086 /// XM_001726380 /// XM_371680 /// XM_941617
3.52	4.04	0.52	8.76E-03	1.89E-01	EVI5L	ecotropic viral integration site 5-like	chr19p13.2	244500_s_at	NM_145245
3.06	3.63	0.57	8.77E-03	1.89E-01	CLPS	colipase, pancreatic	chr6pter-p21.1	206131_at	NM_001832
2.85	3.24	0.39	8.82E-03	1.89E-01	---	---	---	242841_at	---
4.23	5.84	1.60	8.84E-03	1.89E-01	INSIG1	insulin induced gene 1	chr7q36	201625_s_at	NM_005542 /// NM_198336 /// NM_198337
3.76	4.49	0.73	8.83E-03	1.89E-01	---	---	---	1558783_at	---
1.91	2.34	0.44	8.84E-03	1.89E-01	---	---	---	1566638_at	---
5.29	6.03	0.74	8.86E-03	1.90E-01	---	---	---	242366_at	---
1.89	2.32	0.43	8.86E-03	1.90E-01	---	---	---	241860_at	---
3.61	4.02	0.41	8.86E-03	1.90E-01	VCX2	variable charge, X-linked 2	chrXp22.32	211403_x_at	NM_016378
2.32	2.65	0.34	8.89E-03	1.90E-01	LOC131185 /// RAD23B	similar to RAD23B protein /// RAD23 homolog B (S. cerevisiae)	chr3p24.3 /// chr9q31.2	214422_at	NM_002874 /// XR_016694 /// XR_018936 /// XR_039641
5.42	6.62	1.20	8.90E-03	1.90E-01	AQP11	aquaporin 11	chr11q14.1	229526_at	NM_173039
4.85	5.68	0.83	8.89E-03	1.90E-01	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	chr14q32.3-qter|14q32	229115_at	NM_001376
3.99	4.52	0.53	8.91E-03	1.90E-01	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	chr19q13.2	210610_at	NM_001024912 /// NM_001712
4.51	4.99	0.48	8.91E-03	1.90E-01	LOC652821 /// VCX3A /// VCY /// VCY1B	hypothetical protein LOC652821 /// variable charge, X-linked 3A /// variable charge, Y-linked /// variable charge, Y-linked 1B	chrXp22 /// chrYq11.21 /// chrYq11.221	206922_at	NM_004679 /// NM_016379 /// NM_181880 /// XM_946051
4.98	5.53	0.54	8.96E-03	1.91E-01	---	---	---	215701_at	---
3.11	3.52	0.41	8.96E-03	1.91E-01	TNP1	transition protein 1 (during histone to protamine replacement)	chr2q35-q36	206568_at	NM_003284
4.33	6.03	1.70	8.97E-03	1.91E-01	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	chr10q24.31	211708_s_at	NM_005063 /// XM_001723785 /// XM_001725202 /// XM_001725496
4.17	4.86	0.69	8.98E-03	1.91E-01	ZNF606	zinc finger protein 606	chr19q13.4	219635_at	NM_025027
2.36	2.82	0.46	8.98E-03	1.91E-01	TRIM37	tripartite motif-containing 37	chr17q23.2	1554001_at	NM_001005207 /// NM_015294
2.28	2.64	0.36	8.98E-03	1.91E-01	---	---	---	239292_at	---
3.59	4.33	0.75	9.01E-03	1.91E-01	EPHB2	EPH receptor B2	chr1p36.1-p35	209589_s_at	NM_004442 /// NM_017449
4.25	4.88	0.63	9.01E-03	1.91E-01	IL17RE	interleukin 17 receptor E	chr3p25.3	236186_x_at	NM_153480 /// NM_153481 /// NM_153483
3.26	3.84	0.58	9.00E-03	1.91E-01	ITGB1BP3	integrin beta 1 binding protein 3	chr19p13.3	221051_s_at	NM_170678
2.20	2.71	0.51	8.99E-03	1.91E-01	---	---	---	240215_at	---
5.82	6.32	0.50	9.01E-03	1.91E-01	ATXN2L	ataxin 2-like	chr16p11	201806_s_at	NM_007245 /// NM_145714 /// NM_148414 /// NM_148415 /// NM_148416
2.18	2.62	0.44	9.00E-03	1.91E-01	---	---	---	242025_at	---
2.40	2.90	0.50	9.04E-03	1.91E-01	ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	chr2q33.1-q33.2	1555391_a_at	NM_001104586 /// NM_024744
4.37	5.00	0.63	9.13E-03	1.92E-01	ZNF148	zinc finger protein 148	chr3q21	238711_s_at	NM_021964

4.78	5.26	0.48	9.13E-03	1.92E-01	IGLV4-3	immunoglobulin lambda variable 4-3	chr22q11.2	234381_at	---
6.27	6.75	0.48	9.11E-03	1.92E-01	C1orf170	chromosome 1 open reading frame 170	chr1p36.33	224501_at	XR_039825 /// XR_039826 /// XR_039827
2.83	3.29	0.46	9.12E-03	1.92E-01	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	chr16q13	225109_at	NM_018233
2.51	2.94	0.43	9.12E-03	1.92E-01	FGF22	fibroblast growth factor 22	chr19p13.3	221315_s_at	NM_020637
3.19	3.54	0.35	9.12E-03	1.92E-01	ST7L	Suppression of tumorigenicity 7 like	chr1p13.2	236123_at	NM_017744 /// NM_138727 /// NM_138728 /// NM_138729
2.50	2.91	0.41	9.15E-03	1.92E-01	DKFZp547G183	hypothetical LOC55525	chr11q13.5	220572_at	---
2.37	2.86	0.49	9.17E-03	1.92E-01	---	---	---	236732_at	---
2.24	2.66	0.42	9.18E-03	1.92E-01	---	---	---	228934_x_at	---
3.00	3.41	0.41	9.17E-03	1.92E-01	---	---	---	1562937_at	---
4.79	5.74	0.95	9.18E-03	1.92E-01	PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	chr12p12.1	219802_at	NM_024854
3.70	4.26	0.56	9.18E-03	1.92E-01	GDAP1L1	ganglioside-induced differentiation-associated protein 1-like 1	chr20q12	219668_at	NM_024034
3.73	4.24	0.51	9.20E-03	1.92E-01	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	chr1p34	221083_at	NM_004700 /// NM_172163
3.09	3.75	0.67	9.24E-03	1.92E-01	---	---	---	241292_at	---
3.89	4.28	0.38	9.25E-03	1.92E-01	---	---	---	215439_x_at	---
2.28	2.57	0.29	9.27E-03	1.93E-01	---	---	---	215846_at	---
2.43	2.88	0.45	9.29E-03	1.93E-01	GRM5	glutamate receptor, metabotropic 5	chr11q14.2-q14.3	207235_s_at	NM_000842
5.79	6.19	0.40	9.30E-03	1.93E-01	---	---	---	234425_at	---
3.99	4.52	0.53	9.35E-03	1.93E-01	SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	chr19p13.3	223567_at	NM_032108
2.25	2.68	0.43	9.38E-03	1.93E-01	LCP2	Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	chr5q33.1-qter	244251_at	NM_005565
5.64	6.07	0.43	9.37E-03	1.93E-01	UPB1	ureidopropionase, beta	chr22q11.2	228219_s_at	NM_016327
3.62	4.34	0.72	9.41E-03	1.94E-01	---	---	---	238915_at	---
3.74	4.42	0.67	9.41E-03	1.94E-01	---	---	---	236781_at	---
5.57	6.17	0.60	9.41E-03	1.94E-01	TP53I11	tumor protein p53 inducible protein 11	chr11p11.2	203421_at	NM_001076787 /// NM_006034
2.01	2.44	0.44	9.41E-03	1.94E-01	MMP2	Matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	chr16q13-q21	1566677_at	NM_001127891 /// NM_004530
3.77	4.30	0.53	9.42E-03	1.94E-01	FOXD4 /// FOXD4L1	forkhead box D4 /// forkhead box D4-like 1	chr2q14.1 /// chr9p11-q11	217032_at	NM_012184 /// NM_207305
3.59	4.15	0.55	9.43E-03	1.94E-01	TOR1AIP2	torsin A interacting protein 2	chr1q25.2	240700_at	NM_145034
3.50	3.97	0.47	9.47E-03	1.94E-01	---	---	---	238515_at	---
4.53	5.31	0.79	9.50E-03	1.94E-01	ZBTB43	zinc finger and BTB domain containing 43	chr9q33-q34	204182_s_at	NM_014007
9.30	10.01	0.71	9.50E-03	1.94E-01	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	chr6p21.1-p12.1	208788_at	NM_021814
4.67	5.35	0.68	9.49E-03	1.94E-01	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	chr6q24	205231_s_at	NM_001018041 /// NM_005670
4.16	4.72	0.56	9.52E-03	1.94E-01	KIRREL	kin of IRRE like (Drosophila)	chr1q21-q25	232467_at	NM_018240
4.06	4.99	0.93	9.52E-03	1.95E-01	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	chr12q24	238975_at	NM_052845
3.78	5.08	1.30	9.53E-03	1.95E-01	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	chr5q13.1	212249_at	NM_181504 /// NM_181523 /// NM_181524
3.99	4.35	0.36	9.54E-03	1.95E-01	LOC100132244	Hypothetical protein LOC100132244	chr7p22.3	229438_at	XM_001714003 /// XM_001720467 /// XM_001720628
7.12	7.72	0.60	9.56E-03	1.95E-01	CLDN6	claudin 6	chr16p13.3	208474_at	NM_021195
4.71	5.11	0.40	9.56E-03	1.95E-01	CNIH4	cornichon homolog 4 (Drosophila)	chr1q42.11	228306_at	NM_014184
3.76	4.23	0.47	9.58E-03	1.95E-01	EXPH5	Exophilin 5	chr11q22.3	215226_at	NM_015065
6.76	8.39	1.63	9.60E-03	1.95E-01	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	chr11q23.3	211423_s_at	NM_001024956 /// NM_006918
3.20	3.89	0.69	9.65E-03	1.96E-01	---	---	---	244876_at	---
3.16	3.79	0.63	9.65E-03	1.96E-01	GPSM2	G-protein signaling modulator 2 (AGS3-like, C. elegans)	chr1p13.3	205240_at	NM_013296
5.28	5.83	0.55	9.67E-03	1.96E-01	---	---	---	240664_at	---
3.91	4.46	0.56	9.69E-03	1.96E-01	---	---	---	1557797_a_at	---
2.44	2.82	0.37	9.69E-03	1.96E-01	JAK2	Janus kinase 2 (a protein tyrosine kinase)	chr9p24	1562031_at	NM_004972
6.66	8.76	2.09	9.71E-03	1.96E-01	SC4MOL	sterol-C4-methyl oxidase-like	chr4q32-q34	209146_at	NM_001017369 /// NM_006745
3.80	4.83	1.03	9.72E-03	1.96E-01	NCF2	neutrophil cytosolic factor 2	chr1q25	209949_at	NM_000433 /// NM_001127651
4.85	5.49	0.64	9.71E-03	1.96E-01	---	---	---	240508_at	---

3.97	4.58	0.61	9.72E-03	1.96E-01	NLGN2	neuroligin 2	chr17p13.1	1554428_s_at	NM_020795
3.40	3.96	0.56	9.73E-03	1.96E-01	---	---	---	214809_at	---
4.30	4.91	0.61	9.74E-03	1.96E-01	GNG7	guanine nucleotide binding protein (G protein), gamma 7	chr19p13.3	228831_s_at	NM_052847
5.84	6.44	0.60	9.75E-03	1.96E-01	---	---	---	230805_at	---
2.42	2.77	0.35	9.77E-03	1.97E-01	LZTFL1	leucine zipper transcription factor-like 1	chr3p21.3	232418_at	NM_020347
2.62	3.27	0.65	9.81E-03	1.97E-01	DOCK5	Dedicator of cytokinesis 5	chr8p21.2	222721_at	NM_024940
3.94	4.44	0.50	9.81E-03	1.97E-01	GBX1	gastrulation brain homeobox 1	chr7q36	217011_at	NM_001098834
2.08	2.52	0.44	9.80E-03	1.97E-01	---	---	---	233377_at	---
2.75	3.23	0.48	9.82E-03	1.97E-01	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	---	223814_at	NM_182916
3.96	4.91	0.95	9.83E-03	1.97E-01	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	chr12q13	210807_s_at	NM_004731
6.95	7.96	1.01	9.87E-03	1.97E-01	---	---	---	235381_at	---
2.02	2.37	0.35	9.89E-03	1.97E-01	RNF141	ring finger protein 141	chr11p15.4	1565544_at	NM_016422
2.49	2.86	0.37	9.89E-03	1.97E-01	---	---	---	228078_at	---
4.34	4.99	0.65	9.94E-03	1.98E-01	FLNC	filamin C, gamma (actin binding protein 280)	chr7q32-q35	207876_s_at	NM_001127487 /// NM_001458
4.58	5.38	0.80	9.95E-03	1.98E-01	---	---	---	225543_at	---
4.10	4.56	0.45	9.96E-03	1.98E-01	---	---	---	233580_at	---
2.42	3.54	1.13	9.99E-03	1.98E-01	DLG2	discs, large homolog 2, chapsyn-110 (Drosophila)	chr11q14.1	206253_at	NM_001364
7.54	8.47	0.92	9.99E-03	1.98E-01	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	chr8p21	221479_s_at	NM_004331
3.10	3.79	0.69	9.97E-03	1.98E-01	---	---	---	243964_at	---
2.04	2.43	0.38	9.98E-03	1.98E-01	ZNF718	zinc finger protein 718	chr4p16.3	1559746_a_at	NM_001039127
2.30	2.74	0.44	1.00E-02	1.98E-01	KIAA0509	hypothetical LOC57242	---	215480_at	---
7.26	7.89	0.64	1.01E-02	1.99E-01	CES2	carboxylesterase 2 (intestine, liver)	chr16q22.1	209668_x_at	NM_003869 /// NM_198061
3.36	3.87	0.52	1.01E-02	1.99E-01	---	---	---	230665_at	---
3.88	4.39	0.51	1.01E-02	1.99E-01	MGC50722	hypothetical MGC50722	---	1554681_a_at	NM_203348
2.83	3.32	0.49	1.01E-02	1.99E-01	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	chr10q23-q24	206424_at	NM_000783 /// NM_057157
2.88	3.30	0.42	1.00E-02	1.99E-01	CKAP2L	cytoskeleton associated protein 2-like	chr2q13	229610_at	NM_152515
2.04	2.39	0.35	1.01E-02	1.99E-01	---	---	---	243813_at	---
4.48	4.92	0.44	1.01E-02	1.99E-01	HFE	hemochromatosis	chr6p21.3	211866_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
4.54	5.24	0.70	1.01E-02	1.99E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	214129_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359
6.54	7.10	0.56	1.01E-02	1.99E-01	LTBP3	latent transforming growth factor beta binding protein 3	chr11q12	237144_at	NM_001130144 /// NM_021070
3.12	3.68	0.55	1.01E-02	1.99E-01	---	---	---	236527_at	---
2.20	2.74	0.54	1.02E-02	1.99E-01	SLAMF7	SLAM family member 7	chr1q23.1-q24.1	219159_s_at	NM_021181
2.95	3.45	0.49	1.01E-02	1.99E-01	PRSS27	protease, serine 27	chr16p13.3	232074_at	NM_031948
3.05	3.54	0.49	1.01E-02	1.99E-01	CSPG4	chondroitin sulfate proteoglycan 4	chr15q24.2	204736_s_at	NM_001897
3.88	4.30	0.42	1.02E-02	1.99E-01	AIPL1	aryl hydrocarbon receptor interacting protein-like 1	chr17p13.1	235731_at	NM_001033054 /// NM_001033055 /// NM_014336
2.40	2.77	0.37	1.02E-02	1.99E-01	MST075 /// RPA1	MSTP075 /// replication protein A1, 70kDa	chr17p13.3	236675_at	NM_002945 /// XM_001717905
4.77	5.89	1.13	1.02E-02	1.99E-01	RPP25	ribonuclease P/MRP 25kDa subunit	chr15q24.1	219143_s_at	NM_017793
7.87	8.29	0.42	1.02E-02	1.99E-01	---	---	---	221419_s_at	---
2.47	3.28	0.81	1.02E-02	1.99E-01	---	---	---	1557224_at	---
4.81	6.28	1.47	1.02E-02	2.00E-01	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	chr16q22.1	207173_x_at	NM_001797
5.23	5.66	0.43	1.02E-02	2.00E-01	KLK8 /// KLK9	kallikrein-related peptidase 8 /// kallikrein-related peptidase 9	chr19q13.3-q13.4 /// chr19q13.33	233687_s_at	NM_007196 /// NM_012315 /// NM_144505 /// NM_144506 /// NM_144507
2.37	2.76	0.38	1.03E-02	2.00E-01	---	---	---	237181_at	---

2.85	3.41	0.56	1.03E-02	2.00E-01	LOC100130654	hypothetical protein LOC100130654	chr17q21.2	1562017_at	XM_001721506 /// XM_001723501 /// XM_001725839
1.87	2.23	0.36	1.03E-02	2.00E-01	CRYZL1	crystallin, zeta (quinone reductase)-like 1	chr21q21.3	1560609_at	NM_145858
6.57	7.19	0.62	1.03E-02	2.01E-01	FUT7	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	chr9q34.3	217696_at	NM_004479
3.78	4.31	0.53	1.03E-02	2.01E-01	TACC1	transforming, acidic coiled-coil containing protein 1	chr8p11	217437_s_at	NM_001122824 /// NM_006283
3.08	3.67	0.60	1.04E-02	2.01E-01	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	chr15q21.3	219508_at	NM_004751
5.19	5.94	0.75	1.04E-02	2.01E-01	SRPRB	Signal recognition particle receptor, B subunit	chr3q22.1	227737_at	NM_021203
2.02	2.36	0.34	1.04E-02	2.01E-01	DSC3	desmocollin 3	chr18q12.1	206033_s_at	NM_001941 /// NM_024423
3.30	4.13	0.83	1.04E-02	2.01E-01	RAB18	RAB18, member RAS oncogene family	chr10p12.1	243496_at	NM_021252
3.21	3.90	0.69	1.04E-02	2.02E-01	---	---	---	235581_at	---
3.07	3.53	0.46	1.04E-02	2.02E-01	---	---	---	1557889_at	---
4.38	4.83	0.45	1.04E-02	2.02E-01	---	---	---	234858_at	---
1.96	2.33	0.37	1.04E-02	2.02E-01	---	---	---	1561307_at	---
2.05	2.38	0.33	1.04E-02	2.02E-01	---	---	---	1569512_at	---
6.62	7.19	0.57	1.05E-02	2.02E-01	CFB	complement factor B	chr6p21.3	211920_at	NM_001710
3.39	3.80	0.41	1.05E-02	2.02E-01	---	---	---	232828_at	---
8.94	9.59	0.65	1.05E-02	2.02E-01	BSG	basigin (Ok blood group)	chr19p13.3	208677_s_at	NM_001728 /// NM_198589 /// NM_198590 /// NM_198591
3.66	4.21	0.55	1.05E-02	2.02E-01	BEGAIN	brain-enriched guanylate kinase-associated homolog (rat)	chr14q32.2	220795_s_at	NM_020836
2.61	3.00	0.40	1.05E-02	2.02E-01	ITPR3	Inositol 1,4,5-triphosphate receptor, type 3	chr6p21	239542_at	NM_002224
4.09	4.61	0.52	1.05E-02	2.02E-01	PDE4A	Phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	chr19p13.2	242435_at	NM_001111307 /// NM_001111308 /// NM_001111309 /// NM_006202
3.17	3.55	0.38	1.05E-02	2.03E-01	---	---	---	241143_at	---
2.39	2.70	0.32	1.05E-02	2.03E-01	HRNBP3 /// LOC100130312 /// LOC100133332	hexaribonucleotide binding protein 3 /// hypothetical protein LOC100130312 /// hypothetical protein LOC100133332	chr17q25.3	229406_at	NM_001082575 /// XM_001713646 /// XM_001713647
6.18	6.88	0.70	1.06E-02	2.03E-01	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	chr21q22.3	209979_at	NM_001033049 /// NM_001112 /// NM_015833 /// NM_015834
2.37	2.74	0.38	1.06E-02	2.03E-01	---	---	---	229150_at	---
5.37	7.27	1.90	1.06E-02	2.03E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	224567_x_at	NR_002819
3.47	4.47	1.00	1.06E-02	2.03E-01	CPN2	carboxypeptidase N, polypeptide 2	chr3q29	216223_at	NM_001080513
2.93	3.50	0.57	1.06E-02	2.03E-01	---	---	---	242797_x_at	---
4.43	4.85	0.42	1.06E-02	2.03E-01	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	chr3q27-q28	213749_at	NM_001031849 /// NM_001879 /// NM_139125
4.32	4.81	0.49	1.07E-02	2.03E-01	---	---	---	231168_at	---
3.13	3.59	0.46	1.07E-02	2.03E-01	NRXN1	neurexin 1	chr2p16.3	209914_s_at	NM_004801 /// NM_138735
4.21	5.60	1.39	1.08E-02	2.03E-01	---	---	---	228390_at	---
5.51	6.47	0.96	1.07E-02	2.03E-01	FAM173B	family with sequence similarity 173, member B	chr5p15.2	225670_at	NM_199133
4.65	5.42	0.77	1.07E-02	2.03E-01	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	chr4q25	227491_at	NM_001130721 /// NM_024090
4.08	4.85	0.76	1.08E-02	2.03E-01	ACSM5	acyl-CoA synthetase medium-chain family member 5	chr16p12.3	220061_at	NM_017888
2.37	3.06	0.69	1.07E-02	2.03E-01	NRG1	neuregulin 1	chr8p12	208241_at	NM_004495 /// NM_013956 /// NM_013957 /// NM_013958 /// NM_013959 /// NM_013960 /// NM_013961 /// NM_013962 /// NM_013964
6.62	7.26	0.64	1.08E-02	2.03E-01	BTBD14B	BTB (POZ) domain containing 14B	chr19p13.13	235047_x_at	NM_052876
2.03	2.61	0.57	1.07E-02	2.03E-01	---	---	---	237544_at	---

4.94	5.49	0.55	1.07E-02	2.03E-01	BMP7	bone morphogenetic protein 7	chr20q13	211259_s_at	NM_001719
6.70	7.24	0.54	1.08E-02	2.03E-01	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	chr9q34.3	210782_x_at	NM_000832 /// NM_007327 /// NM_021569
4.56	5.08	0.52	1.07E-02	2.03E-01	MMP17	matrix metallopeptidase 17 (membrane-inserted)	chr12q24.3	206234_s_at	NM_016155
3.51	4.01	0.50	1.07E-02	2.03E-01	NFKBIL2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	chr8q24.3	207137_at	NM_013432
4.93	5.41	0.48	1.08E-02	2.03E-01	CCDC40	coiled-coil domain containing 40	chr17q25.3	239254_at	NM_017950
6.27	6.74	0.47	1.07E-02	2.03E-01	---	---	---	221099_at	---
3.44	3.91	0.47	1.08E-02	2.03E-01	COL23A1	collagen, type XXIII, alpha 1	chr5q35.3	229168_at	NM_173465
2.57	2.96	0.40	1.08E-02	2.03E-01	---	---	---	241004_at	---
2.05	2.42	0.37	1.07E-02	2.03E-01	---	---	---	1563241_at	---
2.71	3.08	0.37	1.07E-02	2.03E-01	---	---	---	237321_at	---
3.18	3.94	0.76	1.08E-02	2.04E-01	OSBPL8	oxysterol binding protein-like 8	chr12q14	228986_at	NM_001003712 /// NM_020841
2.12	2.57	0.45	1.08E-02	2.04E-01	---	---	---	1564056_at	---
2.39	2.79	0.40	1.08E-02	2.04E-01	---	---	---	217474_at	---
4.40	5.09	0.69	1.08E-02	2.04E-01	---	---	---	238656_at	---
2.37	2.84	0.47	1.09E-02	2.04E-01	---	---	---	233007_at	---
1.78	2.08	0.30	1.09E-02	2.05E-01	UBE2U	ubiquitin-conjugating enzyme E2U (putative)	chr1p31.3	1553776_at	NM_152489
6.71	7.96	1.24	1.10E-02	2.05E-01	ZNF148	zinc finger protein 148	chr3q21	203318_s_at	NM_021964
2.71	3.14	0.43	1.09E-02	2.05E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	228052_x_at	NM_003200
2.18	2.53	0.35	1.10E-02	2.05E-01	PTEN	phosphatase and tensin homolog	chr10q23.3	222176_at	NM_000314
3.18	3.60	0.42	1.10E-02	2.05E-01	---	---	---	216022_at	---
5.89	6.42	0.54	1.10E-02	2.06E-01	TRIM2	tripartite motif-containing 2	chr4q31.3	215945_s_at	NM_001130067 /// NM_015271
2.48	2.92	0.44	1.10E-02	2.06E-01	TRAV20	T cell receptor alpha variable 20	chr14q11	234860_at	---
4.69	5.93	1.24	1.10E-02	2.06E-01	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	chr16q22.1	207172_s_at	NM_001797
5.35	6.44	1.09	1.10E-02	2.06E-01	IGF1	insulin-like growth factor 1 (somatomedin C)	chr12q22-q23	211577_s_at	NM_000618 /// NM_001111283 /// NM_001111284 /// NM_001111285
5.37	5.99	0.62	1.11E-02	2.06E-01	FLJ21767 /// LOC100133005 /// LOC100134722 /// RASA4	RAS p21 protein activator 4 pseudogene /// similar to RAS p21 protein activator 4 /// similar to HSPC047 protein /// RAS p21 protein activator 4	chr7p13 /// chr7q22 /// chr7q22.1	212707_s_at	NM_001079877 /// NM_006989 /// NR_024116 /// XM_001713977 /// XM_001718200 /// XM_001724280 /// XM_001725218
2.37	2.79	0.42	1.11E-02	2.06E-01	KNG1	kininogen 1	chr3q27	206054_at	NM_000893 /// NM_001102416
2.11	2.46	0.35	1.11E-02	2.06E-01	---	---	---	1570301_at	---
1.85	2.18	0.34	1.11E-02	2.06E-01	---	---	---	240267_at	---
3.28	4.04	0.76	1.11E-02	2.06E-01	---	---	---	236883_at	---
6.70	7.22	0.52	1.11E-02	2.06E-01	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	chr12q23-q24.1	239996_x_at	NM_001681 /// NM_170665
2.41	2.81	0.40	1.11E-02	2.06E-01	---	---	---	242459_at	---
7.12	8.29	1.17	1.12E-02	2.07E-01	FOLR2	folate receptor 2 (fetal)	chr11q13.3-q13.5	204829_s_at	NM_000803 /// NM_001113534 /// NM_001113535 /// NM_001113536
5.51	6.19	0.68	1.12E-02	2.07E-01	MAPK12	mitogen-activated protein kinase 12	chr22q13.33	1556340_at	NM_002969
4.12	4.73	0.61	1.12E-02	2.07E-01	TCEA2	transcription elongation factor A (SII), 2	chr20q13.33	238173_at	NM_003195 /// NM_198723
4.67	5.19	0.52	1.12E-02	2.07E-01	TSSK6	testis-specific serine kinase 6	chr19p13.11	224409_s_at	NM_032037
2.41	2.81	0.40	1.12E-02	2.07E-01	---	---	---	1565768_at	---
1.77	2.11	0.34	1.12E-02	2.07E-01	ADK	adenosine kinase	chr10q22|10q11-q24	204120_s_at	NM_001123 /// NM_006721
3.68	4.21	0.53	1.12E-02	2.07E-01	FAM126B	family with sequence similarity 126, member B	chr2q33.1	1554178_a_at	NM_173822
2.10	2.50	0.40	1.12E-02	2.07E-01	HCG11	HLA complex group 11	chr6p21	1557169_x_at	---
5.85	6.53	0.68	1.13E-02	2.08E-01	MEGF9	multiple EGF-like-domains 9	chr9q32-q33.3	212830_at	NM_001080497
5.62	6.20	0.58	1.13E-02	2.08E-01	CHCHD5	Coiled-coil-helix-coiled-coil-helix domain containing 5	chr2q13	237993_at	NM_032309

4.91	5.49	0.58	1.13E-02	2.08E-01	FRS2	fibroblast growth factor receptor substrate 2	chr12q15	226045_at	NM_001042555 /// NM_006654
4.01	4.53	0.51	1.13E-02	2.08E-01	NKX2-5	NK2 transcription factor related, locus 5 (Drosophila)	chr5q34	206578_at	NM_004387
3.48	3.87	0.39	1.13E-02	2.08E-01	---	---	---	243078_at	---
4.33	4.81	0.48	1.13E-02	2.08E-01	LOC100133142	similar to hCG2008267	chr19q13.42	241964_at	XM_001718400
6.30	7.50	1.20	1.13E-02	2.08E-01	LOC647121	embigin homolog (mouse) pseudogene	chr1p11.2	226789_at	NR_003955
6.36	6.92	0.56	1.13E-02	2.08E-01	SLC12A3	Solute carrier family 12 (sodium/chloride transporters), member 3	chr16q13	244477_at	NM_000339 /// NM_001126107 /// NM_001126108
3.91	4.47	0.56	1.13E-02	2.08E-01	CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11p11	235297_at	NM_001025596 /// NM_006560 /// NM_198700
3.56	4.18	0.62	1.14E-02	2.08E-01	INPP5F	inositol polyphosphate-5-phosphatase F	chr10q26.11	203607_at	NM_014937 /// NR_003251 /// NR_003252
1.84	2.19	0.35	1.14E-02	2.08E-01	---	---	---	233808_at	---
3.06	4.10	1.04	1.14E-02	2.09E-01	ANGPT1	angiopoietin 1	chr8q22.3-q23	205608_s_at	NM_001146
2.67	3.20	0.53	1.14E-02	2.09E-01	ARHGAP22	Rho GTPase activating protein 22	chr10q11.22	1560765_a_at	NM_021226
4.88	5.32	0.44	1.14E-02	2.09E-01	ACCN4	amiloride-sensitive cation channel 4, pituitary	chr2q35	221226_s_at	NM_018674 /// NM_182847
2.68	3.22	0.54	1.14E-02	2.09E-01	POF1B	premature ovarian failure, 1B	chrXq21.1-q21.2	219756_s_at	NM_024921
4.85	5.77	0.92	1.15E-02	2.09E-01	NRP1	neuropilin 1	chr10p12	210510_s_at	NM_001024628 /// NM_001024629 /// NM_003873
4.86	5.43	0.57	1.15E-02	2.09E-01	RAB3IL1	RAB3A interacting protein (rabin3)-like 1	chr11q12-q13.1	219579_at	NM_013401
6.09	6.51	0.42	1.15E-02	2.09E-01	MORN1	MORN repeat containing 1	chr1p36.33-p36.32	219852_s_at	NM_024848
3.01	4.62	1.61	1.15E-02	2.10E-01	CHRNA3	cholinergic receptor, nicotinic, alpha 3	chr15q24	210221_at	NM_000743
4.89	6.05	1.15	1.16E-02	2.10E-01	---	---	---	229072_at	---
5.72	6.21	0.49	1.15E-02	2.10E-01	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	235792_x_at	NM_002645
3.62	4.08	0.46	1.16E-02	2.10E-01	SENP8	SUMO/sentrin specific peptidase family member 8	chr15q23	228398_at	NM_145204
3.52	3.91	0.38	1.16E-02	2.10E-01	---	---	---	1558011_at	---
2.79	3.24	0.45	1.16E-02	2.10E-01	---	---	---	243012_at	---
4.90	5.74	0.84	1.16E-02	2.10E-01	---	---	---	232778_at	---
3.77	4.31	0.54	1.16E-02	2.10E-01	MBD5	methyl-CpG binding domain protein 5	chr2q23.1	220195_at	NM_018328
3.83	4.35	0.52	1.16E-02	2.10E-01	DIO3	deiodinase, iodothyronine, type III	chr14q32	207154_at	NM_001362
5.91	7.54	1.63	1.16E-02	2.10E-01	TPR	translocated promoter region (to activated MET oncogene)	chr1q25	201730_s_at	NM_003292
4.26	4.97	0.70	1.16E-02	2.10E-01	---	---	---	239011_at	---
2.38	2.80	0.42	1.17E-02	2.11E-01	C9orf38	chromosome 9 open reading frame 38	chr9p24.1	208077_at	XM_927012 /// XM_939946
2.17	2.78	0.61	1.17E-02	2.11E-01	---	---	---	241745_at	---
1.99	2.38	0.39	1.17E-02	2.11E-01	USP12	ubiquitin specific peptidase 12	chr13q12.13	215886_x_at	NM_182488
2.69	3.11	0.43	1.17E-02	2.11E-01	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	chr3q26.3	231854_at	NM_006218
4.20	4.92	0.72	1.17E-02	2.11E-01	GGT7	gamma-glutamyltransferase 7	chr20q11.22	226470_at	NM_178026
3.75	4.15	0.39	1.17E-02	2.11E-01	ATP11A	ATPase, class VI, type 11A	chr13q34	215842_s_at	NM_015205 /// NM_032189
3.60	4.01	0.42	1.18E-02	2.11E-01	GPRC5C	G protein-coupled receptor, family C, group 5, member C	chr17q25	230907_at	NM_018653 /// NM_022036
1.77	2.08	0.31	1.18E-02	2.11E-01	PLA2R1	phospholipase A2 receptor 1, 180kDa	chr2q23-q24	210194_at	NM_001007267 /// NM_007366
1.94	2.25	0.32	1.18E-02	2.12E-01	C3orf66	chromosome 3 open reading frame 66	chr3q13.13	1569332_at	NM_001040054
2.98	3.37	0.38	1.18E-02	2.12E-01	CRYBB2P1	crystallin, beta B2 pseudogene 1	chr22q11.2-q12.1	222048_at	---
4.94	6.19	1.26	1.18E-02	2.12E-01	SYNPO2	synaptopodin 2	chr4q26	225895_at	NM_001128933 /// NM_001128934 /// NM_133477
4.32	4.73	0.41	1.18E-02	2.12E-01	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	chr22q13.33	208603_s_at	NM_012324 /// NM_016431
3.85	4.43	0.57	1.18E-02	2.12E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	208878_s_at	NM_002577
4.30	4.70	0.40	1.19E-02	2.13E-01	LOC440330	hypothetical protein LOC440330	chr16p13.3	223911_at	XM_001720977 /// XM_496109 /// XM_944152
6.65	7.35	0.70	1.19E-02	2.13E-01	SCFD2	sec1 family domain containing 2	chr4q12	226923_at	NM_152540

2.83	3.35	0.52	1.19E-02	2.13E-01	IGHA1 /// IGHG1 /// LOC100133862	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// similar to hCG1773549	chr14q32.33	211648_at	XM_001720441
4.57	5.09	0.51	1.19E-02	2.13E-01	ATP9A	ATPase, class II, type 9A	chr20q13.2	216129_at	NM_006045
2.99	3.43	0.44	1.19E-02	2.13E-01	VASH1	vasohibin 1	chr14q24.3	242566_at	NM_014909
2.60	2.97	0.37	1.19E-02	2.13E-01	OTP	orthopedia homeobox	chr5q13.3	231488_at	NM_032109
1.93	2.26	0.34	1.19E-02	2.13E-01	---	---	---	1562076_at	---
1.71	2.04	0.32	1.19E-02	2.13E-01	PRKAG2	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	chr7q36.1	215231_at	NM_001040633 /// NM_016203 /// NM_024429
9.65	10.45	0.80	1.20E-02	2.13E-01	ANXA2	annexin A2	chr15q21-q22	201590_x_at	NM_001002857 /// NM_001002858 /// NM_004039
3.69	4.12	0.43	1.20E-02	2.13E-01	TMEM176B	transmembrane protein 176B	chr7q36.1	236348_at	NM_001101311 /// NM_001101312 /// NM_001101313 /// NM_001101314 /// NM_014020
4.66	5.18	0.52	1.20E-02	2.13E-01	PRR4	proline rich 4 (lacrimal)	chr12p13	204919_at	NM_001098538 /// NM_007244
3.39	3.84	0.45	1.21E-02	2.14E-01	GFRA2	GDNF family receptor alpha 2	chr8p21.3	205722_s_at	NM_001495
1.97	2.35	0.37	1.21E-02	2.14E-01	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	chr16q22.1	201131_s_at	NM_004360
3.39	4.01	0.62	1.21E-02	2.14E-01	TPK1	thiamin pyrophosphokinase 1	chr7q34-q35	223686_at	NM_001042482 /// NM_022445
6.83	7.44	0.61	1.21E-02	2.14E-01	SNF1LK	SNF1-like kinase	chr21q22.3	232470_at	NM_173354
2.06	2.55	0.48	1.21E-02	2.14E-01	C3orf57 /// LOC100129285	chromosome 3 open reading frame 57 /// hypothetical protein LOC100129285	chr3q26.1	238702_at	NM_001040100 /// XM_001723839 /// XM_001725832 /// XM_001726160
2.36	2.72	0.35	1.21E-02	2.14E-01	FAR2	Fatty acyl CoA reductase 2	chr12p11.22	239108_at	NM_018099
2.64	3.00	0.36	1.22E-02	2.15E-01	KLHL1	kelch-like 1 (Drosophila)	chr13q21	216391_s_at	NM_020866
4.80	5.35	0.55	1.22E-02	2.15E-01	ZFP82	zinc finger protein 82 homolog (mouse)	chr19q13.12	235176_at	NM_133466
2.59	2.99	0.40	1.22E-02	2.15E-01	---	---	---	243473_at	---
2.15	2.47	0.32	1.22E-02	2.15E-01	---	---	---	224067_at	---
7.32	8.54	1.22	1.22E-02	2.15E-01	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	chr11q12	223344_s_at	NM_021201 /// NM_206938 /// NM_206939 /// NM_206940
2.68	3.09	0.41	1.22E-02	2.15E-01	---	---	---	241838_at	---
2.45	2.77	0.32	1.22E-02	2.15E-01	---	---	---	243728_at	---
3.16	4.08	0.92	1.22E-02	2.15E-01	MACROD2	MACRO domain containing 2	chr20p12.1	1563209_a_at	NM_001033087 /// NM_080676
4.88	5.75	0.87	1.22E-02	2.16E-01	---	---	---	242188_at	---
3.13	3.80	0.67	1.23E-02	2.16E-01	LRRFIP2	Leucine rich repeat (in FLII) interacting protein 2	chr3p22.2	232705_at	NM_001134369 /// NM_006309 /// NM_017724
3.76	4.63	0.86	1.23E-02	2.16E-01	RTN2	reticulon 2	chr19q13.32	204217_s_at	NM_005619 /// NM_206900 /// NM_206901
2.74	3.41	0.67	1.23E-02	2.16E-01	LOC344595	hypothetical LOC344595	chr3q13.12	235606_at	XM_001128525 /// XM_943541
6.49	7.00	0.51	1.23E-02	2.16E-01	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	chr11q23.3	225211_at	NM_002855 /// NM_203285 /// NM_203286
2.14	2.61	0.47	1.23E-02	2.16E-01	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	chrXp22.11	232553_at	NM_004845
2.16	2.54	0.38	1.23E-02	2.16E-01	---	---	---	1558934_a_at	---
1.98	2.33	0.35	1.23E-02	2.16E-01	ICA1L	islet cell autoantigen 1,69kDa-like	chr2q33.1	1555671_at	NM_138468 /// NM_178231
1.95	2.23	0.28	1.23E-02	2.16E-01	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	chr6p22.3-p22.2	206265_s_at	NM_001503 /// NM_177483

4.14	5.24	1.09	1.23E-02	2.16E-01	MGA	MAX gene associated	chr15q14	235409_at	NM_001080541
2.42	2.89	0.47	1.23E-02	2.16E-01	---	---	---	238277_at	---
6.45	7.14	0.69	1.24E-02	2.16E-01	SH3KBP1	SH3-domain kinase binding protein 1	chrXp22.1-p21.3	223082_at	NM_001024666 /// NM_031892
5.19	5.80	0.61	1.24E-02	2.16E-01	VSTM2L	V-set and transmembrane domain containing 2 like	chr20q11.23	226973_at	NM_080607
4.97	5.57	0.60	1.24E-02	2.16E-01	FREQ	frequenin homolog (Drosophila)	chr9q34	222570_at	NM_001128826 /// NM_014286
3.62	4.16	0.54	1.24E-02	2.16E-01	EML3	echinoderm microtubule associated protein like 3	chr11q12.3	203443_at	NM_153265
4.68	5.19	0.50	1.24E-02	2.16E-01	---	---	---	243091_at	---
2.65	3.08	0.42	1.24E-02	2.16E-01	---	---	---	1559880_at	---
3.14	3.49	0.35	1.24E-02	2.16E-01	---	---	---	238341_at	---
6.35	6.93	0.58	1.25E-02	2.17E-01	SCUBE1	signal peptide, CUB domain, EGF-like 1	chr22q13	233988_x_at	NM_173050
2.80	3.22	0.41	1.25E-02	2.17E-01	FOXO3	Forkhead box O3	chr6q21	231548_at	NM_001455 /// NM_201559
7.69	8.36	0.67	1.25E-02	2.17E-01	CES2	carboxylesterase 2 (intestine, liver)	chr16q22.1	209667_at	NM_003869 /// NM_198061
3.62	4.08	0.46	1.25E-02	2.17E-01	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	chr7p14.3	234232_at	NM_015483
6.04	6.61	0.57	1.25E-02	2.17E-01	ELMOD2	ELMO/CED-12 domain containing 2	chr4q31.1	226502_at	NM_153702
2.07	2.43	0.36	1.25E-02	2.17E-01	GIF	gastric intrinsic factor (vitamin B synthesis)	chr11q13	207033_at	NM_005142
7.71	8.21	0.50	1.26E-02	2.18E-01	CES2	carboxylesterase 2 (intestine, liver)	chr16q22.1	213509_x_at	NM_003869 /// NM_198061
3.03	3.46	0.43	1.26E-02	2.18E-01	EGR4	early growth response 4	chr2p13	207767_s_at	NM_001965
2.85	3.25	0.40	1.26E-02	2.18E-01	RBPJL	recombination signal binding protein for immunoglobulin kappa J region-like	chr20q12-q13.1	221377_s_at	NM_014276
6.68	7.34	0.66	1.26E-02	2.18E-01	ZNF665	zinc finger protein 665	chr19q13.41	220760_x_at	NM_024733
3.51	4.13	0.62	1.26E-02	2.18E-01	---	---	---	210030_at	---
2.64	3.15	0.51	1.27E-02	2.18E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	234851_at	---
2.53	3.01	0.48	1.27E-02	2.18E-01	---	---	---	1560178_at	---
5.67	6.28	0.61	1.27E-02	2.19E-01	LOC729345	hypothetical LOC729345	chr4q28.1	230212_at	XM_001126202 /// XM_001714219 /// XM_001718011
4.51	5.04	0.53	1.27E-02	2.19E-01	TSHZ2	teashirt zinc finger homeobox 2	chr20q13.2	235815_at	NM_173485
2.52	2.88	0.36	1.28E-02	2.19E-01	PADI4	peptidyl arginine deiminase, type IV	chr1p36.13	211413_s_at	NM_012387
4.94	5.36	0.42	1.28E-02	2.19E-01	LOC100132947 /// LOC100134435 /// LOC339742 /// LOC648761	similar to LOC339742 protein /// similar to LOC339742 protein /// hypothetical protein LOC339742 /// similar to LOC339742 protein	chr2q21.2 /// chr9p11.2 /// chr9q12	1569008_at	XM_001714261 /// XM_929883 /// XM_937204 /// XR_036963 /// XR_037042 /// XR_038435 /// XR_042364 /// XR_042374 /// XR_042382
3.49	3.91	0.42	1.28E-02	2.19E-01	RPAIN	RPA interacting protein	chr17p13.2	216961_s_at	NM_001033002
4.00	4.55	0.54	1.29E-02	2.20E-01	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	chr7q21.3-q22.1	214900_at	NM_003439
2.31	2.67	0.36	1.29E-02	2.20E-01	---	---	---	234073_at	---
3.70	4.08	0.38	1.29E-02	2.20E-01	NPAS3	neuronal PAS domain protein 3	chr14q12-q13	1554635_a_at	NM_022123 /// NM_173159
6.94	7.67	0.73	1.29E-02	2.21E-01	PROSC	proline synthetase co-transcribed homolog (bacterial)	chr8p11.2	209385_s_at	NM_007198
3.12	4.00	0.88	1.29E-02	2.21E-01	---	---	---	233607_at	---
2.30	2.74	0.44	1.29E-02	2.21E-01	---	---	---	234118_at	---
4.56	4.96	0.40	1.30E-02	2.21E-01	NOTCH4	Notch homolog 4 (Drosophila)	chr6p21.3	240786_at	NM_004557
4.63	5.42	0.79	1.30E-02	2.22E-01	LGALS2	lectin, galactoside-binding, soluble, 2	chr22q12-q13|22q13.1	208450_at	NM_006498
2.43	3.37	0.95	1.30E-02	2.22E-01	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2	chr5q34	1557122_s_at	NM_000813 /// NM_021911
2.26	2.58	0.32	1.31E-02	2.22E-01	---	---	---	232476_at	---
4.20	4.67	0.47	1.31E-02	2.22E-01	TMEM54	transmembrane protein 54	chr1p35-p34	225536_at	NM_033504
2.50	2.83	0.33	1.31E-02	2.22E-01	---	---	---	243440_at	---
5.55	6.02	0.47	1.31E-02	2.22E-01	B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	chr12q24	221240_s_at	NM_030765
4.19	4.62	0.43	1.31E-02	2.22E-01	---	---	---	244220_at	---
9.21	10.06	0.86	1.31E-02	2.22E-01	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	chr17p11.2	202054_s_at	NM_000382 /// NM_001031806
2.51	2.95	0.44	1.31E-02	2.22E-01	C8orf6	chromosome 8 open reading frame 6	chr8p23.1	1552563_a_at	XR_040215 /// XR_040216 /// XR_040217
2.66	4.31	1.65	1.31E-02	2.22E-01	SQLE	squalene epoxidase	chr8q24.1	213562_s_at	NM_003129

9.52	10.28	0.76	1.32E-02	2.23E-01	ANXA2	annexin A2	chr15q21-q22	213503_x_at	NM_001002857 /// NM_001002858 /// NM_004039																				
3.52	4.06	0.54	1.32E-02	2.23E-01	ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	chr17q23.3	227463_at	NM_000789 /// NM_152830																				
1.71	2.02	0.31	1.32E-02	2.23E-01	---	---	---	1561473_at	---																				
2.63	3.11	0.48	1.32E-02	2.23E-01	RBM12B	RNA binding motif protein 12B	chr8q22.1	51226_at	NM_203390																				
2.65	3.37	0.71	1.32E-02	2.23E-01	---	---	---	231199_at	---																				
4.05	4.68	0.63	1.33E-02	2.23E-01	---	---	---	236755_at	---																				
4.40	4.99	0.59	1.32E-02	2.23E-01	SUSD3	Sushi domain containing 3	chr9q22.31	243956_at	NM_145006																				
3.33	3.90	0.57	1.33E-02	2.23E-01	ROR1	receptor tyrosine kinase-like orphan receptor 1	chr1p32-p31	205805_s_at	NM_001083592 /// NM_005012																				
5.81	6.34	0.54	1.32E-02	2.23E-01	PSD	pleckstrin and Sec7 domain containing	chr10q24	208102_s_at	NM_002779																				
3.59	4.12	0.53	1.32E-02	2.23E-01	TTC9	tetratricopeptide repeat domain 9	chr14q24.2	213174_at	NM_015351																				
2.77	3.21	0.45	1.32E-02	2.23E-01	CDRT15L1	CMT1A duplicated region transcript 15-like 1	chr17p12	240889_at	XM_001725421 /// XM_932309																				
3.13	3.54	0.42	1.32E-02	2.23E-01	CTD-2267G17.3 /// XAGE2	X antigen family, member 2-like /// X antigen family, member 2	chrXp11.22	229469_at	NM_001079538 /// NM_130777																				
4.35	4.74	0.38	1.33E-02	2.23E-01	---	---	---	234761_at	---																				
2.55	2.88	0.33	1.33E-02	2.23E-01	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	chr13q33-q34	211349_at	NM_005073																				
7.06	7.62	0.56	1.33E-02	2.23E-01	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	chr2p24.3-p24.1	222436_s_at	NM_001005753 /// NM_016079																				
3.02	3.49	0.47	1.33E-02	2.23E-01	---	---	---	234598_at	---																				
4.34	5.30	0.96	1.33E-02	2.24E-01	---	---	---	222371_at	---																				
2.29	2.69	0.39	1.33E-02	2.24E-01	---	---	---	220871_at	---																				
3.70	4.36	0.66	1.34E-02	2.24E-01	HIP1	huntingtin interacting protein 1	chr7q11.23	205425_at	NM_005338																				
3.16	3.53	0.37	1.34E-02	2.24E-01	---	---	---	1570361_a_at	---																				
1.97	2.32	0.35	1.34E-02	2.24E-01	LOC645261	PP565	chr5q14.3	1555400_at	NM_001039781																				
8.79	9.91	1.12	1.34E-02	2.24E-01	TNPO1	transportin 1	chr5q13.2	221829_s_at	NM_002270 /// NM_153188																				
4.03	4.48	0.45	1.34E-02	2.24E-01	YBX2	Y box binding protein 2	chr17p11.2-p13.1	219704_at	NM_015982																				
2.46	2.83	0.37	1.34E-02	2.24E-01	FNIP2	folliculin interacting protein 2	chr4q32.1	1569352_at	NM_020840																				
9.34	9.63	0.29	1.34E-02	2.24E-01	CHP	calcium binding protein P22	chr15q13.3	214665_s_at	NM_007236																				
2.97	3.29	0.33	1.34E-02	2.24E-01	FOXP3	forkhead box P3	chrXp11.23	224211_at	NM_001114377 /// NM_014009																				
6.79	7.26	0.47	1.35E-02	2.24E-01	SMG5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr1q21.2	212147_at	NM_015327																				
3.02	3.69	0.67	1.35E-02	2.25E-01	STGC3	hypothetical STGC3	---	230587_at	XR_017846 /// XR_017950 /// XR_041447																				
4.27	5.61	1.34	1.35E-02	2.25E-01	---	---	---	238774_at	---																				
3.20	3.87	0.66	1.36E-02	2.25E-01	DNM1	dynamin 1	chr9q34	215116_s_at	NM_001005336 /// NM_004408																				
2.33	2.87	0.54	1.36E-02	2.25E-01	---	---	---	242664_at	---																				
5.48	6.00	0.53	1.35E-02	2.25E-01	IPP	intracisternal A particle-promoted polypeptide	chr1p34-p32	219843_at	NM_005897																				
3.39	3.92	0.53	1.35E-02	2.25E-01	RAB1A	RAB1A, member RAS oncogene family	chr2p14	239428_at	NM_004161																				
5.36	5.87	0.51	1.35E-02	2.25E-01	---	---	---	242362_at	---																				
3.36	3.84	0.47	1.35E-02	2.25E-01	PLXNA2	plexin A2	chr1q32.2	213030_s_at	NM_025179																				
2.50	2.93	0.44	1.35E-02	2.25E-01	FAM123C	family with sequence similarity 123C	chr2q21.1	236638_at	NM_001105193 /// NM_001105194 /// NM_001105195 /// NM_152698																				
4.72	5.36	0.65	1.36E-02	2.25E-01	GTPBP4 /// IDI2	GTP binding protein 4 /// isopentenyl-diphosphate delta isomerase 2	chr10p15-p14 /// chr10p15.3	217631_at	NM_012341 /// NM_033261																				
3.49	5.03	1.54	1.36E-02	2.25E-01	RCAN2	regulator of calcineurin 2	chr6p12.3	203498_at	NM_005822																				
2.43	2.89	0.46	1.36E-02	2.25E-01	---	---	---	240326_at	---																				
3.89	4.34	0.45	1.36E-02	2.25E-01	---	---	---	1559237_a_at	---																				
2.00	2.37	0.37	1.36E-02	2.25E-01	GRM7	glutamate receptor, metabotropic 7	chr3p26.1-p25.1	207548_at	NM_000844 /// NM_181874																				
2.55	3.12	0.56	1.37E-02	2.25E-01	---	---	---	243046_at	---																				
2.84	3.40	0.56	1.37E-02	2.25E-01	---	---	---	1557279_at	---																				
2.98	3.43	0.45	1.36E-02	2.25E-01	FLJ39582	Hypothetical LOC439931	chr22q11.21	239015_at	---																				
4.41	4.77	0.35	1.37E-02	2.25E-01	RIC8B	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	chr12q23.3	229637_at	NM_018157																				

7.00	7.55	0.55	1.37E-02	2.25E-01	GPR144	G protein-coupled receptor 144	chr9q33.3	216289_at	XR_042072 /// XR_042073 /// XR_042074
1.95	2.43	0.48	1.37E-02	2.25E-01	---	---	---	242206_at	---
2.89	3.29	0.40	1.37E-02	2.25E-01	---	---	---	237140_x_at	---
5.14	6.47	1.33	1.37E-02	2.25E-01	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	chr12q12-q13.11	209376_x_at	NM_004719
2.77	3.54	0.77	1.37E-02	2.25E-01	CP	ceruloplasmin (ferroxidase)	chr3q23-q25	204846_at	NM_000096
6.16	6.93	0.77	1.39E-02	2.26E-01	SAR1B	SAR1 gene homolog B (S. cerevisiae)	chr5q31.1	218254_s_at	NM_001033503 /// NM_016103
3.67	4.32	0.65	1.39E-02	2.26E-01	---	---	---	1557512_at	---
6.31	6.87	0.56	1.39E-02	2.26E-01	NPB	Neuropeptide B	chr17q25.3	230044_at	NM_148896
5.22	5.75	0.53	1.39E-02	2.26E-01	TMEM132A	Transmembrane protein 132A	chr11q12.2	229486_s_at	NM_017870 /// NM_178031
5.35	5.88	0.53	1.39E-02	2.26E-01	STAC3	SH3 and cysteine rich domain 3	chr12q13.3	230852_at	NM_145064
5.34	5.85	0.51	1.38E-02	2.26E-01	---	---	---	241636_x_at	---
2.16	2.66	0.49	1.39E-02	2.26E-01	ZNF596	zinc finger protein 596	chr8p23.3	232641_at	NM_001042415 /// NM_001042416 /// NM_173539
4.00	4.49	0.49	1.39E-02	2.26E-01	---	---	---	1557194_a_at	---
5.82	6.30	0.48	1.39E-02	2.26E-01	---	---	---	241125_at	---
2.62	3.09	0.47	1.38E-02	2.26E-01	KIF26B	kinesin family member 26B	chr1q44	1555164_at	NM_018012
2.62	3.06	0.45	1.39E-02	2.26E-01	---	---	---	242803_at	---
4.24	4.68	0.44	1.39E-02	2.26E-01	RHBG	Rh family, B glycoprotein	chr1q21.3	220510_at	NM_020407
5.56	6.00	0.44	1.39E-02	2.26E-01	PTCRA	pre T-cell antigen receptor alpha	chr6p21.3	211837_s_at	NM_138296
4.22	4.63	0.41	1.38E-02	2.26E-01	SNX24	sorting nexin 24	chr5q23.2	233883_at	NM_014035
2.58	2.99	0.40	1.38E-02	2.26E-01	---	---	---	1568870_at	---
5.86	6.81	0.95	1.40E-02	2.26E-01	APOOL	apolipoprotein O-like	chrXq21.1	235433_at	NM_198450
2.20	2.61	0.41	1.40E-02	2.26E-01	---	---	---	242801_at	---
8.41	8.98	0.57	1.40E-02	2.26E-01	GPSN2	glycoprotein, synaptic 2	chr19p13.12	208336_s_at	NM_138501
3.31	3.66	0.35	1.40E-02	2.26E-01	---	---	---	238186_at	---
6.66	8.07	1.41	1.40E-02	2.26E-01	CALD1	caldesmon 1	chr7q33	201616_s_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
2.17	2.48	0.31	1.40E-02	2.26E-01	---	---	---	230517_at	---
2.21	2.69	0.48	1.41E-02	2.26E-01	---	---	---	238932_at	---
2.15	2.59	0.44	1.41E-02	2.26E-01	CAMTA1	calmodulin binding transcription activator 1	chr1p36.31-p36.23	213268_at	NM_015215
3.53	3.86	0.33	1.41E-02	2.26E-01	---	---	---	233773_at	---
3.31	3.79	0.48	1.41E-02	2.26E-01	FLJ44606	Hypothetical gene supported by AK126569	chr5q23.2	244761_at	XM_001722994 /// XM_932789 /// XM_943643
5.03	6.82	1.79	1.41E-02	2.27E-01	SQLE	squalene epoxidase	chr8q24.1	213577_at	NM_003129
3.93	4.90	0.96	1.41E-02	2.27E-01	INF2	inverted formin, FH2 and WH2 domain containing	chr14q32.33	224469_s_at	NM_001031714 /// NM_022489 /// NM_032714
2.40	2.92	0.52	1.41E-02	2.27E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	236620_at	NM_018151
2.16	2.59	0.43	1.41E-02	2.27E-01	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	chr5q33-q34	210330_at	NM_000337 /// NM_001128209 /// NM_172244
2.11	2.52	0.40	1.41E-02	2.27E-01	CFHR4	complement factor H-related 4	chr1q32	207874_s_at	NM_006684
2.14	2.48	0.34	1.41E-02	2.27E-01	PERP	PERP, TP53 apoptosis effector	chr6q24	1556990_at	NM_022121
2.21	2.54	0.33	1.41E-02	2.27E-01	LOC730432 /// STYX	similar to serine/threonine/tyrosine interacting protein /// serine/threonine/tyrosine interacting protein	---	242408_at	NM_001130701 /// NM_145251 /// XM_001125680
2.65	3.21	0.56	1.42E-02	2.27E-01	---	---	---	243342_at	---
4.70	5.19	0.49	1.42E-02	2.27E-01	RBM27	RNA binding motif protein 27	chr5q32	243295_at	NM_018989 /// XM_001720239 /// XM_001723796 /// XM_001723897
3.14	3.50	0.36	1.42E-02	2.27E-01	FAM91A2	family with sequence similarity 91, member A2	chr1q21.1	1564204_at	XR_040635

6.30	6.92	0.61	1.42E-02	2.28E-01	LOC284801	hypothetical protein LOC284801	chr20p11.1	225762_x_at	XM_001714287 /// XM_378973 /// XM_944897																					
2.30	2.77	0.47	1.42E-02	2.28E-01	---	---	---	1558748_at	---																					
2.39	2.74	0.35	1.42E-02	2.28E-01	---	---	---	230088_at	---																					
9.47	10.16	0.69	1.43E-02	2.28E-01	CYB5R3	cytochrome b5 reductase 3	chr22q13.31-qter|22q13.2-q13.31	201885_s_at	NM_000398 /// NM_001129819 /// NM_007326																					
8.53	9.18	0.66	1.43E-02	2.28E-01	IL1R1	interleukin 1 receptor, type I	chr2q12	202948_at	NM_000877																					
5.55	6.00	0.45	1.43E-02	2.28E-01	FGGY	FGGY carbohydrate kinase domain containing	chr1p32.1	219718_at	NM_001113411 /// NM_018291																					
3.27	3.69	0.42	1.43E-02	2.28E-01	ANKRD5	ankyrin repeat domain 5	chr20pter-q11.23	220144_s_at	NM_022096 /// NM_198798																					
5.24	5.73	0.49	1.43E-02	2.28E-01	GPATCH8	G patch domain containing 8	chr17q21.31	212487_at	NM_001002909																					
2.63	3.05	0.42	1.43E-02	2.28E-01	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	chr1p34.1	241325_at	NM_001114172 /// NM_003629																					
3.15	3.66	0.51	1.43E-02	2.28E-01	TRIML2	tripartite motif family-like 2	chr4q35.2	1552580_at	NM_173553																					
3.95	4.48	0.53	1.43E-02	2.28E-01	PTMS	parathymosin	chr12p13	218044_x_at	NM_002824																					
2.27	2.65	0.38	1.44E-02	2.28E-01	FLRT3	fibronectin leucine rich transmembrane protein 3	chr20p11	219250_s_at	NM_013281 /// NM_198391																					
3.55	4.00	0.46	1.44E-02	2.29E-01	ESD	esterase D/formylglutathione hydrolase	chr13q14.1-q14.2	240808_at	NM_001984																					
6.04	6.42	0.39	1.44E-02	2.29E-01	RUFY1	RUN and FYVE domain containing 1	chr5q35.3	233380_s_at	NM_001040451 /// NM_001040452 /// NM_025158																					
5.10	5.64	0.55	1.44E-02	2.29E-01	---	---	---	228013_at	---																					
4.91	5.39	0.47	1.44E-02	2.29E-01	SNX22	sorting nexin 22	chr15q22.31	235460_at	NM_024798																					
3.29	3.93	0.64	1.44E-02	2.29E-01	CCDC46	coiled-coil domain containing 46	chr17q24.1-q24.2	213644_at	NM_001037325 /// NM_145036																					
4.53	4.89	0.37	1.44E-02	2.29E-01	KLK2	kallikrein-related peptidase 2	chr19q13.41	209855_s_at	NM_001002231 /// NM_005551																					
3.79	4.17	0.38	1.45E-02	2.29E-01	---	---	---	213525_at	---																					
4.66	5.24	0.58	1.45E-02	2.30E-01	---	---	---	230902_at	---																					
4.23	4.81	0.58	1.45E-02	2.30E-01	GUCA2A	guanylate cyclase activator 2A (guanylin)	chr1p35-p34	207003_at	NM_033553																					
3.73	4.59	0.86	1.45E-02	2.30E-01	PXDN	peroxidasin homolog (Drosophila)	chr2p25	212013_at	NM_012293																					
2.66	3.05	0.39	1.45E-02	2.30E-01	SP100	SP100 nuclear antigen	chr2q37.1	210985_s_at	NM_001080391 /// NM_003113																					
2.35	3.30	0.95	1.45E-02	2.30E-01	ASPN	asporin	chr9q22	224396_s_at	NM_017680																					
2.92	3.45	0.54	1.46E-02	2.30E-01	FAM162A	family with sequence similarity 162, member A	chr3q21.1	221533_at	NM_014367																					
2.47	2.80	0.33	1.46E-02	2.30E-01	VNN3	vanin 3	chr6q23-q24	1553514_a_at	NM_001024460 /// NM_018399 /// NM_078625																					
6.00	6.87	0.87	1.46E-02	2.30E-01	CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	chr1p32	217870_s_at	NM_016308																					
9.71	10.46	0.76	1.46E-02	2.31E-01	ANXA2	annexin A2	chr15q21-q22	210427_x_at	NM_001002857 /// NM_001002858 /// NM_004039																					
4.75	5.24	0.49	1.46E-02	2.31E-01	FAM59B	family with sequence similarity 59, member B	chr2p23.3	228028_at	XR_041887 /// XR_041888 /// XR_041889																					
2.51	2.94	0.43	1.46E-02	2.31E-01	RASGEF1A	RasGEF domain family, member 1A	chr10q11.21	242917_at	NM_145313																					
2.55	2.88	0.33	1.46E-02	2.31E-01	CDH23	cadherin-like 23	chr10q21-q22	224527_at	NM_022124 /// NM_052836																					
2.15	2.48	0.33	1.47E-02	2.31E-01	---	---	---	244415_at	---																					
9.44	10.09	0.65	1.47E-02	2.31E-01	CAT	catalase	chr11p13	201432_at	NM_001752																					
2.19	2.71	0.52	1.47E-02	2.31E-01	---	---	---	213841_at	---																					
2.98	3.44	0.46	1.47E-02	2.31E-01	---	---	---	1568488_at	---																					
3.16	3.62	0.45	1.47E-02	2.31E-01	---	---	---	240249_at	---																					
2.15	2.51	0.36	1.47E-02	2.31E-01	---	---	---	233783_at	---																					
2.56	2.92	0.37	1.47E-02	2.31E-01	---	---	---	243769_at	---																					
2.24	3.13	0.89	1.48E-02	2.31E-01	LRRC39	leucine rich repeat containing 39	chr1p21.2	227532_at	NM_144620																					
6.55	7.43	0.88	1.48E-02	2.31E-01	ZFP106	zinc finger protein 106 homolog (mouse)	chr15q15.1	222407_s_at	NM_022473																					
2.91	3.79	0.87	1.48E-02	2.31E-01	NELL2	NEL-like 2 (chicken)	chr12q13.11-q13.12	203413_at	NM_006159																					
6.36	7.13	0.77	1.48E-02	2.31E-01	MRPS10	mitochondrial ribosomal protein S10	chr6p21.1	218106_s_at	NM_018141																					

3.65	4.40	0.75	1.47E-02	2.31E-01	---	---	---	239264_at	---
3.20	3.86	0.67	1.48E-02	2.31E-01	PCSK2	proprotein convertase subtilisin/kexin type 2	chr20p11.2	204870_s_at	NM_002594
6.92	7.58	0.66	1.47E-02	2.31E-01	CENTB1	centaurin, beta 1	chr17p13.1	205212_s_at	NM_014716
7.87	8.52	0.65	1.48E-02	2.31E-01	PTP4A2	protein tyrosine phosphatase type IVA, member 2	chr1p35	216988_s_at	NM_080391 /// NM_080392
3.50	4.14	0.64	1.48E-02	2.31E-01	FBXL16	F-box and leucine-rich repeat protein 16	chr16p13.3	227641_at	NM_153350
1.93	2.46	0.54	1.48E-02	2.31E-01	---	---	---	243794_at	---
3.79	4.22	0.43	1.48E-02	2.31E-01	---	---	---	234828_at	---
2.72	3.10	0.38	1.48E-02	2.31E-01	---	---	---	233067_at	---
2.33	2.68	0.35	1.48E-02	2.31E-01	---	---	---	240901_at	---
2.27	2.57	0.30	1.48E-02	2.31E-01	---	---	---	243130_at	---
6.37	6.94	0.57	1.49E-02	2.31E-01	KCNIP3	Kv channel interacting protein 3, calsenilin	chr2q21.1	231774_at	NM_001034914 /// NM_013434
4.80	5.21	0.41	1.49E-02	2.32E-01	C19orf36	chromosome 19 open reading frame 36	chr19p13.3	214296_x_at	NM_001031735 /// NM_001039846
4.05	4.41	0.35	1.49E-02	2.32E-01	H1FNT	H1 histone family, member N, testis-specific	chr12q13.11	238373_at	NM_181788
3.43	4.42	0.98	1.49E-02	2.32E-01	BNC2	basonuclin 2	chr9p22.3-p22.2	230722_at	NM_017637
5.14	5.64	0.50	1.49E-02	2.32E-01	---	---	---	215908_at	---
3.72	4.06	0.35	1.49E-02	2.32E-01	GLRX3	glutaredoxin 3	chr10q26	207506_at	NM_006541
5.69	8.28	2.58	1.49E-02	2.32E-01	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	chr7q21.2-q21.3|7q21.2	216607_s_at	NM_000786
3.24	3.75	0.51	1.49E-02	2.32E-01	ZNF25	zinc finger protein 25	chr10p11.21	235164_at	NM_145011
3.92	4.49	0.57	1.49E-02	2.32E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	1566775_at	NM_015512
3.39	3.83	0.44	1.49E-02	2.32E-01	---	---	---	240302_at	---
8.24	9.15	0.91	1.49E-02	2.32E-01	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	chr14q23-q24.2	208898_at	NM_015994
4.02	4.46	0.44	1.50E-02	2.32E-01	CARD14	caspase recruitment domain family, member 14	chr17q25	220598_at	NM_024110 /// NM_052819
3.33	3.66	0.32	1.50E-02	2.32E-01	ENTPD4 /// LOXL2	ectonucleoside triphosphate diphosphohydrolase 4 /// lysyl oxidase-like 2	chr8p21.3 /// chr8p21.3-p21.2	202999_s_at	NM_001128930 /// NM_002318 /// NM_004901
3.58	4.19	0.62	1.50E-02	2.32E-01	---	---	---	242671_at	---
6.00	6.57	0.57	1.50E-02	2.32E-01	ATF6	activating transcription factor 6	chr1q22-q23	203952_at	NM_007348
5.01	5.48	0.46	1.50E-02	2.32E-01	---	---	---	1557710_at	---
3.49	3.96	0.47	1.50E-02	2.33E-01	UBE3A	Ubiquitin protein ligase E3A	chr15q11-q13	214980_at	NM_000462 /// NM_130838 /// NM_130839
2.01	2.35	0.34	1.51E-02	2.34E-01	---	---	---	241962_at	---
5.13	6.60	1.47	1.51E-02	2.34E-01	CFH	complement factor H	chr1q32	213800_at	NM_000186 /// NM_001014975
6.90	7.74	0.84	1.51E-02	2.34E-01	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	chr12q24	225826_at	NM_052845
3.78	4.35	0.57	1.52E-02	2.34E-01	SLC38A6	solute carrier family 38, member 6	chr14q23.1	214830_at	NM_153811
3.85	4.32	0.48	1.51E-02	2.34E-01	NIN	ninein (GSK3B interacting protein)	chr14q22.1	224304_x_at	NM_016350 /// NM_020921 /// NM_182944 /// NM_182946
2.83	3.30	0.47	1.51E-02	2.34E-01	FANCI	Fanconi anemia, complementation group I	chr15q26.1	213008_at	NM_001113378 /// NM_018193
3.89	4.33	0.43	1.51E-02	2.34E-01	---	---	---	236719_at	---
3.81	4.18	0.38	1.51E-02	2.34E-01	MAPK15	mitogen-activated protein kinase 15	---	241357_at	NM_139021
1.80	2.12	0.33	1.52E-02	2.34E-01	---	---	---	1559287_at	---
5.61	6.69	1.08	1.53E-02	2.35E-01	---	---	---	224348_s_at	---
8.55	9.24	0.68	1.53E-02	2.35E-01	CREG1	cellular repressor of E1A-stimulated genes 1	chr1q24	201200_at	NM_003851
5.25	5.85	0.60	1.52E-02	2.35E-01	---	---	---	226183_at	---
3.00	3.47	0.46	1.53E-02	2.35E-01	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	chr5p13.2	230893_at	NM_001012339 /// NM_194283
4.15	4.59	0.44	1.52E-02	2.35E-01	---	---	---	235886_at	---
5.66	6.08	0.43	1.53E-02	2.35E-01	CRHR1	corticotropin releasing hormone receptor 1	chr17q12-q22	214619_at	NM_004382
6.04	6.45	0.40	1.53E-02	2.35E-01	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	chr7q22	221956_at	NM_002319
2.00	2.34	0.34	1.53E-02	2.35E-01	---	---	---	236506_at	---
4.77	5.18	0.42	1.53E-02	2.35E-01	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	chr20q12-q13.1	205244_s_at	NM_001011554 /// NM_022829
5.06	6.80	1.74	1.54E-02	2.35E-01	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	chr7q32	235067_at	NM_013255
3.12	3.93	0.80	1.54E-02	2.35E-01	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	chr13q12.3	215888_at	NM_015032
2.80	3.58	0.78	1.53E-02	2.35E-01	IKZF2	IKAROS family zinc finger 2 (Helios)	chr2q34	231929_at	NM_001079526 /// NM_016260
4.91	5.45	0.54	1.53E-02	2.35E-01	C11orf30	chromosome 11 open reading frame 30	chr11q13.5	234669_x_at	NM_020193

6.07	6.57	0.50	1.54E-02	2.35E-01	C20orf151	chromosome 20 open reading frame 151	chr20q13.33	236258_at	NM_080833
3.26	3.75	0.50	1.54E-02	2.35E-01	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	chr17q21-q23	215402_at	NM_006380
4.07	4.56	0.50	1.54E-02	2.35E-01	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	chr8p23	1554703_at	NM_014629
2.88	3.30	0.42	1.54E-02	2.35E-01	SESTD1	SEC14 and spectrin domains 1	chr2q31.2	228088_at	NM_178123
4.25	4.67	0.41	1.53E-02	2.35E-01	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	chr4p16-p15.3	240223_at	NM_001001290 /// NM_020041
1.97	2.36	0.38	1.54E-02	2.35E-01	---	---	---	240103_at	---
2.36	2.72	0.37	1.54E-02	2.35E-01	---	---	---	236512_at	---
1.78	2.08	0.30	1.54E-02	2.35E-01	---	---	---	1563643_at	---
2.65	3.28	0.63	1.55E-02	2.35E-01	LAMA3	laminin, alpha 3	chr18q11.2	203726_s_at	NM_000227 /// NM_001127717 /// NM_001127718 /// NM_198129
5.63	6.75	1.12	1.55E-02	2.35E-01	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	chr12q12-q13.11	213850_s_at	NM_004719
3.88	4.99	1.11	1.55E-02	2.35E-01	---	---	---	235757_at	---
2.11	2.84	0.73	1.55E-02	2.35E-01	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	chr7p15.1-p14.3	243564_at	NM_005020
5.18	5.69	0.51	1.55E-02	2.35E-01	KRIT1	KRIT1, ankyrin repeat containing	chr7q21-q22	204738_s_at	NM_001013406 /// NM_004912 /// NM_194454 /// NM_194455 /// NM_194456
3.43	3.81	0.38	1.55E-02	2.35E-01	ZBTB10	Zinc finger and BTB domain containing 10	chr8q13-q21.1	235491_at	NM_001105539 /// NM_023929
5.29	6.38	1.09	1.56E-02	2.35E-01	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	chr1pter-q31.3	204720_s_at	NM_014787
3.05	3.48	0.43	1.56E-02	2.35E-01	---	---	---	236820_at	---
6.93	7.51	0.58	1.57E-02	2.36E-01	MAPRE3	microtubule-associated protein, RP/EB family, member 3	chr2p23.3-p23.1	203842_s_at	NM_012326
3.40	3.92	0.52	1.56E-02	2.36E-01	---	---	---	243749_s_at	---
4.81	5.24	0.43	1.57E-02	2.36E-01	SNX29	sorting nexin 29	chr16p13.13-p13.12	225624_at	NM_001080530
4.20	5.70	1.50	1.58E-02	2.36E-01	---	---	---	226834_at	---
8.93	10.29	1.37	1.57E-02	2.36E-01	RAB31	RAB31, member RAS oncogene family	chr18p11.3	217762_s_at	NM_006868
9.55	10.69	1.14	1.57E-02	2.36E-01	TXNIP	thioredoxin interacting protein	chr1q21.1	201009_s_at	NM_006472
4.16	5.14	0.98	1.57E-02	2.36E-01	C2orf74	chromosome 2 open reading frame 74	chr2p15	1568658_at	XM_001725951 /// XM_291016 /// XM_941655
4.40	5.32	0.91	1.58E-02	2.36E-01	RAB3IP	RAB3A interacting protein (rabin3)	chr12q14.3	238853_at	NM_001024647 /// NM_022456 /// NM_175623 /// NM_175624 /// NM_175625
6.06	6.75	0.69	1.58E-02	2.36E-01	TMEM151A	transmembrane protein 151A	chr11q13.1	235614_at	NM_153266
4.86	5.51	0.66	1.57E-02	2.36E-01	ZC3H6	zinc finger CCCH-type containing 6	chr2q13	227809_at	NM_198581
3.90	4.52	0.63	1.58E-02	2.36E-01	---	---	---	228457_at	---
6.41	7.00	0.59	1.58E-02	2.36E-01	ACAA2	acetyl-Coenzyme A acyltransferase 2	chr18q21.1	202002_at	NM_006111
4.60	5.19	0.59	1.58E-02	2.36E-01	ZFP1	zinc finger protein 1 homolog (mouse)	chr16q23.1	226807_at	NM_153688
3.75	4.30	0.54	1.58E-02	2.36E-01	---	---	---	239268_at	---
4.20	4.58	0.39	1.58E-02	2.36E-01	TBX6	T-box 6	chr16p11.2	207684_at	NM_004608 /// NM_080758
2.96	3.33	0.37	1.58E-02	2.36E-01	---	---	---	233676_at	---
4.44	4.79	0.35	1.57E-02	2.36E-01	TRIM67	tripartite motif-containing 67	chr1q42.2	233357_at	NM_001004342
2.11	2.43	0.33	1.58E-02	2.36E-01	---	---	---	216788_at	---
4.69	5.38	0.68	1.58E-02	2.36E-01	ZNF771	Zinc finger protein 771	chr16p11.2	221968_s_at	NM_016643 /// XM_001721231 /// XM_001721234
2.85	3.29	0.44	1.58E-02	2.36E-01	LYRM7	Lyrm7 homolog (mouse)	chr5q31.1	231840_x_at	NM_181705
2.58	3.00	0.42	1.59E-02	2.36E-01	WDR65	WD repeat domain 65	chr1p34.2	1553425_at	NM_152498
2.54	3.10	0.57	1.59E-02	2.37E-01	---	---	---	233239_at	---
5.10	5.66	0.56	1.59E-02	2.37E-01	---	---	---	243910_x_at	---
3.92	4.60	0.68	1.60E-02	2.37E-01	ANKRD12	ankyrin repeat domain 12	chr18p11.22	212289_at	NM_001083625 /// NM_015208
3.56	4.09	0.53	1.60E-02	2.37E-01	RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	chr17q25.3	206103_at	NM_005052
4.47	5.06	0.59	1.60E-02	2.37E-01	ZNF277	zinc finger protein 277	chr7q31.1	215887_at	NM_021994
5.78	6.26	0.48	1.60E-02	2.37E-01	MDFI	MyoD family inhibitor	chr6p21	205375_at	NM_005586
7.43	9.18	1.75	1.60E-02	2.37E-01	TMEM97	transmembrane protein 97	chr17q11.2	212279_at	NM_014573

3.46	4.34	0.87	1.60E-02	2.37E-01	---	---	---	229554_at	---
3.81	4.33	0.52	1.60E-02	2.37E-01	TSGA10IP	testis specific, 10 interacting protein	chr11q13.1	1553483_at	NM_152762
3.82	4.19	0.37	1.60E-02	2.37E-01	B4GALNT3	beta-1,4-N-acetyl-galactosaminyl transferase 3	chr12p13.33	229203_at	NM_173593
2.81	3.14	0.33	1.61E-02	2.38E-01	NPC1L1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	chr7p13	224306_at	NM_001101648 /// NM_013389
4.14	4.65	0.50	1.61E-02	2.38E-01	LOC100131347	hypothetical protein LOC100131347	chr17q12	240963_x_at	XM_001714887 /// XM_001716669 /// XM_001718360
1.96	2.29	0.34	1.61E-02	2.38E-01	---	---	---	240856_at	---
4.01	5.47	1.46	1.61E-02	2.38E-01	IGF1	insulin-like growth factor 1 (somatomedin C)	chr12q22-q23	209540_at	NM_000618 /// NM_001111283 /// NM_001111284 /// NM_001111285
3.15	3.77	0.61	1.61E-02	2.38E-01	---	---	---	238078_at	---
4.32	4.81	0.49	1.62E-02	2.38E-01	LOC100131141	hypothetical LOC100131141	chr19q12	235322_at	XR_036860 /// XR_036861 /// XR_038528
3.99	4.41	0.42	1.62E-02	2.38E-01	AVP	arginine vasopressin	chr20p13	207848_at	NM_000490
3.06	3.48	0.42	1.62E-02	2.38E-01	---	---	---	1566501_at	---
4.99	6.27	1.28	1.62E-02	2.38E-01	LOC440731	similar to hCG1817424	chr1q42.2	237563_s_at	XM_933693
2.63	3.03	0.41	1.62E-02	2.38E-01	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	chr12q24.31	244400_at	NM_022916
5.18	6.93	1.75	1.63E-02	2.38E-01	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)	chrXq22.3	219771_at	NM_017752 /// NM_198881
4.08	5.23	1.15	1.63E-02	2.38E-01	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	chr18q12.2	222558_at	NM_018170
7.72	8.58	0.87	1.63E-02	2.38E-01	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	chr2p21	202305_s_at	NM_001042548 /// NM_005102
3.28	3.98	0.70	1.64E-02	2.38E-01	SETBP1	SET binding protein 1	chr18q21.1	205933_at	NM_001130110 /// NM_015559
4.69	5.25	0.57	1.63E-02	2.38E-01	KIAA0746 /// SERINC2	KIAA0746 protein /// serine incorporator 2	chr1p35.1 /// chr4p15.2	224762_at	NM_015187 /// NM_178865
5.21	5.74	0.53	1.63E-02	2.38E-01	LOC100134498	hypothetical protein LOC100134498	---	210332_at	XM_001716631
2.79	3.31	0.52	1.64E-02	2.38E-01	PCDHGA4	protocadherin gamma subfamily A, 4	chr5q31	1552735_at	NM_018917 /// NM_032053
2.59	3.10	0.51	1.64E-02	2.38E-01	---	---	---	233513_at	---
12.75	13.25	0.51	1.63E-02	2.38E-01	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	chr10q24.3	205502_at	NM_000102
6.10	6.59	0.49	1.62E-02	2.38E-01	---	---	---	237882_at	---
2.44	2.91	0.48	1.63E-02	2.38E-01	KIAA0825	KIAA0825 protein	chr5q15	233915_at	XM_376412 /// XM_938750
2.05	2.53	0.47	1.64E-02	2.38E-01	---	---	---	233264_at	---
2.80	3.25	0.45	1.63E-02	2.38E-01	PKDREJ	polycystic kidney disease (polycystin) and REJ homolog (sperm receptor for egg jelly homolog, sea urchin)	chr22q13.31	220548_at	NM_006071
5.27	5.72	0.44	1.64E-02	2.38E-01	---	---	---	243470_at	---
3.47	3.91	0.44	1.63E-02	2.38E-01	---	---	---	237594_at	---
5.09	5.51	0.42	1.64E-02	2.38E-01	CLCF1	cardiotrophin-like cytokine factor 1	chr11q13.3	219500_at	NM_013246
4.58	4.99	0.41	1.63E-02	2.38E-01	HDLBP	High density lipoprotein binding protein	chr2q37.3	235624_at	NM_005336 /// NM_203346
3.20	3.59	0.39	1.63E-02	2.38E-01	---	---	---	215335_at	---
2.96	3.35	0.39	1.64E-02	2.38E-01	CEP152	Centrosomal protein 152kDa	chr15q21.1	215882_at	NM_014985
2.86	3.25	0.39	1.63E-02	2.38E-01	FLJ37638	Hypothetical gene supported by AK094957	chr18q23	244564_at	XM_001127308
4.88	5.23	0.35	1.62E-02	2.38E-01	HOXB1	homeobox B1	chr17q21.3	208224_at	NM_002144
4.19	4.53	0.34	1.64E-02	2.38E-01	NPBWR1	neuropeptides B/W receptor 1	chr8p22-q21.13	231752_at	NM_005285
2.03	2.36	0.33	1.63E-02	2.38E-01	---	---	---	242682_at	---
2.97	3.48	0.51	1.64E-02	2.38E-01	---	---	---	215791_at	---
3.26	3.66	0.40	1.65E-02	2.38E-01	SPEM1	spermatid maturation 1	chr17p13.1	240878_at	NM_199339
3.91	4.47	0.56	1.65E-02	2.38E-01	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	chr9p21	207530_s_at	NM_004936 /// NM_078487
2.20	2.47	0.27	1.65E-02	2.38E-01	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	chr3p14.1	206144_at	NM_001033057 /// NM_004742 /// NM_015520
2.89	3.36	0.47	1.65E-02	2.39E-01	---	---	---	220906_at	---
2.54	2.86	0.33	1.65E-02	2.39E-01	BHLHB4	basic helix-loop-helix domain containing, class B, 4	chr20q13.33	234045_x_at	NM_080606

2.36	2.66	0.30	1.65E-02	2.39E-01	CXorf64	chromosome X open reading frame 64	chrXq25	240043_at	NM_001122716 /// XM_001719075 /// XM_001720449 /// XM_001720573
3.31	3.99	0.68	1.66E-02	2.39E-01	SR140	U2-associated SR140 protein	chr3q23	236696_at	NM_001080415
5.82	6.27	0.45	1.66E-02	2.39E-01	WDR89	WD repeat domain 89	chr14q23.2	238650_x_at	NM_001008726 /// NM_080666
2.87	3.31	0.44	1.66E-02	2.39E-01	WNT8B	wingless-type MMTV integration site family, member 8B	chr10q24	207612_at	NM_003393
2.62	3.02	0.40	1.66E-02	2.39E-01	---	---	---	233958_at	---
3.09	3.44	0.35	1.66E-02	2.39E-01	---	---	---	1562314_at	---
3.38	4.68	1.30	1.67E-02	2.40E-01	---	---	---	240788_at	---
4.10	4.50	0.40	1.67E-02	2.40E-01	CCDC64	coiled-coil domain containing 64	chr12q24.23	228320_x_at	NM_207311
3.76	4.15	0.39	1.67E-02	2.40E-01	---	---	---	234643_x_at	---
5.42	5.94	0.52	1.67E-02	2.40E-01	SORD	sorbitol dehydrogenase	chr15q15.3	201562_s_at	NM_003104
4.99	6.37	1.38	1.67E-02	2.40E-01	---	---	---	230918_at	---
3.94	5.07	1.13	1.67E-02	2.40E-01	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	chr20p12.1	218859_s_at	NM_016649
6.28	6.93	0.65	1.67E-02	2.40E-01	SCCPDH	saccharopine dehydrogenase (putative)	chr1q44	201826_s_at	NM_016002
6.51	7.14	0.63	1.67E-02	2.40E-01	SEZ6L2	Seizure related 6 homolog (mouse)-like 2	chr16p11.2	238404_x_at	NM_001114099 /// NM_001114100 /// NM_012410 /// NM_201575
6.19	6.81	0.62	1.67E-02	2.40E-01	---	---	---	241427_x_at	---
3.47	3.98	0.52	1.67E-02	2.40E-01	CBX6 /// NPTXR	chromobox homolog 6 /// neuronal pentraxin receptor	chr22q13.1	213040_s_at	NM_014292 /// NM_014293
2.36	2.87	0.51	1.67E-02	2.40E-01	---	---	---	217458_at	---
2.65	3.09	0.44	1.67E-02	2.40E-01	MPHOSPH9	M-phase phosphoprotein 9	chr12q24.31	206205_at	NM_022782
1.80	2.17	0.37	1.67E-02	2.40E-01	---	---	---	243013_at	---
3.74	4.15	0.42	1.68E-02	2.40E-01	LOC100129502	Hypothetical protein LOC100129502	chr15q26.1	217548_at	XM_001720085 /// XM_001721688 /// XM_001721701
5.72	6.13	0.41	1.68E-02	2.40E-01	FAM3D	family with sequence similarity 3, member D	chr3p14.2	227676_at	NM_138805
2.46	2.86	0.40	1.68E-02	2.40E-01	---	---	---	1556294_at	---
3.20	3.59	0.39	1.68E-02	2.40E-01	---	---	---	239498_at	---
2.58	2.95	0.38	1.68E-02	2.40E-01	ITIH5L	inter-alpha (globulin) inhibitor H5-like	chrXp11.21	234894_at	NM_198510
2.41	2.74	0.33	1.68E-02	2.40E-01	---	---	---	1563590_at	---
2.01	2.32	0.31	1.68E-02	2.40E-01	---	---	---	239664_at	---
3.77	4.30	0.53	1.69E-02	2.40E-01	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	chr3q24	242587_at	NM_173653
3.68	4.36	0.68	1.69E-02	2.40E-01	SLC25A34	solute carrier family 25, member 34	chr1p36.21	1559977_a_at	NM_207348
3.87	4.90	1.03	1.69E-02	2.41E-01	TM4SF18	transmembrane 4 L six family member 18	chr3q25.1	228489_at	NM_138786
6.36	6.95	0.59	1.69E-02	2.41E-01	MAP3K7IP1	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1	chr22q13.1	233679_at	NM_006116 /// NM_153497
3.43	3.86	0.42	1.69E-02	2.41E-01	POLH	polymerase (DNA directed), eta	chr6p21.1	219380_x_at	NM_006502
2.51	2.92	0.42	1.69E-02	2.41E-01	---	---	---	244662_at	---
6.85	7.42	0.57	1.69E-02	2.41E-01	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	chr2p11.2	218124_at	NM_017750
2.62	3.12	0.49	1.70E-02	2.41E-01	LOC100130175	hypothetical protein LOC100130175	chr10q25.2	236043_at	XM_001722452 /// XM_001725810 /// XM_001726027
8.37	9.38	1.00	1.70E-02	2.41E-01	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	chr4q21-q23	209612_s_at	NM_000668
7.80	8.78	0.98	1.70E-02	2.41E-01	TMEM106B	transmembrane protein 106B	chr7p21.3	222787_s_at	NM_001134232 /// NM_018374
2.62	2.98	0.37	1.70E-02	2.41E-01	---	---	---	233908_x_at	---
4.53	5.36	0.83	1.70E-02	2.41E-01	---	---	---	213598_at	---
5.13	5.97	0.84	1.70E-02	2.41E-01	---	---	---	228959_at	---
2.12	2.55	0.44	1.70E-02	2.41E-01	GJB2	gap junction protein, beta 2, 26kDa	chr13q11-q12	223278_at	NM_004004
3.18	3.61	0.43	1.70E-02	2.41E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	239397_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735

2.81	3.12	0.31	1.70E-02	2.41E-01	C14orf138	chromosome 14 open reading frame 138	chr14q22.1	237640_at	NM_001040662 /// NM_024558
3.56	4.07	0.51	1.71E-02	2.41E-01	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	chr7q22	223994_s_at	NM_020246
5.49	6.08	0.60	1.72E-02	2.41E-01	C14orf45	chromosome 14 open reading frame 45	chr14q24.3	239933_x_at	NM_025057
7.06	7.57	0.51	1.72E-02	2.41E-01	FAM129B	family with sequence similarity 129, member B	chr9q34.11	233974_s_at	NM_001035534 /// NM_022833
2.52	2.95	0.43	1.72E-02	2.41E-01	LOC100132941 /// LOC647187 /// LOC647224	hypothetical protein LOC100132941 /// hypothetical LOC647187 /// hypothetical LOC647224	chr16p11.2	217384_x_at	XM_001718037 /// XR_037895 /// XR_037918
3.23	3.66	0.42	1.72E-02	2.41E-01	LOC442075	hypothetical LOC442075	chr3p25.3	237005_at	XM_001720051 /// XM_001720351 /// XM_001721526
2.69	3.11	0.42	1.72E-02	2.41E-01	---	---	---	243716_at	---
2.50	2.91	0.41	1.72E-02	2.41E-01	CYMP	chymosin pseudogene	chr1p13.3	242902_at	NR_003599
4.65	5.05	0.40	1.72E-02	2.41E-01	TMPRSS6	transmembrane protease, serine 6	chr22q12.3	214955_at	NM_153609
3.98	4.38	0.40	1.72E-02	2.41E-01	USP51	ubiquitin specific peptidase 51	chrXp11.21	237247_at	NM_201286
3.37	3.70	0.33	1.72E-02	2.41E-01	PSG1	pregnancy specific beta-1-glycoprotein 1	chr19q13.2	239583_x_at	NM_006905
2.16	2.50	0.34	1.72E-02	2.41E-01	---	---	---	237953_at	---
2.47	2.88	0.41	1.72E-02	2.41E-01	---	---	---	233765_at	---
2.95	3.36	0.41	1.73E-02	2.41E-01	LOC283454	hypothetical protein LOC283454	chr12q24.23	229552_at	---
2.06	2.50	0.44	1.73E-02	2.42E-01	NMU	neuromedin U	chr4q12	206023_at	NM_006681
4.96	6.49	1.53	1.73E-02	2.42E-01	ACSL3	acyl-CoA synthetase long-chain family member 3	chr2q34-q35	201661_s_at	NM_004457 /// NM_203372
6.28	6.85	0.57	1.73E-02	2.42E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	211862_x_at	NM_001127183 /// NM_001127184 /// NM_003879
3.69	4.02	0.33	1.74E-02	2.42E-01	KIAA0495	KIAA0495	chr1p36.32	213339_at	NM_207306
4.28	4.68	0.41	1.74E-02	2.42E-01	IL1RN	interleukin 1 receptor antagonist	chr2q14.2	212659_s_at	NM_000577 /// NM_173841 /// NM_173842 /// NM_173843
2.50	3.02	0.52	1.74E-02	2.42E-01	---	---	---	241940_at	---
5.36	6.16	0.80	1.75E-02	2.42E-01	HSPB8	heat shock 22kDa protein 8	chr12q24.23	221667_s_at	NM_014365 /// XR_017379 /// XR_019602 /// XR_038402
4.23	4.77	0.54	1.75E-02	2.42E-01	---	---	---	242223_at	---
2.57	2.92	0.36	1.75E-02	2.42E-01	---	---	---	1560836_at	---
3.80	4.23	0.44	1.75E-02	2.43E-01	PLAC2	placenta-specific 2 (non-protein coding)	chr19p13.3	244374_at	XR_040439 /// XR_040440 /// XR_040441
2.33	2.76	0.43	1.75E-02	2.43E-01	---	---	---	1570040_at	---
2.93	3.35	0.42	1.75E-02	2.43E-01	WDR44	WD repeat domain 44	chrXq24	235485_at	NM_019045
2.89	3.21	0.32	1.75E-02	2.43E-01	CHD7	chromodomain helicase DNA binding protein 7	chr8q12.2	218829_s_at	NM_017780
5.12	6.24	1.12	1.75E-02	2.43E-01	UHMK1	U2AF homology motif (UHM) kinase 1	chr1q23.3	235003_at	NM_175866
2.40	2.78	0.38	1.76E-02	2.43E-01	---	---	---	241012_at	---
4.19	5.50	1.30	1.77E-02	2.43E-01	ASAM	adipocyte-specific adhesion molecule	chr11q24.1	228082_at	NM_024769
4.60	5.41	0.81	1.76E-02	2.43E-01	ZDHHC19	zinc finger, DHHC-type containing 19	chr3q29	231122_x_at	NM_001039617
2.46	2.97	0.51	1.76E-02	2.43E-01	---	---	---	236879_at	---
4.14	4.63	0.49	1.77E-02	2.43E-01	LGI2	leucine-rich repeat LGI family, member 2	chr4p15.2	219699_at	NM_018176
7.26	7.72	0.46	1.76E-02	2.43E-01	OSBPL1A	oxysterol binding protein-like 1A	chr18q11.1	208158_s_at	NM_018030 /// NM_080597
2.65	3.10	0.45	1.77E-02	2.43E-01	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	chr3p21.3	234291_s_at	NM_020208 /// NM_022405
2.64	3.05	0.42	1.77E-02	2.43E-01	MPZL3	myelin protein zero-like 3	chr11q23.3	227747_at	NM_198275
2.75	3.12	0.37	1.77E-02	2.43E-01	C16orf70	chromosome 16 open reading frame 70	chr16q22.1	220601_at	NM_025187
2.64	3.01	0.37	1.77E-02	2.43E-01	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	chr10q11.21	237294_at	NM_032023
2.24	2.58	0.35	1.76E-02	2.43E-01	ADRA1B	adrenergic, alpha-1B-, receptor	chr5q23-q32	207589_at	NM_000679
2.96	3.30	0.34	1.76E-02	2.43E-01	---	---	---	1556453_at	---
2.02	2.38	0.36	1.77E-02	2.43E-01	---	---	---	241323_at	---
2.45	2.80	0.34	1.77E-02	2.44E-01	C1orf135	chromosome 1 open reading frame 135	chr1p36.11	222946_s_at	NM_024037
2.50	2.94	0.44	1.77E-02	2.44E-01	C14orf85	chromosome 14 open reading frame 85	chr14q32.12	234594_at	NR_002808
6.61	7.04	0.44	1.78E-02	2.44E-01	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)	chr19p13.13	215844_at	NM_013433
2.40	2.75	0.34	1.78E-02	2.44E-01	WFDC5	WAP four-disulfide core domain 5	chr20q13.12	242204_at	NM_145652
2.15	2.64	0.49	1.78E-02	2.44E-01	STK33	serine/threonine kinase 33	chr11p15.3	228086_at	NM_030906
4.97	5.40	0.43	1.78E-02	2.44E-01	WWC2	WW and C2 domain containing 2	chr4q35.1	1554762_a_at	NM_024949
2.53	3.38	0.85	1.78E-02	2.44E-01	RHOJ	ras homolog gene family, member J	chr14q23.2	1555233_at	NM_020663

3.56	4.04	0.48	1.78E-02	2.44E-01	LOC400236	Hypothetical LOC400236	chr14q32.11	227885_at	XM_001715158 /// XM_378472 /// XM_944198
4.78	5.20	0.42	1.78E-02	2.44E-01	BTNL3	butyrophilin-like 3	chr5q35.3	217207_s_at	NM_197975
3.19	3.52	0.33	1.78E-02	2.44E-01	---	---	---	232784_at	---
9.39	11.09	1.71	1.79E-02	2.44E-01	H19	H19, imprinted maternally expressed transcript (non-protein coding)	chr11p15.5	224646_x_at	NR_002196
7.79	8.72	0.94	1.79E-02	2.44E-01	PALMD	palmdelphin	chr1p22-p21	218736_s_at	NM_017734
6.56	7.28	0.72	1.79E-02	2.44E-01	PEMT	phosphatidylethanolamine N-methyltransferase	chr17p11.2	207621_s_at	NM_007169 /// NM_148172 /// NM_148173
4.25	4.72	0.47	1.79E-02	2.44E-01	LOC100132161 /// LOC100132167 /// LOC100132678 /// LOC643630	similar to hCG1993567 /// similar to hCG1993567 /// similar to hCG1993567 /// similar to hCG1993567	chr9p11.2 /// chr9p12	224519_at	XM_001715998 /// XM_001719500 /// XM_001719650 /// XM_001719822
2.19	2.53	0.33	1.79E-02	2.44E-01	---	---	---	1560832_at	---
1.84	2.15	0.31	1.79E-02	2.44E-01	LOC399959	Hypothetical gene supported by BX647608	chr11q24.1	241975_at	---
2.87	3.71	0.84	1.79E-02	2.44E-01	THRSP	thyroid hormone responsive (SPOT14 homolog, rat)	chr11q13.5	229476_s_at	NM_003251
5.35	6.29	0.94	1.79E-02	2.44E-01	TMCC1	transmembrane and coiled-coil domain family 1	chr3q21.3	227112_at	NM_001017395 /// NM_001128224 /// NM_015008
6.16	6.72	0.56	1.80E-02	2.44E-01	LHB	luteinizing hormone beta polypeptide	chr19q13.32	214471_x_at	NM_000894
4.23	4.75	0.52	1.80E-02	2.44E-01	---	---	---	1565639_a_at	---
2.93	3.40	0.46	1.79E-02	2.44E-01	---	---	---	235787_at	---
3.59	4.02	0.43	1.80E-02	2.44E-01	ZBTB32	zinc finger and BTB domain containing 32	chr19q13.1	220118_at	NM_014383
3.57	3.96	0.38	1.80E-02	2.44E-01	ZBP1	Z-DNA binding protein 1	chr20q13.31	208087_s_at	NM_030776
3.32	3.67	0.35	1.80E-02	2.44E-01	MPL	myeloproliferative leukemia virus oncogene	chr1p34	211903_s_at	NM_005373
3.80	4.13	0.33	1.80E-02	2.44E-01	CD274	CD274 molecule	chr9p24	223834_at	NM_014143
1.93	2.25	0.32	1.79E-02	2.44E-01	OR1E1	olfactory receptor, family 1, subfamily E, member 1	chr17p13.3	214515_at	NM_003553
2.10	2.43	0.34	1.80E-02	2.44E-01	LOC644222	hypothetical LOC644222	chr12q13.13	240346_at	XM_001715807 /// XM_932052
6.03	6.56	0.53	1.80E-02	2.44E-01	FLJ22536	hypothetical locus LOC401237	chr6p22.3	241671_x_at	XM_379398
2.59	2.99	0.40	1.80E-02	2.44E-01	TMLHE	trimethyllysine hydroxylase, epsilon	chrXq28	1554206_at	NM_018196
3.78	4.20	0.43	1.81E-02	2.45E-01	ADAL	adenosine deaminase-like	chr15q15.3	238424_at	NM_001012969
4.67	6.00	1.32	1.81E-02	2.45E-01	LOC644246	hypothetical protein LOC644246	chr17q21.31	230388_s_at	XM_927427
4.19	4.95	0.76	1.81E-02	2.45E-01	---	---	---	233223_at	---
3.14	3.58	0.44	1.81E-02	2.45E-01	---	---	---	234037_s_at	---
3.55	3.98	0.43	1.81E-02	2.45E-01	NUCB2	nucleobindin 2	chr11p15.1-p14	229838_at	NM_005013
3.40	3.78	0.38	1.81E-02	2.45E-01	WDR1	WD repeat domain 1	chr4p16.1	244672_at	NM_005112 /// NM_017491
5.24	6.88	1.64	1.81E-02	2.45E-01	TTC37	tetratricopeptide repeat domain 37	chr5q15	203048_s_at	NM_014639
5.41	5.96	0.55	1.81E-02	2.45E-01	---	---	---	240175_at	---
2.91	3.32	0.41	1.81E-02	2.45E-01	---	---	---	234578_at	---
2.78	3.13	0.35	1.81E-02	2.45E-01	ASAH2B	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B	chr10q11.23	231791_at	NM_001079516
3.83	4.55	0.72	1.82E-02	2.45E-01	LOC51057	hypothetical protein LOC51057	chr2p15	224180_x_at	NM_001042692 /// NM_015910
5.48	6.18	0.70	1.82E-02	2.45E-01	RALBP1	ralA binding protein 1	chr18p11.3	202844_s_at	NM_006788
5.55	6.12	0.58	1.82E-02	2.45E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	222024_s_at	NM_006738 /// NM_007200 /// NM_144767
4.33	4.86	0.53	1.81E-02	2.45E-01	---	---	---	231457_at	---
3.72	4.21	0.49	1.82E-02	2.45E-01	KIAA0319	KIAA0319	chr6p22.3-p22.2	206017_at	NM_014809
4.01	4.46	0.46	1.82E-02	2.45E-01	---	---	---	1566156_at	---
2.68	3.12	0.44	1.81E-02	2.45E-01	TBCD	Tubulin folding cofactor D	chr17q25.3	229767_at	NM_005993
6.45	6.87	0.41	1.82E-02	2.45E-01	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	chr12p13	215026_x_at	NM_001038
2.25	2.57	0.32	1.82E-02	2.45E-01	---	---	---	208207_at	---
3.06	3.58	0.51	1.82E-02	2.45E-01	KLHL17	kelch-like 17 (Drosophila)	chr1p36.33	229792_at	NM_198317
3.54	3.92	0.38	1.82E-02	2.45E-01	ADRA2B	adrenergic, alpha-2B-, receptor	chr2p13-q13	208544_at	NM_000682
5.12	5.44	0.32	1.82E-02	2.45E-01	CYP2D6	Cytochrome P450, family 2, subfamily D, polypeptide 6	chr22q13.1	217468_at	NM_000106 /// NM_001025161
1.96	2.27	0.31	1.83E-02	2.45E-01	---	---	---	233512_at	---
3.65	4.44	0.79	1.83E-02	2.45E-01	---	---	---	233417_at	---
5.51	6.17	0.67	1.83E-02	2.45E-01	SLC39A8	solute carrier family 39 (zinc transporter), member 8	chr4q22-q24	209266_s_at	NM_022154
2.96	3.50	0.54	1.83E-02	2.45E-01	JAG1	jagged 1 (Alagille syndrome)	chr20p12.1-p11.23	209097_s_at	NM_000214

3.00	3.46	0.46	1.83E-02	2.46E-01	TREH	trehalase (brush-border membrane glycoprotein)	chr11q23.3	207378_at	NM_007180
2.90	3.51	0.61	1.84E-02	2.46E-01	FIBCD1	fibrinogen C domain containing 1	chr9q34.12-q34.13	240042_at	NM_032843
6.51	7.10	0.59	1.84E-02	2.46E-01	SFTPC	surfactant protein C	chr8p21	215454_x_at	NM_003018
4.54	5.10	0.57	1.84E-02	2.46E-01	DKFZp434K191 /// DKFZP434P211 /// LOC100133536 /// LOC440821 /// LOC646074 /// LOC728093 /// LOC729915 /// POM121L1 /// POM121L3	hypothetical locus DKFZp434K191 /// POM121-like protein /// similar to hCG2002956 /// similar to POM121 membrane glycoprotein-like 1 /// similar to POM121-like 1 /// hypothetical LOC728093 /// hypothetical LOC729915 /// POM121 membrane glycoprotein-like 1 (rat) /// POM121 membrane glycoprotein-like 3 (rat)	chr20p11.21 /// chr22q11.2 /// chr22q11.22 /// chr22q11.23 /// chr5p13.3 /// chr5q21.1	214570_x_at	NR_003714 /// XM_001719304 /// XM_001722873 /// XM_001724140 /// XM_929034 /// XR_019113 /// XR_036930 /// XR_038038 /// XR_040035 /// XR_042337 /// XR_042405
4.02	4.46	0.45	1.84E-02	2.46E-01	KLK13	kallikrein-related peptidase 13	chr19q13.3-q13.4	217315_s_at	NM_015596
2.64	3.08	0.44	1.84E-02	2.46E-01	---	---	---	230269_at	---
6.01	6.43	0.42	1.84E-02	2.46E-01	---	---	---	234753_x_at	---
6.23	6.64	0.40	1.84E-02	2.46E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	214486_x_at	NM_001127183 /// NM_001127184 /// NM_003879
4.29	4.69	0.40	1.84E-02	2.46E-01	LOC642031	Hypothetical protein LOC642031	---	242415_at	XM_936101
3.31	3.65	0.34	1.84E-02	2.46E-01	ZNF776	Zinc finger protein 776	chr19q13.43	239838_at	NM_173632
3.18	3.69	0.51	1.85E-02	2.46E-01	FANK1	fibronectin type III and ankyrin repeat domains 1	chr10q26.2	232968_at	NM_145235
3.22	3.85	0.63	1.85E-02	2.46E-01	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	chr3p24.2	229657_at	NM_000461 /// NM_001128176 /// NM_001128177
4.30	4.83	0.52	1.85E-02	2.46E-01	---	---	---	238754_at	---
2.50	2.93	0.43	1.85E-02	2.46E-01	ALS2CR12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12	chr2q33.1	242661_x_at	NM_001127391 /// NM_139163
4.17	5.39	1.22	1.85E-02	2.46E-01	FLJ39051	Hypothetical gene supported by AK096370	chr11q24.2	227925_at	---
2.37	2.70	0.34	1.85E-02	2.46E-01	---	---	---	237709_at	---
4.04	4.53	0.49	1.85E-02	2.46E-01	C1QL1	complement component 1, q subcomponent-like 1	chr17q21	205575_at	NM_006688
4.36	4.93	0.57	1.85E-02	2.46E-01	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	chr6p22.3	214877_at	NM_017774
5.72	6.20	0.48	1.85E-02	2.46E-01	N6AMT2	N-6 adenine-specific DNA methyltransferase 2 (putative)	chr13q12.11	227054_at	NM_174928
7.31	7.86	0.54	1.86E-02	2.47E-01	BBC3	BCL2 binding component 3	chr19q13.3-q13.4	211692_s_at	NM_001127240 /// NM_001127241 /// NM_001127242 /// NM_014417
2.41	3.00	0.59	1.86E-02	2.47E-01	NT5E	5'-nucleotidase, ecto (CD73)	chr6q14-q21	1553995_a_at	NM_002526
3.17	3.53	0.37	1.86E-02	2.47E-01	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	chr11q25	235649_at	NM_007037
7.00	7.41	0.42	1.86E-02	2.47E-01	SLC11A1	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	chr2q35	230382_at	NM_000578
3.68	4.08	0.41	1.86E-02	2.47E-01	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	chr17q22	211314_at	NM_018896 /// NM_198376 /// NM_198377 /// NM_198378 /// NM_198379 /// NM_198380 /// NM_198382 /// NM_198383 /// NM_198384 /// NM_198385 /// NM_198386 /// NM_198387 /// NM_198388 /// NM_198396 /// NM_198397
3.10	3.62	0.52	1.87E-02	2.47E-01	LCN8	lipocalin 8	chr9q34.3	1569614_s_at	NM_178469
3.12	3.52	0.40	1.87E-02	2.47E-01	SPG11	spastic paraplegia 11 (autosomal recessive)	chr15q14	1559747_at	NM_025137
3.05	3.67	0.62	1.87E-02	2.48E-01	KIDINS220	kinase D-interacting substrate of 220 kDa	chr2p24	1557246_at	NM_020738
7.88	9.25	1.37	1.87E-02	2.48E-01	PGRMC1	progesterone receptor membrane component 1	chrXq22-q24	201120_s_at	NM_006667
3.90	4.33	0.44	1.88E-02	2.48E-01	---	---	---	221179_at	---

4.14	4.54	0.40	1.88E-02	2.48E-01	NR1I2	nuclear receptor subfamily 1, group I, member 2	chr3q12-q13.3	207203_s_at	NM_003889 /// NM_022002 /// NM_033013
5.68	6.49	0.81	1.88E-02	2.49E-01	CPD	carboxypeptidase D	chr17q11.2	201941_at	NM_001304
2.80	3.20	0.40	1.88E-02	2.49E-01	GHSR	growth hormone secretagogue receptor	chr3q26.31	221360_s_at	NM_004122 /// NM_198407
2.99	3.30	0.31	1.88E-02	2.49E-01	KIAA2026	KIAA2026	chr9p24.1	235021_at	NM_001017969
2.76	3.31	0.55	1.89E-02	2.49E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	241640_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844
5.37	5.82	0.46	1.89E-02	2.49E-01	BCL6B	B-cell CLL/lymphoma 6, member B (zinc finger protein)	chr17p13.1	242148_at	NM_181844
2.48	2.83	0.35	1.89E-02	2.49E-01	C2orf71	chromosome 2 open reading frame 71	chr2p23.2	1556312_at	NM_001029883
4.85	5.18	0.33	1.89E-02	2.49E-01	IL11	interleukin 11	chr19q13.3-q13.4	206926_s_at	NM_000641
2.61	2.94	0.33	1.89E-02	2.49E-01	TRIM36	tripartite motif-containing 36	chr5q22.3	231123_at	NM_001017397 /// NM_001017398 /// NM_018700
3.43	3.89	0.46	1.90E-02	2.49E-01	LOC100133315	Similar to hCG1640299	chr11q13.4	232586_x_at	XM_001717628 /// XM_001723215 /// XM_001723302
5.85	6.89	1.03	1.90E-02	2.50E-01	ACSL3	acyl-CoA synthetase long-chain family member 3	chr2q34-q35	201660_at	NM_004457 /// NM_203372
3.02	3.46	0.45	1.90E-02	2.50E-01	TRIM26	Tripartite motif-containing 26	chr6p21.3	1558967_s_at	NM_003449
3.28	3.63	0.36	1.90E-02	2.50E-01	LARP7	La ribonucleoprotein domain family, member 7	chr4q25	215246_at	NM_015454 /// NM_016648
1.78	2.06	0.28	1.90E-02	2.50E-01	DCDC5	doublecortin domain containing 5	chr11p14.1-p13	232603_at	NM_198462
2.49	2.94	0.45	1.90E-02	2.50E-01	---	---	---	1560409_at	---
3.17	3.66	0.49	1.91E-02	2.50E-01	THBS1	thrombospondin 1	chr15q15	201107_s_at	NM_003246
5.88	6.31	0.42	1.91E-02	2.50E-01	AATK	apoptosis-associated tyrosine kinase	chr17q25.3	205986_at	NM_001080395 /// XM_001714082
3.78	4.27	0.49	1.91E-02	2.50E-01	---	---	---	233265_at	---
3.86	4.32	0.46	1.91E-02	2.50E-01	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	chr1p34.1	231659_at	NM_006279 /// NM_174963 /// NM_174964 /// NM_174965 /// NM_174966 /// NM_174967 /// NM_174968 /// NM_174969 /// NM_174970 /// NM_174971
2.38	2.67	0.29	1.91E-02	2.50E-01	SERPINB3 /// SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 3 /// serpin peptidase inhibitor, clade B (ovalbumin), member 4	chr18q21.3	210413_x_at	NM_002974 /// NM_006919
2.08	2.46	0.39	1.91E-02	2.50E-01	---	---	---	242017_at	---
2.03	2.51	0.47	1.92E-02	2.51E-01	---	---	---	239301_at	---
4.94	5.39	0.45	1.92E-02	2.51E-01	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	chr6q14-q15	221041_s_at	NM_012434
2.74	3.15	0.41	1.92E-02	2.51E-01	PDE12	Phosphodiesterase 12	chr3p14.3	235091_at	NM_177966
2.44	2.83	0.39	1.92E-02	2.51E-01	DLX1	distal-less homeobox 1	chr2q32	242138_at	NM_001038493 /// NM_178120
4.53	5.35	0.82	1.92E-02	2.51E-01	ANKRD57	ankyrin repeat domain 57	chr2q13	219496_at	NM_023016
5.77	6.26	0.49	1.92E-02	2.51E-01	NPPA	natriuretic peptide precursor A	chr1p36.21	209957_s_at	NM_006172
3.52	4.08	0.56	1.93E-02	2.51E-01	GGT7	gamma-glutamyltransferase 7	chr20q11.22	226469_s_at	NM_178026
5.23	5.76	0.53	1.93E-02	2.51E-01	KIAA1656	KIAA1656 protein	---	1569365_a_at	XR_040413 /// XR_040414 /// XR_040415
3.40	3.75	0.35	1.93E-02	2.51E-01	LOC440792	proline dehydrogenase (oxidase) 1 pseudogene	chr22q11.21	215678_at	---
1.97	2.29	0.32	1.93E-02	2.51E-01	MYSM1	Myb-like, SWIRM and MPN domains 1	chr1p32.1	1569706_at	NM_001085487
2.15	2.45	0.30	1.93E-02	2.51E-01	C8orf81	chromosome 8 open reading frame 81	chr8q24.11	1560207_at	XR_040078 /// XR_040079 /// XR_040080

2.64	3.12	0.48	1.93E-02	2.51E-01	---	---	---	237742_at	---
2.86	3.53	0.67	1.94E-02	2.52E-01	FLJ41170	hypothetical LOC440200	chr14q32.31	232955_at	XR_041854 /// XR_041855 /// XR_041856
2.78	3.26	0.48	1.94E-02	2.52E-01	KCNE1L	KCNE1-like	chrXq22.3	220010_at	NM_012282
2.11	2.52	0.41	1.94E-02	2.52E-01	AYP1p1	AYP1 pseudogene 1	chrYp11.31	234931_at	NR_002820
1.98	2.27	0.29	1.94E-02	2.52E-01	CLLU1	chronic lymphocytic leukemia up-regulated 1	chr12q22	1558186_s_at	NM_001025233
3.63	4.38	0.75	1.94E-02	2.52E-01	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	chrXq13.1	204116_at	NM_000206
3.07	3.55	0.48	1.94E-02	2.52E-01	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	chr10q23.31-q23.32	221232_s_at	NM_001129981 /// NM_020349
2.70	3.13	0.43	1.95E-02	2.52E-01	---	---	---	239414_at	---
5.80	6.50	0.70	1.95E-02	2.52E-01	SRPK2	SFRS protein kinase 2	chr7q22-q31.1	203181_x_at	NM_182691 /// NM_182692
3.72	4.34	0.61	1.95E-02	2.52E-01	FAM48A	Family with sequence similarity 48, member A	chr13q13.3	216682_s_at	NM_001014286 /// NM_017569
2.43	3.02	0.59	1.95E-02	2.52E-01	---	---	---	238000_at	---
4.80	5.27	0.47	1.95E-02	2.52E-01	PBX2	pre-B-cell leukemia homeobox 2	chr6p21.3	211096_at	NM_002586
3.83	4.23	0.40	1.95E-02	2.52E-01	MUC3A	mucin 3A, cell surface associated	chr7q22	214676_x_at	XM_001719499 /// XM_001725354
2.30	2.68	0.38	1.95E-02	2.52E-01	OTOR	otoraplin	chr20p12.1-p11.23	221209_s_at	NM_020157
2.40	2.74	0.33	1.95E-02	2.52E-01	MEG3	Maternally expressed 3 (non-protein coding)	chr14q32	231529_at	NR_002766 /// NR_003530 /// NR_003531
4.10	4.59	0.49	1.95E-02	2.52E-01	---	---	---	214977_at	---
5.19	5.62	0.42	1.95E-02	2.52E-01	LRRN2	leucine rich repeat neuronal 2	chr1q32.1	205154_at	NM_006338 /// NM_201630
2.41	2.74	0.33	1.96E-02	2.52E-01	ECT2	epithelial cell transforming sequence 2 oncogene	chr3q26.1-q26.2	219787_s_at	NM_018098
3.44	3.75	0.30	1.96E-02	2.52E-01	---	---	---	237396_at	---
6.58	7.78	1.21	1.96E-02	2.52E-01	PEX3	peroxisomal biogenesis factor 3	chr6q24.2	203972_s_at	NM_003630
5.27	6.33	1.07	1.96E-02	2.52E-01	ACSL1	acyl-CoA synthetase long-chain family member 1	chr4q34-q35	207275_s_at	NM_001995
4.51	5.03	0.52	1.96E-02	2.52E-01	---	---	---	238709_at	---
3.84	4.30	0.46	1.96E-02	2.52E-01	RPAP2	RNA polymerase II associated protein 2	chr1p22.1	219504_s_at	NM_024813
2.53	2.91	0.37	1.96E-02	2.52E-01	---	---	---	1556253_s_at	---
3.50	3.83	0.33	1.96E-02	2.52E-01	---	---	---	244827_at	---
2.94	3.30	0.37	1.97E-02	2.52E-01	TRIMP1	tripartite motif-containing pseudogene 1	chr11p15	232464_at	NR_002777
5.59	7.03	1.44	1.97E-02	2.52E-01	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	chr2p21	202436_s_at	NM_000104
5.38	6.28	0.90	1.97E-02	2.52E-01	PDGFA	Platelet-derived growth factor alpha polypeptide	chr7p22	229830_at	NM_002607 /// NM_033023
2.34	2.83	0.49	1.97E-02	2.52E-01	MET	met proto-oncogene (hepatocyte growth factor receptor)	chr7q31	203510_at	NM_000245 /// NM_001127500
4.99	5.88	0.88	1.97E-02	2.52E-01	---	---	---	237624_at	---
3.90	4.57	0.67	1.97E-02	2.52E-01	---	---	---	243280_at	---
3.90	4.29	0.40	1.97E-02	2.52E-01	---	---	---	241522_at	---
2.04	2.46	0.42	1.98E-02	2.53E-01	PTPRK	Protein tyrosine phosphatase, receptor type, K	chr6q22.2-q22.3	233609_at	NM_002844
4.03	4.44	0.41	1.98E-02	2.53E-01	ASXL2	additional sex combs like 2 (Drosophila)	chr2p24.1	237095_at	NM_018263
5.92	6.41	0.49	1.98E-02	2.53E-01	C14orf115	chromosome 14 open reading frame 115	chr14q24.3	220536_at	NM_018228
6.53	6.99	0.46	1.98E-02	2.53E-01	RBBP9	retinoblastoma binding protein 9	chr20p11.2	226696_at	NM_006606
4.51	6.34	1.83	1.99E-02	2.53E-01	LOC100129762 /// PRUNE2	similar to KIAA0367 /// prune homolog 2 (Drosophila)	chr9q21.13	212805_at	NM_015225 /// NM_138818 /// XM_001715010 /// XM_001719626 /// XM_001719633 /// XM_001722398 /// XM_001722406
2.23	2.62	0.40	1.99E-02	2.53E-01	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	chr3p21.3	206191_at	NM_001248
3.85	4.25	0.40	1.99E-02	2.53E-01	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	chr16q12.2	239394_at	NM_001043

2.08	2.39	0.32	1.99E-02	2.54E-01	NPHP1	nephronophthisis 1 (juvenile)	chr2q13	206285_at	NM_000272 /// NM_001128178 /// NM_001128179 /// NM_207181																				
2.85	3.24	0.38	1.99E-02	2.54E-01	GSTCD	glutathione S-transferase, C-terminal domain containing	chr4q24	220063_at	NM_001031720 /// NM_024751																				
4.36	5.82	1.46	2.00E-02	2.54E-01	---	---	---	225685_at	---																				
4.46	5.00	0.54	2.00E-02	2.54E-01	INTS9	Integrator complex subunit 9	chr8p21.1	237286_at	NM_018250																				
6.09	6.59	0.50	1.99E-02	2.54E-01	SEMA3F	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	chr3p21.3	209730_at	NM_004186																				
4.79	5.56	0.76	2.00E-02	2.54E-01	C1orf156	chromosome 1 open reading frame 156	chr1q24.2	213528_at	NM_033418																				
4.07	4.60	0.53	2.00E-02	2.54E-01	FLJ00049	FLJ00049 protein	chr7p22.2	216460_at	XM_928411																				
4.26	5.08	0.82	2.00E-02	2.54E-01	---	---	---	242677_at	---																				
3.91	4.43	0.52	2.00E-02	2.54E-01	NIPBL	Nipped-B homolog (Drosophila)	chr5p13.2	242352_at	NM_015384 /// NM_133433																				
3.68	4.39	0.70	2.00E-02	2.54E-01	---	---	---	239409_at	---																				
2.62	2.99	0.37	2.00E-02	2.54E-01	PLEKHA6	pleckstrin homology domain containing, family A member 6	chr1q32.1	205093_at	NM_014935																				
2.26	2.62	0.36	2.00E-02	2.54E-01	---	---	---	242638_at	---																				
4.47	4.90	0.43	2.00E-02	2.54E-01	---	---	---	236147_at	---																				
5.94	6.46	0.52	2.00E-02	2.54E-01	LOC440836	Similar to MGC52679 protein	chr22q13.33	238325_s_at	NM_001014440																				
2.76	3.15	0.39	2.01E-02	2.55E-01	---	---	---	243447_at	---																				
2.81	3.49	0.68	2.01E-02	2.55E-01	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	chr1q41	243851_at	NM_012414																				
3.38	3.88	0.50	2.01E-02	2.55E-01	IL4I1 /// NUP62	interleukin 4 induced 1 /// nucleoporin 62kDa	chr19q13.33 /// chr19q13.3|19q13.3-q13.4	214935_at	NM_012346 /// NM_016553 /// NM_152899 /// NM_153718 /// NM_153719 /// NM_172374																				
5.24	6.14	0.90	2.02E-02	2.55E-01	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	chr14q23.1	227728_at	NM_021003 /// NM_177951 /// NM_177952																				
4.67	5.49	0.82	2.02E-02	2.55E-01	---	---	---	215786_at	---																				
7.26	9.13	1.87	2.02E-02	2.55E-01	TMEM97	transmembrane protein 97	chr17q11.2	212282_at	NM_014573																				
2.66	3.38	0.71	2.02E-02	2.55E-01	PHCA	phytoceramidase, alkaline	chr11q13.5	222689_at	NM_018367																				
4.45	5.00	0.55	2.03E-02	2.55E-01	GLTPD2	glycolipid transfer protein domain containing 2	chr17p13.2	230971_x_at	NM_001014985																				
3.44	3.84	0.41	2.03E-02	2.55E-01	SNIP	SNAP25-interacting protein	chr17q12	1554759_at	NM_025248																				
2.86	3.26	0.40	2.02E-02	2.55E-01	---	---	---	232699_at	---																				
2.51	2.80	0.29	2.03E-02	2.55E-01	---	---	---	237090_at	---																				
3.22	3.92	0.70	2.03E-02	2.56E-01	IQGAP3	IQ motif containing GTPase activating protein 3	chr1q22-q23.1	1569061_at	NM_178229																				
4.42	5.02	0.60	2.03E-02	2.56E-01	RORC	RAR-related orphan receptor C	chr1q21	228806_at	NM_001001523 /// NM_005060																				
3.49	3.88	0.38	2.03E-02	2.56E-01	KRT3	keratin 3	chr12q12-q13	217325_at	NM_057088																				
2.68	3.42	0.74	2.04E-02	2.56E-01	---	---	---	237035_at	---																				
3.52	3.96	0.44	2.04E-02	2.56E-01	LCN10	lipocalin 10	chr9q34.3	238071_at	NM_001001712																				
3.43	3.84	0.41	2.03E-02	2.56E-01	PHKG1	phosphorylase kinase, gamma 1 (muscle)	chr7p11.2	234729_at	NM_006213																				
1.69	1.96	0.27	2.04E-02	2.56E-01	C12orf40	chromosome 12 open reading frame 40	chr12q12	1561721_a_at	NM_001031748																				
5.66	6.11	0.45	2.04E-02	2.56E-01	MOBKL2A	MOB1, Mps One Binder kinase activator-like 2A (yeast)	chr19p13.3	235163_at	NM_130807																				
4.20	4.87	0.66	2.04E-02	2.56E-01	YIPF6	Yip1 domain family, member 6	chrXq12	212340_at	NM_173834																				
6.99	7.39	0.40	2.04E-02	2.56E-01	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	chr12q24.13	225428_s_at	NM_001111322 /// NM_024072																				
2.12	2.48	0.36	2.04E-02	2.56E-01	---	---	---	233425_at	---																				
3.15	3.48	0.33	2.04E-02	2.56E-01	DGCR5	DiGeorge syndrome critical region gene 5 (non-protein coding)	chr22q11	1558118_at	NR_002733																				
9.88	10.88	0.99	2.05E-02	2.57E-01	RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	chr14q11.2	201785_at	NM_002933 /// NM_198232 /// NM_198234 /// NM_198235																				
4.37	5.12	0.75	2.05E-02	2.57E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	229642_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735																				
2.45	2.84	0.38	2.05E-02	2.57E-01	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	chr15q24	215688_at	NM_002891 /// NM_153815																				

2.67	3.20	0.53	2.05E-02	2.57E-01	LOC283788	hypothetical protein LOC283788	---	229007_at	XM_001721615 /// XM_001723582 /// XM_001723589
3.38	3.81	0.43	2.05E-02	2.57E-01	HRASLS	HRAS-like suppressor	chr3q29	219983_at	NM_020386
3.19	3.58	0.40	2.05E-02	2.57E-01	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	chr9q33	207216_at	NM_001244
2.41	2.80	0.39	2.05E-02	2.57E-01	BAGE2 /// BAGE4	B melanoma antigen family, member 2 /// B melanoma antigen family, member 4	chr21p /// chr21p11.1	1555408_at	NM_181704 /// NM_182482
2.06	2.43	0.37	2.05E-02	2.57E-01	---	---	---	223889_at	---
2.02	2.36	0.34	2.05E-02	2.57E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	234418_x_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392
2.05	2.38	0.33	2.05E-02	2.57E-01	TADA1L	Transcriptional adaptor 1 (HFI1 homolog, yeast)-like	chr1q24.1	1559289_at	NM_053053
2.27	2.59	0.32	2.05E-02	2.57E-01	---	---	---	236531_at	---
6.27	7.72	1.45	2.06E-02	2.57E-01	ZNF148	zinc finger protein 148	chr3q21	228545_at	NM_021964
4.19	4.93	0.74	2.06E-02	2.57E-01	GGPS1	geranylgeranyl diphosphate synthase 1	chr1q43	202321_at	NM_001037277 /// NM_001037278 /// NM_004837
3.36	4.00	0.64	2.06E-02	2.57E-01	---	---	---	235735_at	---
2.27	2.65	0.38	2.06E-02	2.57E-01	WBSCR28	Williams-Beuren syndrome chromosome region 28	chr7q11.23	238258_at	NM_182504
3.08	3.50	0.42	2.06E-02	2.57E-01	C9orf44	chromosome 9 open reading frame 44	chr9q22.31	233524_at	---
2.10	2.43	0.33	2.07E-02	2.57E-01	C2orf77	chromosome 2 open reading frame 77	chr2q31.1	236909_at	NM_001085447
4.28	4.80	0.52	2.07E-02	2.58E-01	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	chr4q31.22	236347_at	NM_172250
5.58	6.43	0.85	2.07E-02	2.58E-01	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	chr18p11.32	201671_x_at	NM_001037334 /// NM_005151
2.92	3.23	0.31	2.07E-02	2.58E-01	GLUL	glutamate-ammonia ligase (glutamine synthetase)	chr1q31	242281_at	NM_001033044 /// NM_001033056 /// NM_002065
3.69	4.68	0.99	2.07E-02	2.58E-01	PCNX	pecanex homolog (Drosophila)	chr14q24.2	215175_at	NM_014982
2.89	3.41	0.52	2.07E-02	2.58E-01	KIAA1409	KIAA1409	chr14q32.13	229550_at	NM_020818
4.12	4.62	0.50	2.08E-02	2.58E-01	---	---	---	233997_at	---
4.37	5.10	0.73	2.08E-02	2.58E-01	---	---	---	244354_at	---
5.32	5.81	0.48	2.08E-02	2.58E-01	ARL4C	ADP-ribosylation factor-like 4C	chr2q37.1	202208_s_at	NM_005737
5.00	5.98	0.98	2.08E-02	2.58E-01	---	---	---	227765_at	---
4.31	4.93	0.62	2.08E-02	2.58E-01	---	---	---	237370_at	---
3.92	4.37	0.44	2.08E-02	2.58E-01	MAST2	microtubule associated serine/threonine kinase 2	chr1p34.1	215661_at	NM_015112
4.47	5.16	0.70	2.09E-02	2.59E-01	RENBP	renin binding protein	chrXq28	206617_s_at	NM_002910
5.37	6.06	0.69	2.09E-02	2.59E-01	WWC2	WW and C2 domain containing 2	chr4q35.1	218775_s_at	NM_024949
2.12	2.47	0.35	2.09E-02	2.59E-01	NOX4	NADPH oxidase 4	chr11q14.2-q21	219773_at	NM_016931
2.11	2.44	0.33	2.09E-02	2.59E-01	ZNF347	zinc finger protein 347	chr19q13.41	237061_at	NM_032584
4.66	5.11	0.45	2.09E-02	2.59E-01	MICALL2	MICAL-like 2	chr7p22.3	241478_at	NM_182924
6.95	8.46	1.51	2.10E-02	2.59E-01	PEG3 /// ZIM2	paternally expressed 3 /// zinc finger, imprinted 2	chr19q13.4	209243_s_at	NM_006210 /// NM_015363
2.69	3.01	0.32	2.10E-02	2.59E-01	ZNF221	zinc finger protein 221	chr19q13.2	220847_x_at	NM_013359
2.76	3.41	0.65	2.10E-02	2.59E-01	GPR123	G protein-coupled receptor 123	chr10q26	239221_at	NM_001083909
2.43	2.95	0.52	2.10E-02	2.59E-01	LOC146795	hypothetical protein LOC146795	chr17q24.3	1564402_at	---
6.66	7.18	0.51	2.10E-02	2.59E-01	DES /// FAM48A	desmin /// family with sequence similarity 48, member A	chr13q13.3 /// chr2q35	214027_x_at	NM_001014286 /// NM_001927 /// NM_017569
2.49	2.88	0.39	2.10E-02	2.59E-01	hCG_2007354	hCG2007354	---	1556960_a_at	XR_041592 /// XR_041593
3.36	3.72	0.36	2.10E-02	2.59E-01	EPS8L1	EPS8-like 1	chr19q13.42	221665_s_at	NM_017729 /// NM_133180
2.23	2.60	0.37	2.11E-02	2.59E-01	GRIA3	glutamate receptor, ionotrophic, AMPA 3	chrXq25-q26	217565_at	NM_000828 /// NM_007325
2.62	3.09	0.47	2.11E-02	2.59E-01	---	---	---	1561963_at	---
2.53	2.90	0.37	2.11E-02	2.60E-01	ADD1	adducin 1 (alpha)	chr4p16.3	238939_at	NM_001119 /// NM_014189 /// NM_014190 /// NM_176801

8.84	10.04	1.20	2.11E-02	2.60E-01	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	chr2q32	223044_at	NM_014585
3.20	3.71	0.51	2.11E-02	2.60E-01	LCORL	ligand dependent nuclear receptor corepressor-like	chr4p15.32	232293_at	NM_153686
3.44	3.91	0.47	2.11E-02	2.60E-01	SFTPB	surfactant protein B	chr2p12-p11.2	209810_at	NM_000542 /// NM_198843
2.08	2.45	0.37	2.12E-02	2.60E-01	---	---	---	242849_at	---
2.82	3.17	0.35	2.12E-02	2.60E-01	P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	chr12q24.33	221372_s_at	NM_012226 /// NM_016318 /// NM_170682 /// NM_170683 /// NM_174872 /// NM_174873
2.97	3.58	0.62	2.12E-02	2.60E-01	CTSC	cathepsin C	chr11q14.1-q14.3	231234_at	NM_001114173 /// NM_001814 /// NM_148170
4.71	5.59	0.88	2.12E-02	2.60E-01	PRICKLE1	prickle homolog 1 (Drosophila)	chr12q12	226065_at	NM_153026
3.46	3.88	0.42	2.12E-02	2.60E-01	---	---	---	233618_at	---
2.30	2.82	0.51	2.12E-02	2.60E-01	ZFYVE28	zinc finger, FYVE domain containing 28	chr4p16.3	1569369_at	NM_020972
3.20	3.58	0.38	2.13E-02	2.60E-01	LOC646522	Hypothetical LOC646522	chr11q25	237662_at	XR_040072 /// XR_040073 /// XR_040074
3.21	3.53	0.32	2.13E-02	2.60E-01	---	---	---	238235_at	---
2.78	3.36	0.58	2.13E-02	2.60E-01	---	---	---	240557_at	---
5.38	6.31	0.93	2.14E-02	2.60E-01	ATF6	Activating transcription factor 6	chr1q22-q23	217550_at	NM_007348
2.96	3.84	0.88	2.14E-02	2.60E-01	---	---	---	232759_at	---
6.08	6.69	0.61	2.14E-02	2.60E-01	CNPY4	Canopy 4 homolog (zebrafish)	chr7q22.1	217700_at	NM_152755
3.50	4.05	0.56	2.14E-02	2.60E-01	---	---	---	230413_s_at	---
3.83	4.33	0.50	2.13E-02	2.60E-01	---	---	---	241230_at	---
2.12	2.61	0.49	2.13E-02	2.60E-01	LCMT2	leucine carboxyl methyltransferase 2	chr15q15.3	204013_s_at	NM_014793
2.64	3.02	0.38	2.14E-02	2.60E-01	ANXA2	annexin A2	chr15q21-q22	1568126_at	NM_001002857 /// NM_001002858 /// NM_004039
1.76	2.08	0.32	2.14E-02	2.60E-01	KIAA1211	KIAA1211 protein	chr4q12	227231_at	NM_020722
3.02	3.34	0.32	2.13E-02	2.60E-01	MARK2	MAP/microtubule affinity-regulating kinase 2	chr11q12-q13	211082_x_at	NM_001039468 /// NM_001039469 /// NM_004954 /// NM_017490
2.20	2.48	0.28	2.14E-02	2.60E-01	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	chr14q22	206631_at	NM_000956
1.91	2.18	0.27	2.13E-02	2.60E-01	TMEM182	transmembrane protein 182	chr2q12.1	1553301_a_at	NM_144632
3.88	4.40	0.52	2.14E-02	2.60E-01	NAV1	neuron navigator 1	chr1q32.3	224773_at	NM_020443
1.81	2.07	0.26	2.14E-02	2.61E-01	---	---	---	216319_at	---
3.58	4.27	0.69	2.14E-02	2.61E-01	---	---	---	241722_x_at	---
2.45	2.94	0.49	2.15E-02	2.61E-01	SFRS2B	Splicing factor, arginine/serine-rich 2B	chr11q22	229471_s_at	NM_032102
6.03	7.51	1.48	2.15E-02	2.61E-01	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	chr8q11.23	232382_s_at	NM_052937
4.09	5.38	1.29	2.15E-02	2.61E-01	RASEF	RAS and EF-hand domain containing	chr9q21.32	1553185_at	NM_152573
2.85	3.97	1.13	2.16E-02	2.61E-01	COL3A1	Collagen, type III, alpha 1	chr2q31	232458_at	NM_000090
5.21	6.24	1.02	2.15E-02	2.61E-01	WDR32	WD repeat domain 32	chr9p13.2	219001_s_at	NM_024345
4.18	4.80	0.62	2.15E-02	2.61E-01	CCDC13	coiled-coil domain containing 13	chr3p22.1	1553396_a_at	NM_144719
3.59	4.08	0.50	2.16E-02	2.61E-01	MAML3	mastermind-like 3 (Drosophila)	chr4q28	207946_at	NM_018717
3.28	3.70	0.42	2.16E-02	2.61E-01	---	---	---	235894_at	---
4.37	4.79	0.42	2.16E-02	2.61E-01	REG3A /// REG3G	regenerating islet-derived 3 alpha /// regenerating islet-derived 3 gamma	chr2p12	234280_at	NM_001008387 /// NM_002580 /// NM_138937 /// NM_138938 /// NM_198448
3.15	3.54	0.39	2.16E-02	2.61E-01	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	chr9q22.2	1554053_at	NM_006415 /// NM_178324
3.59	3.96	0.37	2.16E-02	2.61E-01	NAV2	neuron navigator 2	chr11p15.1	222598_s_at	NM_001111018 /// NM_001111019 /// NM_145117 /// NM_182964
4.65	5.03	0.37	2.16E-02	2.61E-01	SLAMF9	SLAM family member 9	chr1q23.2	1553770_a_at	NM_033438
2.68	3.02	0.34	2.15E-02	2.61E-01	---	---	---	242616_at	---
2.31	2.63	0.33	2.16E-02	2.61E-01	---	---	---	220582_at	---
2.13	2.44	0.31	2.15E-02	2.61E-01	---	---	---	234223_at	---
1.93	2.20	0.27	2.16E-02	2.61E-01	---	---	---	231308_at	---
2.78	3.43	0.65	2.17E-02	2.61E-01	ALPL	alkaline phosphatase, liver/bone/kidney	chr1p36.12	1557924_s_at	NM_000478 /// NM_001127501
1.87	2.32	0.45	2.17E-02	2.61E-01	LOC644135	hypothetical LOC644135	chr6q23.3	1559124_at	XR_039968

6.40	6.98	0.58	2.17E-02	2.62E-01	PDIA2	protein disulfide isomerase family A, member 2	chr16p13.3	206889_at	NM_006849
2.49	2.97	0.48	2.17E-02	2.62E-01	---	---	---	217570_x_at	---
4.18	4.65	0.47	2.17E-02	2.62E-01	PDZD7	PDZ domain containing 7	chr10q24.31	220555_s_at	NM_024895
2.98	3.40	0.42	2.17E-02	2.62E-01	LOC220594	TL132 protein	chr17p11.2	1559324_at	NR_003554
2.11	2.41	0.29	2.17E-02	2.62E-01	---	---	---	238236_at	---
2.11	2.37	0.26	2.17E-02	2.62E-01	---	---	---	240522_at	---
5.81	6.08	0.27	2.17E-02	2.62E-01	ALPK1	alpha-kinase 1	chr4q25	207133_x_at	NM_001102406 /// NM_025144
2.93	3.30	0.38	2.18E-02	2.62E-01	---	---	---	215630_at	---
3.29	4.49	1.19	2.18E-02	2.62E-01	C6orf142	chromosome 6 open reading frame 142	chr6p12.1	235377_at	NM_138569
4.03	4.65	0.62	2.18E-02	2.62E-01	TNRC6B	trinucleotide repeat containing 6B	chr22q13.1	238468_at	NM_001024843 /// NM_015088
2.39	2.96	0.57	2.18E-02	2.62E-01	LOC728485	hypothetical protein LOC728485	chr19q13.12	242070_at	XR_041661 /// XR_041662 /// XR_041663
2.90	3.38	0.48	2.18E-02	2.62E-01	RNF151	ring finger protein 151	chr16p13.3	236689_at	NM_174903
6.24	6.63	0.39	2.19E-02	2.62E-01	ALS2CL	ALS2 C-terminal like	chr3p21.31	222333_at	NM_147129 /// NM_182775
2.83	3.20	0.37	2.19E-02	2.62E-01	SCML4	sex comb on midleg-like 4 (Drosophila)	chr6q21	1556472_s_at	NM_198081
3.81	4.17	0.36	2.19E-02	2.62E-01	---	---	---	215874_at	---
2.46	2.80	0.34	2.18E-02	2.62E-01	DENND1B	DENN/MADD domain containing 1B	chr1q31.3	1564164_at	NM_019049 /// NM_144977
2.04	2.33	0.29	2.18E-02	2.62E-01	---	---	---	244545_at	---
3.45	3.89	0.44	2.19E-02	2.62E-01	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	chr2q33.3	1553190_s_at	NM_057177 /// NM_152526 /// NM_205863
3.46	3.77	0.31	2.19E-02	2.62E-01	---	---	---	229917_at	---
3.60	4.72	1.13	2.19E-02	2.62E-01	FLJ21272	hypothetical protein FLJ21272	chr1q21.1	220467_at	XR_040830 /// XR_040831 /// XR_040832
1.87	2.29	0.42	2.19E-02	2.62E-01	PTPRR	protein tyrosine phosphatase, receptor type, R	chr12q15	210675_s_at	NM_002849 /// NM_130846
1.86	2.19	0.33	2.19E-02	2.62E-01	---	---	---	1560107_at	---
3.55	4.55	1.01	2.19E-02	2.62E-01	EHBP1	EH domain binding protein 1	chr2p15	212650_at	NM_015252
6.79	7.38	0.59	2.20E-02	2.63E-01	PWWP2B	PWWP domain containing 2B	chr10q26.3	238051_x_at	NM_001098637 /// NM_138499
3.24	3.61	0.38	2.20E-02	2.63E-01	NAV2	neuron navigator 2	chr11p15.1	222599_s_at	NM_001111018 /// NM_001111019 /// NM_145117 /// NM_182964
3.85	4.21	0.36	2.20E-02	2.63E-01	DNAH5	dynein, axonemal, heavy chain 5	chr5p15.2	232381_s_at	NM_001369
3.96	4.43	0.47	2.20E-02	2.63E-01	TNRC6B	trinucleotide repeat containing 6B	chr22q13.1	228998_at	NM_001024843 /// NM_015088
2.47	2.82	0.36	2.20E-02	2.63E-01	KCNK6	potassium channel, subfamily K, member 6	chr19q13.1	223658_at	NM_004823
4.71	5.06	0.35	2.20E-02	2.63E-01	ZBTB7B	zinc finger and BTB domain containing 7B	chr1q21.3	205853_at	NM_015872
2.88	3.39	0.51	2.21E-02	2.63E-01	NT5E	5'-nucleotidase, ecto (CD73)	chr6q14-q21	227486_at	NM_002526
1.79	2.13	0.34	2.21E-02	2.63E-01	---	---	---	241856_at	---
7.90	9.07	1.17	2.21E-02	2.63E-01	TNPO1	transportin 1	chr5q13.2	207657_x_at	NM_002270 /// NM_153188
4.40	4.94	0.54	2.21E-02	2.63E-01	PROCA1	proline-rich cyclin A1-interacting protein	chr17q11.2	236286_at	NM_152465
3.92	4.38	0.45	2.21E-02	2.63E-01	RASA3	RAS p21 protein activator 3	chr13q34	206220_s_at	NM_007368
2.62	2.97	0.35	2.21E-02	2.63E-01	MBP	Myelin basic protein	chr18q23	236324_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385
3.39	3.94	0.55	2.22E-02	2.63E-01	RTN4R	reticulon 4 receptor	chr22q11.21	228550_at	NM_023004
6.11	6.56	0.45	2.22E-02	2.63E-01	CARD10	caspase recruitment domain family, member 10	chr22q13.1	210025_s_at	NM_014550
3.58	4.84	1.25	2.22E-02	2.63E-01	LOC728264	Hypothetical protein LOC728264	chr5q33.1	1558828_s_at	XR_041006 /// XR_041007 /// XR_041008
3.49	4.08	0.59	2.22E-02	2.63E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	211908_x_at	---
4.24	4.78	0.54	2.22E-02	2.63E-01	LOC100134089	similar to protein phosphatase 2 (formerly 2A), regulatory subunit B, beta	---	1566630_at	XR_038350
3.90	4.38	0.48	2.23E-02	2.63E-01	CCDC69	Coiled-coil domain containing 69	chr5q33.1	242430_at	NM_015621

2.56	3.01	0.45	2.23E-02	2.63E-01	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	chr1q25.2	220338_at	NM_018037 /// NM_152663
2.41	2.86	0.44	2.23E-02	2.63E-01	---	---	---	217536_x_at	---
3.23	3.82	0.59	2.23E-02	2.63E-01	TPD52	tumor protein D52	chr8q21	201690_s_at	NM_001025252 /// NM_001025253 /// NM_005079
4.63	5.16	0.53	2.23E-02	2.64E-01	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	chr13q12-q14	212292_at	NM_003045
2.35	2.84	0.50	2.23E-02	2.64E-01	LIN7A	lin-7 homolog A (C. elegans)	chr12q21	206440_at	NM_004664
2.83	3.21	0.37	2.23E-02	2.64E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	207046_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054
2.09	2.44	0.35	2.23E-02	2.64E-01	---	---	---	215298_at	---
3.75	4.16	0.41	2.24E-02	2.64E-01	STX7	syntaxin 7	chr6q23.1	203457_at	NM_003569
6.10	7.00	0.90	2.24E-02	2.64E-01	TMTC1	transmembrane and tetratricopeptide repeat containing 1	chr12p11.22	226931_at	NM_175861
2.99	3.55	0.56	2.24E-02	2.64E-01	ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	chr12p13-p12	207220_at	NM_021071
2.44	2.83	0.39	2.24E-02	2.64E-01	---	---	---	241161_at	---
8.45	9.18	0.73	2.25E-02	2.64E-01	FADS1 /// FADS3	fatty acid desaturase 1 /// fatty acid desaturase 3	chr11q12-q13.1 /// chr11q12.2-q13.1	208962_s_at	NM_013402 /// NM_021727
4.72	5.31	0.58	2.25E-02	2.64E-01	PCSK6	proprotein convertase subtilisin/kexin type 6	chr15q26.3	211263_s_at	NM_002570 /// NM_138319 /// NM_138320 /// NM_138321 /// NM_138322 /// NM_138323 /// NM_138324 /// NM_138325
2.85	3.41	0.56	2.25E-02	2.64E-01	---	---	---	1563596_at	---
5.38	5.83	0.45	2.24E-02	2.64E-01	DKKL1	dickkopf-like 1 (soggy)	chr19q13.33	220284_at	NM_014419
2.62	3.07	0.45	2.25E-02	2.64E-01	LEPR	leptin receptor	chr1p31	211356_x_at	NM_001003679 /// NM_001003680 /// NM_002303
2.94	3.36	0.43	2.25E-02	2.64E-01	---	---	---	232064_at	---
3.53	3.92	0.39	2.25E-02	2.64E-01	---	---	---	233816_at	---
1.97	2.25	0.28	2.25E-02	2.64E-01	MEOX2	mesenchyme homeobox 2	chr7p22.1-p21.3	206201_s_at	NM_005924
7.48	8.93	1.45	2.25E-02	2.64E-01	PTGDS	prostaglandin D2 synthase 21kDa (brain)	chr9q34.2-q34.3	212187_x_at	NM_000954
5.49	6.41	0.92	2.25E-02	2.64E-01	FOXP1	forkhead box P1	chr3p14.1	223287_s_at	NM_001012505 /// NM_032682
3.53	4.12	0.59	2.25E-02	2.64E-01	---	---	---	1561181_at	---
2.60	2.95	0.35	2.25E-02	2.64E-01	INO80D	INO80 complex subunit D	chr2q33.3	243070_at	NM_017759
2.88	3.24	0.36	2.26E-02	2.64E-01	PTPRA	Protein tyrosine phosphatase, receptor type, A	chr20p13	239419_at	NM_002836 /// NM_080840 /// NM_080841
2.88	3.23	0.35	2.26E-02	2.64E-01	---	---	---	238531_x_at	---
2.40	2.88	0.48	2.26E-02	2.65E-01	---	---	---	215525_at	---
1.99	2.36	0.38	2.26E-02	2.65E-01	---	---	---	1554636_at	---
5.06	5.65	0.59	2.26E-02	2.65E-01	---	---	---	230980_x_at	---
3.28	4.02	0.74	2.27E-02	2.65E-01	DPYS	dihydropyrimidinase	chr8q22	206065_s_at	NM_001385

5.11	5.68	0.58	2.27E-02	2.65E-01	CALD1	Caldesmon 1	chr7q33	235834_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
2.35	2.68	0.34	2.27E-02	2.65E-01	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	chr12p12.2-p11.2	224204_x_at	NM_020183
5.91	6.29	0.38	2.27E-02	2.65E-01	CEND1	cell cycle exit and neuronal differentiation 1	chr11p15.5	219591_at	NM_016564
5.68	6.03	0.35	2.27E-02	2.65E-01	---	---	---	202881_x_at	---
4.50	4.89	0.39	2.27E-02	2.65E-01	---	---	---	240321_at	---
4.78	5.73	0.95	2.28E-02	2.65E-01	MBP	myelin basic protein	chr18q23	210136_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385
2.53	2.87	0.34	2.28E-02	2.65E-01	ZNF382	zinc finger protein 382	chr19q13.12	1561687_a_at	NM_032825
6.65	7.21	0.56	2.28E-02	2.65E-01	SRCRB4D	scavenger receptor cysteine rich domain containing, group B (4 domains)	chr7q11.23	236529_at	NM_080744
2.05	2.36	0.32	2.28E-02	2.66E-01	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	chr5q12	220866_at	NM_197941
3.61	4.01	0.40	2.28E-02	2.66E-01	---	---	---	1566136_at	---
2.87	3.22	0.36	2.28E-02	2.66E-01	CDT1	chromatin licensing and DNA replication factor 1	chr16q24.3	209832_s_at	NM_030928
13.42	13.71	0.29	2.28E-02	2.66E-01	IQWD1 /// ND4 /// UNC5B	IQ motif and WD repeats 1 /// NADH dehydrogenase, subunit 4 (complex I) /// unc-5 homolog B (C. elegans)	chr10q22.1 /// chr1q24.2	224372_at	NM_001017977 /// NM_018442 /// NM_170744
2.59	3.05	0.46	2.29E-02	2.66E-01	---	---	---	243902_at	---
3.67	4.04	0.37	2.29E-02	2.66E-01	---	---	---	236643_s_at	---
2.81	3.13	0.32	2.29E-02	2.66E-01	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	chr15q11.2-q12	205850_s_at	NM_000814 /// NM_021912
3.58	4.01	0.43	2.29E-02	2.66E-01	---	---	---	242011_at	---
5.59	6.21	0.62	2.29E-02	2.66E-01	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	chr16p12-p11.2	222817_at	NM_025193
2.24	2.59	0.34	2.29E-02	2.66E-01	ZNF148	zinc finger protein 148	chr3q21	235166_at	NM_021964
1.87	2.19	0.32	2.29E-02	2.66E-01	---	---	---	240821_at	---
6.57	6.97	0.41	2.30E-02	2.67E-01	---	---	---	240919_at	---
2.09	2.50	0.41	2.30E-02	2.67E-01	---	---	---	243043_at	---
2.78	3.09	0.31	2.30E-02	2.67E-01	SYNPO2	synaptopodin 2	chr4q26	244108_at	NM_001128933 /// NM_001128934 /// NM_133477
2.47	2.92	0.45	2.31E-02	2.67E-01	---	---	---	1556306_at	---
4.09	4.44	0.35	2.31E-02	2.67E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	209639_s_at	NM_002926 /// NM_198227 /// NM_198229
3.31	3.62	0.31	2.31E-02	2.67E-01	TIFAB	TRAF-interacting protein with forkhead-associated domain, family member B	chr5q31.1	236673_at	NM_001099221
5.02	5.97	0.95	2.31E-02	2.67E-01	BHMT2	betaine-homocysteine methyltransferase 2	chr5q13	219902_at	NM_017614
2.53	3.07	0.54	2.31E-02	2.68E-01	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	chr16q22.1	239286_at	NM_001797
3.73	4.13	0.40	2.31E-02	2.68E-01	FBN3	fibrillin 3	chr19p13	240117_at	NM_032447
7.40	7.79	0.39	2.31E-02	2.68E-01	LMNA	Lamin A/C	chr1q21.2-q21.3	214213_x_at	NM_005572 /// NM_170707 /// NM_170708
5.60	6.02	0.42	2.32E-02	2.68E-01	---	---	---	235279_at	---
4.27	5.03	0.76	2.32E-02	2.68E-01	---	---	---	232975_at	---
5.25	6.73	1.49	2.32E-02	2.68E-01	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	chr5q13.1	212240_s_at	NM_181504 /// NM_181523 /// NM_181524
4.62	5.02	0.41	2.32E-02	2.68E-01	---	---	---	234788_x_at	---
2.12	2.60	0.48	2.32E-02	2.68E-01	---	---	---	242244_at	---
7.48	7.81	0.33	2.32E-02	2.68E-01	---	---	---	216524_x_at	---
6.14	7.09	0.94	2.33E-02	2.68E-01	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	chr9q31-q32	220161_s_at	NM_018424 /// NM_019114
5.34	5.83	0.49	2.33E-02	2.68E-01	LOC100128862	Hypothetical protein LOC100128862	chr16q24.3	1558728_at	XM_001714089 /// XM_001714383
3.74	4.13	0.40	2.33E-02	2.68E-01	RNFT2	ring finger protein, transmembrane 2	chr12q24.22	221909_at	NM_001109903 /// NM_032814

1.90	2.16	0.26	2.33E-02	2.68E-01	DSC3	desmocollin 3	chr18q12.1	206032_at	NM_001941 /// NM_024423
4.35	5.65	1.31	2.33E-02	2.68E-01	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	chr2q24.2	223519_at	NM_016653 /// NM_133646
3.57	4.29	0.73	2.33E-02	2.68E-01	---	---	---	1552829_at	---
2.66	3.09	0.43	2.34E-02	2.68E-01	---	---	---	235561_at	---
5.94	6.32	0.38	2.34E-02	2.68E-01	RHBDD3	rhomboid domain containing 3	chr22q12.1-q12.2	217622_at	NM_012265
2.33	2.66	0.33	2.34E-02	2.68E-01	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	chr21q22.1|21q22.11	217445_s_at	NM_000819 /// NM_175085
2.96	3.31	0.35	2.34E-02	2.68E-01	CCKAR	cholecystokinin A receptor	chr4p15.1-p15.2	211173_at	NM_000730
5.06	5.76	0.70	2.35E-02	2.69E-01	C5orf30	chromosome 5 open reading frame 30	chr5q21.1	221823_at	NM_033211
5.33	5.65	0.31	2.35E-02	2.69E-01	---	---	---	232186_at	---
2.30	3.04	0.74	2.35E-02	2.69E-01	GATA5	GATA binding protein 5	chr20q13.33	238197_at	NM_080473
5.82	6.39	0.57	2.35E-02	2.69E-01	CD79A	CD79a molecule, immunoglobulin-associated alpha	chr19q13.2	205049_s_at	NM_001783 /// NM_021601
2.51	3.00	0.49	2.35E-02	2.69E-01	---	---	---	227318_at	---
3.47	3.88	0.41	2.35E-02	2.69E-01	LOC645757	hypothetical LOC645757	chr1p32.1	236176_at	XM_001718638 /// XM_001719181 /// XM_933122
2.82	3.17	0.35	2.35E-02	2.69E-01	VWA1	von Willebrand factor A domain containing 1	chr1p36.33	222724_at	NM_022834 /// NM_199121
2.93	3.25	0.32	2.35E-02	2.69E-01	---	---	---	1563274_at	---
2.33	2.63	0.30	2.35E-02	2.69E-01	KIAA1267	KIAA1267	chr17q21.31	224489_at	NM_015443
4.43	5.11	0.67	2.36E-02	2.69E-01	KIAA1128	KIAA1128	chr10q23.1	209379_s_at	NM_018999
7.02	7.69	0.67	2.35E-02	2.69E-01	PROSC	proline synthetase co-transcribed homolog (bacterial)	chr8p11.2	209384_at	NM_007198
2.03	2.52	0.49	2.36E-02	2.69E-01	ENPEP	glutamyl aminopeptidase (aminopeptidase A)	chr4q25	204845_s_at	NM_001977
6.53	7.07	0.54	2.36E-02	2.69E-01	PLA2G4F	phospholipase A2, group IVF	chr15q15.1	235958_at	NM_213600
2.24	2.60	0.36	2.36E-02	2.69E-01	PRND	prion protein 2 (dublet)	chr20pter-p12	222106_at	NM_012409
2.62	2.94	0.31	2.36E-02	2.69E-01	---	---	---	229048_at	---
2.97	3.47	0.50	2.36E-02	2.69E-01	STX17	syntaxin 17	chr9q31.1	226655_at	NM_017919
2.98	3.47	0.49	2.37E-02	2.69E-01	PRB4 /// PRH1 /// PRH2	proline-rich protein BstNI subfamily 4 /// proline-rich protein HaeIII subfamily 1 /// proline-rich protein HaeIII subfamily 2	chr12p13.2	243389_at	NM_001110213 /// NM_002723 /// NM_005042 /// NM_006250
2.74	3.19	0.44	2.37E-02	2.69E-01	---	---	---	242413_at	---
2.22	2.56	0.34	2.36E-02	2.69E-01	---	---	---	236412_at	---
2.94	3.52	0.57	2.37E-02	2.69E-01	---	---	---	238317_x_at	---
2.39	3.02	0.63	2.37E-02	2.69E-01	PDZD2	PDZ domain containing 2	chr5p13.3	209493_at	NM_178140
2.52	2.88	0.36	2.37E-02	2.69E-01	---	---	---	232344_at	---
6.54	8.36	1.83	2.37E-02	2.70E-01	TMEM97	transmembrane protein 97	chr17q11.2	212281_s_at	NM_014573
4.45	4.87	0.42	2.37E-02	2.70E-01	CALU	Calumenin	chr7q32.1	238908_at	NM_001130674 /// NM_001219
3.55	4.06	0.51	2.37E-02	2.70E-01	---	---	---	226139_at	---
4.27	4.61	0.35	2.37E-02	2.70E-01	HARBI1	harbinger transposase derived 1	chr11p11.2	241498_at	NM_173811
4.52	4.90	0.39	2.38E-02	2.70E-01	P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	chr12q24.33	224557_x_at	NM_012226 /// NM_016318 /// NM_170682 /// NM_170683 /// NM_174872 /// NM_174873
4.77	5.10	0.33	2.38E-02	2.70E-01	---	---	---	240792_at	---
7.11	7.99	0.88	2.38E-02	2.70E-01	TNPO1	transportin 1	chr5q13.2	209225_x_at	NM_002270 /// NM_153188
2.38	2.78	0.40	2.38E-02	2.70E-01	PDCD1LG2	programmed cell death 1 ligand 2	chr9p24.2	224399_at	NM_025239
1.86	2.11	0.25	2.38E-02	2.70E-01	LOC441208	hypothetical gene supported by AK094370	chr7p14.3	1556404_a_at	NR_003502
3.38	4.30	0.92	2.38E-02	2.70E-01	ZNF117	zinc finger protein 117	chr7q11.21	207605_x_at	NM_015852
3.45	4.04	0.59	2.38E-02	2.70E-01	---	---	---	230321_at	---
2.28	2.78	0.51	2.38E-02	2.70E-01	ONECUT2	one cut homeobox 2	chr18q21.1-q21.2	233446_at	NM_004852
2.40	2.71	0.30	2.38E-02	2.70E-01	NLRC4	NLR family, CARD domain containing 4	chr2p22-p21	1552554_a_at	NM_021209
2.35	2.88	0.53	2.39E-02	2.70E-01	MGC24103	hypothetical protein MGC24103	chr9p22.3	232568_at	XR_041890 /// XR_041891 /// XR_041892
2.88	3.18	0.30	2.39E-02	2.70E-01	FOXP2	forkhead box P2	chr7q31	1552902_a_at	NM_014491 /// NM_148898 /// NM_148899
1.92	2.21	0.29	2.39E-02	2.70E-01	C9orf14	Chromosome 9 open reading frame 14	chr9p21	1559292_s_at	XM_376821 /// XM_938938
2.38	2.75	0.37	2.39E-02	2.70E-01	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	chr12q13	241866_at	NM_004731

3.09	3.50	0.41	2.39E-02	2.70E-01	CST1	cystatin SN	chr20p11.21	206224_at	NM_001898
5.14	5.74	0.59	2.39E-02	2.70E-01	TLN2	talin 2	chr15q15-q21	212703_at	NM_015059
2.66	3.24	0.58	2.39E-02	2.70E-01	---	---	---	239519_at	---
3.83	4.45	0.63	2.40E-02	2.71E-01	GP1BB /// SEPT5	glycoprotein Ib (platelet), beta polypeptide /// septin 5	chr22q11.21 /// chr22q11.21-q11.23|22q11.21	206655_s_at	NM_000407 /// NM_002688
6.40	7.03	0.63	2.40E-02	2.71E-01	GOLPH3L	golgi phosphoprotein 3-like	chr1q21.2	218361_at	NM_018178
3.35	4.19	0.84	2.40E-02	2.71E-01	MACROD2	MACRO domain containing 2	chr20p12.1	235278_at	NM_001033087 /// NM_080676
3.21	3.57	0.36	2.40E-02	2.71E-01	EML2	echinoderm microtubule associated protein like 2	chr19q13.32	204397_at	NM_012155
5.97	6.52	0.54	2.41E-02	2.71E-01	---	---	---	232592_at	---
2.22	2.57	0.35	2.41E-02	2.71E-01	---	---	---	244637_at	---
8.27	9.10	0.83	2.41E-02	2.71E-01	FDFT1	farnesyl-diphosphate farnesyltransferase 1	chr8p23.1-p22	208647_at	NM_004462
2.68	3.24	0.56	2.41E-02	2.71E-01	---	---	---	1562467_at	---
2.33	2.82	0.49	2.41E-02	2.71E-01	---	---	---	240725_at	---
5.00	5.47	0.46	2.41E-02	2.71E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	227039_at	NM_006738 /// NM_007200 /// NM_144767
2.00	2.43	0.42	2.41E-02	2.71E-01	C1orf180	chromosome 1 open reading frame 180	chr1p22.3	1563743_at	NM_001033660
2.84	3.22	0.37	2.41E-02	2.71E-01	SHD	Src homology 2 domain containing transforming protein D	chr19p13.3	227845_s_at	NM_020209
3.76	4.12	0.36	2.41E-02	2.71E-01	ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	chr9q34.1-q34.2	216716_at	NM_020469
2.05	2.41	0.36	2.41E-02	2.71E-01	WDR78	WD repeat domain 78	chr1p31.3	220769_s_at	NM_024763 /// NM_207014
1.78	2.09	0.30	2.41E-02	2.71E-01	ZNF271	zinc finger protein 271	chr18q12	236231_at	NM_001112663 /// NM_006629
1.88	2.14	0.25	2.41E-02	2.71E-01	RSU1	Ras suppressor protein 1	chr10p13	1569543_at	NM_012425 /// NM_152724
1.93	2.24	0.31	2.42E-02	2.71E-01	KRT25	keratin 25	chr17q21.2	237905_at	NM_181534
3.70	4.16	0.46	2.42E-02	2.71E-01	---	---	---	238242_at	---
2.59	3.02	0.44	2.42E-02	2.71E-01	EIF3B	eukaryotic translation initiation factor 3, subunit B	chr7p22.2	237457_at	NM_001037283 /// NM_003751
2.44	2.83	0.39	2.42E-02	2.71E-01	41524	Septin 7	chr7p14.3-p14.1	244508_at	NM_001011553 /// NM_001788
2.02	2.28	0.27	2.42E-02	2.71E-01	---	---	---	1562023_at	---
3.10	3.53	0.43	2.43E-02	2.71E-01	---	---	---	237026_at	---
2.61	3.01	0.40	2.43E-02	2.72E-01	PCDHA9	protocadherin alpha 9	chr5q31	208205_at	NM_014005 /// NM_031857
1.98	2.34	0.37	2.43E-02	2.72E-01	KCNIP2	Kv channel interacting protein 2	chr10q24	224528_s_at	NM_014591 /// NM_173191 /// NM_173192 /// NM_173193 /// NM_173194 /// NM_173195 /// NM_173197
2.30	2.83	0.53	2.43E-02	2.72E-01	LINGO1	leucine rich repeat and Ig domain containing 1	chr15q24.3	227933_at	NM_032808
5.32	5.82	0.51	2.44E-02	2.72E-01	---	---	---	241010_x_at	---
2.13	2.51	0.38	2.44E-02	2.72E-01	NRP1	Neuropilin 1	chr10p12	1561365_at	NM_001024628 /// NM_001024629 /// NM_003873
2.29	2.54	0.25	2.44E-02	2.72E-01	FAM38B	Family with sequence similarity 38, member B	chr18p11.22	1565774_at	NM_022068
5.16	5.75	0.59	2.45E-02	2.73E-01	---	---	---	243074_at	---
4.36	4.74	0.38	2.45E-02	2.73E-01	CLDN14	claudin 14	chr21q22.3	210689_at	NM_012130 /// NM_144492
6.00	6.37	0.36	2.45E-02	2.73E-01	SDK2	sidekick homolog 2 (chicken)	chr17q25.1	220628_s_at	NM_019064
1.85	2.14	0.30	2.45E-02	2.73E-01	---	---	---	1567059_at	---
6.32	6.86	0.53	2.45E-02	2.73E-01	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	chr6q23.3	227287_at	NM_006079
5.70	6.87	1.17	2.46E-02	2.73E-01	CPE	carboxypeptidase E	chr4q32.3	201116_s_at	NM_001873
6.77	7.55	0.78	2.46E-02	2.73E-01	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	chr17p13.3	202224_at	NM_005206 /// NM_016823
1.92	2.31	0.39	2.46E-02	2.73E-01	ACVR1C	activin A receptor, type IC	chr2q24.1	1563182_at	NM_001111031 /// NM_001111032 /// NM_001111033 /// NM_145259
2.49	2.83	0.34	2.46E-02	2.73E-01	---	---	---	236511_at	---

3.50	3.82	0.32	2.46E-02	2.73E-01	F11R	F11 receptor	chr1q21.2-q21.3	222354_at	NM_016946 /// NM_144503
2.00	2.40	0.39	2.46E-02	2.73E-01	---	---	---	241780_at	---
8.76	9.81	1.05	2.46E-02	2.73E-01	RAB31	RAB31, member RAS oncogene family	chr18p11.3	217764_s_at	NM_006868
4.97	5.81	0.84	2.46E-02	2.73E-01	EIF2C3	eukaryotic translation initiation factor 2C, 3	chr1p34.3	219426_at	NM_024852 /// NM_177422
6.62	7.27	0.65	2.46E-02	2.73E-01	NFIA	nuclear factor I/A	chr1p31.3-p31.2	224975_at	NM_001134673 /// NM_005595
4.59	5.23	0.65	2.46E-02	2.73E-01	PARP11	poly (ADP-ribose) polymerase family, member 11	chr12p13.3	229138_at	NM_020367
3.81	4.45	0.64	2.47E-02	2.73E-01	CTTNBP2NL	CTTNBP2 N-terminal like	chr1p13.2	231822_at	NM_018704
1.98	2.34	0.36	2.47E-02	2.73E-01	---	---	---	1556903_at	---
3.55	3.86	0.31	2.47E-02	2.73E-01	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	chr3p25.3	232869_at	NM_001033117 /// NM_014850
2.66	2.96	0.31	2.46E-02	2.73E-01	TPRG1	tumor protein p63 regulated 1	chr3q28	229764_at	NM_198485
2.87	3.65	0.78	2.47E-02	2.73E-01	FGF7 /// KGFLP1 /// KGFLP2	fibroblast growth factor 7 (keratinocyte growth factor) /// keratinocyte growth factor-like protein 1 /// keratinocyte growth factor-like protein 2	chr15q15-q21.1 /// chr9p11.2 /// chr9p12	1554741_s_at	NM_002009 /// NR_003670 /// NR_003674
5.76	6.79	1.03	2.47E-02	2.73E-01	TPM1	tropomyosin 1 (alpha)	chr15q22.1	206116_s_at	NM_000366 /// NM_001018004 /// NM_001018005 /// NM_001018006 /// NM_001018007 /// NM_001018008 /// NM_001018020
3.76	4.34	0.58	2.47E-02	2.73E-01	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	chr14q23.1	235344_at	NM_021003 /// NM_177951 /// NM_177952
3.85	4.41	0.57	2.47E-02	2.73E-01	HSPA1L	Heat shock 70kDa protein 1-like	chr6p21.3	233694_at	NM_005527
6.35	6.85	0.49	2.47E-02	2.73E-01	FAM84A	Family with sequence similarity 84, member A	chr2p24.3	228319_at	NM_145175
3.87	4.61	0.74	2.48E-02	2.73E-01	ZFP82	zinc finger protein 82 homolog (mouse)	chr19q13.12	1555793_a_at	NM_133466
2.30	2.62	0.32	2.47E-02	2.73E-01	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	chr4q32.1	238176_at	NM_014247
2.10	2.41	0.31	2.48E-02	2.73E-01	---	---	---	240645_at	---
4.70	5.25	0.55	2.48E-02	2.74E-01	SEC14L2	SEC14-like 2 (S. cerevisiae)	chr22q12.2	232895_s_at	NM_012429
6.90	7.85	0.95	2.48E-02	2.74E-01	ZYG11B	zyg-11 homolog B (C. elegans)	chr1p32.3	225350_s_at	NM_024646
2.52	3.05	0.53	2.48E-02	2.74E-01	---	---	---	238861_at	---
2.98	3.40	0.42	2.48E-02	2.74E-01	---	---	---	230476_at	---
2.86	3.23	0.36	2.48E-02	2.74E-01	LOC100134025 /// SPEF2	hypothetical protein LOC100134025 /// sperm flagellar 2	chr5p13.2	1552716_at	NM_024867 /// NM_144722 /// XM_001713757
6.64	7.30	0.66	2.49E-02	2.74E-01	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	chr11p15.1	207180_s_at	NM_001098520 /// NM_001098521 /// NM_001098522 /// NM_001098523 /// NM_006410
6.48	7.30	0.82	2.49E-02	2.74E-01	EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	chr1p34.1	218488_at	NM_020365
2.61	3.18	0.57	2.49E-02	2.74E-01	ZNF271	zinc finger protein 271	chr18q12	238007_at	NM_001112663 /// NM_006629
4.62	5.04	0.41	2.49E-02	2.74E-01	UBXN10	UBX domain protein 10	chr1p36.12	230092_at	NM_152376
5.10	5.49	0.39	2.49E-02	2.74E-01	DCDC2B	doublecortin domain containing 2B	chr1p35.1	233918_at	NM_001099434
4.22	4.59	0.37	2.49E-02	2.74E-01	FAM69B	family with sequence similarity 69, member B	chr9q34.3	227652_at	NM_152421
2.48	2.82	0.34	2.49E-02	2.74E-01	---	---	---	1569849_at	---
2.18	2.50	0.31	2.50E-02	2.74E-01	---	---	---	237141_x_at	---
3.01	3.70	0.68	2.50E-02	2.74E-01	---	---	---	230892_at	---
5.71	6.26	0.55	2.50E-02	2.74E-01	IQCC	IQ motif containing C	chr1p36.11-p34.2	206650_at	NM_018134
2.47	2.85	0.38	2.50E-02	2.74E-01	C1orf211	chromosome 1 open reading frame 211	chr1p36.31	1553741_at	XR_040929 /// XR_040930 /// XR_040931
6.09	6.52	0.43	2.51E-02	2.74E-01	MAP2K7	mitogen-activated protein kinase kinase 7	chr19p13.3-p13.2	226023_at	NM_145185
2.56	2.97	0.41	2.51E-02	2.74E-01	---	---	---	1566427_at	---

2.12	2.43	0.31	2.51E-02	2.74E-01	---	---	---	236943_at	---
3.39	4.06	0.67	2.51E-02	2.74E-01	PRIM1	primase, DNA, polypeptide 1 (49kDa)	chr12q13	205053_at	NM_000946
4.54	6.14	1.59	2.52E-02	2.75E-01	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	chr4p14	201387_s_at	NM_004181
6.94	8.24	1.30	2.53E-02	2.75E-01	RIMS2	regulating synaptic membrane exocytosis 2	chr8q22.3	206137_at	NM_001100117 /// NM_014677
5.54	6.50	0.96	2.53E-02	2.75E-01	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	chr6q21	202512_s_at	NM_004849
3.99	4.55	0.56	2.53E-02	2.75E-01	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	chr3p22.2	232704_s_at	NM_001134369 /// NM_006309 /// NM_017724
4.55	5.05	0.50	2.52E-02	2.75E-01	PCDHA10	protocadherin alpha 10	chr5q31	211867_s_at	NM_018901 /// NM_031859 /// NM_031860
4.26	4.74	0.48	2.52E-02	2.75E-01	CD79B	CD79b molecule, immunoglobulin-associated beta	chr17q23	205297_s_at	NM_000626 /// NM_001039933 /// NM_021602
3.09	3.56	0.47	2.52E-02	2.75E-01	LOC729070	Similar to hCG2030186	chr6q24.1	1555868_at	XM_001132470 /// XM_001133421 /// XM_001723282
3.19	3.65	0.46	2.53E-02	2.75E-01	---	---	---	242399_at	---
2.94	3.38	0.44	2.53E-02	2.75E-01	---	---	---	234748_x_at	---
4.02	4.46	0.43	2.53E-02	2.75E-01	LOC401317	hypothetical LOC401317	chr7p15.1	242329_at	XM_379479 /// XM_380095 /// XM_938320
2.94	3.37	0.42	2.53E-02	2.75E-01	SMA4	Glucuronidase, beta pseudogene	chr5q13	238446_at	---
2.81	3.20	0.39	2.53E-02	2.75E-01	YY2	YY2 transcription factor	chrXp22.2-p22.1	216531_at	NM_206923
2.67	3.04	0.38	2.53E-02	2.75E-01	PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	chr7p21-p11.2	231543_at	NM_032639
2.58	2.96	0.38	2.52E-02	2.75E-01	ACVR1B	activin A receptor, type IB	chr12q13	208218_s_at	NM_004302 /// NM_020327 /// NM_020328
2.75	3.11	0.36	2.52E-02	2.75E-01	---	---	---	232789_at	---
3.08	3.44	0.35	2.53E-02	2.75E-01	TM4SF5	transmembrane 4 L six family member 5	chr17p13.3	206242_at	NM_003963
3.28	3.62	0.34	2.53E-02	2.75E-01	C20orf26	chromosome 20 open reading frame 26	chr20p11.23	1554657_a_at	NM_015585
2.36	2.69	0.33	2.53E-02	2.75E-01	CDH18	cadherin 18, type 2	chr5p15.2-p15.1	206280_at	NM_004934
2.45	2.70	0.25	2.53E-02	2.75E-01	MAP2K5	Mitogen-activated protein kinase kinase 5	chr15q23	216765_at	NM_002757 /// NM_145160
5.25	5.80	0.55	2.53E-02	2.75E-01	KIAA0913	KIAA0913	chr10q22.2	216345_at	NM_015037
3.09	3.46	0.37	2.53E-02	2.75E-01	KIF5A	kinesin family member 5A	chr12q13.13	223933_at	NM_004984
3.97	5.02	1.05	2.54E-02	2.75E-01	ZFP90	zinc finger protein 90 homolog (mouse)	chr16q22.1	235698_at	NM_133458
2.75	3.10	0.36	2.54E-02	2.75E-01	SLC6A5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	chr11p15.2-p15.1	210810_s_at	NM_004211
3.22	3.50	0.28	2.55E-02	2.75E-01	---	---	---	240171_at	---
6.38	7.18	0.79	2.55E-02	2.75E-01	ORC3L	origin recognition complex, subunit 3-like (yeast)	chr6q14.3-q16.1	210028_s_at	NM_012381 /// NM_181837
2.49	3.23	0.74	2.55E-02	2.75E-01	---	---	---	229907_at	---
2.29	2.71	0.42	2.55E-02	2.75E-01	---	---	---	241484_x_at	---
4.47	4.85	0.38	2.55E-02	2.75E-01	PSG9	pregnancy specific beta-1-glycoprotein 9	chr19q13.2	210126_at	NM_002784
3.00	3.45	0.45	2.55E-02	2.76E-01	---	---	---	229301_at	---
1.86	2.13	0.27	2.55E-02	2.76E-01	MGC32805	hypothetical protein MGC32805	chr5q23.2	1554781_at	---
5.41	6.31	0.91	2.56E-02	2.76E-01	---	---	---	225880_at	---
3.96	4.43	0.46	2.56E-02	2.76E-01	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	chr7p22.2	215270_at	NM_001040167 /// NM_001040168
4.69	5.07	0.39	2.56E-02	2.76E-01	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	chr11p14-p13	222596_s_at	NM_018490
3.51	3.97	0.46	2.56E-02	2.76E-01	AP1M2	adaptor-related protein complex 1, mu 2 subunit	chr19p13.2	65517_at	NM_005498
3.90	4.28	0.37	2.57E-02	2.76E-01	---	---	---	236772_s_at	---
2.90	3.27	0.36	2.57E-02	2.77E-01	LOC154822	hypothetical LOC154822	chr7q36.3	1570376_at	---
5.90	6.76	0.86	2.57E-02	2.77E-01	CREB1	cAMP responsive element binding protein 1	chr2q34	225565_at	NM_004379 /// NM_134442
2.69	3.53	0.83	2.57E-02	2.77E-01	---	---	---	240146_at	---
3.16	3.94	0.78	2.57E-02	2.77E-01	C13orf31	chromosome 13 open reading frame 31	chr13q14.11	228937_at	NM_001128303 /// NM_153218
5.12	5.52	0.40	2.57E-02	2.77E-01	CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	chr19q13.2	208327_at	NM_000766

3.93	4.37	0.44	2.57E-02	2.77E-01	GSG1L	GSG1-like	chr16p11.2	236701_at	NM_001109763 /// NM_144675																					
6.58	7.10	0.51	2.58E-02	2.77E-01	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	chr2p24.3-p24.1	217837_s_at	NM_001005753 /// NM_016079																					
4.04	4.48	0.44	2.58E-02	2.77E-01	---	---	---	241849_at	---																					
2.77	3.08	0.31	2.58E-02	2.77E-01	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	chr10q26	229827_at	NM_001007793 /// NM_004725																					
2.14	2.50	0.35	2.58E-02	2.77E-01	---	---	---	229051_at	---																					
2.96	3.68	0.71	2.59E-02	2.77E-01	PPM1E	protein phosphatase 1E (PP2C domain containing)	chr17q22	205938_at	NM_014906																					
5.31	5.87	0.57	2.59E-02	2.77E-01	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	chr19p13.2	211901_s_at	NM_001111307 /// NM_001111308 /// NM_001111309 /// NM_006202																					
2.59	3.15	0.56	2.59E-02	2.77E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31 /// LOC100126583 /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant gamma 4 (G4m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical LOC100126583 /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	211638_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001724554 /// XM_941465																					
6.52	6.89	0.38	2.58E-02	2.77E-01	GRIK5	glutamate receptor, ionotropic, kainate 5	chr19q13.2	217509_x_at	NM_002088																					
2.02	2.48	0.46	2.59E-02	2.77E-01	LOC284100	Hypothetical protein LOC284100	chr17q12	240979_at	NM_001129906 /// XM_001716065 /// XM_001718301 /// XM_375443																					
3.26	3.94	0.68	2.59E-02	2.77E-01	---	---	---	243271_at	---																					
4.53	5.17	0.64	2.59E-02	2.77E-01	PEX3	peroxisomal biogenesis factor 3	chr6q24.2	203969_at	NM_003630																					
3.05	3.38	0.33	2.59E-02	2.77E-01	---	---	---	1563075_s_at	---																					
4.58	5.78	1.20	2.60E-02	2.77E-01	NBN	nibrin	chr8q21	202905_x_at	NM_001024688 /// NM_002485																					
4.47	5.52	1.05	2.60E-02	2.77E-01	ETFDH	electron-transferring-flavoprotein dehydrogenase	chr4q32-q35	205530_at	NM_004453																					
3.50	4.52	1.01	2.60E-02	2.77E-01	ZYG11B	zyg-11 homolog B (C. elegans)	chr1p32.3	227918_s_at	NM_024646																					
5.04	5.93	0.89	2.60E-02	2.77E-01	---	---	---	227533_at	---																					
3.82	4.67	0.85	2.60E-02	2.77E-01	TACC1	transforming, acidic coiled-coil containing protein 1	chr8p11	1554690_a_at	NM_001122824 /// NM_006283																					
4.94	5.58	0.64	2.60E-02	2.77E-01	LPIN1	lipin 1	chr2p25.1	212276_at	NM_145693																					
7.01	7.51	0.49	2.60E-02	2.77E-01	DUX4 /// LOC653548	double homeobox, 4 /// double homeobox, 4-like	chr4q35 /// chr4q35.2	216473_x_at	NM_033178 /// XM_928023																					
5.24	5.74	0.49	2.60E-02	2.77E-01	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	chr19p13.2-p13.1	206399_x_at	NM_000068 /// NM_001127221 /// NM_001127222 /// NM_023035																					
6.59	7.04	0.45	2.59E-02	2.77E-01	POU2F2	POU class 2 homeobox 2	chr19q13.2	211660_at	NM_002698																					
5.79	6.22	0.44	2.60E-02	2.77E-01	CRTC1	CREB regulated transcription coactivator 1	chr19p13.11	213091_at	NM_001098482 /// NM_015321																					
2.41	2.83	0.43	2.60E-02	2.77E-01	---	---	---	216626_at	---																					
2.56	2.96	0.40	2.60E-02	2.77E-01	---	---	---	242894_at	---																					
2.31	2.62	0.32	2.60E-02	2.77E-01	COLEC10	collectin sub-family member 10 (C-type lectin)	chr8q23-q24.1	207420_at	NM_006438																					
2.71	3.15	0.43	2.61E-02	2.78E-01	ZFYVE9	zinc finger, FYVE domain containing 9	chr1p32.3	208446_s_at	NM_004799 /// NM_007323 /// NM_007324																					
3.11	3.40	0.30	2.61E-02	2.78E-01	---	---	---	213961_s_at	---																					
3.78	4.24	0.47	2.61E-02	2.78E-01	DTX1	deltex homolog 1 (Drosophila)	chr12q24.13	227336_at	NM_004416																					

5.58	6.67	1.10	2.62E-02	2.78E-01	NRP1	neuropilin 1	chr10p12	212298_at	NM_001024628 /// NM_001024629 /// NM_003873																				
4.02	4.72	0.71	2.62E-02	2.78E-01	USP32	ubiquitin specific peptidase 32	chr17q23.2	244871_s_at	NM_032582																				
2.49	3.03	0.54	2.62E-02	2.78E-01	FHL5	four and a half LIM domains 5	chr6q16.1-q16.3	220170_at	NM_020482																				
4.80	5.13	0.32	2.62E-02	2.78E-01	VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	chr10q25.2	235034_at	NM_145206																				
3.81	4.23	0.42	2.62E-02	2.78E-01	TMCC2	transmembrane and coiled-coil domain family 2	chr1q32.1	1555503_a_at	NM_014858																				
3.81	4.14	0.34	2.62E-02	2.78E-01	TNK2	tyrosine kinase, non-receptor, 2	chr3q29	216439_at	NM_001010938 /// NM_005781																				
3.30	3.74	0.44	2.63E-02	2.79E-01	ANO5	anoctamin 5	chr11p14.3	229313_at	NM_213599																				
2.72	3.09	0.38	2.63E-02	2.79E-01	LY9	lymphocyte antigen 9	chr1q21.3-q22	215967_s_at	NM_001033667 /// NM_002348																				
3.09	3.82	0.74	2.63E-02	2.79E-01	---	---	---	229327_s_at	---																				
3.78	4.56	0.78	2.64E-02	2.79E-01	---	---	---	230072_at	---																				
2.72	3.12	0.40	2.64E-02	2.79E-01	ATE1	Arginyltransferase 1	chr10q26.13	238857_at	NM_001001976 /// NM_007041																				
2.85	3.21	0.36	2.64E-02	2.79E-01	---	---	---	1562853_x_at	---																				
2.44	2.86	0.42	2.65E-02	2.80E-01	SAMD5	sterile alpha motif domain containing 5	chr6q24.3	228653_at	NM_001030060																				
4.04	4.47	0.43	2.65E-02	2.80E-01	GPR27	G protein-coupled receptor 27	chr3p21-p14	221306_at	NM_018971																				
4.07	4.57	0.51	2.65E-02	2.80E-01	NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	chr19q13.1	228388_at	NM_001001716 /// NM_002503																				
2.70	3.50	0.80	2.65E-02	2.80E-01	---	---	---	228504_at	---																				
3.44	3.71	0.27	2.66E-02	2.80E-01	DNASE1	deoxyribonuclease I	chr16p13.3	1557189_at	NM_005223																				
2.25	3.08	0.84	2.66E-02	2.80E-01	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	chr12q14.2	1554473_at	NM_020762																				
3.74	4.67	0.93	2.67E-02	2.81E-01	---	---	---	243149_at	---																				
3.55	4.18	0.63	2.67E-02	2.81E-01	---	---	---	239228_at	---																				
6.29	6.75	0.46	2.67E-02	2.81E-01	QSOX1	quiescin Q6 sulfhydryl oxidase 1	chr1q24	226706_at	NM_001004128 /// NM_002826																				
2.86	3.27	0.41	2.67E-02	2.81E-01	C20orf96	chromosome 20 open reading frame 96	chr20p13	231905_at	NM_153269																				
2.92	3.31	0.39	2.67E-02	2.81E-01	STS	steroid sulfatase (microsomal), isozyme S	chrXp22.32	203770_s_at	NM_000351																				
7.53	8.96	1.43	2.67E-02	2.81E-01	PTGDS	prostaglandin D2 synthase 21kDa (brain)	chr9q34.2-q34.3	211748_x_at	NM_000954																				
6.93	7.50	0.57	2.67E-02	2.81E-01	APOL2	apolipoprotein L, 2	chr22q12	221013_s_at	NM_030882 /// NM_145637																				
3.82	4.27	0.45	2.67E-02	2.81E-01	C19orf20	Chromosome 19 open reading frame 20	chr19p13.3	243600_at	NM_033513																				
2.55	2.90	0.35	2.67E-02	2.81E-01	GM2A	GM2 ganglioside activator	chr5q31.3-q33.1	215890_at	NM_000405																				
2.07	2.50	0.44	2.68E-02	2.81E-01	---	---	---	236354_at	---																				
3.03	3.51	0.48	2.68E-02	2.81E-01	---	---	---	244590_at	---																				
7.46	8.58	1.11	2.68E-02	2.81E-01	SEC62	SEC62 homolog (S. cerevisiae)	chr3q26.2	208942_s_at	NM_003262																				
5.35	5.76	0.41	2.68E-02	2.81E-01	MESP1	mesoderm posterior 1 homolog (mouse)	chr15q26.1	243387_at	NM_018670																				
5.66	6.61	0.95	2.68E-02	2.82E-01	SRGAP2P1	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 1	chr1p11.2	228628_at	---																				
3.61	4.05	0.44	2.68E-02	2.82E-01	---	---	---	244652_at	---																				
3.16	3.59	0.42	2.68E-02	2.82E-01	KLK12	kallikrein-related peptidase 12	chr19q13.3-q13.4	233586_s_at	NM_019598 /// NM_145894 /// NM_145895																				
3.22	3.55	0.33	2.68E-02	2.82E-01	SLC10A7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	chr4q31.22	235143_at	NM_001029998 /// NM_032128																				
3.47	3.95	0.48	2.69E-02	2.82E-01	PGAM2	phosphoglycerate mutase 2 (muscle)	chr7p13-p12|7p13	205736_at	NM_000290																				
3.35	3.82	0.48	2.69E-02	2.82E-01	PCDH1	protocadherin 1	chr5q32-q33	215277_at	NM_002587 /// NM_032420																				
2.82	3.17	0.35	2.69E-02	2.82E-01	---	---	---	216465_at	---																				
5.46	5.97	0.51	2.69E-02	2.82E-01	PHF20	PHD finger protein 20	chr20q11.22-q11.23	206567_s_at	NM_016436																				
2.35	2.73	0.38	2.69E-02	2.82E-01	---	---	---	234131_at	---																				
2.09	2.42	0.33	2.69E-02	2.82E-01	CUX2	cut-like homeobox 2	chr12q24.11-q24.12	213920_at	NM_015267																				
1.97	2.29	0.32	2.69E-02	2.82E-01	---	---	---	231615_at	---																				
3.75	4.07	0.32	2.69E-02	2.82E-01	MED27	mediator complex subunit 27	chr9q34.1-q34.3	215371_at	NM_004269																				
5.48	6.01	0.53	2.69E-02	2.82E-01	ZFP90	zinc finger protein 90 homolog (mouse)	chr16q22.1	226124_at	NM_133458																				
3.11	3.45	0.33	2.69E-02	2.82E-01	---	---	---	229904_at	---																				
3.83	4.26	0.43	2.70E-02	2.82E-01	PROC	protein C (inactivator of coagulation factors Va and VIIIa)	chr2q13-q14	206259_at	NM_000312																				
4.75	5.26	0.51	2.70E-02	2.82E-01	RGS6	regulator of G-protein signaling 6	chr14q24.3	211448_s_at	NM_004296																				
2.76	3.26	0.50	2.70E-02	2.82E-01	---	---	---	233291_at	---																				

2.47	2.81	0.34	2.70E-02	2.82E-01	ARNT	aryl hydrocarbon receptor nuclear translocator	chr1q21	233724_at	NM_001668 /// NM_178426 /// NM_178427																				
7.67	8.57	0.90	2.70E-02	2.82E-01	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	chr3q26.2-q26.3	205356_at	NM_003940																				
5.85	6.72	0.87	2.71E-02	2.82E-01	PEG3	Paternally expressed 3	chr19q13.4	230068_s_at	NM_006210																				
4.54	5.30	0.76	2.71E-02	2.82E-01	PTPRF	protein tyrosine phosphatase, receptor type, F	chr1p34	200635_s_at	NM_002840 /// NM_130440																				
3.32	3.88	0.57	2.71E-02	2.82E-01	FRMD4A	FERM domain containing 4A	chr10p13	208476_s_at	NM_018027																				
5.97	6.48	0.50	2.71E-02	2.82E-01	FAM57B	family with sequence similarity 57, member B	chr16p11.2	227781_x_at	NM_031478																				
4.41	4.90	0.49	2.71E-02	2.82E-01	BCAS4	breast carcinoma amplified sequence 4	chr20q13.13	228787_s_at	NM_001010974 /// NM_017843 /// NM_198799																				
4.12	4.54	0.41	2.71E-02	2.82E-01	TRPM7	Transient receptor potential cation channel, subfamily M, member 7	chr15q21	231689_at	NM_017672																				
2.42	2.78	0.36	2.71E-02	2.82E-01	---	---	---	242279_at	---																				
2.44	2.72	0.28	2.71E-02	2.82E-01	---	---	---	239637_at	---																				
3.44	3.88	0.43	2.71E-02	2.82E-01	FAM49B	family with sequence similarity 49, member B	chr8q24.21	217534_at	NM_016623																				
6.82	7.25	0.43	2.71E-02	2.82E-01	ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	chr19p13.3-p13.2	230341_x_at	NM_030957																				
5.21	6.57	1.36	2.73E-02	2.82E-01	OXR1	oxidation resistance 1	chr8q23	218197_s_at	NM_018002 /// NM_181354																				
4.89	5.73	0.84	2.73E-02	2.82E-01	SYP	synaptophysin	chrXp11.23-p11.22	213200_at	NM_003179																				
4.58	5.24	0.66	2.72E-02	2.82E-01	KNDC1	kinase non-catalytic C-lobe domain (KIND) containing 1	chr10q26.3	230359_at	NM_152643																				
3.47	4.09	0.62	2.72E-02	2.82E-01	CPNE8	copine VIII	chr12q12	241706_at	NM_153634																				
3.67	4.16	0.49	2.73E-02	2.82E-01	PIK3CA	Phosphoinositide-3-kinase, catalytic, alpha polypeptide	chr3q26.3	235980_at	NM_006218																				
6.82	7.30	0.48	2.73E-02	2.82E-01	KLF16	Kruppel-like factor 16	chr19p13.3	224111_x_at	NM_031918																				
3.46	3.94	0.48	2.73E-02	2.82E-01	SLC22A23	solute carrier family 22, member 23	chr6p25.2	1568719_s_at	NM_015482 /// NM_021945																				
3.48	3.91	0.43	2.72E-02	2.82E-01	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	chr10p12	215365_at	NM_000724 /// NM_201570 /// NM_201571 /// NM_201572 /// NM_201590 /// NM_201593 /// NM_201596 /// NM_201597																				
4.22	4.63	0.41	2.73E-02	2.82E-01	PCDHGB5	protocadherin gamma subfamily B, 5	chr5q31	211807_x_at	NM_018925 /// NM_032099																				
4.69	5.08	0.39	2.73E-02	2.82E-01	SCAMP5	secretory carrier membrane protein 5	chr15q24.1-q24.2	234241_at	NM_138967																				
4.45	4.83	0.38	2.73E-02	2.82E-01	ERICH1	glutamate-rich 1	chr8p23.3	1556356_at	NM_207332																				
2.75	3.11	0.36	2.72E-02	2.82E-01	DENND1A	DENN/MADD domain containing 1A	chr9q33.2	219763_at	NM_020946 /// NM_024820																				
3.07	3.37	0.30	2.72E-02	2.82E-01	LOC728411	similar to Beta-glucuronidase precursor	chr5p14.3	1556742_at	XR_041632 /// XR_041633																				
1.97	2.26	0.29	2.72E-02	2.82E-01	---	---	---	1566215_at	---																				
2.14	2.42	0.28	2.73E-02	2.82E-01	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	chr13q14-q21	211616_s_at	NM_000621																				
2.70	3.35	0.65	2.73E-02	2.83E-01	USP31	ubiquitin specific peptidase 31	chr16p12.1	1558117_s_at	NM_020718																				
3.85	4.27	0.42	2.73E-02	2.83E-01	---	---	---	230627_at	---																				
4.62	5.03	0.40	2.73E-02	2.83E-01	CTAGE4 /// LOC100142659 /// LOC441294	CTAGE family, member 4 /// CTAGE family member /// similar to CTAGE6	chr7q /// chr7q35	214355_x_at	NM_001008747 /// NM_198495 /// XM_001713619 /// XM_001726736 /// XR_038147 /// XR_039265																				
7.05	7.48	0.43	2.74E-02	2.83E-01	BAT2	HLA-B associated transcript 2	chr6p21.3	214201_x_at	NM_080686																				
4.82	6.26	1.44	2.74E-02	2.83E-01	LMO3	LIM domain only 3 (rhombotin-like 2)	chr12p12.3	204424_s_at	NM_001001395 /// NM_018640																				
3.17	4.38	1.21	2.75E-02	2.83E-01	FAM69A	family with sequence similarity 69, member A	chr1p22.1	216044_x_at	NM_001006605																				
4.90	6.08	1.18	2.75E-02	2.83E-01	DAAM1	dishevelled associated activator of morphogenesis 1	chr14q23.1	216060_s_at	NM_014992																				
3.28	4.38	1.10	2.75E-02	2.83E-01	BNC2	basonuclin 2	chr9p22.3-p22.2	238478_at	NM_017637																				
4.66	5.70	1.03	2.74E-02	2.83E-01	LYRM2	LYR motif containing 2	chr6q14.2-q16.1	227712_at	NM_020466																				
2.19	3.11	0.92	2.75E-02	2.83E-01	---	---	---	242379_at	---																				
4.54	5.19	0.64	2.74E-02	2.83E-01	KIAA1715	KIAA1715	chr2q31	225718_at	NM_030650																				

6.96	7.51	0.55	2.74E-02	2.83E-01	SEZ6L2	seizure related 6 homolog (mouse)-like 2	chr16p11.2	238406_x_at	NM_001114099 /// NM_001114100 /// NM_012410 /// NM_201575																				
3.60	4.14	0.53	2.75E-02	2.83E-01	PPP1R1B	protein phosphatase 1, regulatory (inhibitor) subunit 1B	chr17q12	225165_at	NM_032192 /// NM_181505																				
3.81	4.25	0.44	2.76E-02	2.83E-01	---	---	---	243596_at	---																				
4.92	5.37	0.44	2.75E-02	2.83E-01	---	---	---	1566957_at	---																				
4.61	5.04	0.42	2.76E-02	2.83E-01	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4	chr3q23	229929_at	NM_080862																				
3.41	3.83	0.41	2.75E-02	2.83E-01	SPOCD1	SPOC domain containing 1	chr1p35.2	235417_at	NM_144569																				
3.15	3.56	0.41	2.74E-02	2.83E-01	PLEKHB1	Pleckstrin homology domain containing, family B (evectins) member 1	chr11q13.5-q14.1	229046_s_at	NM_001130033 /// NM_001130034 /// NM_001130035 /// NM_001130036 /// NM_021200																				
2.43	2.81	0.38	2.74E-02	2.83E-01	FAM63B	family with sequence similarity 63, member B	chr15q22.1	214691_x_at	NM_001040450 /// NM_001040453																				
3.00	3.36	0.37	2.75E-02	2.83E-01	---	---	---	1556970_at	---																				
3.30	3.66	0.36	2.75E-02	2.83E-01	---	---	---	244847_at	---																				
4.89	5.24	0.34	2.75E-02	2.83E-01	RABGAP1	RAB GTPase activating protein 1	chr9q33.2	215070_x_at	NM_012197																				
4.77	5.09	0.32	2.75E-02	2.83E-01	LOC146429	hypothetical protein LOC146429	chr16q24.3	232765_x_at	XM_001714568 /// XM_370997 /// XM_946336																				
2.03	2.33	0.29	2.75E-02	2.83E-01	C21orf23	chromosome 21 open reading frame 23	chr21q21.3	231491_at	---																				
4.02	4.56	0.53	2.76E-02	2.83E-01	---	---	---	229135_at	---																				
2.81	3.31	0.50	2.76E-02	2.83E-01	GCC1	GRIP and coiled-coil domain containing 1	chr7q32.1	243437_at	NM_024523																				
5.60	6.04	0.44	2.76E-02	2.83E-01	---	---	---	237176_at	---																				
2.27	2.54	0.27	2.76E-02	2.83E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	210305_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359																				
5.26	6.39	1.13	2.76E-02	2.83E-01	---	---	---	224549_x_at	---																				
2.77	3.12	0.35	2.76E-02	2.83E-01	PDIA2	protein disulfide isomerase family A, member 2	chr16p13.3	216127_at	NM_006849																				
2.08	2.38	0.30	2.76E-02	2.83E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	234542_at	NM_015313																				
4.04	4.42	0.37	2.76E-02	2.83E-01	HMGA1	high mobility group AT-hook 1	chr6p21	206074_s_at	NM_002131 /// NM_145899 /// NM_145901 /// NM_145902 /// NM_145903 /// NM_145904 /// NM_145905																				
9.26	10.90	1.64	2.77E-02	2.83E-01	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	chr14q32.33	211969_at	NM_001017963 /// NM_005348																				
4.15	4.93	0.78	2.77E-02	2.83E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	1559400_s_at	NM_002581																				
2.15	2.85	0.70	2.77E-02	2.83E-01	---	---	---	240450_at	---																				
6.87	7.35	0.48	2.77E-02	2.83E-01	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	chr16p11.2	228798_x_at	NM_001042539 /// NM_002383																				
5.99	6.44	0.44	2.77E-02	2.83E-01	C9orf44	chromosome 9 open reading frame 44	chr9q22.31	233525_s_at	---																				
2.24	2.63	0.38	2.77E-02	2.83E-01	---	---	---	237950_s_at	---																				
6.15	6.47	0.32	2.77E-02	2.83E-01	SPG21	spastic paraplegia 21 (autosomal recessive, Mast syndrome)	chr15q21-q22	215383_x_at	NM_001127889 /// NM_001127890 /// NM_016630																				
2.59	2.86	0.27	2.77E-02	2.83E-01	UBE2DNL	ubiquitin-conjugating enzyme E2D N-terminal like pseudogene	chrXq21.1	1554763_at	NR_024062 /// XM_001716039 /// XM_001716422 /// XM_001717602																				
5.51	6.12	0.61	2.77E-02	2.83E-01	XPA	xeroderma pigmentosum, complementation group A	chr9q22.3	205672_at	NM_000380																				

2.58	2.99	0.42	2.77E-02	2.83E-01	41526	septin 9	chr17q25	1559025_at	NM_001113491 /// NM_001113492 /// NM_001113493 /// NM_001113494 /// NM_001113495 /// NM_001113496 /// NM_006640
3.07	3.56	0.49	2.77E-02	2.84E-01	XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	chrXq25	216910_at	NM_003399
3.72	4.11	0.39	2.78E-02	2.84E-01	RREB1	ras responsive element binding protein 1	chr6p25	215620_at	NM_001003698 /// NM_001003699 /// NM_002955
4.03	5.66	1.63	2.78E-02	2.84E-01	KLHL4	kelch-like 4 (Drosophila)	chrXq21.3	214591_at	NM_019117 /// NM_057162
8.24	9.38	1.13	2.78E-02	2.84E-01	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	chr5q21	201413_at	NM_000414
2.89	3.37	0.48	2.78E-02	2.84E-01	PRSS2	protease, serine, 2 (trypsin 2)	chr7q34	205402_x_at	NM_002770
3.36	3.76	0.40	2.78E-02	2.84E-01	VSIG2	V-set and immunoglobulin domain containing 2	chr11q24	228232_s_at	NM_014312
4.68	5.08	0.40	2.78E-02	2.84E-01	SLC26A1	solute carrier family 26 (sulfate transporter), member 1	chr4p16.3	220733_at	NM_022042 /// NM_134425 /// NM_213613
5.66	7.15	1.49	2.79E-02	2.84E-01	HSPH1	heat shock 105kDa/110kDa protein 1	chr13q12.3	208744_x_at	NM_006644
4.50	5.20	0.70	2.79E-02	2.84E-01	---	---	---	1560500_at	---
4.91	5.28	0.37	2.79E-02	2.84E-01	RHBDD1	rhomboid domain containing 1	chr2q36.3	227414_at	NM_032276
2.17	2.49	0.32	2.79E-02	2.84E-01	GYPA	glycophorin A (MNS blood group)	chr4q28.2-q31.1	211821_x_at	NM_002099
3.41	3.72	0.31	2.79E-02	2.84E-01	BCL2L10	BCL2-like 10 (apoptosis facilitator)	chr15q21	221320_at	NM_020396
2.48	3.14	0.66	2.79E-02	2.84E-01	---	---	---	215612_at	---
2.22	2.75	0.53	2.79E-02	2.84E-01	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	chr8q21.12	204612_at	NM_006823 /// NM_181839
3.87	4.36	0.49	2.79E-02	2.84E-01	LOC200772	hypothetical protein LOC200772	chr2q37.3	241525_at	---
3.32	4.49	1.17	2.80E-02	2.84E-01	PGDS	prostaglandin D2 synthase, hematopoietic	chr4q22.3	206726_at	NM_014485
6.32	6.89	0.56	2.80E-02	2.84E-01	---	---	---	242810_x_at	---
4.76	5.37	0.61	2.80E-02	2.85E-01	SOS1	son of sevenless homolog 1 (Drosophila)	chr2p22-p21	230337_at	NM_005633
2.38	2.71	0.33	2.81E-02	2.85E-01	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	chrXq28	242036_x_at	NM_001001344 /// NM_021949
5.18	5.60	0.43	2.81E-02	2.85E-01	ETV7	ets variant gene 7 (TEL2 oncogene)	chr6p21	221680_s_at	NM_016135
2.74	3.09	0.34	2.81E-02	2.85E-01	---	---	---	233433_at	---
1.85	2.14	0.29	2.81E-02	2.85E-01	CCDC14	coiled-coil domain containing 14	chr3q21.1	240884_at	NM_022757
2.70	3.02	0.31	2.81E-02	2.85E-01	OPN5	opsin 5	chr6p12.3	233657_at	NM_001030051 /// NM_181744
4.59	5.16	0.57	2.82E-02	2.85E-01	TBC1D19	TBC1 domain family, member 19	chr4p15.2	220260_at	NM_018317
3.08	3.56	0.48	2.82E-02	2.85E-01	JPH2	junctophilin 2	chr20q13.12	229578_at	NM_020433 /// NM_175913
5.77	6.13	0.36	2.82E-02	2.85E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	200767_s_at	NM_014612
4.09	4.45	0.35	2.82E-02	2.85E-01	RIPK5	receptor interacting protein kinase 5	chr1q32.1	211515_s_at	NM_015375 /// NM_199462
4.16	4.49	0.32	2.82E-02	2.85E-01	---	---	---	240134_at	---
2.65	3.05	0.40	2.82E-02	2.85E-01	FAM38B	family with sequence similarity 38, member B	chr18p11.22	222908_at	NM_022068
2.86	3.23	0.37	2.82E-02	2.85E-01	---	---	---	244576_at	---
2.24	2.56	0.32	2.82E-02	2.85E-01	---	---	---	241063_at	---
2.30	2.59	0.29	2.82E-02	2.85E-01	---	---	---	242980_at	---
2.11	2.45	0.34	2.83E-02	2.86E-01	PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma	chr12p13	206841_at	NM_006205
2.98	3.33	0.34	2.83E-02	2.86E-01	---	---	---	233922_at	---
3.29	4.06	0.76	2.83E-02	2.86E-01	---	---	---	242342_at	---
7.05	7.63	0.58	2.83E-02	2.86E-01	GLTSCR2	glioma tumor suppressor candidate region gene 2	chr19q13.3	234918_at	NM_015710
3.93	4.45	0.52	2.83E-02	2.86E-01	---	---	---	1556846_at	---
2.80	3.21	0.40	2.83E-02	2.86E-01	PLXNA4	plexin A4	chr7q32.3	1562240_at	NM_001105543 /// NM_020911 /// NM_181775
4.60	5.04	0.44	2.84E-02	2.86E-01	BICD1	bicaudal D homolog 1 (Drosophila)	chr12p11.2-p11.1	204741_at	NM_001003398 /// NM_001714
2.23	2.55	0.33	2.84E-02	2.86E-01	---	---	---	241176_at	---
4.40	5.25	0.85	2.84E-02	2.86E-01	DUSP16	Dual specificity phosphatase 16	chr12p13	1563505_at	NM_030640

6.17	6.90	0.73	2.84E-02	2.86E-01	ERC1	ELKS/RAB6-interacting/CAST family member 1	chr12p13.3	215606_s_at	NM_015064 /// NM_178037 /// NM_178038 /// NM_178039 /// NM_178040																			
2.26	3.58	1.32	2.84E-02	2.86E-01	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	chr9q22.1	221795_at	NM_001007097 /// NM_001018064 /// NM_001018065 /// NM_001018066 /// NM_006180																			
3.25	3.71	0.46	2.85E-02	2.86E-01	---	---	---	230750_at	---																			
4.27	4.73	0.45	2.85E-02	2.86E-01	CCDC108	coiled-coil domain containing 108	chr2q35	239508_x_at	NM_152389 /// NM_194302																			
2.73	3.18	0.45	2.85E-02	2.86E-01	IGL@ /// IGLC1 /// IGLV3-12 /// IGLV3-21	immunoglobulin lambda locus /// immunoglobulin lambda constant 1 (Mcg marker) /// immunoglobulin lambda variable 3-12 /// immunoglobulin lambda variable 3-21	chr22q11.1-q11.2 /// chr22q11.2	234350_at	---																			
2.69	3.11	0.43	2.85E-02	2.86E-01	SCGN	secretagogin, EF-hand calcium binding protein	chr6p22.3-p22.1	205697_at	NM_006998																			
2.39	2.80	0.42	2.84E-02	2.86E-01	---	---	---	221159_at	---																			
4.24	4.62	0.37	2.85E-02	2.86E-01	---	---	---	239149_at	---																			
1.96	2.26	0.29	2.85E-02	2.86E-01	OVOL2	ovo-like 2 (Drosophila)	chr20pter-q11.23	206048_at	NM_021220																			
3.24	3.51	0.27	2.85E-02	2.86E-01	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	chr11p13	207291_at	NM_024081																			
6.73	8.16	1.43	2.85E-02	2.86E-01	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	chr5q13.3	223466_x_at	NM_001130105 /// NM_005713 /// NM_031361																			
3.90	5.10	1.20	2.85E-02	2.86E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	203242_s_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257																			
3.57	4.16	0.59	2.85E-02	2.86E-01	GNG4	guanine nucleotide binding protein (G protein), gamma 4	chr1q42.3	205184_at	NM_001098721 /// NM_001098722 /// NM_004485																			
3.59	3.99	0.39	2.85E-02	2.86E-01	HIST1H2BB	histone cluster 1, H2bb	chr6p21.3	208547_at	NM_021062																			
5.56	5.94	0.38	2.86E-02	2.86E-01	CADM4	cell adhesion molecule 4	chr19q13.31	229335_at	NM_145296																			
2.42	2.81	0.39	2.86E-02	2.87E-01	TCERG1	transcription elongation regulator 1	chr5q31	229706_at	NM_001040006 /// NM_006706																			
5.21	5.80	0.59	2.86E-02	2.87E-01	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	chr10q22.2	214496_x_at	NM_012330																			
2.10	2.48	0.39	2.86E-02	2.87E-01	---	---	---	231511_at	---																			
3.86	4.27	0.41	2.86E-02	2.87E-01	---	---	---	236812_at	---																			
5.71	7.11	1.40	2.87E-02	2.87E-01	BAT2D1	BAT2 domain containing 1	chr1q23.3	211948_x_at	NM_015172																			
3.77	4.39	0.62	2.87E-02	2.87E-01	KPNA1	karyopherin alpha 1 (importin alpha 5)	chr3q21	213741_s_at	NM_002264																			
5.16	5.65	0.49	2.87E-02	2.87E-01	PTEN	phosphatase and tensin homolog	chr10q23.3	233254_x_at	NM_000314																			
3.32	3.58	0.27	2.87E-02	2.87E-01	---	---	---	1559676_a_at	---																			
2.26	2.77	0.52	2.87E-02	2.87E-01	SFRS15	Splicing factor, arginine/serine-rich 15	chr21q22.1	243759_at	NM_020706																			
6.78	7.60	0.82	2.87E-02	2.87E-01	TPM1	tropomyosin 1 (alpha)	chr15q22.1	210987_x_at	NM_000366 /// NM_001018004 /// NM_001018005 /// NM_001018006 /// NM_001018007 /// NM_001018008 /// NM_001018020																			
6.53	7.06	0.53	2.88E-02	2.87E-01	DLG4	discs, large homolog 4 (Drosophila)	chr17p13.1	210684_s_at	NM_001128827 /// NM_001365																			
5.44	5.88	0.43	2.88E-02	2.87E-01	---	---	---	229612_at	---																			
3.60	4.01	0.40	2.88E-02	2.87E-01	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	chr5p15.2	230995_at	NM_138809																			
3.90	4.28	0.38	2.88E-02	2.87E-01	---	---	---	240393_at	---																			

1.99	2.34	0.35	2.88E-02	2.87E-01	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	chrXp11.3-p11.23	1558120_at	NM_001356
4.62	4.96	0.34	2.88E-02	2.87E-01	THAP6	THAP domain containing 6	chr4q21.1	235218_x_at	NM_144721
2.49	2.83	0.34	2.88E-02	2.87E-01	DNAJC28	DnaJ (Hsp40) homolog, subfamily C, member 28	chr21q22.11	220372_at	NM_001040192 /// NM_017833
2.74	3.06	0.32	2.88E-02	2.87E-01	PI15	peptidase inhibitor 15	chr8q21.11	207938_at	NM_015886
2.35	2.64	0.29	2.88E-02	2.87E-01	---	---	---	215345_x_at	---
2.57	2.90	0.33	2.88E-02	2.87E-01	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)	chr12p13	240284_x_at	NM_006331
3.61	4.58	0.97	2.89E-02	2.87E-01	APC	adenomatous polyposis coli	chr5q21-q22	203526_s_at	NM_000038 /// NM_001127510 /// NM_001127511
2.73	3.06	0.33	2.89E-02	2.87E-01	CELSR3 /// SLC26A6	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) /// solute carrier family 26, member 6	chr3p21.3 /// chr3p24.1-p21.2	205165_at	NM_001040454 /// NM_001407 /// NM_022911 /// NM_134263 /// NM_134426
4.24	4.69	0.45	2.89E-02	2.87E-01	---	---	---	231584_s_at	---
3.52	4.37	0.85	2.89E-02	2.88E-01	SV2A	synaptic vesicle glycoprotein 2A	chr1q21.2	203069_at	NM_014849
6.85	7.30	0.45	2.89E-02	2.88E-01	RHEB	Ras homolog enriched in brain	chr7q36	241795_at	NM_005614
3.24	3.63	0.39	2.89E-02	2.88E-01	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	chr19p13.3	207592_s_at	NM_001194
1.86	2.19	0.33	2.89E-02	2.88E-01	---	---	---	216618_at	---
3.95	4.28	0.33	2.89E-02	2.88E-01	DDA1	DET1 and DDB1 associated 1	chr19p13.11	227457_at	NM_024050
3.29	3.80	0.51	2.90E-02	2.88E-01	ACSL4	Acyl-CoA synthetase long-chain family member 4	chrXq22.3-q23	1557419_a_at	NM_004458 /// NM_022977
2.38	2.79	0.41	2.90E-02	2.88E-01	CTAG2	cancer/testis antigen 2	chrXq28	207337_at	NM_020994 /// NM_172377 /// XM_001714637
2.54	3.13	0.59	2.90E-02	2.88E-01	---	---	---	1570412_at	---
3.56	4.13	0.57	2.90E-02	2.88E-01	CD163L1	CD163 molecule-like 1	chr12p13.3	223655_at	NM_174941
3.84	4.39	0.55	2.90E-02	2.88E-01	ZNF222	zinc finger protein 222	chr19q13.2	206175_x_at	NM_001129996 /// NM_013360
5.09	5.61	0.53	2.90E-02	2.88E-01	LGI4	leucine-rich repeat LGI family, member 4	chr19q13.12|19q13.11	242670_at	NM_139284
3.15	3.67	0.52	2.90E-02	2.88E-01	NDRG2	NDRG family member 2	chr14q11.2	214278_s_at	NM_016250 /// NM_201535 /// NM_201536 /// NM_201537 /// NM_201538 /// NM_201539 /// NM_201540 /// NM_201541
2.76	3.15	0.39	2.90E-02	2.88E-01	---	---	---	1560410_at	---
2.35	2.73	0.38	2.90E-02	2.88E-01	---	---	---	243823_at	---
1.87	2.19	0.33	2.90E-02	2.88E-01	DKFZP434B061	DKFZP434B061 protein	chr13p13	233092_s_at	XR_015528 /// XR_040812
2.95	3.33	0.38	2.91E-02	2.88E-01	AP1GBP1	AP1 gamma subunit binding protein 1	chr17q12	232387_at	NM_007247 /// NM_080550
2.59	2.95	0.36	2.91E-02	2.88E-01	---	---	---	241508_at	---
4.32	5.32	1.00	2.91E-02	2.88E-01	---	---	---	243931_at	---
3.69	4.40	0.71	2.91E-02	2.88E-01	CALD1	caldesmon 1	chr7q33	205525_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
3.85	4.55	0.71	2.91E-02	2.88E-01	OSGIN2	oxidative stress induced growth inhibitor family member 2	chr8q21	1554414_a_at	NM_001126111 /// NM_004337
4.45	4.91	0.45	2.91E-02	2.88E-01	LOC147343	Hypothetical protein LOC147343	chr18q21.1	217514_at	---
2.44	2.72	0.29	2.91E-02	2.88E-01	UPP2	uridine phosphorylase 2	chr2q24.1	233155_at	NM_173355
4.63	5.58	0.95	2.92E-02	2.88E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	223438_s_at	NM_001001928 /// NM_005036
3.38	3.73	0.36	2.92E-02	2.88E-01	C10orf132	chromosome 10 open reading frame 132	chr10q24.2	228068_at	NM_001010917
3.60	3.96	0.35	2.92E-02	2.88E-01	GAB1	GRB2-associated binding protein 1	chr4q31.21	1560382_at	NM_002039 /// NM_207123
1.76	1.99	0.23	2.92E-02	2.88E-01	---	---	---	222249_at	---
5.76	6.08	0.32	2.92E-02	2.88E-01	UBQLN4	ubiquilin 4	chr1q21	222252_x_at	NM_020131
5.03	6.01	0.98	2.92E-02	2.88E-01	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	chr1p31.3	205176_s_at	NM_014288

6.50	7.02	0.52	2.92E-02	2.88E-01	RUNX3	runt-related transcription factor 3	chr1p36	234928_x_at	NM_001031680 /// NM_004350																				
5.06	6.61	1.55	2.93E-02	2.88E-01	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	226094_at	NM_002645																				
2.15	2.56	0.42	2.93E-02	2.89E-01	BRS3	bombesin-like receptor 3	chrXq26-q28	207369_at	NM_001727																				
5.99	6.73	0.74	2.93E-02	2.89E-01	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	chr16q22.2	210555_s_at	NM_004555 /// NM_173163 /// NM_173164 /// NM_173165																				
2.05	2.39	0.33	2.93E-02	2.89E-01	---	---	---	239819_at	---																				
7.35	7.77	0.43	2.93E-02	2.89E-01	SIL1	SIL1 homolog, endoplasmic reticulum chaperone (S. cerevisiae)	chr5q31	218436_at	NM_001037633 /// NM_022464																				
2.71	3.01	0.30	2.94E-02	2.89E-01	GYPB	glycophorin B (MNS blood group)	chr4q28-q31	207459_x_at	NM_002100																				
4.72	5.32	0.60	2.94E-02	2.89E-01	SDCCAG10	serologically defined colon cancer antigen 10	chr5q12.3	223337_at	NM_005869																				
5.21	5.77	0.56	2.94E-02	2.89E-01	BTBD7	BTB (POZ) domain containing 7	chr14q32.12-q32.13	1556000_s_at	NM_001002860 /// NM_018167																				
2.27	2.62	0.34	2.94E-02	2.89E-01	WT1	Wilms tumor 1	chr11p13	216953_s_at	NM_000378 /// NM_024424 /// NM_024425 /// NM_024426																				
3.49	3.86	0.36	2.94E-02	2.89E-01	---	---	---	244458_at	---																				
4.61	5.02	0.41	2.94E-02	2.89E-01	LOC100128977	similar to hCG1654542	chr17q21.31	237536_at	XM_001715841 /// XM_001717446 /// XM_001719146																				
2.55	2.88	0.33	2.95E-02	2.89E-01	IGL@ /// IGLV2-18 /// IGLV3-19	immunoglobulin lambda locus /// immunoglobulin lambda variable 2-18 /// immunoglobulin lambda variable 3-19	chr22q11.1-q11.2 /// chr22q11.2	216846_at	---																				
4.02	4.44	0.42	2.95E-02	2.90E-01	C14orf28	chromosome 14 open reading frame 28	chr14q21.3	235369_at	NM_001017923																				
5.22	5.84	0.62	2.95E-02	2.90E-01	DIAPH2	diaphanous homolog 2 (Drosophila)	chrXq21.33	205726_at	NM_006729 /// NM_007309																				
3.16	3.58	0.42	2.95E-02	2.90E-01	C10orf62	chromosome 10 open reading frame 62	chr10q24.2	240235_at	NM_001009997																				
4.52	4.86	0.35	2.96E-02	2.90E-01	TGFB1	transforming growth factor, beta 1	chr19q13.2|19q13.1	203084_at	NM_000660																				
2.51	2.85	0.34	2.95E-02	2.90E-01	---	---	---	1560241_at	---																				
6.35	6.68	0.33	2.96E-02	2.90E-01	MMP14	matrix metallopeptidase 14 (membrane-inserted)	chr14q11-q12	202828_s_at	NM_004995																				
5.03	6.25	1.22	2.97E-02	2.90E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	216804_s_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257																				
4.83	5.71	0.89	2.96E-02	2.90E-01	FRMD3	FERM domain containing 3	chr9q21.32	229893_at	NM_174938																				
3.60	4.18	0.58	2.96E-02	2.90E-01	---	---	---	217671_at	---																				
8.40	8.90	0.50	2.96E-02	2.90E-01	EZR	ezrin	chr6q25.2-q26	208622_s_at	NM_001111077 /// NM_003379																				
2.61	3.07	0.47	2.96E-02	2.90E-01	STAG1	stromal antigen 1	chr3q22.3	232588_at	NM_005862																				
4.37	4.79	0.42	2.97E-02	2.90E-01	SPEF1	sperm flagellar 1	chr20pter-q11.23	216119_s_at	NM_015417																				
5.32	5.73	0.41	2.97E-02	2.90E-01	TUSC5	tumor suppressor candidate 5	chr17p13.3	239523_at	NM_172367																				
2.81	3.22	0.40	2.96E-02	2.90E-01	ZNF587	Zinc finger protein 587	chr19q13.43	1557248_at	NM_032828																				
7.09	7.49	0.40	2.97E-02	2.90E-01	INF2	inverted formin, FH2 and WH2 domain containing	chr14q32.33	218144_s_at	NM_001031714 /// NM_022489 /// NM_032714																				
2.35	2.74	0.38	2.97E-02	2.90E-01	---	---	---	237198_at	---																				
2.69	3.06	0.38	2.97E-02	2.90E-01	---	---	---	238210_at	---																				
2.36	2.73	0.37	2.97E-02	2.90E-01	NPNT	nephronectin	chr4q24	244747_at	NM_001033047																				
2.61	2.96	0.35	2.96E-02	2.90E-01	---	---	---	242779_at	---																				
2.15	2.48	0.33	2.97E-02	2.90E-01	LRP2	low density lipoprotein-related protein 2	chr2q24-q31	230863_at	NM_004525																				
2.39	2.70	0.31	2.97E-02	2.90E-01	TSPAN16	tetraspanin 16	chr19p13.2	242179_s_at	NM_012466																				

4.10	4.43	0.33	2.97E-02	2.90E-01	LOC100131081	hypothetical protein LOC100131081	chr14q21.1	235790_at	XM_001721889 /// XM_001722148 /// XM_001724274																				
5.45	6.09	0.64	2.97E-02	2.90E-01	HYAL1	hyaluronoglucosaminidase 1	chr3p21.3-p21.2	210619_s_at	NM_007312 /// NM_033159 /// NM_153281 /// NM_153282 /// NM_153283 /// NM_153285																				
1.99	2.40	0.41	2.98E-02	2.90E-01	THADA	Thyroid adenoma associated	chr2p21	1566889_at	NM_001083953 /// NM_022065																				
5.17	5.61	0.44	2.98E-02	2.91E-01	KREMEN1	kringle containing transmembrane protein 1	chr22q12.1	243029_at	NM_001039570 /// NM_001039571																				
4.66	5.44	0.78	2.98E-02	2.91E-01	---	---	---	235600_at	---																				
2.61	3.01	0.40	2.98E-02	2.91E-01	TGM4	transglutaminase 4 (prostate)	chr3p22-p21.33	217567_at	NM_003241																				
2.47	2.84	0.38	2.98E-02	2.91E-01	SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	chr19q13.3-q13.4	205861_at	NM_003121																				
2.52	2.99	0.47	2.99E-02	2.91E-01	GTF2A2	general transcription factor IIA, 2, 12kDa	chr15q22.2	243985_at	NM_004492																				
4.15	5.15	0.99	2.99E-02	2.91E-01	INSR	insulin receptor	chr19p13.3-p13.2	207851_s_at	NM_000208 /// NM_001079817																				
4.10	4.56	0.46	2.99E-02	2.91E-01	---	---	---	235673_at	---																				
4.71	5.15	0.45	2.99E-02	2.91E-01	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	chr7p15	244131_at	NM_002137 /// NM_031243																				
3.67	4.09	0.42	2.99E-02	2.91E-01	---	---	---	230222_at	---																				
2.73	3.12	0.38	3.00E-02	2.91E-01	---	---	---	230794_at	---																				
4.41	4.79	0.38	2.99E-02	2.91E-01	---	---	---	234156_at	---																				
2.72	3.07	0.34	2.99E-02	2.91E-01	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	chr14q32.2	1559485_at	NM_018036																				
1.88	2.21	0.33	3.00E-02	2.91E-01	---	---	---	1566600_at	---																				
2.20	2.51	0.31	2.99E-02	2.91E-01	---	---	---	1561763_at	---																				
2.09	2.42	0.33	3.00E-02	2.91E-01	ABI3BP	ABI gene family, member 3 (NESH) binding protein	chr3q12	220518_at	NM_015429																				
3.81	4.40	0.59	3.00E-02	2.91E-01	WDR5B	WD repeat domain 5B	chr3q21.1	235850_at	NM_019069																				
4.61	5.85	1.24	3.01E-02	2.92E-01	---	---	---	238536_at	---																				
4.55	5.67	1.12	3.01E-02	2.92E-01	FRMD3	FERM domain containing 3	chr9q21.32	230645_at	NM_174938																				
7.51	8.37	0.86	3.01E-02	2.92E-01	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	chr20q13.1	217717_s_at	NM_003404 /// NM_139323																				
4.87	5.35	0.48	3.01E-02	2.92E-01	LOC100130955	hypothetical protein LOC100130955	chr14q32.2	210795_s_at	XM_001723690 /// XM_001725000 /// XM_001726513																				
4.66	5.12	0.46	3.01E-02	2.92E-01	RASGRP4	RAS guanyl releasing protein 4	chr19q13.1	231328_s_at	NM_170604																				
2.06	2.51	0.45	3.01E-02	2.92E-01	---	---	---	1564776_at	---																				
3.88	4.32	0.44	3.01E-02	2.92E-01	LOC645700 /// ZNF815	similar to hCG1786132 /// zinc finger protein 815	chr7p22.1	232863_at	NR_023382 /// XM_001714471 /// XM_001714535 /// XM_001716167 /// XM_001716200 /// XM_001716517 /// XM_928774 /// XM_935668																				
2.27	2.67	0.40	3.01E-02	2.92E-01	PCDHGA11	protocadherin gamma subfamily A, 11	chr5q31	211877_s_at	NM_018914 /// NM_032091 /// NM_032092																				
2.44	2.79	0.36	3.01E-02	2.92E-01	---	---	---	237117_at	---																				
4.13	4.48	0.35	3.01E-02	2.92E-01	---	---	---	231103_at	---																				
2.09	2.34	0.25	3.01E-02	2.92E-01	SOS1	son of sevenless homolog 1 (Drosophila)	chr2p22-p21	1557354_at	NM_005633																				
4.65	5.67	1.02	3.01E-02	2.92E-01	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	chr2p21	209288_s_at	NM_006449																				
2.51	2.83	0.32	3.01E-02	2.92E-01	ANKRD22	ankyrin repeat domain 22	chr10q23.31	238439_at	NM_144590																				
4.18	4.94	0.75	3.02E-02	2.92E-01	---	---	---	241435_at	---																				
2.31	2.77	0.47	3.02E-02	2.92E-01	WRNIP1	Werner helicase interacting protein 1	chr6p25.2	218015_s_at	NM_020135 /// NM_130395																				
3.54	4.30	0.76	3.02E-02	2.92E-01	ZNF600	zinc finger protein 600	chr19q13.41	242463_x_at	NM_198457																				
2.84	3.20	0.36	3.02E-02	2.92E-01	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	chr14q11.2	206008_at	NM_000359																				
2.75	3.07	0.33	3.03E-02	2.92E-01	ALK	anaplastic lymphoma receptor tyrosine kinase	chr2p23	208211_s_at	NM_004304																				

4.07	4.52	0.45	3.03E-02	2.92E-01	LOC222070	hypothetical protein LOC222070	chr7p13	221949_at	---
3.30	3.65	0.35	3.03E-02	2.93E-01	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	chr2q24.2	218833_at	NM_016653 /// NM_133646
2.24	2.59	0.35	3.03E-02	2.93E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	211655_at	---
2.72	3.14	0.42	3.04E-02	2.93E-01	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	chr14q24.1	207185_at	NM_003049
3.98	4.34	0.36	3.04E-02	2.93E-01	NPHP4	nephronophthisis 4	chr1p36.22	216344_at	NM_015102
1.99	2.45	0.46	3.04E-02	2.93E-01	MMP13	matrix metallopeptidase 13 (collagenase 3)	chr11q22.3	205959_at	NM_002427
2.19	2.55	0.36	3.04E-02	2.93E-01	SVIP	small VCP/p97-interacting protein	chr11p14.2	230005_at	NM_148893
1.76	2.06	0.30	3.04E-02	2.93E-01	ESR1	estrogen receptor 1	chr6q25.1	211627_x_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742
2.41	2.68	0.26	3.04E-02	2.93E-01	---	---	---	217498_at	---
4.67	5.37	0.70	3.05E-02	2.93E-01	USP47	ubiquitin specific peptidase 47	chr11p15.3	223119_s_at	NM_017944
7.01	7.50	0.49	3.05E-02	2.93E-01	CNTROB	centrobin, centrosomal BRCA2 interacting protein	chr17p13.1	231884_at	NM_001037144 /// NM_053051
6.47	6.82	0.34	3.05E-02	2.93E-01	WBSCR23	Williams-Beuren syndrome chromosome region 23	chr7q11.23	221176_x_at	XR_040833 /// XR_040834 /// XR_040835 /// XR_040836
1.88	2.14	0.26	3.05E-02	2.93E-01	---	---	---	1558170_at	---
4.43	4.87	0.44	3.05E-02	2.93E-01	TMPRSS3	transmembrane protease, serine 3	chr21q22.3	223948_s_at	NM_024022 /// NM_032401 /// NM_032404 /// NM_032405
3.51	4.04	0.52	3.06E-02	2.93E-01	HRB	HIV-1 Rev binding protein	chr2q36.3	213926_s_at	NM_004504
5.06	5.49	0.43	3.06E-02	2.93E-01	PTGER1	prostaglandin E receptor 1 (subtype EP1), 42kDa	chr19p13.1	214391_x_at	NM_000955
3.32	3.67	0.35	3.06E-02	2.93E-01	TCF3	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	213809_x_at	NM_003200
5.13	5.85	0.72	3.06E-02	2.93E-01	WDFY1	WD repeat and FYVE domain containing 1	chr2q36.1	233559_s_at	NM_020830
5.32	6.26	0.94	3.07E-02	2.94E-01	ITGA8	integrin, alpha 8	chr10p13	214265_at	NM_003638
5.32	5.91	0.59	3.07E-02	2.94E-01	SH3KBP1	SH3-domain kinase binding protein 1	chrXp22.1-p21.3	1554168_a_at	NM_001024666 /// NM_031892
4.95	5.48	0.53	3.07E-02	2.94E-01	IGHD /// IGHM /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy constant delta /// immunoglobulin heavy constant mu /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	211632_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001724554 /// XM_941465
3.69	4.21	0.52	3.07E-02	2.94E-01	FOXP1	forkhead box P1	chr3p14.1	223937_at	NM_001012505 /// NM_032682
5.79	6.29	0.49	3.07E-02	2.94E-01	TSEN15	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	chr1q25	230257_s_at	NM_001127394 /// NM_052965 /// NR_023349
2.21	2.65	0.44	3.07E-02	2.94E-01	---	---	---	233684_at	---
1.91	2.35	0.44	3.07E-02	2.94E-01	LOC644213	Similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	chr1p12	233791_at	XR_016570 /// XR_018856 /// XR_040026
3.12	3.50	0.39	3.07E-02	2.94E-01	RFC3	replication factor C (activator 1) 3, 38kDa	chr13q12.3-q13	231119_at	NM_002915 /// NM_181558
2.60	2.99	0.38	3.07E-02	2.94E-01	PAPPA2	pappalysin 2	chr1q23-q25	213332_at	NM_020318 /// NM_021936
3.96	4.33	0.37	3.07E-02	2.94E-01	---	---	---	235702_at	---
3.28	3.59	0.32	3.06E-02	2.94E-01	DNM1DN11-6	DNM1DN11.6 duplicon	chr15q25.2	232143_at	---
2.47	2.76	0.30	3.07E-02	2.94E-01	HBS1L	HBS1-like (S. cerevisiae)	chr6q23-q24	209315_at	NM_006620
5.01	5.48	0.47	3.07E-02	2.94E-01	CENTG1	centaurin, gamma 1	chr12q14.1	206152_at	NM_001122772 /// NM_014770
2.39	2.68	0.29	3.07E-02	2.94E-01	TRIM31	Tripartite motif-containing 31	chr6p21.3	1557151_at	NM_007028
7.80	8.52	0.72	3.08E-02	2.94E-01	SCAP	SREBF chaperone	chr3p21.31	212329_at	NM_012235
7.39	8.11	0.72	3.08E-02	2.94E-01	CYB5R3	cytochrome b5 reductase 3	chr22q13.31-qter|22q13.2-q13.31	1554574_a_at	NM_000398 /// NM_001129819 /// NM_007326

7.38	8.02	0.63	3.08E-02	2.94E-01	PTP4A2	protein tyrosine phosphatase type IVA, member 2	chr1p35	208617_s_at	NM_080391 /// NM_080392
3.50	4.04	0.55	3.08E-02	2.94E-01	C14orf118	chromosome 14 open reading frame 118	chr14q22.1-q24.3	229514_at	NM_017926 /// NM_017972
5.92	6.34	0.42	3.08E-02	2.94E-01	FAM83G	family with sequence similarity 83, member G	chr17p11.2	228587_at	NM_001039999
3.48	3.84	0.36	3.08E-02	2.94E-01	KCNG1	potassium voltage-gated channel, subfamily G, member 1	chr20q13	211053_at	NM_002237 /// NM_172318
2.39	2.71	0.32	3.08E-02	2.94E-01	---	---	---	1566541_at	---
2.29	2.79	0.50	3.08E-02	2.94E-01	SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	chr9p22.3	222286_at	NM_001039697
3.31	3.75	0.44	3.09E-02	2.94E-01	---	---	---	236747_at	---
2.75	3.11	0.36	3.09E-02	2.95E-01	GVIN1	GTPase, very large interferon inducible 1	chr11p15.4	220577_at	NR_003945 /// XM_495863 /// XM_940224
5.42	6.65	1.23	3.09E-02	2.95E-01	SMAD1	SMAD family member 1	chr4q31	210993_s_at	NM_001003688 /// NM_005900
2.61	2.91	0.30	3.09E-02	2.95E-01	FAF1	Fas (TNFRSF6) associated factor 1	chr1p33	239749_at	NM_007051
1.83	2.07	0.24	3.09E-02	2.95E-01	---	---	---	244106_at	---
6.24	6.73	0.49	3.09E-02	2.95E-01	---	---	---	223788_at	---
4.36	4.72	0.36	3.09E-02	2.95E-01	---	---	---	231046_at	---
6.79	7.20	0.41	3.09E-02	2.95E-01	SEC14L1	SEC14-like 1 (S. cerevisiae)	chr17q25.1-q25.2	202082_s_at	NM_001039573 /// NM_003003
2.20	2.47	0.28	3.09E-02	2.95E-01	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	chr11q12	210356_x_at	NM_021950 /// NM_152866
2.56	3.00	0.44	3.10E-02	2.95E-01	AKAP6	A kinase (PRKA) anchor protein 6	chr14q13.1	217669_s_at	NM_004274
3.32	3.75	0.43	3.10E-02	2.95E-01	---	---	---	238670_at	---
3.10	3.95	0.85	3.10E-02	2.95E-01	FHL5	four and a half LIM domains 5	chr6q16.1-q16.3	1555191_a_at	NM_020482
4.68	5.05	0.37	3.10E-02	2.95E-01	RAB23	RAB23, member RAS oncogene family	chr6p11	223463_at	NM_016277 /// NM_183227
4.92	5.28	0.36	3.10E-02	2.95E-01	C6orf162	chromosome 6 open reading frame 162	chr6q15-q16.1	213312_at	NM_001042493 /// NM_020425
4.67	5.22	0.55	3.10E-02	2.95E-01	C17orf46	chromosome 17 open reading frame 46	chr17q21.31	1553803_at	NM_152343
2.26	2.63	0.37	3.11E-02	2.95E-01	RAB14	RAB14, member RAS oncogene family	chr9q32-q34.11	200928_s_at	NM_016322
3.12	3.40	0.28	3.11E-02	2.95E-01	---	---	---	237283_at	---
6.43	6.89	0.46	3.11E-02	2.95E-01	DOHH	deoxyhypusine hydroxylase/monooxygenase	chr19p13.3	208141_s_at	NM_031304
3.14	3.53	0.39	3.11E-02	2.95E-01	CYP4A11 /// CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 11 /// cytochrome P450, family 4, subfamily A, polypeptide 22	chr1p33	1554837_a_at	NM_000778 /// NM_001010969
4.74	5.12	0.38	3.11E-02	2.95E-01	CASP10	caspase 10, apoptosis-related cysteine peptidase	chr2q33-q34	205467_at	NM_001230 /// NM_032974 /// NM_032977
2.49	2.79	0.31	3.11E-02	2.95E-01	---	---	---	232951_at	---
2.62	2.95	0.33	3.12E-02	2.95E-01	---	---	---	240071_at	---
2.29	2.69	0.40	3.12E-02	2.95E-01	CNOT4	CCR4-NOT transcription complex, subunit 4	chr7q22-qter	210204_s_at	NM_001008225 /// NM_013316
5.74	6.11	0.37	3.12E-02	2.96E-01	---	---	---	231998_at	---
5.84	6.86	1.02	3.12E-02	2.96E-01	EIF5B	eukaryotic translation initiation factor 5B	chr2q11.2	201024_x_at	NM_015904
2.42	2.71	0.28	3.13E-02	2.96E-01	---	---	---	237969_at	---
3.56	3.92	0.36	3.13E-02	2.96E-01	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	chr10p12	1559420_x_at	NM_000724 /// NM_201570 /// NM_201571 /// NM_201572 /// NM_201590 /// NM_201593 /// NM_201596 /// NM_201597
3.03	3.69	0.66	3.13E-02	2.96E-01	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	chr4q11-q12	205051_s_at	NM_000222 /// NM_001093772
3.08	3.50	0.41	3.13E-02	2.96E-01	CAV2	Caveolin 2	chr7q31.1	213426_s_at	NM_001233 /// NM_198212
2.80	3.27	0.47	3.13E-02	2.96E-01	---	---	---	239661_at	---
1.86	2.09	0.24	3.13E-02	2.96E-01	C9orf11	chromosome 9 open reading frame 11	chr9p21	1554982_a_at	NM_020641
2.75	3.11	0.37	3.14E-02	2.96E-01	---	---	---	244081_at	---
5.61	6.11	0.51	3.14E-02	2.96E-01	---	---	---	240441_at	---
2.47	2.87	0.41	3.14E-02	2.96E-01	---	---	---	234160_at	---
2.27	2.52	0.25	3.14E-02	2.96E-01	---	---	---	1559303_at	---
3.76	4.15	0.39	3.14E-02	2.96E-01	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	chr15q24.2	220706_at	NM_014272

4.92	5.86	0.94	3.14E-02	2.96E-01	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	chr2q24.2	225662_at	NM_016653 /// NM_133646
4.29	4.72	0.42	3.15E-02	2.97E-01	FGD2	FYVE, RhoGEF and PH domain containing 2	chr6p21.2	242632_at	NM_173558
1.78	2.05	0.27	3.15E-02	2.97E-01	---	---	---	231495_at	---
2.07	2.34	0.27	3.15E-02	2.97E-01	---	---	---	234532_at	---
3.30	3.74	0.44	3.16E-02	2.97E-01	---	---	---	233756_at	---
2.69	3.11	0.42	3.16E-02	2.97E-01	---	---	---	1561944_at	---
2.99	3.33	0.34	3.16E-02	2.97E-01	GOLGA2L1	golgi autoantigen, golgin subfamily a, 2-like 1	chr12q23.1	219876_s_at	NM_017600
3.29	3.62	0.33	3.16E-02	2.97E-01	---	---	---	237940_s_at	---
7.33	7.93	0.60	3.17E-02	2.98E-01	PLEKHB2	pleckstrin homology domain containing, family B (evectins) member 2	chr2q21.1	201410_at	NM_001100623 /// NM_017958
3.49	3.93	0.44	3.17E-02	2.98E-01	---	---	---	229648_at	---
5.52	5.88	0.37	3.17E-02	2.98E-01	ANKRD13B	ankyrin repeat domain 13B	chr17q11.2	227720_at	NM_152345
2.14	2.43	0.29	3.17E-02	2.98E-01	---	---	---	217571_at	---
4.42	5.32	0.90	3.18E-02	2.98E-01	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	chr8q22.2	236254_at	NM_015243 /// NM_017890 /// NM_152564 /// NM_181661
3.32	3.78	0.45	3.18E-02	2.98E-01	---	---	---	1557457_at	---
2.10	2.45	0.35	3.18E-02	2.98E-01	ABCC6P1	ATP-binding cassette, sub-family C, member 6 pseudogene 1	chr16p12.3	236205_at	NR_003569
2.19	2.53	0.34	3.18E-02	2.98E-01	CTNND2	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	chr5p15.2	209617_s_at	NM_001332
2.08	2.38	0.30	3.18E-02	2.98E-01	---	---	---	244511_at	---
4.71	4.99	0.29	3.18E-02	2.98E-01	CNGB1	cyclic nucleotide gated channel beta 1	chr16q13	210769_at	NM_001297
2.25	2.72	0.46	3.18E-02	2.98E-01	---	---	---	242572_at	---
5.22	5.73	0.50	3.18E-02	2.98E-01	TTTY14	testis-specific transcript, Y-linked 14	chrYq11.222	224003_at	NR_001543
3.06	3.42	0.36	3.19E-02	2.98E-01	---	---	---	236458_at	---
6.65	7.09	0.45	3.19E-02	2.99E-01	RASL10B	RAS-like, family 10, member B	chr17q12	244656_at	NM_033315
3.26	3.63	0.38	3.19E-02	2.99E-01	---	---	---	1557630_s_at	---
6.36	7.59	1.23	3.20E-02	2.99E-01	HRSP12	heat-responsive protein 12	chr8q22	203790_s_at	NM_005836
3.24	3.80	0.56	3.20E-02	2.99E-01	DCBLD2	discoidin, CUB and LCCL domain containing 2	chr3q12.1|3	213865_at	NM_080927
2.01	2.29	0.28	3.20E-02	2.99E-01	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	chr10p11.23	238451_at	NM_173496
4.05	4.49	0.43	3.20E-02	2.99E-01	ZNF75A	zinc finger protein 75a	chr16p13.11	239204_at	NM_153028
4.80	5.28	0.48	3.20E-02	2.99E-01	---	---	---	238082_at	---
4.13	4.48	0.35	3.20E-02	2.99E-01	CARD11	caspase recruitment domain family, member 11	chr7p22	1562368_at	NM_032415
1.98	2.22	0.24	3.20E-02	2.99E-01	ANKRD12	Ankyrin repeat domain 12	chr18p11.22	216563_at	NM_001083625 /// NM_015208
4.79	5.46	0.67	3.21E-02	2.99E-01	ACP5	acid phosphatase 5, tartrate resistant	chr19p13.3-p13.2	204638_at	NM_001111034 /// NM_001111035 /// NM_001111036 /// NM_001611
2.73	3.07	0.34	3.21E-02	3.00E-01	ARL10	ADP-ribosylation factor-like 10	chr5q35.2	1553207_at	NM_173664
4.02	4.60	0.58	3.21E-02	3.00E-01	RAB18	RAB18, member RAS oncogene family	chr10p12.1	229398_at	NM_021252
1.92	2.24	0.32	3.22E-02	3.00E-01	---	---	---	241068_at	---
3.95	4.29	0.34	3.22E-02	3.00E-01	---	---	---	237913_at	---
2.22	2.56	0.34	3.22E-02	3.00E-01	SNRK	SNF related kinase	chr3p22.1	207474_at	NM_001100594 /// NM_017719
5.14	5.62	0.48	3.22E-02	3.00E-01	CYP4V2	Cytochrome P450, family 4, subfamily V, polypeptide 2	chr4q35.2	229959_at	NM_207352
3.76	4.17	0.42	3.22E-02	3.00E-01	SLCO4A1	Solute carrier organic anion transporter family, member 4A1	chr20q13.33	229239_x_at	NM_016354
2.75	3.13	0.37	3.22E-02	3.00E-01	---	---	---	241131_at	---
3.10	3.39	0.29	3.22E-02	3.00E-01	C1orf115	Chromosome 1 open reading frame 115	chr1q41	230159_at	NM_024709
7.82	8.86	1.03	3.23E-02	3.00E-01	OSBPL8	oxysterol binding protein-like 8	chr12q14	212582_at	NM_001003712 /// NM_020841
4.51	4.97	0.46	3.23E-02	3.00E-01	DEGS2	degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)	chr14q32.2	236496_at	NM_206918
5.41	6.56	1.15	3.24E-02	3.00E-01	FNIP2	folliculin interacting protein 2	chr4q32.1	226460_at	NM_020840
5.74	6.26	0.51	3.24E-02	3.00E-01	PLEKHN1	pleckstrin homology domain containing, family N member 1	chr1p36.33	224125_at	NM_032129
10.03	10.53	0.50	3.23E-02	3.00E-01	---	---	---	AFFX-BioDn-3_at	---
2.88	3.35	0.47	3.23E-02	3.00E-01	ZNHIT2	zinc finger, HIT type 2	chr11q13	227734_s_at	NM_014205
2.77	3.23	0.46	3.23E-02	3.00E-01	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	chr1q22	234072_at	NM_022367
7.11	7.54	0.43	3.23E-02	3.00E-01	---	---	---	241799_x_at	---
1.93	2.29	0.37	3.23E-02	3.00E-01	---	---	---	237762_at	---
2.38	2.72	0.35	3.23E-02	3.00E-01	RIPK5	receptor interacting protein kinase 5	chr1q32.1	211514_at	NM_015375 /// NM_199462

2.44	2.77	0.33	3.24E-02	3.00E-01	SLC22A24	solute carrier family 22, member 24	chr11q12.3	1553923_at	XM_001720378 /// XM_001720395 /// XM_001720420																				
2.94	3.23	0.29	3.23E-02	3.00E-01	LOC100131721	hypothetical protein LOC100131721	chr8q21.13	236271_at	XM_001716076 /// XM_001716120 /// XM_001716134																				
2.59	3.11	0.51	3.24E-02	3.00E-01	C2orf72	chromosome 2 open reading frame 72	chr2q37.1	213148_at	XM_001129456 /// XM_001132119 /// XM_001715135																				
5.12	5.54	0.43	3.24E-02	3.00E-01	STAT2	signal transducer and activator of transcription 2, 113kDa	chr12q13.2	217199_s_at	NM_005419																				
4.49	4.84	0.35	3.24E-02	3.00E-01	LOC90586	AOC3 pseudogene	chr17q21.31	216601_at	NR_002773																				
2.83	3.10	0.27	3.24E-02	3.00E-01	HGD /// LOC100132552 /// LOC727722	homogentisate 1,2-dioxygenase (homogentisate oxidase) /// similar to homogentisate 1,2-dioxygenase /// homogentisate 1,2-dioxygenase like	chr3q13.33	237029_at	NM_000187 /// XM_001713606 /// XM_001719739																				
2.57	2.82	0.26	3.24E-02	3.00E-01	ASCL1	achaete-scute complex homolog 1 (Drosophila)	chr12q23.2	209986_at	NM_004316																				
2.90	3.45	0.55	3.25E-02	3.00E-01	USP25	ubiquitin specific peptidase 25	chr21q11.2	1563497_at	NM_013396																				
2.78	3.30	0.52	3.25E-02	3.00E-01	TMEM20	transmembrane protein 20	chr10q23.33	231012_at	NM_001134658 /// NM_153226																				
3.89	4.31	0.42	3.25E-02	3.00E-01	C1orf86	Hypothetical protein LOC100129828	chr1p36.33	228197_at	NM_182533 /// XM_001718861																				
3.04	3.46	0.42	3.25E-02	3.00E-01	BRD7P3	bromodomain containing 7 pseudogene 3	chr6q22.1-q22.33	221093_at	---																				
2.53	2.86	0.33	3.25E-02	3.00E-01	ODZ1	odz, odd Oz/ten-m homolog 1(Drosophila)	chrXq25	1553007_a_at	NM_014253																				
1.94	2.23	0.29	3.25E-02	3.00E-01	---	---	---	1563339_at	---																				
4.30	4.66	0.36	3.25E-02	3.00E-01	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	chr11q23.3	211845_at	NM_002855 /// NM_203285 /// NM_203286																				
6.51	6.90	0.39	3.25E-02	3.00E-01	TRPV6	transient receptor potential cation channel, subfamily V, member 6	chr7q33-q34	206827_s_at	NM_018646																				
3.63	4.08	0.45	3.26E-02	3.00E-01	KRT6A /// KRT6B /// KRT6C	keratin 6A /// keratin 6B /// keratin 6C	chr12q12-q13 /// chr12q13.13	214580_x_at	NM_005554 /// NM_005555 /// NM_173086																				
3.83	4.24	0.41	3.26E-02	3.01E-01	SLC44A1	solute carrier family 44, member 1	chr9q31.2	228485_s_at	NM_080546																				
3.07	3.49	0.42	3.26E-02	3.01E-01	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	chr11q13.5-q14.1	206277_at	NM_002564 /// NM_176071 /// NM_176072																				
4.32	4.76	0.44	3.26E-02	3.01E-01	ZFYVE28	zinc finger, FYVE domain containing 28	chr4p16.3	232408_at	NM_020972																				
2.32	2.66	0.34	3.27E-02	3.01E-01	HHLA2	HERV-H LTR-associating 2	chr3q13.13	220812_s_at	NM_007072																				
5.77	6.42	0.65	3.27E-02	3.01E-01	CEP68	centrosomal protein 68kDa	chr2p14	212677_s_at	NM_015147																				
5.52	6.89	1.37	3.28E-02	3.01E-01	ANKHD1 /// ANKHD1-EIF4EBP3 /// EIF4EBP3	ankyrin repeat and KH domain containing 1 /// ANKHD1-EIF4EBP3 /// eukaryotic translation initiation factor 4E binding protein 3	chr5q31.3	208772_at	NM_003732 /// NM_017747 /// NM_017978 /// NM_020690 /// NM_024668																				
7.52	8.72	1.19	3.28E-02	3.01E-01	KIF5B	kinesin family member 5B	chr10pter-q22.1	201991_s_at	NM_004521																				
3.21	3.86	0.64	3.28E-02	3.01E-01	LDHD	lactate dehydrogenase D	chr16q23.1	229241_at	NM_153486 /// NM_194436																				
3.19	3.83	0.64	3.29E-02	3.02E-01	---	---	---	1560026_at	---																				
2.70	3.09	0.40	3.29E-02	3.02E-01	DENND5B	DENN/MADD domain containing 5B	chr12p11.21	215058_at	NM_144973																				
6.49	7.32	0.84	3.29E-02	3.02E-01	CRYAB	crystallin, alpha B	chr11q22.3-q23.1	209283_at	NM_001885																				
2.31	2.71	0.40	3.29E-02	3.02E-01	SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	chr11q13.4	243570_at	NM_014752																				
4.32	5.14	0.82	3.30E-02	3.02E-01	PSMB7	Proteasome (prosome, macropain) subunit, beta type, 7	chr9q34.11-q34.12	244801_at	NM_002799																				
2.71	3.02	0.31	3.30E-02	3.02E-01	---	---	---	231141_at	---																				
2.24	2.59	0.35	3.30E-02	3.03E-01	ARHGAP24	Rho GTPase activating protein 24	chr4q21.23-q21.3	230802_at	NM_001025616 /// NM_001042669 /// NM_031305																				
10.89	11.30	0.41	3.30E-02	3.03E-01	---	---	---	AFFX-CreX-5_at	---																				
2.18	2.56	0.38	3.31E-02	3.03E-01	ZNF233	zinc finger protein 233	chr19q13.31	232986_at	NM_181756																				
4.66	5.17	0.51	3.31E-02	3.03E-01	PPAPDC2	phosphatidic acid phosphatase type 2 domain containing 2	chr9p24.1	227385_at	NM_203453																				

3.51	3.89	0.38	3.31E-02	3.03E-01	GRIN3B	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B	chr19p13.3	233892_at	NM_138690
4.32	4.67	0.35	3.31E-02	3.03E-01	---	---	---	243633_at	---
3.35	3.66	0.31	3.31E-02	3.03E-01	FKBP6	FK506 binding protein 6, 36kDa	chr7q11.23	206763_at	NM_003602
2.94	3.41	0.46	3.31E-02	3.03E-01	ATAD2B	ATPase family, AAA domain containing 2B	chr2p24.1-p23.3	232908_at	NM_017552
2.48	2.79	0.31	3.31E-02	3.03E-01	---	---	---	241737_x_at	---
2.40	2.79	0.39	3.31E-02	3.03E-01	---	---	---	231621_at	---
7.17	7.85	0.68	3.32E-02	3.03E-01	ACAA2	acetyl-Coenzyme A acyltransferase 2	chr18q21.1	202003_s_at	NM_006111
6.64	7.17	0.54	3.32E-02	3.03E-01	RRAGD	Ras-related GTP binding D	chr6q15-q16	221524_s_at	NM_021244
4.69	5.90	1.20	3.32E-02	3.03E-01	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	chr1q22	222667_s_at	NM_018489
2.61	2.99	0.38	3.32E-02	3.03E-01	---	---	---	236342_at	---
2.31	2.64	0.33	3.32E-02	3.03E-01	C7orf34	chromosome 7 open reading frame 34	chr7q34	231435_at	NM_178829
3.47	3.94	0.47	3.32E-02	3.03E-01	---	---	---	243233_at	---
2.60	3.04	0.44	3.32E-02	3.03E-01	DOCK3	dedicator of cytokinesis 3	chr3p21.31	213482_at	NM_004947
3.24	3.62	0.38	3.32E-02	3.03E-01	---	---	---	216749_at	---
2.80	3.12	0.32	3.32E-02	3.03E-01	EYA2	eyes absent homolog 2 (Drosophila)	chr20q13.1	209692_at	NM_005244 /// NM_172110 /// NM_172111 /// NM_172112 /// NM_172113
5.43	5.93	0.50	3.33E-02	3.03E-01	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	chr11q12	224357_s_at	NM_024021 /// NM_148975
2.57	2.99	0.42	3.33E-02	3.03E-01	LOC285300	hypothetical protein LOC285300	chr3p14.1	1563691_at	---
4.64	5.12	0.47	3.33E-02	3.04E-01	---	---	---	220691_at	---
3.32	3.81	0.49	3.33E-02	3.04E-01	---	---	---	239966_at	---
2.54	2.97	0.43	3.33E-02	3.04E-01	SCNN1B	sodium channel, nonvoltage-gated 1, beta	chr16p12.2-p12.1	205464_at	NM_000336
3.01	3.41	0.40	3.33E-02	3.04E-01	---	---	---	210921_at	---
2.67	3.09	0.42	3.33E-02	3.04E-01	ATP11A	ATPase, class VI, type 11A	chr13q34	241603_at	NM_015205 /// NM_032189
3.04	3.33	0.28	3.34E-02	3.04E-01	EFTUD2	elongation factor Tu GTP binding domain containing 2	chr17q21.31	222397_at	NM_004247
3.04	3.75	0.72	3.34E-02	3.04E-01	---	---	---	232431_at	---
2.97	3.48	0.51	3.34E-02	3.04E-01	SNORA71A	small nucleolar RNA, H/ACA box 71A	chr20q11.23	1565859_at	NR_002911
2.89	3.34	0.46	3.34E-02	3.04E-01	AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	chr12p11.21 /// chr1p31.3	204348_s_at	NM_001002921 /// NM_001005353 /// NM_013410 /// NM_203464 /// XM_001132080 /// XM_001725174 /// XM_928632
2.69	3.13	0.44	3.34E-02	3.04E-01	LRRC37A /// LRRC37A2	leucine rich repeat containing 37A /// leucine rich repeat containing 37, member A2	chr17q21.31 /// chr17q21.32	206088_at	NM_001006607 /// NM_014834
2.22	2.51	0.30	3.34E-02	3.04E-01	---	---	---	1562230_at	---
2.02	2.29	0.27	3.34E-02	3.04E-01	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	chr6q27	215904_at	NM_001040000 /// NM_001040001 /// NM_005936
2.60	3.01	0.41	3.35E-02	3.04E-01	---	---	---	242839_at	---
2.12	2.61	0.49	3.35E-02	3.04E-01	ZNF385B	zinc finger protein 385B	chr2q31.2-q31.3	1555801_s_at	NM_001113397 /// NM_001113398 /// NM_152520
3.84	4.28	0.44	3.35E-02	3.04E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	206870_at	NM_001001928 /// NM_005036
2.31	2.69	0.37	3.35E-02	3.04E-01	HIST1H2BL /// HIST1H2BN /// HIST2H3PS2	histone cluster 1, H2bl /// histone cluster 1, H2bn /// histone cluster 2, H3, pseudogene 2	chr1q21.1 /// chr6p22-p21.3	207611_at	NM_003519 /// NM_003520
2.02	2.31	0.29	3.35E-02	3.04E-01	WDR78	WD repeat domain 78	chr1p31.3	1554140_at	NM_024763 /// NM_207014
5.01	5.28	0.27	3.35E-02	3.04E-01	LOC340085	hypothetical protein LOC340085	chr5q11.2	232455_x_at	---
5.00	5.43	0.43	3.35E-02	3.04E-01	SMOC1	SPARC related modular calcium binding 1	chr14q24.2	222784_at	NM_001034852 /// NM_022137
3.17	3.58	0.41	3.36E-02	3.04E-01	VPS8	Vacuolar protein sorting 8 homolog (S. cerevisiae)	chr3q27.2	239917_at	NM_001009921 /// NM_015303
6.69	7.86	1.18	3.36E-02	3.05E-01	USP47	ubiquitin specific peptidase 47	chr11p15.3	221518_s_at	NM_017944
2.57	3.02	0.46	3.36E-02	3.05E-01	KBTBD7	kelch repeat and BTB (POZ) domain containing 7	chr13q14.11	229970_at	NM_032138
3.02	3.40	0.38	3.36E-02	3.05E-01	---	---	---	1561910_at	---

2.16	2.46	0.30	3.36E-02	3.05E-01	---	---	---	237677_at	---
3.66	4.32	0.66	3.36E-02	3.05E-01	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	chrXq22.3	226421_at	NM_001025580 /// NM_015365
5.22	5.58	0.36	3.37E-02	3.05E-01	PLEKHB1	Pleckstrin homology domain containing, family B (evectins) member 1	chr11q13.5-q14.1	229047_at	NM_001130033 /// NM_001130034 /// NM_001130035 /// NM_001130036 /// NM_021200
3.21	3.60	0.40	3.37E-02	3.05E-01	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	chr6p25	1556950_s_at	NM_004568
2.09	2.78	0.69	3.37E-02	3.05E-01	KCNT2	Potassium channel, subfamily T, member 2	chr1q31.3	234103_at	NM_198503
2.78	3.16	0.37	3.37E-02	3.05E-01	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17p13.3	1557112_a_at	NM_001128159 /// NM_018289
3.89	5.14	1.25	3.38E-02	3.05E-01	RASEF	RAS and EF-hand domain containing	chr9q21.32	1553186_x_at	NM_152573
5.69	6.70	1.00	3.38E-02	3.05E-01	ANKRD46	ankyrin repeat domain 46	chr8q22.3	212731_at	NM_198401
5.87	6.22	0.35	3.38E-02	3.05E-01	GJC2	gap junction protein, gamma 2, 47kDa	chr1q42.13	207025_at	NM_020435
1.85	2.15	0.30	3.38E-02	3.05E-01	---	---	---	240741_x_at	---
2.01	3.18	1.17	3.39E-02	3.05E-01	AK7	adenylate kinase 7	chr14q32.2	1553734_at	NM_152327
3.29	3.93	0.64	3.38E-02	3.05E-01	RAB3B	RAB3B, member RAS oncogene family	chr1p32-p31	205924_at	NM_002867
2.68	3.31	0.62	3.38E-02	3.05E-01	---	---	---	243751_at	---
3.18	3.61	0.42	3.39E-02	3.05E-01	ADCY10	adenylate cyclase 10 (soluble)	chr1q24	214547_at	NM_018417
3.03	3.43	0.40	3.38E-02	3.05E-01	---	---	---	1563539_at	---
3.75	4.09	0.34	3.39E-02	3.05E-01	FRMD8	FERM domain containing 8	chr11q13	210043_at	NM_031904
4.12	4.46	0.33	3.39E-02	3.05E-01	TMEM39A	transmembrane protein 39A	chr3q13.33	241374_at	NM_018266
2.58	2.86	0.27	3.39E-02	3.05E-01	CHP2	calcineurin B homologous protein 2	chr16p12.1	206149_at	NM_022097
1.84	2.19	0.35	3.39E-02	3.05E-01	FLJ11996	hypothetical protein FLJ11996	chr18p11.23	207487_at	XR_040967 /// XR_040968 /// XR_040969
6.50	6.92	0.42	3.40E-02	3.05E-01	RAB7L1	RAB7, member RAS oncogene family-like 1	chr1q32	243777_at	NM_003929
5.71	6.28	0.56	3.40E-02	3.06E-01	SARDH	sarcosine dehydrogenase	chr9q33-q34	234536_at	NM_001134707 /// NM_007101
4.32	4.81	0.49	3.40E-02	3.06E-01	ZMIZ1	zinc finger, MIZ-type containing 1	chr10q22.3	232508_at	NM_020338
2.64	3.12	0.48	3.40E-02	3.06E-01	---	---	---	232286_at	---
1.80	2.09	0.29	3.40E-02	3.06E-01	---	---	---	1563649_at	---
2.37	2.66	0.29	3.40E-02	3.06E-01	---	---	---	239990_at	---
2.35	2.80	0.45	3.41E-02	3.06E-01	CBLN1	cerebellin 1 precursor	chr16q12.1	205747_at	NM_004352
2.49	2.89	0.40	3.41E-02	3.06E-01	ROPN1 /// ROPN1B	ropporin, rhophilin associated protein 1 /// ropporin, rhophilin associated protein 1B	chr3q21.1 /// chr3q21.2	220425_x_at	NM_001012337 /// NM_017578
4.23	4.71	0.48	3.41E-02	3.06E-01	UBE3A	ubiquitin protein ligase E3A	chr15q11-q13	212278_x_at	NM_000462 /// NM_130838 /// NM_130839
6.18	6.84	0.66	3.41E-02	3.06E-01	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	chr11q23.1-q23.2	223989_s_at	NM_015523
3.73	4.22	0.49	3.41E-02	3.06E-01	---	---	---	237311_at	---
2.25	2.59	0.34	3.41E-02	3.06E-01	---	---	---	1569052_at	---
2.50	2.88	0.38	3.42E-02	3.06E-01	C12orf51	Chromosome 12 open reading frame 51	chr12q24.13	230216_at	NM_001109662
5.73	6.18	0.45	3.42E-02	3.06E-01	RNASET2	ribonuclease T2	chr6q27	220096_at	NM_003730
2.18	2.51	0.33	3.42E-02	3.06E-01	SMAD1	SMAD family member 1	chr4q31	208015_at	NM_001003688 /// NM_005900
2.60	2.93	0.33	3.42E-02	3.06E-01	C10orf71 /// LOC100130757	chromosome 10 open reading frame 71 /// similar to hCG1996658	chr10q11.23	232456_at	NM_199459 /// XM_001718949 /// XM_001719012 /// XM_001719395
2.50	2.81	0.31	3.42E-02	3.06E-01	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	chr1q32.1	201958_s_at	NM_002481 /// NM_032103 /// NM_032104 /// NM_032105
4.31	4.97	0.66	3.43E-02	3.06E-01	PRKCA	protein kinase C, alpha	chr17q22-q23.2	215195_at	NM_002737
3.37	3.60	0.23	3.43E-02	3.06E-01	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	chr12q15	202970_at	NM_003583 /// NM_006482
3.94	4.62	0.68	3.44E-02	3.06E-01	RAB6B	RAB6B, member RAS oncogene family	chr3q22.1	225259_at	NM_016577
2.87	3.49	0.62	3.43E-02	3.06E-01	---	---	---	1556595_at	---
9.60	10.17	0.57	3.44E-02	3.06E-01	SKP1	S-phase kinase-associated protein 1	chr5q31	207974_s_at	NM_006930 /// NM_170679
5.38	5.79	0.41	3.43E-02	3.06E-01	HAX1	HCLS1 associated protein X-1	chr1q21.3	244865_at	NM_001018837 /// NM_006118

1.82	2.16	0.34	3.44E-02	3.06E-01	---	---	---	232325_at	---
3.00	3.28	0.28	3.44E-02	3.06E-01	SLC34A1	solute carrier family 34 (sodium phosphate), member 1	chr5q35	217530_at	NM_003052
1.71	1.97	0.26	3.43E-02	3.06E-01	---	---	---	1557772_at	---
5.63	6.12	0.49	3.44E-02	3.06E-01	ZFPL1	zinc finger protein-like 1	chr11q13	214311_at	NM_006782
4.40	4.64	0.24	3.44E-02	3.06E-01	---	---	---	241515_at	---
5.87	7.12	1.25	3.44E-02	3.06E-01	EPRS	glutamyl-prolyl-tRNA synthetase	chr1q41-q42	200842_s_at	NM_004446
7.18	8.10	0.93	3.44E-02	3.06E-01	CETN2	centrin, EF-hand protein, 2	chrXq28	209194_at	NM_004344
3.58	4.50	0.92	3.44E-02	3.07E-01	TRPS1	trichorhinophalangeal syndrome I	chr8q24.12	224218_s_at	NM_014112
4.95	6.16	1.20	3.45E-02	3.07E-01	GALNTL1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	chr14q24.1	230418_s_at	NM_020692
2.10	2.39	0.29	3.45E-02	3.07E-01	TACR1	tachykinin receptor 1	chr2p13.1	208048_at	NM_001058 /// NM_015727
1.85	2.14	0.29	3.45E-02	3.07E-01	OR2J2	olfactory receptor, family 2, subfamily J, member 2	chr6p22.2-p21.31	208508_s_at	NM_030905
5.88	6.34	0.46	3.46E-02	3.07E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	209534_x_at	NM_006738 /// NM_007200 /// NM_144767
3.85	4.28	0.43	3.46E-02	3.07E-01	ZNF577	zinc finger protein 577	chr19q13.33	223581_at	NM_032679
4.66	5.06	0.40	3.46E-02	3.07E-01	LOC100132739 /// ZIC1	hypothetical protein LOC100132739 /// Zic family member 1 (odd-paired homolog, Drosophila)	chr3q24	234716_at	NM_003412 /// XM_001717528 /// XM_001718250 /// XM_001718465
4.57	4.97	0.40	3.46E-02	3.07E-01	NNAT	neuronatin	chr20q11.2-q12	204239_s_at	NM_005386 /// NM_181689
3.70	4.08	0.38	3.46E-02	3.07E-01	GDAP1	ganglioside-induced differentiation-associated protein 1	chr8q21.11	226271_at	NM_001040875 /// NM_018972
4.81	5.19	0.38	3.46E-02	3.07E-01	---	---	---	238359_at	---
3.22	3.58	0.36	3.46E-02	3.07E-01	IGHG1 /// LOC90925	immunoglobulin heavy constant gamma 1 (G1m marker) /// hypothetical protein LOC90925	chr14q32.33	215721_at	XR_017976
4.60	4.95	0.34	3.45E-02	3.07E-01	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	chr22q13.2	214210_at	NM_006358
2.02	2.31	0.30	3.46E-02	3.07E-01	---	---	---	1559932_at	---
2.36	2.63	0.28	3.46E-02	3.07E-01	---	---	---	1561352_at	---
2.01	2.40	0.39	3.47E-02	3.07E-01	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	chr4q31.22	239852_at	NM_172250
2.78	3.08	0.30	3.47E-02	3.07E-01	BSND	Bartter syndrome, infantile, with sensorineural deafness (Barttin)	chr1p32.1	1552548_at	NM_057176
2.35	3.10	0.75	3.47E-02	3.07E-01	GPATCH2	G patch domain containing 2	chr1q41	1556126_s_at	NM_018040
2.39	2.68	0.29	3.47E-02	3.07E-01	---	---	---	239338_x_at	---
5.85	6.26	0.41	3.48E-02	3.08E-01	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	chr11q13	211004_s_at	NM_000694 /// NM_001030010
3.71	4.10	0.40	3.47E-02	3.08E-01	MIB2	Mindbomb homolog 2 (Drosophila)	chr1p36.33	241378_at	NM_080875
2.45	2.82	0.37	3.47E-02	3.08E-01	---	---	---	241850_at	---
3.21	3.51	0.30	3.47E-02	3.08E-01	AIG1	androgen-induced 1	chr6q24.2	232810_at	NM_016108
6.01	7.70	1.69	3.48E-02	3.08E-01	EDIL3	EGF-like repeats and discoidin I-like domains 3	chr5q14	225275_at	NM_005711
4.30	5.23	0.93	3.48E-02	3.08E-01	---	---	---	227395_at	---
10.57	11.13	0.57	3.48E-02	3.08E-01	TncRNA	trophoblast-derived noncoding RNA	chr11q13.1	234989_at	NR_002802
2.37	2.70	0.33	3.48E-02	3.08E-01	KIF2C	kinesin family member 2C	chr1p34.1	211519_s_at	NM_006845
6.80	7.38	0.58	3.48E-02	3.08E-01	LOC348162 /// LOC642799 /// LOC729602	hypothetical protein 348162 /// hypothetical LOC642799 /// similar to nuclear pore complex interacting protein	chr16p11.2 /// chr16p13.11 /// chr18p11.21	215123_at	XM_001717235 /// XM_001720898 /// XM_001720909 /// XM_001720910 /// XR_016550
4.53	5.18	0.65	3.50E-02	3.08E-01	---	---	---	229670_at	---
4.43	5.05	0.62	3.49E-02	3.08E-01	C1orf97	chromosome 1 open reading frame 97	chr1q32.3	224444_s_at	XR_040057 /// XR_040058 /// XR_040059
4.99	5.56	0.57	3.49E-02	3.08E-01	DERL3	Der1-like domain family, member 3	chr22q11.23	229719_s_at	NM_001002862 /// NM_198440
5.64	6.10	0.46	3.49E-02	3.08E-01	MVK	mevalonate kinase	chr12q24	204056_s_at	NM_000431 /// NM_001114185
3.01	3.47	0.46	3.50E-02	3.08E-01	---	---	---	238185_at	---

3.53	3.95	0.43	3.49E-02	3.08E-01	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	chr11p15.5	214385_s_at	NM_017511 /// XM_001134429 /// XM_001714104 /// XM_001714774
3.13	3.49	0.36	3.49E-02	3.08E-01	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	chr5q14.2	223677_at	NM_001131028 /// NM_031482
4.37	4.72	0.35	3.49E-02	3.08E-01	CASR	Calcium-sensing receptor	chr3q13	240886_at	NM_000388
1.93	2.24	0.31	3.49E-02	3.08E-01	LPPR4	plasticity related gene 1	chr1p21.2	213496_at	NM_014839
3.45	3.98	0.53	3.50E-02	3.08E-01	RBM41	RNA binding motif protein 41	chrXq22.1-q24	219754_at	NM_018301
2.51	2.79	0.28	3.50E-02	3.08E-01	---	---	---	237432_at	---
4.01	4.45	0.44	3.50E-02	3.08E-01	LOC729397	hypothetical LOC729397	chr1q42.3	225854_x_at	XM_001716181 /// XM_001716365
5.71	6.42	0.71	3.50E-02	3.08E-01	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	chr5q13.1	212239_at	NM_181504 /// NM_181523 /// NM_181524
4.64	5.25	0.61	3.51E-02	3.08E-01	LRP5	low density lipoprotein receptor-related protein 5	chr11q13.4	209468_at	NM_002335
2.96	3.36	0.40	3.50E-02	3.08E-01	CCDC36	coiled-coil domain containing 36	chr3p21.31	1554909_at	NM_178173
4.46	4.85	0.39	3.50E-02	3.08E-01	C11orf16	chromosome 11 open reading frame 16	chr11p15.3	220344_at	NM_020643
3.06	3.39	0.33	3.50E-02	3.08E-01	---	---	---	1556304_s_at	---
2.28	2.59	0.30	3.50E-02	3.08E-01	---	---	---	244438_at	---
2.04	2.30	0.27	3.51E-02	3.08E-01	---	---	---	1563129_at	---
2.48	2.84	0.37	3.51E-02	3.08E-01	---	---	---	208360_s_at	---
4.10	4.60	0.50	3.51E-02	3.09E-01	RHAG	Rh-associated glycoprotein	chr6p21.1-p11	206146_s_at	NM_000324
4.31	4.68	0.37	3.51E-02	3.09E-01	DBT	dihydrolipoamide branched chain transacylase E2	chr1p31	231919_at	NM_001918
4.10	4.44	0.34	3.51E-02	3.09E-01	GRM4	glutamate receptor, metabotropic 4	chr6p21.3	210234_at	NM_000841
5.89	7.44	1.54	3.52E-02	3.09E-01	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	chr5q13.3	219625_s_at	NM_001130105 /// NM_005713 /// NM_031361
6.12	6.63	0.51	3.52E-02	3.09E-01	ANKRD11	ankyrin repeat domain 11	chr16q24.3	228356_at	NM_013275
6.03	6.52	0.49	3.51E-02	3.09E-01	MUC3A	mucin 3A, cell surface associated	chr7q22	217117_x_at	XM_001719499 /// XM_001725354
3.10	3.56	0.47	3.52E-02	3.09E-01	MSR1	macrophage scavenger receptor 1	chr8p22	208423_s_at	NM_002445 /// NM_138715 /// NM_138716
2.88	3.31	0.43	3.52E-02	3.09E-01	TTLL6	tubulin tyrosine ligase-like family, member 6	chr17q21.32	230924_at	NM_001130918 /// NM_173623
2.97	3.33	0.37	3.52E-02	3.09E-01	---	---	---	233053_at	---
2.16	2.49	0.33	3.51E-02	3.09E-01	CAPN6	calpain 6	chrXq23	202966_at	NM_014289
1.91	2.17	0.26	3.52E-02	3.09E-01	SLCO5A1	solute carrier organic anion transporter family, member 5A1	chr8q13.3	220984_s_at	NM_030958
5.22	6.74	1.53	3.52E-02	3.09E-01	CCDC3	coiled-coil domain containing 3	chr10p13	223316_at	NM_031455
11.23	11.74	0.51	3.52E-02	3.09E-01	MGST1	microsomal glutathione S-transferase 1	chr12p12.3-p12.1	231736_x_at	NM_020300 /// NM_145764 /// NM_145791 /// NM_145792
2.53	2.83	0.30	3.52E-02	3.09E-01	LOC100131402	hypothetical protein LOC100131402	chr1q32.1	243648_at	XM_001725069 /// XM_001726819
6.45	7.08	0.63	3.52E-02	3.09E-01	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	chr8q22.2	204068_at	NM_006281
4.60	5.70	1.10	3.52E-02	3.09E-01	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	chr12q15-q21	201602_s_at	NM_002480
2.36	2.84	0.49	3.52E-02	3.09E-01	CP	ceruloplasmin (ferroxidase)	chr3q23-q25	1558034_s_at	NM_000096
9.18	10.22	1.04	3.53E-02	3.09E-01	TXNIP	thioredoxin interacting protein	chr1q21.1	201008_s_at	NM_006472
2.28	2.58	0.30	3.53E-02	3.09E-01	---	---	---	244327_at	---
2.75	3.05	0.30	3.54E-02	3.09E-01	C8orf15	chromosome 8 open reading frame 15	chr8p23.1	240626_at	XR_041594 /// XR_041595 /// XR_041596
2.72	3.23	0.52	3.54E-02	3.09E-01	---	---	---	239714_at	---
4.69	5.11	0.43	3.54E-02	3.09E-01	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	chr19q13.3-q13.4	230531_at	NM_004977
5.34	6.65	1.31	3.54E-02	3.10E-01	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	chr2q33-q34	231873_at	NM_001204
2.65	3.45	0.79	3.54E-02	3.10E-01	---	---	---	1566948_at	---
2.63	3.06	0.43	3.55E-02	3.10E-01	---	---	---	1562955_at	---
2.34	2.71	0.37	3.55E-02	3.10E-01	FLJ30679	hypothetical protein FLJ30679	chr16q24.1	1553258_at	XM_001715503 /// XM_001725647 /// XM_001726881
10.49	10.84	0.35	3.54E-02	3.10E-01	PARK7	Parkinson disease (autosomal recessive, early onset) 7	chr1p36.23	200006_at	NM_001123377 /// NM_007262

1.77	2.02	0.25	3.54E-02	3.10E-01	---	---	---	221144_at	---
3.56	3.78	0.23	3.54E-02	3.10E-01	COL10A1	collagen, type X, alpha 1	chr6q21-q22	205941_s_at	NM_000493
5.81	6.20	0.40	3.55E-02	3.10E-01	UNC13D	unc-13 homolog D (C. elegans)	chr17q25.1	226678_at	NM_199242
6.15	6.56	0.41	3.55E-02	3.10E-01	LARS	leucyl-tRNA synthetase	chr5q32	217810_x_at	NM_020117
2.12	2.45	0.33	3.55E-02	3.10E-01	SIAH1	seven in absentia homolog 1 (Drosophila)	chr16q12	232365_at	NM_001006610 /// NM_003031
3.72	4.24	0.52	3.56E-02	3.10E-01	---	---	---	240594_at	---
5.15	5.52	0.37	3.56E-02	3.10E-01	LOC96610	hypothetical gene LOC96610	chr22q11.22	226802_s_at	XR_040596
4.34	4.70	0.36	3.56E-02	3.10E-01	---	---	---	236569_at	---
2.64	2.95	0.30	3.56E-02	3.10E-01	---	---	---	241106_at	---
3.60	3.98	0.39	3.56E-02	3.10E-01	SMAD6	SMAD family member 6	chr15q21-q22	213565_s_at	NM_005585
6.32	6.89	0.57	3.56E-02	3.10E-01	TRIM25	tripartite motif-containing 25	chr17q23.2	224806_at	NM_005082
7.12	7.58	0.46	3.56E-02	3.10E-01	L3MBTL	l(3)mbt-like (Drosophila)	chr20q13.12	216076_at	NM_015478 /// NM_032107
3.47	3.87	0.41	3.56E-02	3.10E-01	MAP7D3	MAP7 domain containing 3	chrXq26.3	219576_at	NM_024597
8.57	9.59	1.02	3.56E-02	3.10E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	1558678_s_at	NR_002819
5.73	6.83	1.10	3.58E-02	3.10E-01	TMEM135	transmembrane protein 135	chr11q14.2	222209_s_at	NM_022918
6.65	7.10	0.45	3.58E-02	3.10E-01	SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila)	chr19q13.42	224431_s_at	NM_032701
3.07	3.53	0.45	3.57E-02	3.10E-01	LZTS1	leucine zipper, putative tumor suppressor 1	chr8p22	221719_s_at	NM_021020
4.48	4.93	0.45	3.58E-02	3.10E-01	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	chr19p13.3	223317_at	NM_032306
2.44	2.84	0.40	3.58E-02	3.10E-01	NT5E	5'-nucleotidase, ecto (CD73)	chr6q14-q21	1553994_at	NM_002526
2.29	2.66	0.36	3.57E-02	3.10E-01	NEK1	NIMA (never in mitosis gene a)-related kinase 1	chr4q33	1564093_at	NM_012224
2.28	2.62	0.34	3.57E-02	3.10E-01	---	---	---	240531_at	---
2.08	2.41	0.34	3.57E-02	3.10E-01	CNKSR2	connector enhancer of kinase suppressor of Ras 2	chrXp22.12	229116_at	NM_014927
2.33	2.65	0.32	3.58E-02	3.10E-01	---	---	---	238212_at	---
10.21	10.53	0.32	3.58E-02	3.10E-01	YBX1	Y box binding protein 1	chr1p34	208628_s_at	NM_004559
2.67	2.98	0.31	3.57E-02	3.10E-01	SIM2	single-minded homolog 2 (Drosophila)	chr21q22.2|21q22.13	206558_at	NM_005069 /// NM_009586
3.96	4.64	0.68	3.58E-02	3.10E-01	IFT74	intraflagellar transport 74 homolog (Chlamydomonas)	chr9p21.2	219174_at	NM_001099222 /// NM_001099223 /// NM_001099224 /// NM_025103
2.99	3.31	0.32	3.58E-02	3.10E-01	H1FNT	H1 histone family, member N, testis-specific	chr12q13.11	238374_at	NM_181788
5.99	6.43	0.45	3.59E-02	3.11E-01	RANBP3	RAN binding protein 3	chr19p13.3	208272_at	NM_003624 /// NM_007320 /// NM_007322
4.90	5.32	0.42	3.59E-02	3.11E-01	---	---	---	230530_at	---
4.00	4.37	0.37	3.59E-02	3.11E-01	SCN2B	sodium channel, voltage-gated, type II, beta	chr11q23	210364_at	NM_004588
2.00	2.29	0.29	3.59E-02	3.11E-01	---	---	---	236697_at	---
8.70	9.58	0.88	3.60E-02	3.11E-01	FDFT1	farnesyl-diphosphate farnesyltransferase 1	chr8p23.1-p22	210950_s_at	NM_004462
2.75	3.89	1.15	3.60E-02	3.11E-01	---	---	---	1561956_at	---
6.11	6.80	0.69	3.60E-02	3.11E-01	RAB22A	RAB22A, member RAS oncogene family	chr20q13.32	213405_at	NM_020673
6.50	6.96	0.46	3.60E-02	3.11E-01	TNRC4	trinucleotide repeat containing 4	chr1q21	215045_at	NM_007185
4.52	4.93	0.41	3.60E-02	3.11E-01	S1PR2	sphingosine-1-phosphate receptor 2	chr19p13.2	208537_at	NM_004230
3.96	4.51	0.55	3.60E-02	3.11E-01	KIAA0644	KIAA0644 gene product	chr7p15.1	205151_s_at	NM_014817
7.98	8.78	0.80	3.61E-02	3.12E-01	SEC62	SEC62 homolog (S. cerevisiae)	chr3q26.2	208943_s_at	NM_003262
3.58	4.15	0.57	3.61E-02	3.12E-01	KPNA1	karyopherin alpha 1 (importin alpha 5)	chr3q21	202057_at	NM_002264
4.28	4.72	0.44	3.61E-02	3.12E-01	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	chr3p25.3	234714_x_at	NM_001001331 /// NM_001683
2.07	2.71	0.63	3.61E-02	3.12E-01	---	---	---	239591_at	---
4.26	5.39	1.14	3.62E-02	3.12E-01	---	---	---	1558410_s_at	---
6.58	7.24	0.67	3.62E-02	3.12E-01	ZC3HAV1	zinc finger CCCH-type, antiviral 1	chr7q34	225634_at	NM_020119 /// NM_024625
6.69	7.13	0.43	3.62E-02	3.12E-01	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	chr16q22.2	207416_s_at	NM_004555 /// NM_173163 /// NM_173164 /// NM_173165
3.11	3.45	0.35	3.62E-02	3.12E-01	KIF1A	kinesin family member 1A	chr2q37.3	225482_at	NM_004321
2.67	3.00	0.33	3.62E-02	3.12E-01	C5	complement component 5	chr9q33-q34	205500_at	NM_001735
5.54	6.09	0.54	3.62E-02	3.12E-01	LOC100131564	hypothetical protein LOC100131564	chr1p22.1	230073_at	XM_001714658 /// XM_001715045 /// XM_001719527
5.52	6.62	1.10	3.62E-02	3.12E-01	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	chr13q32.2	239246_at	NM_001001715 /// NM_005766

2.84	3.17	0.33	3.62E-02	3.12E-01	LOC100131262	hypothetical protein LOC100131262	---	1558152_at	XM_001717523 /// XM_001719220																				
4.63	5.32	0.69	3.63E-02	3.12E-01	IGLV2-11 /// IGLV2-18 /// IGLV2-23	immunoglobulin lambda variable 2-11 /// immunoglobulin lambda variable 2-18 /// immunoglobulin lambda variable 2-23	chr22q11.2	216984_x_at	---																				
6.22	6.68	0.46	3.63E-02	3.12E-01	LOC389458 /// RBAK	hypothetical LOC389458 /// RB-associated KRAB zinc finger	chr7p22.1	230439_at	NM_021163 /// NM_203393 /// NR_015343																				
2.32	2.65	0.33	3.63E-02	3.12E-01	---	---	---	1558121_at	---																				
3.76	4.08	0.32	3.63E-02	3.12E-01	ARID1A	AT rich interactive domain 1A (SWI-like)	chr1p35.3	207591_s_at	NM_006015 /// NM_139135																				
5.96	7.08	1.12	3.63E-02	3.12E-01	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	chr14q24.1	217775_s_at	NM_016026																				
4.04	4.58	0.54	3.64E-02	3.12E-01	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	chr2p24	211504_x_at	NM_004850																				
3.04	3.55	0.51	3.64E-02	3.12E-01	SGMS2	sphingomyelin synthase 2	chr4q25	227038_at	NM_152621																				
3.77	4.24	0.47	3.64E-02	3.12E-01	SUGT1L1	SGT1, suppressor of G2 allele of SKP1 like 1 (S. cerevisiae)	chr13q14.11	236770_at	NR_003365																				
5.84	6.28	0.44	3.63E-02	3.12E-01	MGC10814	hypothetical protein MGC10814	chr19p13.11	224134_at	---																				
2.47	2.77	0.30	3.64E-02	3.12E-01	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	chr2q11.2-q12	1558732_at	NM_004834 /// NM_145686 /// NM_145687																				
4.24	4.53	0.29	3.64E-02	3.12E-01	---	---	---	243326_at	---																				
4.74	5.03	0.29	3.64E-02	3.12E-01	---	---	---	241285_at	---																				
2.76	3.18	0.43	3.64E-02	3.12E-01	---	---	---	1559332_at	---																				
2.21	2.53	0.32	3.64E-02	3.12E-01	---	---	---	216783_at	---																				
4.00	4.59	0.60	3.65E-02	3.13E-01	---	---	---	239122_at	---																				
7.03	7.63	0.60	3.65E-02	3.13E-01	NFIB	nuclear factor I/B	chr9p24.1	209290_s_at	NM_005596																				
4.61	5.10	0.49	3.65E-02	3.13E-01	SDC2	syndecan 2	chr8q22-q23	212157_at	NM_002998																				
2.04	2.31	0.28	3.65E-02	3.13E-01	---	---	---	1565578_at	---																				
4.20	5.00	0.80	3.66E-02	3.13E-01	C9orf125	chromosome 9 open reading frame 125	chr9q31.1	213386_at	NM_032342																				
4.18	4.73	0.55	3.66E-02	3.13E-01	LBA1	lupus brain antigen 1	chr3p22.2	213261_at	NM_014831																				
2.94	3.43	0.48	3.66E-02	3.13E-01	ZFP28	zinc finger protein 28 homolog (mouse)	---	234937_x_at	NM_020828																				
4.73	5.13	0.40	3.66E-02	3.13E-01	OSM	oncostatin M	chr22q12.2	230170_at	NM_020530																				
4.13	4.50	0.37	3.66E-02	3.13E-01	C19orf2	chromosome 19 open reading frame 2	chr19q12	210157_at	NM_003796 /// NM_134447																				
2.14	2.49	0.35	3.66E-02	3.13E-01	NLRP6	NLR family, pyrin domain containing 6	chr11p15	1552932_at	NM_138329																				
2.02	2.29	0.27	3.66E-02	3.13E-01	---	---	---	1562835_at	---																				
2.76	3.03	0.27	3.66E-02	3.13E-01	MTMR10	myotubularin related protein 10	chr15q13.3	220286_at	NM_017762																				
2.81	3.15	0.34	3.66E-02	3.13E-01	---	---	---	242713_at	---																				
4.13	4.65	0.52	3.67E-02	3.13E-01	TMEM116	transmembrane protein 116	chr12q24.13	227172_at	NM_138341																				
2.48	2.80	0.32	3.67E-02	3.13E-01	HRH1	histamine receptor H1	chr3p25	205579_at	NM_000861 /// NM_001098211 /// NM_001098212 /// NM_001098213																				
3.05	3.68	0.63	3.67E-02	3.13E-01	LOC100130070 /// LOC100130775 /// LOC100131787 /// LOC100131905 /// LOC100132291 /// LOC100132488 /// RPS27	similar to metallopanstimulin /// similar to rCG63653 /// similar to metallopanstimulin /// similar to metallopanstimulin /// similar to hCG2027326 /// similar to rCG63653 /// ribosomal protein S27	chr12q12 /// chr12q23.2 /// chr19p12 /// chr1p13.3 /// chr1q21 /// chr1q25.1 /// chr4p15.31	236621_at	NM_001030 /// XM_001721002 /// XM_001722161 /// XM_001722965 /// XM_001723889 /// XM_001726077 /// XM_001726895 /// XR_037624 /// XR_037631 /// XR_037683 /// XR_038381 /// XR_038623 /// XR_038822 /// XR_039334 /// XR_039557 /// XR_039685 /// XR_039693 /// XR_042325 /// XR_042403																				
4.13	4.60	0.47	3.67E-02	3.13E-01	KCNQ1OT1	KCNQ1 overlapping transcript 1 (non-protein coding)	chr11p15	243428_at	NR_002728																				
3.66	4.13	0.46	3.67E-02	3.13E-01	---	---	---	241932_at	---																				

7.31	8.70	1.39	3.69E-02	3.14E-01	RNF13	ring finger protein 13	chr3q25.1	201779_s_at	NM_007282 /// NM_183381 /// NM_183383 /// NM_183384																				
3.18	3.76	0.58	3.68E-02	3.14E-01	FLJ25076	similar to CG4502-PA	chr5p15.31	226618_at	XR_040585 /// XR_040586																				
4.46	4.90	0.44	3.68E-02	3.14E-01	LEPREL1	leprecan-like 1	chr3q28	230813_at	NM_001134418 /// NM_018192																				
2.09	2.52	0.43	3.68E-02	3.14E-01	PCDHA1 /// PCDHA10 /// PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2	protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	chr5q31	210674_s_at	NM_014005 /// NM_018898 /// NM_018899 /// NM_018900 /// NM_018901 /// NM_018902 /// NM_018903 /// NM_018904 /// NM_018905 /// NM_018906 /// NM_018907 /// NM_018908 /// NM_018909 /// NM_018910 /// NM_018911 /// NM_031410 /// NM_031411 /// NM_031495 /// NM_031496 /// NM_031497 /// NM_031500 /// NM_031501 /// NM_031848 /// NM_031849 /// NM_031852 /// NM_031856 /// NM_031857 /// NM_031859 /// NM_031860 /// NM_031861 /// NM_031864 /// NM_031865 /// NM_031882 /// NM_031883																					
3.11	3.37	0.26	3.68E-02	3.14E-01	CACNG6	calcium channel, voltage-dependent, gamma subunit 6	chr19q13.4	224291_at	NM_031897 /// NM_145814 /// NM_145815																				
4.60	5.19	0.59	3.69E-02	3.14E-01	LRIG2	Leucine-rich repeats and immunoglobulin-like domains 2	chr1p13.1	238653_at	NM_014813																				
2.57	2.87	0.30	3.69E-02	3.14E-01	WDR72	WD repeat domain 72	chr15q21.3	238253_at	NM_182758																				
6.79	7.29	0.50	3.69E-02	3.14E-01	---	---	---	231161_x_at	---																				
4.27	4.87	0.61	3.69E-02	3.14E-01	CLCNKB	chloride channel Kb	chr1p36	1554749_s_at	NM_000085																				
6.61	7.23	0.62	3.70E-02	3.14E-01	PPAP2B	phosphatidic acid phosphatase type 2B	chr1pter-p22.1	212230_at	NM_003713 /// NM_177414																				
5.46	5.90	0.45	3.70E-02	3.14E-01	LOC728649 /// LOC728701	hypothetical LOC728649 /// hypothetical LOC728701	chr9q12	234380_x_at	XM_001128586 /// XM_001128647 /// XM_001732848																				
6.43	6.88	0.44	3.70E-02	3.14E-01	ADCY3	adenylate cyclase 3	chr2p23.3	209320_at	NM_004036																				
1.79	2.05	0.27	3.70E-02	3.14E-01	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	chr2p16.1	241103_at	NM_001122964 /// NM_020463																				
5.59	6.00	0.41	3.70E-02	3.14E-01	IFNAR2	interferon (alpha, beta and omega) receptor 2	chr21q22.1|21q22.11	204786_s_at	NM_000874 /// NM_207584 /// NM_207585																				
3.64	4.11	0.47	3.71E-02	3.14E-01	---	---	---	210598_at	---																				
3.92	4.25	0.33	3.71E-02	3.14E-01	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	chr9q34.3	204543_at	NM_005312 /// NM_198679																				
4.94	6.27	1.33	3.72E-02	3.14E-01	---	---	---	233611_at	---																				
5.39	6.62	1.23	3.73E-02	3.14E-01	TTC3	tetratricopeptide repeat domain 3	chr21q22.2	208663_s_at	NM_001001894 /// NM_003316																				
5.30	6.32	1.02	3.72E-02	3.14E-01	TMEM209	transmembrane protein 209	chr7q32.2	235158_at	NM_032842																				
2.49	3.50	1.01	3.72E-02	3.14E-01	REEP1	receptor accessory protein 1	chr2p11.2	204365_s_at	NM_022912																				

3.75	4.68	0.93	3.71E-02	3.14E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	205084_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844
4.08	4.94	0.87	3.73E-02	3.14E-01	CPLX1	complexin 1	chr4p16.3	223500_at	NM_006651
5.01	5.73	0.73	3.72E-02	3.14E-01	---	---	---	227630_at	---
9.00	9.71	0.71	3.72E-02	3.14E-01	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	chr1p13.2	200850_s_at	NM_006621
4.32	5.02	0.70	3.72E-02	3.14E-01	---	---	---	239404_at	---
3.75	4.42	0.67	3.72E-02	3.14E-01	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	chr18p11.22	242780_at	NM_003574 /// NM_194434
4.19	4.80	0.61	3.72E-02	3.14E-01	---	---	---	240539_at	---
4.24	4.82	0.58	3.73E-02	3.14E-01	---	---	---	243286_at	---
8.79	9.35	0.56	3.72E-02	3.14E-01	POMP	proteasome maturation protein	chr13q12.3	217769_s_at	NM_015932
3.93	4.45	0.52	3.71E-02	3.14E-01	STS	steroid sulfatase (microsomal), isozyme S	chrXp22.32	203768_s_at	NM_000351
4.13	4.60	0.46	3.73E-02	3.14E-01	---	---	---	240116_at	---
2.71	3.12	0.41	3.72E-02	3.14E-01	---	---	---	240099_at	---
6.80	7.21	0.41	3.73E-02	3.14E-01	NRG1	neuregulin 1	chr8p12	208232_x_at	NM_004495 /// NM_013956 /// NM_013957 /// NM_013958 /// NM_013959 /// NM_013960 /// NM_013961 /// NM_013962 /// NM_013964
3.45	3.85	0.40	3.72E-02	3.14E-01	41525	septin 8	chr5q31	226627_at	NM_001098811 /// NM_001098812 /// NM_001098813 /// NM_015146
2.87	3.22	0.35	3.71E-02	3.14E-01	MKNK1	MAP kinase interacting serine/threonine kinase 1	chr1p33	1560720_at	NM_003684 /// NM_198973
7.17	7.49	0.31	3.73E-02	3.14E-01	C10orf104	chromosome 10 open reading frame 104	chr10q22.1	224667_x_at	NM_173473
2.90	3.21	0.31	3.73E-02	3.14E-01	---	---	---	236964_at	---
3.40	3.71	0.31	3.73E-02	3.14E-01	POLR2F	Polymerase (RNA) II (DNA directed) polypeptide F	chr22q13.1	232643_at	NM_021974
1.91	2.22	0.31	3.72E-02	3.14E-01	---	---	---	233667_at	---
2.17	2.47	0.30	3.73E-02	3.14E-01	ZDHHC21	zinc finger, DHHC-type containing 21	chr9p22.3	233215_s_at	NM_178566
2.26	2.55	0.28	3.73E-02	3.14E-01	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	chr2p21	210704_at	NM_001042548 /// NM_005102
2.05	2.32	0.28	3.73E-02	3.14E-01	AARSD1	alanyl-tRNA synthetase domain containing 1	chr17q21.31	238740_at	NM_025267
3.56	4.17	0.61	3.74E-02	3.15E-01	---	---	---	233014_at	---
3.55	3.93	0.38	3.74E-02	3.15E-01	---	---	---	216362_at	---
3.14	3.44	0.30	3.74E-02	3.15E-01	PURA	Purine-rich element binding protein A	chr5q31	213806_at	NM_005859
2.85	3.28	0.43	3.74E-02	3.15E-01	C11orf52	chromosome 11 open reading frame 52	chr11q23.1	238805_at	NM_080659
2.74	3.06	0.32	3.74E-02	3.15E-01	---	---	---	233281_at	---
4.49	5.43	0.93	3.75E-02	3.15E-01	MAP3K13	mitogen-activated protein kinase kinase kinase 13	chr3q27	206249_at	NM_004721
5.70	6.15	0.45	3.75E-02	3.15E-01	ATAD3C	ATPase family, AAA domain containing 3C	chr1p36.33	240210_at	NM_001039211
3.49	3.82	0.32	3.75E-02	3.15E-01	COMMD4	COMM domain containing 4	chr15q24.2	209133_s_at	NM_017828
2.43	2.66	0.24	3.75E-02	3.15E-01	PAPOLG	poly(A) polymerase gamma	chr2p16.1	219160_s_at	NM_022894
8.36	8.82	0.46	3.75E-02	3.15E-01	PTP4A2	protein tyrosine phosphatase type IVA, member 2	chr1p35	208616_s_at	NM_080391 /// NM_080392
3.07	3.37	0.30	3.75E-02	3.15E-01	---	---	---	240818_at	---
5.26	5.66	0.39	3.75E-02	3.15E-01	C16orf84	Chromosome 16 open reading frame 84	chr16q24.3	1561500_at	NM_001012759 /// NM_001012762
3.20	3.58	0.38	3.75E-02	3.15E-01	TMEM134	transmembrane protein 134	chr11q13.1	1558712_at	NM_001078650 /// NM_001078651 /// NM_025124
5.24	5.92	0.68	3.75E-02	3.15E-01	LOC729177	hypothetical LOC729177	chr6p22.3	241670_x_at	XR_041022 /// XR_041023 /// XR_041024
3.89	4.44	0.56	3.76E-02	3.15E-01	COPZ2	coatomer protein complex, subunit zeta 2	chr17q21.32	235897_at	NM_016429
1.82	2.10	0.27	3.76E-02	3.15E-01	LRIG3	leucine-rich repeats and immunoglobulin-like domains 3	chr12q14.1	226908_at	NM_153377
4.23	5.34	1.11	3.76E-02	3.15E-01	DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14	chr4q23	222850_s_at	NM_001031723 /// NM_024920
3.11	3.41	0.29	3.76E-02	3.15E-01	TYR	tyrosinase (oculocutaneous albinism IA)	chr11q14-q21	206630_at	NM_000372
3.40	3.77	0.37	3.76E-02	3.16E-01	FAT2	FAT tumor suppressor homolog 2 (Drosophila)	chr5q32-q33	208153_s_at	NM_001447
5.02	5.44	0.42	3.77E-02	3.16E-01	---	---	---	241629_at	---

7.32	8.05	0.73	3.78E-02	3.16E-01	NRD1	nardilysin (N-arginine dibasic convertase)	chr1p32.2-p32.1	208709_s_at	NM_001101662 /// NM_002525
4.52	5.03	0.51	3.78E-02	3.16E-01	ZNRF4	zinc and ring finger 4	chr19p13.3	215461_at	NM_181710
4.24	4.62	0.38	3.78E-02	3.16E-01	---	---	---	237092_at	---
2.50	2.85	0.35	3.78E-02	3.16E-01	NRP2	Neuropilin 2	chr2q33.3	228103_s_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279
2.78	3.11	0.34	3.78E-02	3.16E-01	---	---	---	1565862_a_at	---
6.39	7.65	1.25	3.79E-02	3.16E-01	---	---	---	235501_at	---
2.47	3.18	0.71	3.79E-02	3.16E-01	---	---	---	232535_at	---
5.38	5.88	0.49	3.79E-02	3.16E-01	KHSRP	KH-type splicing regulatory protein	chr19p13.3	204371_s_at	NM_003685
3.02	3.47	0.45	3.79E-02	3.16E-01	CCDC58	coiled-coil domain containing 58	chr3q21.1	241943_at	NM_001017928
3.90	4.35	0.45	3.79E-02	3.16E-01	LOC729397	hypothetical LOC729397	chr1q42.3	227389_x_at	XM_001716181 /// XM_001716365
2.81	3.21	0.40	3.79E-02	3.16E-01	MYO9A	myosin IXA	chr15q22-q23	242512_at	NM_006901
2.16	2.53	0.37	3.79E-02	3.16E-01	D21S2089E	D21S2089E	chr21q21.1	1563346_at	---
2.49	2.84	0.35	3.79E-02	3.16E-01	---	---	---	241258_at	---
2.78	3.10	0.32	3.79E-02	3.16E-01	---	---	---	242074_at	---
2.38	2.82	0.44	3.79E-02	3.16E-01	PHLDB3	Pleckstrin homology-like domain, family B, member 3	chr19q13.31	228874_at	NM_198850
2.49	2.90	0.42	3.80E-02	3.16E-01	---	---	---	240231_at	---
6.32	7.40	1.08	3.80E-02	3.17E-01	GPNMB	glycoprotein (transmembrane) nmb	chr7p15	201141_at	NM_001005340 /// NM_002510
6.95	7.38	0.43	3.80E-02	3.17E-01	OGFR	opioid growth factor receptor	chr20q13.3	211512_s_at	NM_007346
2.58	2.96	0.38	3.81E-02	3.17E-01	LARP2	La ribonucleoprotein domain family, member 2	chr4q28.2	233764_s_at	NM_018078 /// NM_032239 /// NM_178043
6.97	7.48	0.51	3.81E-02	3.17E-01	CENTD2	centaurin, delta 2	chr11q13.4	242039_at	NM_001040118 /// NM_015242 /// NM_139181
4.74	5.16	0.42	3.81E-02	3.17E-01	TNPO3	transportin 3	chr7q32.1	212317_at	NM_012470
7.12	7.53	0.41	3.81E-02	3.17E-01	EPN1	epsin 1	chr19q13.42	226667_x_at	NM_001130071 /// NM_001130072 /// NM_013333
9.05	9.45	0.40	3.81E-02	3.17E-01	LOC653566 /// SPCS2	signal peptidase complex subunit 2 homolog pseudogene /// signal peptidase complex subunit 2 homolog (S. cerevisiae)	chr11q13.4 /// chr1p35.3	201240_s_at	NM_014752
8.56	8.97	0.40	3.81E-02	3.17E-01	ALAD	aminolevulinate, delta-, dehydratase	chr9q33.1	218487_at	NM_000031 /// NM_001003945
3.20	3.47	0.27	3.81E-02	3.17E-01	---	---	---	233925_at	---
6.04	6.63	0.59	3.81E-02	3.17E-01	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	chr12p12.1	214352_s_at	NM_004985 /// NM_033360
10.51	11.30	0.79	3.81E-02	3.17E-01	TXNIP	thioredoxin interacting protein	chr1q21.1	201010_s_at	NM_006472
4.54	4.93	0.39	3.81E-02	3.17E-01	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	chr8q13	1556228_a_at	NM_025054
3.57	3.96	0.39	3.81E-02	3.17E-01	---	---	---	237931_at	---
1.70	1.91	0.21	3.81E-02	3.17E-01	MAP1D	methionine aminopeptidase 1D	chr2q31.1	1565755_at	NM_199227
3.42	4.03	0.61	3.82E-02	3.17E-01	ZDHHC19	zinc finger, DHHC-type containing 19	chr3q29	1553952_at	NM_001039617
2.87	3.25	0.37	3.82E-02	3.17E-01	ULK4	unc-51-like kinase 4 (C. elegans)	chr3p22.1	244168_s_at	NM_017886
2.63	3.02	0.39	3.83E-02	3.18E-01	LOC728730	Hypothetical LOC728730	chr2p22.1	242313_at	XM_001132276 /// XM_001133148 /// XM_001718734
5.56	5.98	0.42	3.83E-02	3.18E-01	RSBN1	round spermatid basic protein 1	chr1p13.2	222788_s_at	NM_018364
1.76	2.00	0.24	3.83E-02	3.18E-01	---	---	---	1564107_at	---
4.65	5.27	0.62	3.83E-02	3.18E-01	FER	fer (fps/fes related) tyrosine kinase	chr5q21	206412_at	NM_005246
4.09	4.54	0.46	3.84E-02	3.18E-01	---	---	---	239323_at	---
4.39	4.82	0.43	3.84E-02	3.18E-01	ITGB4	Integrin, beta 4	chr17q25	230704_s_at	NM_000213 /// NM_001005619 /// NM_001005731
5.17	5.57	0.40	3.83E-02	3.18E-01	LOC400238	hypothetical gene supported by AK093266	chr14q32.12	1557656_at	---
2.64	3.02	0.38	3.84E-02	3.18E-01	---	---	---	242732_at	---

4.84	5.22	0.37	3.83E-02	3.18E-01	C16orf84	Chromosome 16 open reading frame 84	chr16q24.3	1561502_x_at	NM_001012759 /// NM_001012762																				
7.61	8.28	0.67	3.84E-02	3.18E-01	ZMPSTE24	zinc metallopeptidase (STE24 homolog, S. cerevisiae)	chr1p34	202939_at	NM_005857																				
4.15	4.63	0.48	3.84E-02	3.18E-01	SDAD1	SDA1 domain containing 1	chr4q21.1	242190_at	NM_018115																				
4.34	4.73	0.40	3.84E-02	3.18E-01	GPR161	G protein-coupled receptor 161	chr1q24.2	206972_s_at	NM_007369 /// NM_153832																				
3.11	4.15	1.03	3.85E-02	3.18E-01	EBF1	early B-cell factor 1	chr5q34	229487_at	NM_024007																				
2.94	3.49	0.55	3.85E-02	3.18E-01	STX1B	Syntaxin 1B	chr16p11.2	230691_at	NM_052874																				
11.37	11.75	0.38	3.85E-02	3.18E-01	---	---	---	AFFX-CreX-3_at	---																				
2.77	3.10	0.34	3.85E-02	3.18E-01	ATP10A	ATPase, class V, type 10A	chr15q11.2	214256_at	NM_024490																				
1.95	2.22	0.27	3.85E-02	3.18E-01	---	---	---	224084_at	---																				
3.81	4.21	0.40	3.85E-02	3.18E-01	CSPP1	centrosome and spindle pole associated protein 1	chr8q13.2	220072_at	NM_001077204 /// NM_024790																				
4.80	5.40	0.59	3.86E-02	3.18E-01	RBM25	RNA binding motif protein 25	chr14q24.3	212028_at	NM_021239																				
4.56	5.02	0.46	3.86E-02	3.18E-01	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	chrXq13.1	216711_s_at	NM_004606 /// NM_138923																				
3.73	4.13	0.40	3.86E-02	3.18E-01	---	---	---	1559642_a_at	---																				
6.54	7.36	0.81	3.86E-02	3.18E-01	TBC1D23	TBC1 domain family, member 23	chr3q12.1-q12.2	225121_at	NM_018309																				
2.33	2.61	0.28	3.86E-02	3.18E-01	SYT7	synaptotagmin VII	chr11q12-q13.1	1559392_s_at	NM_004200																				
6.10	6.52	0.42	3.86E-02	3.18E-01	C11orf86	chromosome 11 open reading frame 86	chr11q13.1	233938_at	XM_001129415 /// XM_001129697 /// XM_001721724																				
8.75	9.45	0.70	3.87E-02	3.18E-01	AK3	adenylate kinase 3	chr9p24.1-p24.3	224655_at	NM_016282																				
4.67	5.17	0.50	3.87E-02	3.18E-01	JHDM1D	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	chr7q34	221778_at	NM_030647																				
3.72	4.18	0.47	3.86E-02	3.18E-01	HMGB2	high-mobility group box 2	chr4q31	236091_at	NM_001130688 /// NM_001130689 /// NM_002129																				
2.77	3.17	0.40	3.87E-02	3.18E-01	---	---	---	244665_at	---																				
3.87	4.26	0.39	3.87E-02	3.18E-01	MYH14	myosin, heavy chain 14	chr19q13.33	226988_s_at	NM_001077186 /// NM_024729																				
3.30	3.68	0.37	3.87E-02	3.18E-01	---	---	---	244294_at	---																				
4.43	5.23	0.80	3.87E-02	3.18E-01	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	chr1p36.1	202742_s_at	NM_002731 /// NM_182948 /// NM_207578																				
2.86	3.19	0.33	3.87E-02	3.18E-01	PCDH7	protocadherin 7	chr4p15	210273_at	NM_002589 /// NM_032456 /// NM_032457																				
3.62	4.10	0.48	3.87E-02	3.19E-01	TRIM13	tripartite motif-containing 13	chr13q14	230192_at	NM_001007278 /// NM_005798 /// NM_052811 /// NM_213590																				
6.81	7.23	0.41	3.88E-02	3.19E-01	ESRRA	estrogen-related receptor alpha	chr11q13	203193_at	NM_004451																				
2.94	3.28	0.34	3.88E-02	3.19E-01	ARHGAP8	Rho GTPase activating protein 8	chr22q13.31	232567_at	NM_001017526 /// NM_181335																				
3.48	3.83	0.35	3.88E-02	3.19E-01	FLJ42291	hypothetical LOC346547	chr7q36.2	238648_at	XR_040030 /// XR_040031 /// XR_040032 /// XR_040033																				
2.47	2.92	0.45	3.88E-02	3.19E-01	---	---	---	216744_at	---																				
4.87	5.30	0.42	3.88E-02	3.19E-01	POU2F2	POU class 2 homeobox 2	chr19q13.2	211771_s_at	NM_002698																				
2.98	3.36	0.39	3.88E-02	3.19E-01	---	---	---	242861_at	---																				
3.64	4.01	0.36	3.88E-02	3.19E-01	CLCN1	chloride channel 1, skeletal muscle	chr7q32-qter|7q35	208437_at	NM_000083																				
2.88	3.23	0.35	3.88E-02	3.19E-01	---	---	---	1557661_at	---																				
6.02	6.68	0.66	3.89E-02	3.19E-01	KLHL2	kelch-like 2, Mayven (Drosophila)	chr4q21.2	219157_at	NM_007246																				
5.99	6.53	0.54	3.89E-02	3.19E-01	TNPO3	transportin 3	chr7q32.1	214550_s_at	NM_012470																				
5.64	6.13	0.50	3.89E-02	3.19E-01	LTB4R2	leukotriene B4 receptor 2	chr14q11.2-q12	220130_x_at	NM_019839																				

3.35	3.69	0.34	3.89E-02	3.19E-01	MBP	myelin basic protein	chr18q23	225408_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385
2.38	2.61	0.23	3.89E-02	3.19E-01	MAP1D	methionine aminopeptidase 1D	chr2q31.1	1565756_a_at	NM_199227
6.59	6.97	0.38	3.89E-02	3.19E-01	FARS2	phenylalanyl-tRNA synthetase 2, mitochondrial	chr6p25.1	204282_s_at	NM_006567
2.51	2.81	0.30	3.89E-02	3.19E-01	---	---	---	217453_at	---
2.32	2.70	0.38	3.90E-02	3.19E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	1565306_a_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
2.77	3.14	0.37	3.90E-02	3.19E-01	LOC284912	hypothetical gene supported by BC001801	chr22q12.3	224117_at	XR_041186 /// XR_041187 /// XR_041188
2.58	2.87	0.29	3.91E-02	3.20E-01	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	chr1q32	221854_at	NM_000299 /// NM_001005337
3.92	4.32	0.40	3.91E-02	3.20E-01	FAM124A	family with sequence similarity 124A	chr13q14.3	1553239_at	NM_145019
5.51	5.83	0.33	3.91E-02	3.20E-01	---	---	---	236413_at	---
3.24	3.72	0.48	3.92E-02	3.20E-01	---	---	---	230694_at	---
5.08	5.53	0.45	3.92E-02	3.20E-01	ZNF683	zinc finger protein 683	chr1p36.11	230756_at	NM_001114759 /// NM_173574
3.17	3.61	0.44	3.92E-02	3.20E-01	---	---	---	217614_at	---
4.17	4.59	0.41	3.92E-02	3.20E-01	NEU2	sialidase 2 (cytosolic sialidase)	chr2q37	221368_at	NM_005383
4.37	4.74	0.37	3.92E-02	3.20E-01	---	---	---	238884_at	---
2.28	2.61	0.33	3.92E-02	3.20E-01	---	---	---	1567612_at	---
5.50	6.21	0.71	3.92E-02	3.20E-01	---	---	---	222033_s_at	---
5.23	6.11	0.88	3.92E-02	3.20E-01	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	chr7q36.1	222413_s_at	NM_170606
5.64	6.80	1.16	3.93E-02	3.20E-01	TRIM33	tripartite motif-containing 33	chr1p13.1	210266_s_at	NM_015906 /// NM_033020
3.40	3.85	0.45	3.93E-02	3.20E-01	ARSF	arylsulfatase F	chrXp22.3	214490_at	NM_004042
5.94	6.30	0.36	3.93E-02	3.20E-01	EXOSC3	exosome component 3	chr9p11	227916_x_at	NM_001002269 /// NM_016042
2.87	3.15	0.28	3.92E-02	3.20E-01	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	chr12q24.2	206553_at	NM_001032731 /// NM_002535 /// NM_016817
2.91	3.23	0.32	3.93E-02	3.20E-01	PLXNA3	plexin A3	chrXq28	1567519_at	NM_017514
5.24	6.12	0.88	3.93E-02	3.20E-01	SDCCAG1	serologically defined colon cancer antigen 1	chr14q22	1569594_a_at	NM_004713
6.48	7.02	0.54	3.93E-02	3.20E-01	HELZ	helicase with zinc finger	chr17q24.2	203674_at	NM_014877
3.68	4.14	0.46	3.93E-02	3.20E-01	FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	chr16q22-q24	214520_at	NM_005251
4.94	5.35	0.41	3.93E-02	3.20E-01	KRT8 /// KRT8P9 /// LOC149501 /// LOC647954	keratin 8 /// keratin 8 pseudogene 9 /// similar to keratin 8 /// similar to keratin 8	chr12q13 /// chr15q23 /// chr1q23.1 /// chr5q23.2	216821_at	NM_002273 /// XR_017100 /// XR_017231 /// XR_018597 /// XR_018676 /// XR_019144 /// XR_037556 /// XR_038441 /// XR_039009 /// XR_039426
4.45	4.86	0.41	3.93E-02	3.20E-01	LOC100133503 /// LOC644397 /// LRRC37A /// LRRC37A2 /// LRRC37A3 /// LRRC37A4	similar to LRRC37A3 protein /// similar to hCG2036502 /// leucine rich repeat containing 37A /// leucine rich repeat containing 37, member A2 /// leucine rich repeat containing 37, member A3 /// leucine rich repeat containing 37, member A4 (pseudogene)	chr17q21.31 /// chr17q21.32 /// chr17q24.1	220219_s_at	NM_001006607 /// NM_014834 /// NM_199340 /// NR_002940 /// XM_001719702 /// XR_037772 /// XR_042323 /// XR_042484
4.86	6.38	1.52	3.94E-02	3.20E-01	---	---	---	233300_at	---
3.85	4.35	0.49	3.94E-02	3.20E-01	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	221284_s_at	NM_005417 /// NM_198291
3.46	3.85	0.39	3.94E-02	3.20E-01	FAM65C	family with sequence similarity 65, member C	chr20q13.13	243978_at	NM_080829
3.74	4.12	0.38	3.94E-02	3.20E-01	INADL	InaD-like (Drosophila)	chr1p31.3	214493_s_at	NM_176877
2.43	2.78	0.35	3.94E-02	3.20E-01	---	---	---	237438_at	---

2.46	2.74	0.28	3.94E-02	3.20E-01	ZNF117	Zinc finger protein 117	chr7q11.21	235564_at	NM_015852
3.11	3.53	0.41	3.94E-02	3.20E-01	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	chr11q21-q22.1	1565149_at	NM_001080463
2.09	2.44	0.36	3.94E-02	3.20E-01	---	---	---	243139_at	---
2.37	2.71	0.34	3.94E-02	3.20E-01	ADCY1	adenylate cyclase 1 (brain)	chr7p13-p12	215340_at	NM_021116
2.52	2.85	0.33	3.94E-02	3.20E-01	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	chr4p16-p15.3	232678_at	NM_001001290 /// NM_020041
4.34	4.97	0.63	3.95E-02	3.20E-01	FBXO22	F-box protein 22	chr15q24.2	225734_at	NM_012170 /// NM_147188
2.29	2.62	0.34	3.95E-02	3.20E-01	---	---	---	238985_at	---
2.05	2.30	0.24	3.95E-02	3.20E-01	TP63	tumor protein p63	chr3q28	211194_s_at	NM_001114978 /// NM_001114979 /// NM_001114980 /// NM_001114981 /// NM_001114982 /// NM_003722
2.25	2.55	0.30	3.95E-02	3.21E-01	---	---	---	235986_at	---
7.46	8.26	0.80	3.95E-02	3.21E-01	ASXL2	additional sex combs like 2 (Drosophila)	chr2p24.1	218659_at	NM_018263
4.39	4.78	0.39	3.95E-02	3.21E-01	MSL-1	Male-specific lethal-1 homolog	chr17q21.1	230155_x_at	NM_001012241
3.25	3.59	0.33	3.96E-02	3.21E-01	TNR	tenascin R (restrictin, janusin)	chr1q24	1564897_at	NM_003285
5.37	5.68	0.32	3.96E-02	3.21E-01	VPS37D	vacuolar protein sorting 37 homolog D (S. cerevisiae)	chr7q11.23	235569_at	NM_001077621
2.45	2.76	0.31	3.95E-02	3.21E-01	FLJ33630	hypothetical LOC644873	chr5q23.3	244769_at	NR_015360 /// XM_932475
2.20	2.48	0.27	3.95E-02	3.21E-01	SMCR5	Smith-Magenis syndrome chromosome region, candidate 5 (non-protein coding)	---	1553020_at	NR_024007 /// XM_001719311 /// XM_001722800 /// XM_001725572
2.44	2.82	0.38	3.97E-02	3.21E-01	METTL6	methyltransferase like 6	chr3p24.3	1557991_at	NM_152396
1.98	2.27	0.29	3.97E-02	3.21E-01	---	---	---	232799_at	---
2.86	3.89	1.03	3.97E-02	3.21E-01	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	chr21q22.3	211018_at	NM_001001438 /// NM_002340
6.08	6.75	0.67	3.97E-02	3.21E-01	GTDC1	glycosyltransferase-like domain containing 1	chr2q22.2-q22.3	219770_at	NM_001006636 /// NM_024659
8.94	9.43	0.49	3.97E-02	3.21E-01	ALDH9A1	aldehyde dehydrogenase 9 family, member A1	chr1q23.1	201612_at	NM_000696
6.49	6.93	0.44	3.97E-02	3.21E-01	MLXIPL	MLX interacting protein-like	chr7q11.23	221163_s_at	NM_032951 /// NM_032952 /// NM_032953 /// NM_032954
3.68	4.03	0.35	3.97E-02	3.21E-01	TMEM40	transmembrane protein 40	chr3p25.1	222892_s_at	NM_018306
3.92	4.36	0.43	3.97E-02	3.21E-01	---	---	---	240571_at	---
8.36	9.29	0.93	3.98E-02	3.22E-01	DDR2	discoidin domain receptor tyrosine kinase 2	chr1q23.3	205168_at	NM_001014796 /// NM_006182
4.28	4.86	0.58	3.98E-02	3.22E-01	RTN4IP1	reticulon 4 interacting protein 1	chr6q21	1555679_a_at	NM_032730
3.68	4.17	0.49	3.98E-02	3.22E-01	NEBL	nebulette	chr10p12	216882_s_at	NM_006393 /// NM_213569
4.91	5.33	0.43	3.98E-02	3.22E-01	ZNF696	zinc finger protein 696	chr8q24.3	232162_at	NM_030895
2.77	3.18	0.41	3.99E-02	3.22E-01	---	---	---	1561770_at	---
2.15	2.52	0.38	3.99E-02	3.22E-01	---	---	---	243315_at	---
4.79	5.17	0.38	3.99E-02	3.22E-01	---	---	---	236317_at	---
3.40	3.73	0.33	3.98E-02	3.22E-01	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	chr6p21.2-p21.1	220554_at	NM_006672 /// NM_153320
1.92	2.19	0.27	3.98E-02	3.22E-01	---	---	---	1569482_at	---
1.74	2.01	0.27	3.98E-02	3.22E-01	---	---	---	1556933_at	---
5.15	6.17	1.01	3.99E-02	3.22E-01	PRKD3	protein kinase D3	chr2p21	211084_x_at	NM_005813
2.97	3.27	0.30	3.99E-02	3.22E-01	C3orf34	chromosome 3 open reading frame 34	chr3q29	230860_at	NM_032898
3.18	3.48	0.30	3.99E-02	3.22E-01	---	---	---	1565549_at	---
3.12	3.72	0.61	3.99E-02	3.22E-01	FLI1	Friend leukemia virus integration 1	chr11q24.1-q24.3	210786_s_at	NM_002017
6.80	7.20	0.40	3.99E-02	3.22E-01	SORT1	sortilin 1	chr1p21.3-p13.1|1p21.3-p13.1	224818_at	NM_002959
2.36	2.65	0.29	3.99E-02	3.22E-01	SNORD8	small nucleolar RNA, C/D box 8	chr14q11.2	1566339_at	NR_002916
7.72	8.58	0.86	4.00E-02	3.22E-01	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	chr14q24.1	217776_at	NM_016026

5.93	6.74	0.80	4.00E-02	3.22E-01	FOXP1	forkhead box P1	chr3p14.1	224838_at	NM_001012505 /// NM_032682
4.62	5.43	0.80	4.00E-02	3.22E-01	PNMT	phenylethanolamine N-methyltransferase	chr17q21-q22	206793_at	NM_002686
5.10	5.83	0.74	4.00E-02	3.22E-01	SVIL	supervillin	chr10p11.2	202565_s_at	NM_003174 /// NM_021738
6.28	6.55	0.27	4.00E-02	3.22E-01	LOC650794	similar to FRAS1 related extracellular matrix protein 2	chr13q12.11	243760_at	XM_001716126 /// XM_370711 /// XM_939879
4.47	4.84	0.36	4.00E-02	3.22E-01	IGSF9B	immunoglobulin superfamily, member 9B	chr11q25	215255_at	NM_014987
3.93	4.28	0.35	4.00E-02	3.22E-01	FOXL1	forkhead box L1	chr16q24	243409_at	NM_005250
1.99	2.30	0.31	4.00E-02	3.22E-01	BLZF1	basic leucine zipper nuclear factor 1	chr1q24	32088_at	NM_003666
3.71	4.09	0.38	4.01E-02	3.22E-01	LOC100130740	similar to hCG2042068	chr17q21.32	239791_at	XM_001722876 /// XM_001725076 /// XM_001726544
3.98	4.35	0.37	4.01E-02	3.22E-01	ARID1B	AT rich interactive domain 1B (SWI1-like)	chr6q25.1	1566991_at	NM_017519 /// NM_020732 /// NM_175863
5.95	6.34	0.39	4.02E-02	3.22E-01	---	---	---	217723_x_at	---
3.44	3.77	0.32	4.02E-02	3.22E-01	IQCK	IQ motif containing K	chr16p12.3	215130_s_at	NM_153208
4.31	4.63	0.32	4.02E-02	3.22E-01	LRG1	leucine-rich alpha-2-glycoprotein 1	chr19p13.3	228648_at	NM_052972
2.21	2.43	0.23	4.02E-02	3.22E-01	MARVELD3	MARVEL domain containing 3	chr16q22.3	239148_at	NM_001017967 /// NM_052858
3.71	4.04	0.33	4.02E-02	3.22E-01	---	---	---	215397_x_at	---
5.57	6.20	0.63	4.03E-02	3.23E-01	TMTC1	transmembrane and tetratricopeptide repeat containing 1	chr12p11.22	226322_at	NM_175861
2.15	2.49	0.34	4.03E-02	3.23E-01	FLJ40235	hypothetical protein FLJ40235	chr19q13.33	1553887_at	NM_173635
2.67	3.00	0.33	4.02E-02	3.23E-01	WWC1	WW and C2 domain containing 1	chr5q35.1	213085_s_at	NM_015238
2.04	2.40	0.37	4.03E-02	3.23E-01	ZNF117	zinc finger protein 117	chr7q11.21	207117_at	NM_015852
3.11	3.88	0.77	4.03E-02	3.23E-01	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	chr3p25.3	204685_s_at	NM_001001331 /// NM_001683
4.84	5.47	0.63	4.03E-02	3.23E-01	---	---	---	242480_at	---
6.16	6.55	0.39	4.03E-02	3.23E-01	DCBLD2	discoidin, CUB and LCCL domain containing 2	chr3q12.1|3	239446_x_at	NM_080927
3.09	3.44	0.34	4.03E-02	3.23E-01	LOC282992	hypothetical protein LOC282992	chr10q24.31	244209_at	XM_001723618 /// XM_001725321 /// XM_001725601
2.61	2.88	0.27	4.03E-02	3.23E-01	PTPRN	protein tyrosine phosphatase, receptor type, N	chr2q35-q36.1	204945_at	NM_002846
3.57	4.00	0.43	4.03E-02	3.23E-01	---	---	---	244218_at	---
3.44	3.81	0.36	4.03E-02	3.23E-01	C1orf158	chromosome 1 open reading frame 158	chr1p36.21	231549_at	NM_152290
2.14	2.48	0.34	4.04E-02	3.23E-01	LOC100130360	hypothetical protein LOC100130360	chr6p22.3	230507_at	XM_001717221 /// XM_001718619 /// XM_001718724
6.64	7.08	0.44	4.04E-02	3.23E-01	---	---	---	238105_x_at	---
5.84	6.22	0.38	4.04E-02	3.23E-01	---	---	---	217079_at	---
2.19	2.51	0.33	4.04E-02	3.23E-01	---	---	---	237358_at	---
2.13	2.45	0.32	4.04E-02	3.23E-01	---	---	---	222320_at	---
5.50	5.83	0.32	4.04E-02	3.23E-01	---	---	---	203326_x_at	---
2.25	2.54	0.29	4.04E-02	3.23E-01	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	chr9q33.3	242689_at	NM_014636
4.84	5.29	0.45	4.04E-02	3.23E-01	FLJ20489	hypothetical protein FLJ20489	chr12q13.11	218416_s_at	NM_017842
9.60	10.54	0.94	4.05E-02	3.23E-01	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	chr15q22.2	234000_s_at	NM_016395
4.97	5.31	0.34	4.05E-02	3.23E-01	ANKRD9	Ankyrin repeat domain 9	chr14q32.31	244245_at	NM_152326
2.36	3.54	1.18	4.05E-02	3.23E-01	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	chr9q22.1	221796_at	NM_001007097 /// NM_001018064 /// NM_001018065 /// NM_001018066 /// NM_006180
4.34	5.14	0.80	4.05E-02	3.23E-01	FLJ39653	hypothetical FLJ39653	chr4p15.32	1553145_at	XR_040405 /// XR_040406
6.53	7.85	1.32	4.05E-02	3.23E-01	TTC3	tetratricopeptide repeat domain 3	chr21q22.2	208661_s_at	NM_001001894 /// NM_003316
7.57	8.60	1.03	4.05E-02	3.23E-01	LPP	LIM domain containing preferred translocation partner in lipoma	chr3q28	202822_at	NM_005578
3.61	4.21	0.60	4.05E-02	3.23E-01	PDZK1IP1	PDZK1 interacting protein 1	chr1p33	1553589_a_at	NM_005764

1.94	2.19	0.25	4.05E-02	3.23E-01	LOC728137 /// LOC728395 /// LOC728412 /// TSPY1	similar to testis specific protein, Y-linked 1 /// similar to testis specific protein, Y-linked 1 /// similar to testis specific protein, Y-linked 1 /// testis specific protein, Y-linked 1	chrYp11.2	207918_s_at	NM_001077697 /// NM_003308 /// XM_001126990 /// XM_001127025
3.72	4.22	0.50	4.06E-02	3.24E-01	---	---	---	1566142_at	---
3.54	3.92	0.39	4.06E-02	3.24E-01	ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	chr9q34.1-q34.2	214504_at	NM_020469
3.67	4.10	0.44	4.06E-02	3.24E-01	PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA3 /// PCDHGA5 /// PCDHGA6	protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 6	chr5q31	211876_x_at	NM_003735 /// NM_018913 /// NM_018914 /// NM_018916 /// NM_018918 /// NM_018919 /// NM_032011 /// NM_032054 /// NM_032086 /// NM_032090 /// NM_032091 /// NM_032092 /// NM_032094
5.19	5.80	0.61	4.06E-02	3.24E-01	SRR	serine racemase	chr17p13	219205_at	NM_021947
3.79	4.36	0.56	4.06E-02	3.24E-01	FOXP1	forkhead box P1	chr3p14.1	235444_at	NM_001012505 /// NM_032682
2.62	2.99	0.37	4.07E-02	3.24E-01	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	chr1p31.3-p31.2	205073_at	NM_000775
3.15	3.71	0.56	4.07E-02	3.24E-01	FAM130A2	family with sequence similarity 130, member A2	chr2q24.3	220462_at	NM_024969
5.14	5.67	0.53	4.07E-02	3.24E-01	CLYBL	citrate lyase beta like	chr13q32	238440_at	NM_206808
2.57	3.01	0.44	4.07E-02	3.24E-01	FST	follistatin	chr5q11.2	207345_at	NM_006350 /// NM_013409
2.79	3.18	0.39	4.07E-02	3.24E-01	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	chr6p21.1-p12.1	1567222_x_at	NM_021814
2.35	2.69	0.34	4.07E-02	3.24E-01	SLC24A5	solute carrier family 24, member 5	chr15q21.1	232672_x_at	NM_205850
4.41	4.85	0.44	4.08E-02	3.24E-01	PDE1B	phosphodiesterase 1B, calmodulin-dependent	chr12q13	206444_at	NM_000924
2.84	3.23	0.39	4.08E-02	3.24E-01	ITGB4	integrin, beta 4	chr17q25	214292_at	NM_000213 /// NM_001005619 /// NM_001005731
4.46	4.76	0.30	4.08E-02	3.24E-01	---	---	---	239918_at	---
2.99	3.40	0.41	4.08E-02	3.24E-01	LOC100132634 /// LOC283112	hypothetical protein LOC100132634 /// hypothetical protein LOC283112	chr11p15.1	241317_at	XM_001716851 /// XM_001717348 /// XM_001717384
4.91	5.25	0.34	4.08E-02	3.24E-01	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	chr22q12|7p14.3-p14.1	213276_at	NM_001220 /// NM_172078 /// NM_172079 /// NM_172080 /// NM_172081 /// NM_172082 /// NM_172083 /// NM_172084
5.23	6.30	1.07	4.09E-02	3.24E-01	RBBP6	retinoblastoma binding protein 6	chr16p12.2	205178_s_at	NM_006910 /// NM_018703 /// NM_032626
4.83	5.67	0.84	4.09E-02	3.24E-01	PROSC	proline synthetase co-transcribed homolog (bacterial)	chr8p11.2	214545_s_at	NM_007198
8.26	8.90	0.64	4.09E-02	3.24E-01	MTSS1	metastasis suppressor 1	chr8p22	203037_s_at	NM_014751
4.11	4.73	0.63	4.09E-02	3.24E-01	---	---	---	1556055_at	---
4.96	5.44	0.49	4.09E-02	3.24E-01	LPIN1	lipin 1	chr2p25.1	212274_at	NM_145693
3.39	3.77	0.38	4.09E-02	3.24E-01	CD1E	CD1e molecule	chr1q22-q23	208592_s_at	NM_001042583 /// NM_001042584 /// NM_001042585 /// NM_001042586 /// NM_001042587 /// NM_030893

3.01	3.37	0.35	4.09E-02	3.24E-01	C3orf24	chromosome 3 open reading frame 24	chr3p25.3	231531_at	NM_173472
2.31	2.65	0.33	4.09E-02	3.24E-01	CRB2	crumbs homolog 2 (Drosophila)	chr9q33.2	1552506_at	NM_173689
3.35	3.68	0.33	4.09E-02	3.24E-01	SLITRK2	SLIT and NTRK-like family, member 2	chrXq27.3	233051_at	NM_032539
2.14	2.45	0.31	4.09E-02	3.24E-01	ZNF519	zinc finger protein 519	chr18p11.21	1557283_a_at	NM_145287
1.95	2.21	0.26	4.09E-02	3.24E-01	---	---	---	233282_at	---
2.34	2.76	0.42	4.10E-02	3.25E-01	RHOBTB3	Rho-related BTB domain containing 3	chr5q15	216049_at	NM_014899
3.40	3.78	0.38	4.10E-02	3.25E-01	KLK3	kallikrein-related peptidase 3	chr19q13.41	204582_s_at	NM_001030047 /// NM_001030048 /// NM_001030049 /// NM_001030050 /// NM_001648
2.72	3.08	0.35	4.10E-02	3.25E-01	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	chrXq28	216312_at	NM_001001344 /// NM_021949
2.80	3.18	0.38	4.10E-02	3.25E-01	MEGF9	multiple EGF-like-domains 9	chr9q32-q33.3	212831_at	NM_001080497
3.23	4.22	0.99	4.11E-02	3.25E-01	ASB4	ankyrin repeat and SOCS box-containing 4	chr7q21-q22	208481_at	NM_016116 /// NM_145872
2.27	2.84	0.57	4.11E-02	3.25E-01	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	chr16q22.1	236179_at	NM_001797
4.93	5.53	0.60	4.11E-02	3.25E-01	---	---	---	235847_at	---
3.34	3.73	0.39	4.11E-02	3.25E-01	---	---	---	242475_at	---
2.52	2.81	0.30	4.11E-02	3.25E-01	KLC1	Kinesin light chain 1	chr14q32.3	232036_at	NM_001130107 /// NM_005552 /// NM_182923
3.80	4.18	0.37	4.11E-02	3.25E-01	MESP1	mesoderm posterior 1 homolog (mouse)	chr15q26.1	229195_at	NM_018670
4.07	4.46	0.39	4.12E-02	3.25E-01	ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif, 16	chr5p15	238125_at	NM_139056
5.91	6.99	1.07	4.12E-02	3.25E-01	PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	chr14q23.1	229322_at	NM_006246
2.80	3.20	0.40	4.13E-02	3.26E-01	---	---	---	215866_at	---
4.65	5.10	0.45	4.13E-02	3.26E-01	LOC399904	hypothetical LOC399904	chr11q13.1	213740_s_at	XR_017776
4.34	5.31	0.97	4.13E-02	3.26E-01	CCDC80	coiled-coil domain containing 80	chr3q13.2	225241_at	NM_199511 /// NM_199512
5.71	6.40	0.70	4.13E-02	3.26E-01	CCPG1	cell cycle progression 1	chr15q21.1	221511_x_at	NM_004748 /// NM_020739
3.12	3.78	0.66	4.13E-02	3.26E-01	LIFR	leukemia inhibitory factor receptor alpha	chr5p13-p12	225571_at	NM_001127671 /// NM_002310
2.76	3.05	0.29	4.14E-02	3.26E-01	KIAA0241	KIAA0241	chr7p14.3	1563452_at	NM_015060
2.45	2.82	0.38	4.14E-02	3.26E-01	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	chr2q33.1	1555439_at	NM_012086
2.84	3.31	0.47	4.14E-02	3.26E-01	ST6GALNAC3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	chr1p31.1	235334_at	NM_152996
2.42	2.82	0.40	4.14E-02	3.26E-01	---	---	---	239016_at	---
2.98	3.33	0.35	4.15E-02	3.26E-01	TMEM30B	Transmembrane protein 30B	chr14q23.1	230124_at	NM_001017970
4.58	5.33	0.75	4.15E-02	3.27E-01	GLT8D2	glycosyltransferase 8 domain containing 2	chr12q	221447_s_at	NM_031302
2.55	2.86	0.31	4.15E-02	3.27E-01	BHLHB5	basic helix-loop-helix domain containing, class B, 5	chr8q13	244323_at	NM_152414
2.72	2.99	0.26	4.15E-02	3.27E-01	GRIK4	Glutamate receptor, ionotropic, kainate 4	chr11q22.3	242215_at	NM_014619
4.13	4.57	0.44	4.15E-02	3.27E-01	---	---	---	241556_at	---
6.76	7.15	0.39	4.16E-02	3.27E-01	C7orf50	chromosome 7 open reading frame 50	chr7p22.3	240147_at	NM_001134395 /// NM_001134396 /// NM_032350
2.39	2.78	0.39	4.16E-02	3.27E-01	C14orf56	chromosome 14 open reading frame 56	chr14q24.2	215877_at	XM_001715980 /// XM_001716301 /// XM_001718387
2.24	2.60	0.37	4.16E-02	3.27E-01	---	---	---	237303_at	---
2.78	3.02	0.24	4.16E-02	3.27E-01	TMED4	transmembrane emp24 protein transport domain containing 4	chr7p13	1558052_at	NM_182547
9.46	10.45	0.99	4.17E-02	3.27E-01	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	chr14q32.33	210211_s_at	NM_001017963 /// NM_005348
8.80	9.41	0.62	4.17E-02	3.27E-01	ESD	esterase D/formylglutathione hydrolase	chr13q14.1-q14.2	209009_at	NM_001984
3.05	3.57	0.52	4.17E-02	3.27E-01	SYT12	synaptotagmin XII	chr11q13.1	228072_at	NM_177963
2.31	2.76	0.45	4.17E-02	3.27E-01	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	chr4q21	203908_at	NM_001098484 /// NM_001134742 /// NM_003759
2.03	2.33	0.30	4.17E-02	3.27E-01	---	---	---	1563720_at	---

2.53	2.81	0.29	4.17E-02	3.27E-01	NLRP7	NLR family, pyrin domain containing 7	chr19q13.42	237461_at	NM_001127255 /// NM_139176 /// NM_206828
3.61	3.97	0.36	4.18E-02	3.27E-01	MTSS1	metastasis suppressor 1	chr8p22	210360_s_at	NM_014751
3.13	3.43	0.30	4.17E-02	3.27E-01	KLK7	kallikrein-related peptidase 7	chr19q13.33	239381_at	NM_005046 /// NM_139277
2.65	2.93	0.28	4.18E-02	3.27E-01	ZNF44	zinc finger protein 44	chr19p13.2	228718_at	NM_016264 /// XM_001718561 /// XM_001719479 /// XM_001719639
2.22	2.47	0.24	4.17E-02	3.27E-01	---	---	---	1561141_at	---
2.55	2.96	0.41	4.18E-02	3.27E-01	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma	chr9q13	207228_at	NM_002732
2.34	2.73	0.39	4.18E-02	3.27E-01	GIMAP8	GTPase, IMAP family member 8	chr7q36.1	240646_at	NM_175571
3.29	3.62	0.33	4.18E-02	3.27E-01	SBSN	suprabasin	chr19q13.13	235272_at	NM_198538
2.30	2.75	0.45	4.18E-02	3.27E-01	---	---	---	233289_at	---
5.49	5.87	0.38	4.18E-02	3.27E-01	LOC149773	hypothetical protein LOC149773	chr20q13.32	1556900_at	XR_042084 /// XR_042085 /// XR_042086
3.19	3.73	0.54	4.18E-02	3.27E-01	---	---	---	236648_at	---
1.96	2.45	0.49	4.18E-02	3.27E-01	CHD9	chromodomain helicase DNA binding protein 9	chr16q12.2	235388_at	NM_025134
2.98	3.40	0.41	4.18E-02	3.27E-01	LOC645030	Hypothetical protein LOC645030	chr1p31.3	232932_at	XM_001726217 /// XM_934772 /// XM_946093
2.18	2.45	0.27	4.18E-02	3.27E-01	---	---	---	217351_at	---
8.51	9.00	0.50	4.19E-02	3.27E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	209563_x_at	NM_001743 /// NM_005184 /// NM_006888
3.75	4.11	0.36	4.18E-02	3.27E-01	PHTF1	putative homeodomain transcription factor 1	chr1p13	205702_at	NM_006608
3.04	3.37	0.33	4.19E-02	3.27E-01	C20orf144	chromosome 20 open reading frame 144	chr20q11.22	231522_at	NM_080825
2.07	2.33	0.26	4.19E-02	3.28E-01	MBP	Myelin basic protein	chr18q23	228938_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385
4.54	4.90	0.35	4.19E-02	3.28E-01	IQGAP3	IQ motif containing GTPase activating protein 3	chr1q22-q23.1	241939_at	NM_178229
8.87	9.47	0.60	4.20E-02	3.28E-01	DPYSL2	dihydropyrimidinase-like 2	chr8p22-p21	200762_at	NM_001386
2.79	3.11	0.32	4.20E-02	3.28E-01	IFNW1	interferon, omega 1	chr9p22	207817_at	NM_002177
2.29	2.52	0.23	4.20E-02	3.28E-01	PAX1	paired box 1	chr20p11.2	1553492_a_at	NM_006192
5.02	5.48	0.46	4.21E-02	3.28E-01	---	---	---	228861_at	---
3.76	4.18	0.42	4.21E-02	3.28E-01	LRRK1	leucine-rich repeat kinase 1	chr15q26.3	219441_s_at	NM_024652
3.78	4.10	0.32	4.21E-02	3.28E-01	TP53I11	tumor protein p53 inducible protein 11	chr11p11.2	214667_s_at	NM_001076787 /// NM_006034
3.56	3.95	0.39	4.21E-02	3.28E-01	SPEN	spen homolog, transcriptional regulator (Drosophila)	chr1p36.33-p36.11	201996_s_at	NM_015001
6.10	6.46	0.35	4.21E-02	3.28E-01	---	---	---	233235_x_at	---
2.31	2.65	0.34	4.21E-02	3.28E-01	PRKD3	protein kinase D3	chr2p21	242549_at	NM_005813
3.06	3.38	0.32	4.21E-02	3.28E-01	---	---	---	236636_at	---
5.84	6.33	0.49	4.21E-02	3.29E-01	C9orf98	chromosome 9 open reading frame 98	chr9q34.13	230976_at	NM_152572
4.94	5.37	0.43	4.22E-02	3.29E-01	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17p13.3	227229_at	NM_001128159 /// NM_018289
3.31	3.86	0.54	4.22E-02	3.29E-01	---	---	---	1558409_at	---
3.83	4.49	0.67	4.22E-02	3.29E-01	---	---	---	239557_at	---
2.03	2.26	0.23	4.23E-02	3.29E-01	---	---	---	242831_at	---
4.03	4.55	0.52	4.23E-02	3.29E-01	WDR1	WD repeat domain 1	chr4p16.1	240282_at	NM_005112 /// NM_017491
6.09	6.52	0.43	4.23E-02	3.29E-01	STK11	serine/threonine kinase 11	chr19p13.3	204292_x_at	NM_000455
3.16	3.49	0.33	4.23E-02	3.29E-01	TTLL9	tubulin tyrosine ligase-like family, member 9	chr20q11.21	232357_at	NM_001008409
2.14	2.45	0.31	4.23E-02	3.29E-01	TCTE3	T-complex-associated-testis-expressed 3	chr6q27	232258_at	NM_174910
4.13	5.61	1.47	4.24E-02	3.30E-01	ZCCHC2	zinc finger, CCHC domain containing 2	chr18q21.33	222816_s_at	NM_017742
5.05	5.45	0.40	4.24E-02	3.30E-01	PLCH2	phospholipase C, eta 2	chr1p36.32	206080_at	NM_014638
7.53	7.92	0.39	4.24E-02	3.30E-01	WNK1	WNK lysine deficient protein kinase 1	chr12p13.3	211992_at	NM_018979
4.75	5.15	0.40	4.24E-02	3.30E-01	---	---	---	241322_at	---

4.11	4.55	0.43	4.25E-02	3.30E-01	TNRC18	Trinucleotide repeat containing 18	chr7p22.1	244882_at	NM_001080495																				
2.19	2.62	0.42	4.25E-02	3.30E-01	GALNT17	polypeptide N-acetylgalactosaminyltransferase 17	chr4q34.1	1555273_at	NM_001034845																				
4.73	5.12	0.39	4.25E-02	3.30E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	241646_s_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844																				
3.42	4.04	0.62	4.26E-02	3.30E-01	ZNF678	Zinc finger protein 678	chr1q42.13	232028_at	NM_178549																				
3.86	4.33	0.47	4.26E-02	3.30E-01	---	---	---	243199_at	---																				
2.54	3.00	0.45	4.26E-02	3.30E-01	NMT2	N-myristoyltransferase 2	chr10p13	205006_s_at	NM_004808																				
3.78	4.20	0.42	4.26E-02	3.30E-01	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	chr1p36.3	217071_s_at	NM_005957																				
4.85	5.24	0.39	4.25E-02	3.30E-01	---	---	---	240104_at	---																				
2.35	2.71	0.37	4.26E-02	3.30E-01	---	---	---	244636_at	---																				
2.09	2.40	0.31	4.26E-02	3.30E-01	FBXO40	F-box protein 40	chr3q13.33	220164_s_at	NM_016298																				
3.81	5.00	1.19	4.27E-02	3.31E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	226675_s_at	NR_002819																				
4.47	4.86	0.38	4.27E-02	3.31E-01	RAB37	RAB37, member RAS oncogene family	chr17q25.1	244124_at	NM_001006638 /// NM_175738																				
7.00	7.33	0.33	4.27E-02	3.31E-01	YARS	tyrosyl-tRNA synthetase	chr1p35.1	212048_s_at	NM_003680																				
2.89	3.32	0.42	4.27E-02	3.31E-01	---	---	---	230111_at	---																				
2.33	2.63	0.30	4.27E-02	3.31E-01	---	---	---	242078_at	---																				
7.00	7.34	0.34	4.27E-02	3.31E-01	---	---	---	225917_at	---																				
3.36	3.87	0.51	4.28E-02	3.31E-01	KISS1	KiSS-1 metastasis-suppressor	chr1q32	205563_at	NM_002256																				
5.10	5.84	0.74	4.28E-02	3.31E-01	ACSL1	acyl-CoA synthetase long-chain family member 1	chr4q34-q35	201963_at	NM_001995																				
2.58	3.24	0.66	4.28E-02	3.31E-01	ZMYM1	zinc finger, MYM-type 1	chr1p34.3	220206_at	NM_024772																				
2.14	2.54	0.40	4.28E-02	3.31E-01	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	chr15q15-q21.1	205782_at	NM_002009																				
3.81	4.16	0.35	4.28E-02	3.31E-01	PTCH2	patched homolog 2 (Drosophila)	chr1p33-p34	221292_at	NM_003738																				
2.66	3.02	0.36	4.28E-02	3.31E-01	OR3A2	olfactory receptor, family 3, subfamily A, member 2	chr17p13.3	221386_at	NM_002551																				
5.99	6.53	0.54	4.29E-02	3.31E-01	CDH15	cadherin 15, M-cadherin (myotubule)	chr16q24.3	206328_at	NM_004933																				
3.94	4.30	0.37	4.29E-02	3.31E-01	GPR156	G protein-coupled receptor 156	chr3q13.33	239607_at	NM_153002																				
3.80	4.99	1.19	4.29E-02	3.31E-01	ASB4	ankyrin repeat and SOCS box-containing 4	chr7q21-q22	217228_s_at	NM_016116 /// NM_145872																				
4.86	5.14	0.29	4.29E-02	3.31E-01	---	---	---	240505_at	---																				
3.23	3.68	0.45	4.30E-02	3.32E-01	CSMD2	CUB and Sushi multiple domains 2	chr1p35.1-p34.3	233145_at	NM_052896																				
3.12	3.53	0.42	4.30E-02	3.32E-01	C14orf83	chromosome 14 open reading frame 83	chr14q24.1	238820_at	NM_182526																				
10.75	11.22	0.47	4.30E-02	3.32E-01	HSPA8	heat shock 70kDa protein 8	chr11q24.1	221891_x_at	NM_006597 /// NM_153201																				
2.71	3.10	0.38	4.30E-02	3.32E-01	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	chr7q31.2	205043_at	NM_000492																				
9.20	9.98	0.78	4.30E-02	3.32E-01	A2M	alpha-2-macroglobulin	chr12p13.3-p12.3	217757_at	NM_000014																				
4.58	4.97	0.39	4.30E-02	3.32E-01	GATAD2A	GATA zinc finger domain containing 2A	chr19p13.11	238324_at	NM_017660																				
2.40	2.77	0.37	4.30E-02	3.32E-01	---	---	---	242216_at	---																				
3.07	3.42	0.36	4.30E-02	3.32E-01	---	---	---	217676_at	---																				
6.81	7.55	0.74	4.31E-02	3.32E-01	FAM107B	family with sequence similarity 107, member B	chr10p13	223058_at	NM_031453																				
4.59	4.95	0.36	4.30E-02	3.32E-01	FAM182A	Family with sequence similarity 182, member A	chr20p11.1	216053_x_at	XR_041125 /// XR_041127																				
4.67	5.03	0.36	4.31E-02	3.32E-01	RHOV	ras homolog gene family, member V	chr15q13.3	241990_at	NM_133639																				
4.29	4.65	0.36	4.31E-02	3.32E-01	TICAM2 /// TMED7	toll-like receptor adaptor molecule 2 /// transmembrane emp24 protein transport domain containing 7	chr5q22.3 /// chr5q23.1	239431_at	NM_021649 /// NM_181836																				
4.24	4.64	0.40	4.31E-02	3.32E-01	CD2AP	CD2-associated protein	chr6p12	236257_at	NM_012120																				
4.22	4.95	0.74	4.31E-02	3.32E-01	---	---	---	238875_at	---																				
2.54	2.84	0.30	4.31E-02	3.32E-01	DYX1C1	dyslexia susceptibility 1 candidate 1	chr15q21.3	241713_s_at	NM_001033559 /// NM_001033560 /// NM_130810																				
3.08	4.13	1.05	4.31E-02	3.32E-01	---	---	---	227618_at	---																				
2.19	2.56	0.37	4.31E-02	3.32E-01	---	---	---	231111_at	---																				
2.65	2.98	0.33	4.31E-02	3.32E-01	GLDC	glycine dehydrogenase (decarboxylating)	chr9p22	204836_at	NM_000170																				
2.42	2.80	0.38	4.32E-02	3.32E-01	---	---	---	239584_at	---																				
3.72	4.30	0.58	4.32E-02	3.32E-01	ASAH2B	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B	chr10q11.23	229793_at	NM_001079516																				
2.50	2.95	0.45	4.32E-02	3.32E-01	---	---	---	1560411_at	---																				
2.24	2.60	0.36	4.32E-02	3.32E-01	---	---	---	234043_at	---																				
5.37	5.71	0.34	4.32E-02	3.32E-01	LOC595101	PI-3-kinase-related kinase SMG-1 pseudogene	chr16p11.2	238449_at	NR_002453																				
3.89	4.21	0.32	4.32E-02	3.32E-01	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	chr5q31.2	201344_at	NM_003339 /// NM_181838																				
3.73	4.90	1.18	4.33E-02	3.32E-01	PALMD	palmdelphin	chr1p22-p21	222725_s_at	NM_017734																				
7.74	8.66	0.92	4.32E-02	3.32E-01	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	chr2q37.1	201199_s_at	NM_002807																				
5.07	5.96	0.89	4.33E-02	3.32E-01	C14orf129	chromosome 14 open reading frame 129	chr14q32.2	223239_at	NM_016472																				

3.44	4.18	0.74	4.32E-02	3.32E-01	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	chr3p25-p24	205920_at	NM_001134367 /// NM_001134368 /// NM_003043																				
5.60	6.28	0.68	4.33E-02	3.32E-01	KIF3B	kinesin family member 3B	chr20q11.21	203943_at	NM_004798																				
4.49	4.93	0.44	4.33E-02	3.32E-01	NMNAT3	nicotinamide nucleotide adenylyltransferase 3	chr3q23	243738_at	NM_178177																				
3.98	4.34	0.36	4.33E-02	3.32E-01	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	chr6p21	238543_x_at	NM_153487																				
1.72	2.01	0.29	4.33E-02	3.32E-01	FILIP1	filamin A interacting protein 1	chr6q14.1	1556325_at	NM_015687																				
2.44	2.80	0.37	4.33E-02	3.32E-01	---	---	---	208276_at	---																				
2.29	3.15	0.86	4.33E-02	3.32E-01	GUCY1B3	guanylate cyclase 1, soluble, beta 3	chr4q31.3-q33	211555_s_at	NM_000857																				
5.88	6.54	0.66	4.33E-02	3.32E-01	---	---	---	228775_at	---																				
3.46	3.97	0.51	4.33E-02	3.32E-01	VWA5B2	von Willebrand factor A domain containing 5B2	chr3q27.1	1554850_at	XM_001716350 /// XM_291077 /// XM_941833																				
5.90	7.21	1.32	4.34E-02	3.32E-01	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	chr18q12.1	1568618_a_at	NM_020474																				
5.36	5.92	0.56	4.34E-02	3.32E-01	SP110	SP110 nuclear body protein	chr2q37.1	209761_s_at	NM_004509 /// NM_004510 /// NM_080424																				
2.39	2.69	0.30	4.34E-02	3.32E-01	FAM80A	family with sequence similarity 80, member A	chr1p34.2	236884_at	NM_173642																				
3.84	4.24	0.40	4.35E-02	3.33E-01	---	---	---	234135_x_at	---																				
3.57	3.90	0.33	4.35E-02	3.33E-01	PTPN1	protein tyrosine phosphatase, non-receptor type 1	chr20q13.1-q13.2	217686_at	NM_002827																				
4.16	4.72	0.56	4.35E-02	3.33E-01	ZNF426	zinc finger protein 426	chr19p13.2	205964_at	NM_024106																				
2.18	2.49	0.31	4.35E-02	3.33E-01	ONECUT2	one cut homeobox 2	chr18q21.1-q21.2	239911_at	NM_004852																				
5.88	6.89	1.01	4.36E-02	3.33E-01	ADK	adenosine kinase	chr10q22|10q11-q24	204119_s_at	NM_001123 /// NM_006721																				
4.45	4.83	0.38	4.36E-02	3.33E-01	AP3M1	adaptor-related protein complex 3, mu 1 subunit	chr10q22.2	222517_at	NM_012095 /// NM_207012																				
2.23	2.58	0.35	4.35E-02	3.33E-01	LOC100127980	hypothetical protein LOC100127980	chr19q13.12	1560238_at	XM_001720119 /// XM_001722650																				
1.97	2.32	0.35	4.35E-02	3.33E-01	ERAP1	endoplasmic reticulum aminopeptidase 1	chr5q15	214012_at	NM_001040458 /// NM_016442																				
3.12	3.60	0.49	4.36E-02	3.33E-01	---	---	---	239162_at	---																				
3.14	3.38	0.24	4.36E-02	3.33E-01	ADRA1D	adrenergic, alpha-1D-, receptor	chr20p13	210960_at	NM_000678																				
1.85	2.08	0.23	4.36E-02	3.33E-01	RBM11	RNA binding motif protein 11	chr21q11	232549_at	NM_144770																				
4.49	5.03	0.54	4.36E-02	3.33E-01	---	---	---	229449_at	---																				
4.82	5.28	0.45	4.36E-02	3.33E-01	---	---	---	228910_at	---																				
3.37	3.67	0.30	4.36E-02	3.33E-01	---	---	---	241020_at	---																				
3.89	4.24	0.35	4.37E-02	3.33E-01	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	chr12p12.3	1555811_at	NM_001175																				
2.73	3.11	0.38	4.37E-02	3.33E-01	LZTS2	leucine zipper, putative tumor suppressor 2	chr10q24	225013_at	NM_032429																				
4.18	5.18	1.00	4.37E-02	3.33E-01	SULF2	sulfatase 2	chr20q12-q13.2	233555_s_at	NM_018837 /// NM_198596																				
2.66	3.08	0.43	4.37E-02	3.33E-01	C4orf12	chromosome 4 open reading frame 12	chr4q21.3	241401_at	NR_015359 /// XR_042111 /// XR_042112 /// XR_042113																				
3.81	4.24	0.43	4.37E-02	3.34E-01	IQSEC3 /// LOC100134209 /// LOC731035	IQ motif and Sec7 domain 3 /// similar to IQ motif and Sec7 domain-containing protein 3 /// similar to IQ motif and Sec7 domain 3	chr12p13.33	213834_at	NM_015232 /// XM_001126365 /// XM_001720539																				
2.48	2.80	0.32	4.37E-02	3.34E-01	ZNF707	Zinc finger protein 707	chr8q24.3	1562944_at	NM_001100598 /// NM_001100599 /// NM_173831																				
2.72	2.99	0.27	4.37E-02	3.34E-01	LOC283688	hypothetical protein LOC283688	chr15q25.1	1566526_at	XM_001127453 /// XM_001132532 /// XM_001714631																				
4.53	4.88	0.35	4.37E-02	3.34E-01	PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	chr1p36	205232_s_at	NM_000437																				
3.05	3.43	0.38	4.38E-02	3.34E-01	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	chr11q23.2-q24.2	230707_at	NM_003105																				
2.82	3.13	0.31	4.38E-02	3.34E-01	RUNX2	runt-related transcription factor 2	chr6p21	221282_x_at	NM_001015051 /// NM_001024630 /// NM_004348																				

1.83	2.11	0.28	4.38E-02	3.34E-01	GRIA2	glutamate receptor, ionotropic, AMPA 2	chr4q32-q33	236538_at	NM_000826 /// NM_001083619 /// NM_001083620																				
3.98	4.89	0.91	4.38E-02	3.34E-01	TCF12	Transcription factor 12	chr15q21	235925_at	NM_003205 /// NM_207036 /// NM_207037 /// NM_207038 /// NM_207040																				
6.46	7.34	0.88	4.39E-02	3.34E-01	SECISBP2	SECIS binding protein 2	chr9q22.2	224250_s_at	NM_024077																				
3.77	4.27	0.49	4.39E-02	3.34E-01	HOXD13	homeobox D13	chr2q31.1	236681_at	NM_000523																				
3.81	4.21	0.41	4.38E-02	3.34E-01	PTPDC1	protein tyrosine phosphatase domain containing 1	chr9q22.32	229517_at	NM_152422 /// NM_177995																				
2.40	2.74	0.34	4.38E-02	3.34E-01	TP73	tumor protein p73	chr1p36.3	232546_at	NM_001126240 /// NM_001126241 /// NM_001126242 /// NM_005427																				
7.68	8.50	0.82	4.39E-02	3.34E-01	TNS3	tensin 3	chr7p12.3	217853_at	NM_022748																				
7.42	8.84	1.41	4.39E-02	3.34E-01	TNPO1	transportin 1	chr5q13.2	209226_s_at	NM_002270 /// NM_153188																				
2.61	2.97	0.35	4.39E-02	3.34E-01	C18orf54	chromosome 18 open reading frame 54	chr18q21.2	229442_at	NM_173529																				
5.09	5.53	0.44	4.40E-02	3.34E-01	SORT1	sortilin 1	chr1p21.3-p13.1|1p21.3-p13.1	212807_s_at	NM_002959																				
3.05	3.40	0.34	4.40E-02	3.34E-01	---	---	---	1563077_at	---																				
3.94	4.27	0.33	4.40E-02	3.34E-01	ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	chr16q24.1	214798_at	NM_014861																				
6.79	7.22	0.44	4.41E-02	3.35E-01	ZNF646	zinc finger protein 646	chr16p11.2	204876_at	NM_014699																				
6.05	7.29	1.25	4.41E-02	3.35E-01	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	chr18q12.1	201723_s_at	NM_020474																				
1.97	2.22	0.24	4.41E-02	3.35E-01	---	---	---	1566544_at	---																				
5.25	5.79	0.54	4.42E-02	3.35E-01	---	---	---	227264_at	---																				
5.00	5.41	0.40	4.42E-02	3.35E-01	---	---	---	236709_at	---																				
5.97	6.27	0.30	4.42E-02	3.35E-01	BCL2L1	BCL2-like 1	chr20q11.21	231228_at	NM_001191 /// NM_138578																				
3.14	3.49	0.35	4.42E-02	3.35E-01	LSDP5	Lipid storage droplet protein 5	chr19p13.3	238019_at	NM_001013706																				
6.07	7.04	0.98	4.42E-02	3.35E-01	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	chr14q23.3	201143_s_at	NM_004094																				
4.68	5.32	0.64	4.43E-02	3.35E-01	---	---	---	243184_at	---																				
5.09	5.56	0.47	4.43E-02	3.35E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	240098_at	NM_018151																				
2.38	2.77	0.39	4.43E-02	3.35E-01	TTC30B	tetratricopeptide repeat domain 30B	chr2q31.2	243413_at	NM_152517																				
2.12	2.40	0.28	4.43E-02	3.35E-01	MAP3K2	mitogen-activated protein kinase kinase kinase 2	chr2q14.3	1565131_x_at	NM_006609																				
4.58	5.02	0.45	4.43E-02	3.36E-01	C1orf200	chromosome 1 open reading frame 200	chr1p36.22	1559638_at	NM_001045478																				
2.47	2.81	0.34	4.44E-02	3.36E-01	---	---	---	237629_at	---																				
1.95	2.21	0.25	4.44E-02	3.36E-01	---	---	---	243844_at	---																				
4.93	5.53	0.61	4.44E-02	3.36E-01	TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	chr1q23.2	1553677_a_at	NM_001031800 /// NM_152902																				
3.02	3.46	0.44	4.45E-02	3.36E-01	KIAA1462	KIAA1462	chr10p11.23	231841_s_at	NM_020848																				
5.46	6.34	0.88	4.45E-02	3.36E-01	ZNF415	zinc finger protein 415	chr19q13.41	205514_at	NM_018355																				
6.04	6.49	0.45	4.45E-02	3.36E-01	LOC157860	hypothetical protein LOC157860	chr8p11.23	232040_at	---																				
5.11	5.53	0.42	4.46E-02	3.36E-01	RRP7A /// RRP7B	ribosomal RNA processing 7 homolog A (S. cerevisiae) /// ribosomal RNA processing 7 homolog B (S. cerevisiae)	chr22q13.2 /// chr22q13.2-q13.31	214828_s_at	NM_015703 /// NR_002184																				
2.40	2.78	0.38	4.46E-02	3.36E-01	JHDM1D	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	chr7q34	225142_at	NM_030647																				
3.92	4.29	0.37	4.46E-02	3.36E-01	TP73	tumor protein p73	chr1p36.3	1554379_a_at	NM_001126240 /// NM_001126241 /// NM_001126242 /// NM_005427																				
2.73	3.09	0.36	4.46E-02	3.36E-01	---	---	---	243174_at	---																				
6.07	6.41	0.34	4.46E-02	3.36E-01	ARVCF	armadillo repeat gene deletes in velocardiofacial syndrome	chr22q11.21	205784_x_at	NM_001670																				

2.82	3.09	0.26	4.46E-02	3.36E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	210805_x_at	NM_001001890 /// NM_001122607 /// NM_001754
8.61	9.12	0.51	4.46E-02	3.36E-01	ANAPC13	anaphase promoting complex subunit 13	chr3q22.1	209001_s_at	NM_015391
2.63	3.01	0.38	4.46E-02	3.36E-01	---	---	---	242936_at	---
2.23	2.67	0.44	4.46E-02	3.36E-01	---	---	---	1569558_at	---
4.65	4.98	0.33	4.47E-02	3.36E-01	GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	chr22q13.31	217560_at	NM_001001560 /// NM_001001561 /// NM_013365
2.05	2.37	0.31	4.47E-02	3.37E-01	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	chr13q32.2	237767_at	NM_001001715 /// NM_005766
11.36	11.90	0.54	4.47E-02	3.37E-01	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	chr2q31.2	1555653_at	NM_194247
4.85	5.72	0.87	4.48E-02	3.37E-01	---	---	---	1557813_at	---
3.75	4.48	0.73	4.48E-02	3.37E-01	SRR	serine racemase	chr17p13	219204_s_at	NM_021947
4.64	5.25	0.61	4.48E-02	3.37E-01	---	---	---	233824_at	---
2.97	3.47	0.50	4.48E-02	3.37E-01	---	---	---	233009_at	---
3.13	3.52	0.39	4.48E-02	3.37E-01	---	---	---	1556373_a_at	---
2.78	3.16	0.38	4.48E-02	3.37E-01	LOC150527	hypothetical protein LOC150527	chr2q21.2	1560806_at	---
2.48	2.83	0.34	4.48E-02	3.37E-01	C20orf78 /// LOC100128496 /// LOC100133825	chromosome 20 open reading frame 78 /// similar to chromosome 20 open reading frame 78 /// similar to chromosome 20 open reading frame 78	chr20p11.23	237793_at	XM_001724637 /// XM_001724640 /// XM_001725705 /// XM_001725706
4.50	4.82	0.33	4.48E-02	3.37E-01	---	---	---	217283_at	---
4.05	4.36	0.31	4.48E-02	3.37E-01	FLJ45055 /// LOC100133687	60S ribosomal pseudogene /// similar to hCG15392	chr8p23.3	222225_at	NR_003572 /// XM_001721097
2.47	2.77	0.30	4.48E-02	3.37E-01	---	---	---	230199_at	---
2.63	2.91	0.28	4.48E-02	3.37E-01	---	---	---	237658_at	---
2.39	2.66	0.27	4.48E-02	3.37E-01	---	---	---	238271_x_at	---
4.22	5.42	1.19	4.49E-02	3.37E-01	---	---	---	233219_at	---
2.66	2.96	0.30	4.49E-02	3.37E-01	ZNF614	zinc finger protein 614	chr19q13.33	210599_at	NM_025040
3.94	4.18	0.24	4.49E-02	3.37E-01	---	---	---	1569345_at	---
4.12	4.61	0.48	4.49E-02	3.37E-01	---	---	---	235660_at	---
6.59	7.11	0.51	4.49E-02	3.37E-01	NFIB	nuclear factor I/B	chr9p24.1	209289_at	NM_005596
5.43	5.97	0.54	4.50E-02	3.37E-01	APOL6	apolipoprotein L, 6	chr22q12.3	241869_at	NM_030641
2.29	2.68	0.39	4.50E-02	3.37E-01	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	chr1q21-q22	208605_s_at	NM_001007792 /// NM_001012331 /// NM_002529
4.86	5.21	0.36	4.50E-02	3.37E-01	KIAA0241	KIAA0241	chr7p14.3	212475_at	NM_015060
2.08	2.36	0.28	4.50E-02	3.37E-01	LOC100128729 /// LOC731082 /// TLK2	similar to TLK2 protein /// similar to Serine/threonine-protein kinase tousled-like 2 (Tousled-like kinase 2) /// tousled-like kinase 2	chr17q23 /// chr7q32.1	232585_at	NM_001112707 /// NM_006852 /// XM_001715628 /// XR_042327 /// XR_042485
2.08	2.39	0.31	4.50E-02	3.37E-01	---	---	---	1564083_at	---
6.09	6.59	0.51	4.50E-02	3.37E-01	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	chr1p34.1	225905_s_at	NM_006279 /// NM_174963 /// NM_174964 /// NM_174965 /// NM_174966 /// NM_174967 /// NM_174968 /// NM_174969 /// NM_174970 /// NM_174971
4.84	5.18	0.34	4.50E-02	3.37E-01	C14orf68	chromosome 14 open reading frame 68	chr14q32.2	237765_at	NM_207117
2.19	2.50	0.32	4.51E-02	3.37E-01	PDE3A	phosphodiesterase 3A, cGMP-inhibited	chr12p12	206389_s_at	NM_000921
2.29	2.67	0.39	4.51E-02	3.37E-01	---	---	---	239778_x_at	---
2.21	2.85	0.65	4.52E-02	3.37E-01	KLHL31	kelch-like 31 (Drosophila)	chr6p12.1	239398_at	NM_001003760
4.83	5.27	0.44	4.51E-02	3.37E-01	SPDEF	SAM pointed domain containing ets transcription factor	chr6p21.3	214404_x_at	NM_012391
5.06	5.45	0.39	4.51E-02	3.37E-01	WDR34	WD repeat domain 34	chr9q34.11	237287_at	NM_052844
2.18	2.56	0.39	4.51E-02	3.37E-01	---	---	---	244273_at	---
7.96	8.34	0.37	4.51E-02	3.37E-01	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa	chr6q21	225083_at	NM_138408

3.43	3.75	0.33	4.52E-02	3.37E-01	HGD /// LOC100132552 /// LOC727722	homogentisate 1,2-dioxygenase (homogentisate oxidase) /// similar to homogentisate 1,2-dioxygenase /// homogentisate 1,2-dioxygenase like	chr3q13.33	214308_s_at	NM_000187 /// XM_001713606 /// XM_001719739																				
2.68	2.97	0.29	4.51E-02	3.37E-01	TRIO	triple functional domain (PTPRF interacting)	chr5p15.2	209010_s_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929																				
2.06	2.32	0.26	4.51E-02	3.37E-01	---	---	---	234348_at	---																				
2.43	2.69	0.26	4.52E-02	3.37E-01	CLEC4D	C-type lectin domain family 4, member D	chr12p13.31	1552773_at	NM_080387																				
7.18	8.03	0.85	4.52E-02	3.37E-01	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	chr4q11-q13	203131_at	NM_006206																				
2.92	3.32	0.40	4.52E-02	3.38E-01	---	---	---	1560636_a_at	---																				
2.71	3.00	0.28	4.52E-02	3.38E-01	OVOL2	ovo-like 2 (Drosophila)	chr20pter-q11.23	211778_s_at	NM_021220																				
2.06	2.32	0.26	4.52E-02	3.38E-01	---	---	---	231091_x_at	---																				
3.97	5.20	1.23	4.54E-02	3.38E-01	PPID	Peptidylprolyl isomerase D (cyclophilin D)	chr4q31.3	228469_at	NM_005038																				
7.06	7.67	0.61	4.53E-02	3.38E-01	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	chr11p15.1	209448_at	NM_001098520 /// NM_001098521 /// NM_001098522 /// NM_001098523 /// NM_006410																				
2.61	3.12	0.51	4.53E-02	3.38E-01	---	---	---	239780_at	---																				
3.12	3.49	0.38	4.54E-02	3.38E-01	TTLL10	tubulin tyrosine ligase-like family, member 10	chr1p36.33	1552419_s_at	NM_001130045 /// NM_153254																				
6.82	7.17	0.34	4.53E-02	3.38E-01	IGHM /// LOC652494	immunoglobulin heavy constant mu /// similar to Ig heavy chain V-III region VH26 precursor	chr14q32.33	215949_x_at	XM_001717586 /// XM_001719484																				
2.77	3.09	0.32	4.53E-02	3.38E-01	41528	septin 11	chr4q21.1	230071_at	NM_018243																				
3.21	3.58	0.36	4.54E-02	3.38E-01	SH3GLP2	SH3-domain GRB2-like pseudogene 2	chr17q11.2	1567030_at	---																				
5.84	6.73	0.89	4.54E-02	3.38E-01	ACSL3	acyl-CoA synthetase long-chain family member 3	chr2q34-q35	201662_s_at	NM_004457 /// NM_203372																				
2.77	3.11	0.34	4.54E-02	3.38E-01	ESR2	estrogen receptor 2 (ER beta)	chr14q23.2	211120_x_at	NM_001040275 /// NM_001040276 /// NM_001437																				
1.91	2.16	0.24	4.54E-02	3.38E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	234544_at	NM_015313																				
3.30	3.54	0.25	4.54E-02	3.38E-01	---	---	---	230282_at	---																				
4.13	6.15	2.02	4.55E-02	3.38E-01	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	chr5p14-p13	205822_s_at	NM_001098272 /// NM_002130																				
5.85	6.64	0.79	4.55E-02	3.38E-01	TBXA2R	thromboxane A2 receptor	chr19p13.3	336_at	NM_001060 /// NM_201636																				
2.45	2.75	0.30	4.55E-02	3.38E-01	OR11A1	olfactory receptor, family 11, subfamily A, member 1	chr6p22.2-p21.31	221343_at	NM_013937																				
2.59	2.86	0.27	4.55E-02	3.38E-01	---	---	---	243806_at	---																				
2.13	2.40	0.27	4.55E-02	3.38E-01	---	---	---	233284_at	---																				
7.88	9.07	1.18	4.55E-02	3.38E-01	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	chr14q23-q24.2	208899_x_at	NM_015994																				
5.72	6.22	0.50	4.55E-02	3.38E-01	KIAA1598	KIAA1598	chr10q25.3	221802_s_at	NM_001127211 /// NM_018330																				
3.69	3.98	0.29	4.56E-02	3.38E-01	CCL17	chemokine (C-C motif) ligand 17	chr16q13	207900_at	NM_002987																				
4.74	5.05	0.31	4.56E-02	3.39E-01	TNXB	tenascin XB	chr6p21.3	217413_s_at	NM_019105 /// NM_032470																				
4.10	4.58	0.48	4.56E-02	3.39E-01	MMP25	matrix metallopeptidase 25	chr16p13.3	207890_s_at	NM_022468																				
3.65	4.67	1.02	4.56E-02	3.39E-01	---	---	---	230175_s_at	---																				
2.51	2.88	0.37	4.57E-02	3.39E-01	PRO0132	PRO0132 protein	chr2q34	220479_at	NR_002763																				
2.34	2.85	0.51	4.57E-02	3.39E-01	---	---	---	224254_x_at	---																				
3.21	3.61	0.40	4.57E-02	3.39E-01	---	---	---	238311_at	---																				
3.49	3.86	0.37	4.57E-02	3.39E-01	TMEM151B	transmembrane protein 151B	chr6p21.1	213676_at	XM_001723534 /// XM_001723740 /// XM_001725716																				
2.46	2.75	0.29	4.57E-02	3.39E-01	---	---	---	1560588_at	---																				
4.96	6.45	1.49	4.58E-02	3.39E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	227510_x_at	NR_002819																				

4.16	4.67	0.51	4.58E-02	3.39E-01	ZNF626	zinc finger protein 626	chr19p12	235687_at	NM_001076675 /// NM_145297
2.74	3.17	0.43	4.58E-02	3.39E-01	---	---	---	233130_at	---
4.45	4.84	0.39	4.58E-02	3.39E-01	LAD1	ladinin 1	chr1q25.1-q32.3	216641_s_at	NM_005558
3.74	4.11	0.37	4.58E-02	3.39E-01	---	---	---	244610_x_at	---
2.74	3.07	0.32	4.58E-02	3.39E-01	LOC728084	hypothetical LOC728084	chr12q21.33	1559595_at	XR_040692 /// XR_040693 /// XR_040694
2.15	2.40	0.25	4.58E-02	3.39E-01	---	---	---	237998_at	---
6.54	6.97	0.43	4.59E-02	3.39E-01	C19orf68	chromosome 19 open reading frame 68	chr19q13.32	238866_at	XM_001713770 /// XM_001713771 /// XM_001713772
3.23	3.50	0.27	4.58E-02	3.39E-01	TNK1	tyrosine kinase, non-receptor, 1	chr17p13.1	205793_x_at	NM_003985
1.90	2.14	0.24	4.58E-02	3.39E-01	UPP2	uridine phosphorylase 2	chr2q24.1	231376_at	NM_173355
2.16	2.46	0.31	4.59E-02	3.39E-01	---	---	---	1562873_at	---
3.69	4.14	0.45	4.59E-02	3.39E-01	C14orf50	chromosome 14 open reading frame 50	chr14q23.3	237654_at	NM_172365
2.86	3.27	0.41	4.59E-02	3.39E-01	NPCDR1	nasopharyngeal carcinoma, down-regulated 1	chr3p21.1	224140_at	XR_041781 /// XR_041782 /// XR_041783
3.50	3.88	0.38	4.59E-02	3.39E-01	RPRD1B	Regulation of nuclear pre-mRNA domain containing 1B	chr20q11.21-q12	230801_at	NM_021215
3.25	3.59	0.34	4.59E-02	3.39E-01	GAB1	GRB2-associated binding protein 1	chr4q31.21	214987_at	NM_002039 /// NM_207123
2.82	3.14	0.32	4.59E-02	3.39E-01	F5	coagulation factor V (proaccelerin, labile factor)	chr1q23	204714_s_at	NM_000130
4.00	4.32	0.31	4.59E-02	3.39E-01	LOC100133772 /// SLC16A5	similar to MCT /// solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	chr17q25.1	206599_at	NM_004695 /// XM_001715145
2.32	2.63	0.31	4.59E-02	3.39E-01	DKFZp547H025	hypothetical protein DKFZp547H025	chr2q36.3	208265_at	NM_020161
3.02	3.38	0.36	4.60E-02	3.39E-01	BRD4	bromodomain containing 4	chr19p13.1	240360_at	NM_014299 /// NM_058243
2.56	3.03	0.47	4.60E-02	3.39E-01	KIAA1128	KIAA1128	chr10q23.1	1554132_a_at	NM_018999
5.11	5.48	0.37	4.60E-02	3.39E-01	VIPR2	vasoactive intestinal peptide receptor 2	chr7q36.3	205946_at	NM_003382
2.11	2.35	0.25	4.60E-02	3.39E-01	LOC100134363 /// LOC100134366 /// PLGLA /// PLGLB1 /// PLGLB2	hypothetical protein LOC100134363 /// hypothetical protein LOC100134366 /// plasminogen-like A /// plasminogen-like B1 /// plasminogen-like B2	chr2p11-q11 /// chr2p11.2 /// chr2q12.2	205871_at	NM_001032392 /// NM_002665 /// NR_003506 /// XM_001713633 /// XM_001713689 /// XR_042135
2.82	3.50	0.69	4.61E-02	3.40E-01	KIAA1333	KIAA1333	chr14q12	223258_s_at	NM_017769
3.44	3.78	0.34	4.61E-02	3.40E-01	C3orf45	chromosome 3 open reading frame 45	chr3p21.31	237024_at	NM_153215
2.31	2.55	0.24	4.61E-02	3.40E-01	---	---	---	221146_at	---
2.38	2.66	0.28	4.61E-02	3.40E-01	TRIM9	tripartite motif-containing 9	chr14q22.1	209859_at	NM_015163 /// NM_052978
1.77	2.03	0.26	4.61E-02	3.40E-01	---	---	---	1559214_at	---
2.06	2.29	0.23	4.61E-02	3.40E-01	NR2C1	nuclear receptor subfamily 2, group C, member 1	chr12q22	229956_at	NM_001032287 /// NM_001127362 /// NM_003297
2.99	3.36	0.38	4.61E-02	3.40E-01	---	---	---	216143_at	---
3.62	3.97	0.35	4.61E-02	3.40E-01	---	---	---	216152_at	---
3.20	3.64	0.44	4.62E-02	3.40E-01	ZDHHC22	zinc finger, DHHC-type containing 22	chr14q24.3	229875_at	NM_174976
2.29	2.62	0.32	4.62E-02	3.40E-01	---	---	---	240823_at	---
2.80	3.29	0.49	4.62E-02	3.40E-01	SSTR2	somatostatin receptor 2	chr17q24	239031_at	NM_001050
4.51	4.96	0.45	4.62E-02	3.40E-01	MFSD3	Major facilitator superfamily domain containing 3	chr8q24.3	238947_at	NM_138431
6.22	6.64	0.42	4.62E-02	3.40E-01	SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	chr19p13.3	220778_x_at	NM_032108
2.63	2.88	0.25	4.62E-02	3.40E-01	---	---	---	239606_at	---
2.42	2.91	0.49	4.63E-02	3.40E-01	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	chr7q21.1	210997_at	NM_000601 /// NM_001010931 /// NM_001010932 /// NM_001010933 /// NM_001010934
4.43	4.83	0.39	4.63E-02	3.40E-01	RCOR1	REST corepressor 1	chr14q32.31-q32.32	237041_x_at	NM_015156
2.99	3.35	0.36	4.63E-02	3.40E-01	---	---	---	240351_at	---
3.89	4.24	0.35	4.63E-02	3.40E-01	---	---	---	232394_at	---

2.35	2.67	0.31	4.63E-02	3.40E-01	---	---	---	243663_at	---
3.02	3.32	0.30	4.63E-02	3.40E-01	HRG	histidine-rich glycoprotein	chr3q27	206226_at	NM_000412
3.02	3.32	0.30	4.63E-02	3.40E-01	LPIN3	lipin 3	chr20q12	232966_at	NM_022896
3.14	3.42	0.28	4.63E-02	3.40E-01	---	---	---	244667_at	---
3.75	4.30	0.55	4.64E-02	3.40E-01	LOC142893	hypothetical protein LOC142893	chr10q22.3	233336_at	---
2.55	2.96	0.41	4.64E-02	3.40E-01	---	---	---	242726_at	---
2.35	2.63	0.28	4.64E-02	3.40E-01	OLAH	oleoyl-ACP hydrolase	chr10p13	233126_s_at	NM_001039702 /// NM_018324
5.06	6.89	1.83	4.64E-02	3.40E-01	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	chr3q26.3	204369_at	NM_006218
6.69	7.34	0.66	4.64E-02	3.40E-01	SORD	sorbitol dehydrogenase	chr15q15.3	201563_at	NM_003104
2.37	2.80	0.43	4.64E-02	3.40E-01	---	---	---	231250_at	---
3.44	3.82	0.38	4.64E-02	3.40E-01	---	---	---	217324_at	---
2.51	2.88	0.37	4.64E-02	3.40E-01	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	chr12p13.3	238636_at	NM_000719 /// NM_001129827 /// NM_001129829 /// NM_001129830 /// NM_001129831 /// NM_001129832 /// NM_001129833 /// NM_001129834 /// NM_001129835 /// NM_001129836 /// NM_001129837 /// NM_001129838 /// NM_001129839 /// NM_001129840 /// NM_001129841 /// NM_001129842 /// NM_001129843 /// NM_001129844 /// NM_001129846 /// NM_199460
2.15	2.47	0.32	4.64E-02	3.40E-01	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	chr6q24-q25.1	219813_at	NM_004690
3.20	3.48	0.28	4.64E-02	3.40E-01	IRX2	iroquois homeobox 2	chr5p15.33	228404_at	NM_001134222 /// NM_033267
2.50	2.77	0.27	4.64E-02	3.40E-01	OXTR	oxytocin receptor	chr3p25	206825_at	NM_000916
9.26	10.41	1.15	4.64E-02	3.40E-01	DDR2	discoidin domain receptor tyrosine kinase 2	chr1q23.3	227561_at	NM_001014796 /// NM_006182
5.16	5.61	0.45	4.65E-02	3.40E-01	FBXL18	F-box and leucine-rich repeat protein 18	chr7p22.2	227500_at	NM_024963
4.45	4.82	0.36	4.65E-02	3.40E-01	---	---	---	242386_x_at	---
5.71	6.07	0.36	4.65E-02	3.40E-01	BCCIP	BRCA2 and CDKN1A interacting protein	chr10q26.1	218264_at	NM_016567 /// NM_078468 /// NM_078469
2.90	3.31	0.40	4.65E-02	3.40E-01	---	---	---	233027_at	---
1.82	2.17	0.35	4.65E-02	3.40E-01	GIGYF2	GRB10 interacting GYF protein 2	chr2q37.1	1560133_at	NM_001103146 /// NM_001103147 /// NM_001103148 /// NM_015575
4.98	5.32	0.34	4.65E-02	3.40E-01	TMCC1	transmembrane and coiled-coil domain family 1	chr3q21.3	213349_at	NM_001017395 /// NM_001128224 /// NM_015008

4.47	4.79	0.33	4.65E-02	3.40E-01	---	---	---	241792_x_at	---
3.46	3.73	0.27	4.65E-02	3.40E-01	LOC388948	hypothetical gene supported by BC062774	chr2p21	237840_at	XM_001725424 /// XM_373985 /// XM_945437
2.74	2.99	0.25	4.65E-02	3.40E-01	NRXN3	neurexin 3	chr14q31	215021_s_at	NM_001105250 /// NM_004796 /// NM_138970
6.52	7.55	1.02	4.66E-02	3.40E-01	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	chr7q22.1-q22.3	201067_at	NM_002803
3.05	3.40	0.35	4.66E-02	3.40E-01	ARRB1	arrestin, beta 1	chr11q13	218832_x_at	NM_004041 /// NM_020251
5.27	5.95	0.68	4.66E-02	3.40E-01	UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)	chr2q31.1	234982_at	NM_172070
3.94	4.33	0.39	4.66E-02	3.40E-01	ZSCAN5A	zinc finger and SCAN domain containing 5A	chr19q13.43	1565583_at	NM_024303
6.40	6.77	0.37	4.67E-02	3.40E-01	---	---	---	242246_x_at	---
2.02	2.33	0.30	4.66E-02	3.40E-01	GRIA2	glutamate receptor, ionotropic, AMPA 2	chr4q32-q33	205358_at	NM_000826 /// NM_001083619 /// NM_001083620
1.77	2.06	0.29	4.67E-02	3.40E-01	---	---	---	1560581_at	---
3.87	4.65	0.78	4.67E-02	3.40E-01	SCARA5	scavenger receptor class A, member 5 (putative)	chr8p21.1	235849_at	NM_173833
6.43	6.88	0.45	4.67E-02	3.40E-01	FAM22B	family with sequence similarity 22, member B	chr10q22.3	234695_x_at	XM_001133075 /// XM_001723434
2.66	2.97	0.31	4.67E-02	3.40E-01	---	---	---	242310_at	---
5.89	6.74	0.86	4.68E-02	3.41E-01	EIF4B	eukaryotic translation initiation factor 4B	chr12q13.13	219599_at	NM_001417
3.95	4.41	0.46	4.68E-02	3.41E-01	GIPR	gastric inhibitory polypeptide receptor	chr19q13.3	208105_at	NM_000164
3.46	3.86	0.40	4.68E-02	3.41E-01	SLC38A1	solute carrier family 38, member 1	chr12q13.11	224580_at	NM_001077484 /// NM_030674
2.48	2.80	0.32	4.68E-02	3.41E-01	LOC100133131	hypothetical protein LOC100133131	chr4p16.1	1570411_at	XM_001720390 /// XM_001721325 /// XM_001722499
6.53	7.30	0.77	4.68E-02	3.41E-01	PTRF	polymerase I and transcript release factor	chr17q21.31	1557938_s_at	NM_012232
3.48	4.19	0.71	4.69E-02	3.41E-01	IGHA1 /// IGHG1 /// LOC100133862	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// similar to hCG1773549	chr14q32.33	211647_x_at	XM_001720441
3.61	4.08	0.46	4.68E-02	3.41E-01	ERGIC2	ERGIC and golgi 2	chr12p11.22	240172_at	NM_016570
5.76	6.21	0.45	4.68E-02	3.41E-01	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	chr9q34.3	210678_s_at	NM_001012727 /// NM_006412
2.58	2.99	0.41	4.69E-02	3.41E-01	---	---	---	233619_at	---
2.36	2.76	0.40	4.68E-02	3.41E-01	---	---	---	232671_at	---
6.49	6.88	0.39	4.68E-02	3.41E-01	SRCAP	Snf2-related CREBBP activator protein	chr16p11.2	212275_s_at	NM_006662
4.37	4.72	0.35	4.68E-02	3.41E-01	KSR1	kinase suppressor of ras 1	chr17q11.1	213770_at	NM_014238
2.59	2.93	0.34	4.69E-02	3.41E-01	TRIM50	tripartite motif-containing 50	chr7q11.23	231014_at	NM_178125
1.84	2.15	0.32	4.68E-02	3.41E-01	ARPP-21 /// LOC100130503	cyclic AMP-regulated phosphoprotein, 21 kD /// hypothetical protein LOC100130503	chr3p22.3	1556598_at	NM_001025068 /// NM_001025069 /// NM_016300 /// NM_198399 /// XM_001717149 /// XM_001717791 /// XM_001718042
6.00	6.31	0.31	4.69E-02	3.41E-01	SPDEF	SAM pointed domain containing ets transcription factor	chr6p21.3	213442_x_at	NM_012391
3.75	4.06	0.31	4.69E-02	3.41E-01	---	---	---	242043_s_at	---
2.52	2.83	0.31	4.69E-02	3.41E-01	---	---	---	236375_at	---
2.79	3.09	0.30	4.69E-02	3.41E-01	SLC22A13	solute carrier family 22 (organic anion transporter), member 13	chr3p21.3	207444_at	NM_004256
2.36	2.61	0.25	4.69E-02	3.41E-01	---	---	---	214227_at	---
5.05	5.41	0.36	4.69E-02	3.41E-01	GRIP2	glutamate receptor interacting protein 2	chr3p24-p23	216481_at	NM_001080423
1.87	2.09	0.22	4.69E-02	3.41E-01	---	---	---	1557448_a_at	---
6.30	7.66	1.36	4.70E-02	3.41E-01	PLEK2	pleckstrin 2	chr14q23.3	218644_at	NM_016445
4.56	5.18	0.62	4.70E-02	3.41E-01	PXK	PX domain containing serine/threonine kinase	chr3p14.3	1552274_at	NM_017771

3.76	4.19	0.43	4.70E-02	3.41E-01	FGFR4	fibroblast growth factor receptor 4	chr5q35.1-qter	211237_s_at	NM_002011 /// NM_022963 /// NM_213647
2.50	2.82	0.32	4.70E-02	3.41E-01	REG1P	regenerating islet-derived 1 pseudogene	chr2p12	207778_at	NR_002714
5.68	6.01	0.33	4.70E-02	3.41E-01	ARFRP1 /// IGLJ3	ADP-ribosylation factor related protein 1 /// immunoglobulin lambda joining 3	chr20q13.3 /// chr22q11.1-q11.2	203174_s_at	NM_001134758 /// NM_003224
3.67	3.98	0.31	4.70E-02	3.41E-01	---	---	---	AFFX-PheX-3_at	---
2.75	3.00	0.25	4.70E-02	3.41E-01	---	---	---	234187_at	---
3.89	4.28	0.39	4.70E-02	3.41E-01	MGC12982	hypothetical protein MGC12982	---	224457_at	---
8.48	9.03	0.55	4.71E-02	3.41E-01	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	chr5q31	200765_x_at	NM_001903
6.87	7.29	0.42	4.71E-02	3.41E-01	---	---	---	241944_x_at	---
4.87	5.48	0.61	4.71E-02	3.41E-01	PYGL	phosphorylase, glycogen, liver	chr14q21-q22	202990_at	NM_002863
6.31	7.07	0.76	4.71E-02	3.41E-01	TRIM24	tripartite motif-containing 24	chr7q32-q34	213301_x_at	NM_003852 /// NM_015905
7.56	8.12	0.56	4.71E-02	3.41E-01	SOBP	sine oculis binding protein homolog (Drosophila)	chr6q21	218974_at	NM_018013
5.95	6.45	0.50	4.71E-02	3.41E-01	ARHGAP30	Rho GTPase activating protein 30	chr1q23.3	241346_at	NM_001025598 /// NM_181720
2.96	3.40	0.44	4.71E-02	3.41E-01	STK4	serine/threonine kinase 4	chr20q11.2-q13.2	211085_s_at	NM_006282
5.69	6.12	0.43	4.71E-02	3.41E-01	---	---	---	243640_x_at	---
1.80	2.05	0.25	4.71E-02	3.41E-01	G6PC	glucose-6-phosphatase, catalytic subunit	chr17q21	206952_at	NM_000151
5.10	6.25	1.15	4.72E-02	3.41E-01	ARHGAP15	Rho GTPase activating protein 15	chr2q22.2	218870_at	NM_018460
2.88	3.18	0.30	4.72E-02	3.41E-01	---	---	---	236992_at	---
4.31	4.62	0.31	4.72E-02	3.41E-01	HIF3A	hypoxia inducible factor 3, alpha subunit	chr19q13.32	219319_at	NM_022462 /// NM_152794 /// NM_152795
3.72	4.12	0.40	4.72E-02	3.41E-01	---	---	---	241008_at	---
2.43	2.75	0.33	4.72E-02	3.41E-01	LOC100129857	similar to KIAA1620 protein	chr4q32.1	231671_at	XM_001721864 /// XM_001721903 /// XM_001725995
4.64	5.27	0.63	4.72E-02	3.41E-01	---	---	---	228835_at	---
1.92	2.19	0.26	4.73E-02	3.42E-01	---	---	---	1563494_at	---
4.11	4.48	0.37	4.73E-02	3.42E-01	UNC13D	unc-13 homolog D (C. elegans)	chr17q25.1	228352_at	NM_199242
2.91	4.02	1.11	4.73E-02	3.42E-01	FOXP2	forkhead box P2	chr7q31	235201_at	NM_014491 /// NM_148898 /// NM_148899
3.97	4.85	0.88	4.73E-02	3.42E-01	---	---	---	238666_at	---
1.95	2.31	0.35	4.73E-02	3.42E-01	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	chr12q12	1552694_at	NM_052885
2.21	2.51	0.30	4.73E-02	3.42E-01	DNAL1	dynein, axonemal, light chain 1	chr14q24.3	223958_s_at	NM_031427
3.05	3.39	0.34	4.73E-02	3.42E-01	SEMA6D	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	chr15q21.1	244746_at	NM_020858 /// NM_024966 /// NM_153616 /// NM_153617 /// NM_153618 /// NM_153619
5.68	6.56	0.88	4.74E-02	3.42E-01	SEC62	SEC62 homolog (S. cerevisiae)	chr3q26.2	1552790_a_at	NM_003262
5.00	6.70	1.70	4.74E-02	3.42E-01	COBLL1	COBL-like 1	chr2q24.3	203641_s_at	NM_014900
6.73	7.46	0.73	4.74E-02	3.42E-01	CXXC5	CXXC finger 5	chr5q31.3	224516_s_at	NM_016463
3.05	3.63	0.57	4.74E-02	3.42E-01	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	chr15q21.2	209838_at	NM_004236
2.63	2.98	0.35	4.74E-02	3.42E-01	DST	dystonin	chr6p12.1	220154_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380
3.83	4.20	0.37	4.75E-02	3.42E-01	KLF2	Kruppel-like factor 2 (lung)	chr19p13.13-p13.11	226645_at	NM_016270
3.85	4.31	0.46	4.75E-02	3.42E-01	NCKIPSD	NCK interacting protein with SH3 domain	chr3p21	233165_at	NM_016453 /// NM_184231
2.36	2.68	0.32	4.75E-02	3.42E-01	PIAS2	Protein inhibitor of activated STAT, 2	chr18q21.1	243624_at	NM_004671 /// NM_173206
3.95	4.57	0.62	4.75E-02	3.42E-01	---	---	---	239300_at	---
3.16	3.66	0.50	4.75E-02	3.42E-01	RNF212	ring finger protein 212	chr4p16.3	236454_at	NM_001131034 /// NM_194439
3.37	3.72	0.35	4.75E-02	3.42E-01	C21orf2	Chromosome 21 open reading frame 2	chr21q22.3	238582_at	NM_004928
5.14	6.17	1.03	4.76E-02	3.42E-01	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	chr2q32	213258_at	NM_001032281 /// NM_006287
4.69	5.62	0.93	4.76E-02	3.42E-01	TncRNA	trophoblast-derived noncoding RNA	chr11q13.1	238320_at	NR_002802

6.37	7.24	0.88	4.76E-02	3.42E-01	ACSS2	acyl-CoA synthetase short-chain family member 2	chr20q11.22	234312_s_at	NM_001076552 /// NM_018677
7.03	7.50	0.47	4.75E-02	3.42E-01	---	---	---	AFFX-r2-Ec-bioB-3_at	---
4.86	5.27	0.41	4.76E-02	3.42E-01	BCAM	basal cell adhesion molecule (Lutheran blood group)	chr19q13.2	203009_at	NM_001013257 /// NM_005581
3.03	3.36	0.33	4.76E-02	3.42E-01	ATP8A2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	chr13q12	231395_at	NM_016529
2.29	2.61	0.32	4.76E-02	3.42E-01	TRIML1	tripartite motif family-like 1	chr4q35.2	1557677_a_at	NM_178556
3.47	3.78	0.31	4.76E-02	3.42E-01	FASN	fatty acid synthase	chr17q25	217006_x_at	NM_004104
2.50	2.81	0.31	4.75E-02	3.42E-01	---	---	---	241081_at	---
5.04	5.57	0.53	4.76E-02	3.42E-01	CCNT1	cyclin T1	chr12pter-qter	206967_at	NM_001240
2.87	3.22	0.34	4.76E-02	3.42E-01	TRDMT1	tRNA aspartic acid methyltransferase 1	chr10p15.1	232121_at	NM_004412 /// NM_176081 /// NM_176083
4.10	4.70	0.60	4.77E-02	3.43E-01	---	---	---	214202_at	---
2.98	3.29	0.31	4.77E-02	3.43E-01	---	---	---	244729_at	---
2.09	2.39	0.30	4.77E-02	3.43E-01	---	---	---	244634_at	---
2.78	4.23	1.45	4.78E-02	3.43E-01	REEP1	receptor accessory protein 1	chr2p11.2	204364_s_at	NM_022912
8.00	8.67	0.67	4.77E-02	3.43E-01	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	chr8q21.3	202447_at	NM_001359
5.21	5.62	0.41	4.78E-02	3.43E-01	PTGES	prostaglandin E synthase	chr9q34.3	207388_s_at	NM_004878
3.28	3.64	0.36	4.78E-02	3.43E-01	CHRD	chordin	chr3q27	221674_s_at	NM_003741
7.13	7.49	0.35	4.78E-02	3.43E-01	FOXO4	forkhead box O4	chrXq13.1	205451_at	NM_005938
2.08	2.41	0.33	4.78E-02	3.43E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	232339_at	NM_015726
2.32	2.63	0.32	4.77E-02	3.43E-01	SMR3A /// SMR3B	submaxillary gland androgen regulated protein 3A /// submaxillary gland androgen regulated protein 3B	chr4q13.3	214565_s_at	NM_006685 /// NM_012390
2.18	2.48	0.31	4.77E-02	3.43E-01	---	---	---	1561018_at	---
2.62	2.89	0.27	4.79E-02	3.43E-01	PLAC4	placenta-specific 4	chr21q22.3	231454_at	NM_182832
2.77	3.15	0.38	4.79E-02	3.43E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	1555908_at	NM_014612
3.59	3.95	0.36	4.79E-02	3.43E-01	---	---	---	241839_at	---
6.89	7.25	0.36	4.79E-02	3.43E-01	CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	chr1p32	222448_s_at	NM_016308
6.17	6.97	0.80	4.81E-02	3.44E-01	KIAA0265	KIAA0265 protein	chr7q32.2	209256_s_at	NM_014997
2.80	3.58	0.79	4.81E-02	3.44E-01	ORM1	orosomucoid 1	chr9q31-q32	205040_at	NM_000607
6.29	7.03	0.74	4.80E-02	3.44E-01	CXXC5	CXXC finger 5	chr5q31.3	233955_x_at	NM_016463
5.12	5.84	0.72	4.81E-02	3.44E-01	---	---	---	244648_at	---
2.29	2.65	0.36	4.81E-02	3.44E-01	EIF5B	eukaryotic translation initiation factor 5B	chr2q11.2	201026_at	NM_015904
2.54	2.89	0.35	4.80E-02	3.44E-01	ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	chr4q21-q23	207820_at	NM_000667
4.14	4.49	0.34	4.81E-02	3.44E-01	---	---	---	207488_at	---
2.39	2.65	0.26	4.81E-02	3.44E-01	---	---	---	237753_at	---
7.67	8.64	0.98	4.81E-02	3.44E-01	LOC285986	hypothetical protein LOC285986	chr7q21.3	235619_at	---
2.16	2.48	0.32	4.81E-02	3.44E-01	---	---	---	1555117_at	---
2.11	2.40	0.29	4.82E-02	3.44E-01	---	---	---	234559_at	---
5.31	6.05	0.74	4.82E-02	3.44E-01	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	chr5q31	202733_at	NM_001017973 /// NM_001017974 /// NM_004199
3.48	3.94	0.46	4.82E-02	3.44E-01	SLC7A4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	chr22q11.21	205864_at	NM_004173
2.78	3.21	0.43	4.82E-02	3.44E-01	LOC285827	hypothetical protein LOC285827	chr6p21.33	231571_at	---
2.19	2.48	0.29	4.82E-02	3.44E-01	---	---	---	240341_at	---
3.12	3.57	0.45	4.83E-02	3.44E-01	LOC100130740	similar to hCG2042068	chr17q21.32	240151_at	XM_001722876 /// XM_001725076 /// XM_001726544
3.38	3.82	0.44	4.83E-02	3.44E-01	OR4D1	olfactory receptor, family 4, subfamily D, member 1	chr17q23.2	1567068_at	NM_012374
5.12	5.55	0.42	4.83E-02	3.44E-01	PRKD2	protein kinase D2	chr19q13.3	241669_x_at	NM_001079880 /// NM_001079881 /// NM_001079882 /// NM_016457
2.16	2.48	0.32	4.83E-02	3.44E-01	---	---	---	242563_at	---
3.56	3.89	0.33	4.83E-02	3.44E-01	ERGIC3	ERGIC and golgi 3	chr20pter-q12	1558020_at	NM_015966 /// NM_198398
2.44	2.69	0.25	4.83E-02	3.44E-01	---	---	---	243778_at	---
4.32	4.69	0.37	4.83E-02	3.44E-01	LOC440836	similar to MGC52679 protein	chr22q13.33	235257_at	NM_001014440

2.81	3.20	0.39	4.84E-02	3.45E-01	PTCH1	patched homolog 1 (Drosophila)	chr9q22.3	208522_s_at	NM_000264 /// NM_001083602 /// NM_001083603 /// NM_001083604 /// NM_001083605 /// NM_001083606 /// NM_001083607																				
6.03	7.16	1.13	4.85E-02	3.45E-01	---	---	---	241681_at	---																				
3.21	4.06	0.85	4.84E-02	3.45E-01	CLRN1	clarin 1	chr3q25	1555034_at	NM_052995 /// NM_174878																				
2.43	2.87	0.44	4.85E-02	3.45E-01	SGOL1	shugoshin-like 1 (S. pombe)	chr3p24.3	1553690_at	NM_001012409 /// NM_001012410 /// NM_001012411 /// NM_001012412 /// NM_001012413 /// NM_138484																				
2.86	3.28	0.42	4.84E-02	3.45E-01	C14orf73	chromosome 14 open reading frame 73	chr14q32.32	231209_at	NM_001077594																				
2.96	3.34	0.38	4.84E-02	3.45E-01	ARHGAP28	Rho GTPase activating protein 28	chr18p11.31	227911_at	NM_001010000 /// NM_030672																				
3.53	3.89	0.36	4.84E-02	3.45E-01	---	---	---	233699_at	---																				
2.06	2.31	0.26	4.84E-02	3.45E-01	---	---	---	237121_at	---																				
2.60	3.28	0.68	4.85E-02	3.45E-01	ACSL4	acyl-CoA synthetase long-chain family member 4	chrXq22.3-q23	202422_s_at	NM_004458 /// NM_022977																				
3.16	3.75	0.59	4.85E-02	3.45E-01	CCDC136	coiled-coil domain containing 136	chr7q33	226971_at	NM_022742																				
2.98	3.45	0.47	4.85E-02	3.45E-01	TLK1	tousled-like kinase 1	chr2q31.1	211077_s_at	NM_012290																				
3.16	3.62	0.46	4.85E-02	3.45E-01	---	---	---	238344_at	---																				
4.55	4.94	0.38	4.85E-02	3.45E-01	GRPR	gastrin-releasing peptide receptor	chrXp22.2-p22.13	207929_at	NM_005314																				
2.47	2.77	0.30	4.85E-02	3.45E-01	---	---	---	216376_x_at	---																				
2.18	2.47	0.29	4.85E-02	3.45E-01	FGF5	fibroblast growth factor 5	chr4q21	210311_at	NM_004464 /// NM_033143																				
2.13	2.41	0.28	4.85E-02	3.45E-01	---	---	---	1562173_a_at	---																				
2.46	2.79	0.33	4.87E-02	3.45E-01	FRMPD4	FERM and PDZ domain containing 4	chrXp22.2	215052_at	NM_014728																				
2.25	2.57	0.32	4.87E-02	3.45E-01	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	chr2q11.2-q12	222547_at	NM_004834 /// NM_145686 /// NM_145687																				
2.75	3.03	0.29	4.87E-02	3.45E-01	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	chr11p15.2	214600_at	NM_021961																				
5.94	6.74	0.80	4.87E-02	3.45E-01	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	chr2q24.2	225665_at	NM_016653 /// NM_133646																				
5.36	6.09	0.72	4.87E-02	3.45E-01	UBE2L3	ubiquitin-conjugating enzyme E2L 3	chr22q11.21	200676_s_at	NM_003347 /// NM_198157																				
4.36	5.05	0.69	4.87E-02	3.45E-01	USP1	ubiquitin specific peptidase 1	chr1p31.3	202412_s_at	NM_001017415 /// NM_001017416 /// NM_003368																				
10.81	11.41	0.60	4.88E-02	3.45E-01	SCARB1	scavenger receptor class B, member 1	chr12q24.31	1552256_a_at	NM_001082959 /// NM_005505																				
2.41	2.95	0.55	4.88E-02	3.45E-01	---	---	---	240180_at	---																				
5.20	5.63	0.43	4.88E-02	3.45E-01	BACE1	beta-site APP-cleaving enzyme 1	chr11q23.2-q23.3	222463_s_at	NM_012104 /// NM_138971 /// NM_138972 /// NM_138973																				
5.06	5.45	0.40	4.87E-02	3.45E-01	LOC442142	Similar to SOX30 protein	chr5q33.3	240325_x_at	XM_001723185 /// XR_016528 /// XR_019090																				
2.51	2.85	0.34	4.87E-02	3.45E-01	---	---	---	1567590_at	---																				
2.15	2.46	0.32	4.88E-02	3.45E-01	FUT9	Fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	chr6q16	216185_at	NM_006581																				
2.67	2.98	0.30	4.87E-02	3.45E-01	OTOS	otospiralin	chr2q37.3	242883_at	NM_148961																				
2.02	2.31	0.28	4.88E-02	3.45E-01	---	---	---	241455_at	---																				
2.75	3.07	0.32	4.88E-02	3.45E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	211398_at	NM_000141 /// NM_022970																				

3.96	4.26	0.31	4.88E-02	3.46E-01	UNQ1887	signal peptide peptidase 3	chr12q24.31	1554565_x_at	NM_139015
8.64	9.68	1.04	4.88E-02	3.46E-01	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	chr9q31.2	202468_s_at	NM_003798
3.10	4.11	1.01	4.89E-02	3.46E-01	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	chr3q27-q28	232224_at	NM_001031849 /// NM_001879 /// NM_139125
3.49	3.88	0.40	4.89E-02	3.46E-01	KIF26A	kinesin family member 26A	chr14q32.33	232069_at	NM_015656
4.21	5.69	1.47	4.89E-02	3.46E-01	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	chr8q24.1	210839_s_at	NM_001040092 /// NM_001130863 /// NM_006209
3.91	4.57	0.66	4.89E-02	3.46E-01	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	chr5q33-q34	213543_at	NM_000337 /// NM_001128209 /// NM_172244
4.75	5.50	0.75	4.89E-02	3.46E-01	DOCK11	dedicator of cytokinesis 11	chrXq24	226875_at	NM_144658
2.80	3.11	0.31	4.89E-02	3.46E-01	---	---	---	234119_at	---
2.18	2.41	0.23	4.90E-02	3.46E-01	SPATA17	spermatogenesis associated 17	chr1q41	1552269_at	NM_138796
5.18	6.21	1.02	4.90E-02	3.46E-01	PALM2-AKAP2	PALM2-AKAP2	chr9q31-q33	202760_s_at	NM_007203 /// NM_147150
4.48	4.89	0.41	4.90E-02	3.46E-01	OSBPL5	oxysterol binding protein-like 5	chr11p15.4	223464_at	NM_020896 /// NM_145638
3.34	3.65	0.31	4.90E-02	3.46E-01	KLK12	kallikrein-related peptidase 12	chr19q13.3-q13.4	234316_x_at	NM_019598 /// NM_145894 /// NM_145895
1.95	2.17	0.22	4.91E-02	3.46E-01	PMP2	peripheral myelin protein 2	chr8q21.3-q22.1	206826_at	NM_002677
4.07	4.44	0.37	4.91E-02	3.47E-01	TAL1	T-cell acute lymphocytic leukemia 1	chr1p32	216928_at	NM_003189
2.41	2.69	0.27	4.91E-02	3.47E-01	THTPA	Thiamine triphosphatase	chr14q11.2	214341_at	NM_001126339 /// NM_024328 /// NR_023314
3.73	4.35	0.62	4.91E-02	3.47E-01	---	---	---	244878_at	---
4.56	5.23	0.67	4.92E-02	3.47E-01	FNIP1	folliculin interacting protein 1	chr5q23.3	228250_at	NM_001008738 /// NM_133372
4.09	4.48	0.39	4.92E-02	3.47E-01	EIF1AD	eukaryotic translation initiation factor 1A domain containing	chr11q13.1	223682_s_at	NM_032325
5.76	6.14	0.39	4.92E-02	3.47E-01	FAM176B	Family with sequence similarity 176, member B	chr1p34.3	229998_x_at	NM_018166
2.59	2.89	0.30	4.92E-02	3.47E-01	---	---	---	243090_at	---
6.40	6.95	0.54	4.92E-02	3.47E-01	C20orf149	chromosome 20 open reading frame 149	chr20q13.33	233571_x_at	NM_024299
6.38	7.64	1.26	4.93E-02	3.47E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	221718_s_at	NM_006738 /// NM_007200 /// NM_144767
4.25	4.75	0.49	4.93E-02	3.47E-01	DGAT2	diacylglycerol O-acyltransferase homolog 2 (mouse)	chr11q13.5	224327_s_at	NM_032564
2.78	3.14	0.36	4.93E-02	3.47E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	211017_s_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833
6.52	7.73	1.21	4.94E-02	3.47E-01	ANKRD17	ankyrin repeat domain 17	chr4q13.3	225852_at	NM_032217 /// NM_198889
6.27	7.27	1.00	4.94E-02	3.47E-01	SAR1B	SAR1 gene homolog B (S. cerevisiae)	chr5q31.1	1554482_a_at	NM_001033503 /// NM_016103
3.78	4.49	0.70	4.94E-02	3.47E-01	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	chr5p15.2	205405_at	NM_003966
4.67	5.13	0.46	4.94E-02	3.47E-01	C9orf21	chromosome 9 open reading frame 21	chr9q22.32	227534_at	NM_153698
5.34	5.75	0.40	4.94E-02	3.47E-01	TCAP	titin-cap (telethonin)	chr17q12	205766_at	NM_003673
3.26	3.63	0.37	4.94E-02	3.47E-01	TBCD	tubulin folding cofactor D	chr17q25.3	216128_at	NM_005993
3.37	3.73	0.37	4.94E-02	3.47E-01	---	---	---	228187_at	---
2.84	3.17	0.33	4.93E-02	3.47E-01	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	chr20q13.33	244601_at	NM_025219
3.43	3.76	0.33	4.93E-02	3.47E-01	---	---	---	232852_at	---
3.08	3.36	0.28	4.95E-02	3.47E-01	---	---	---	217637_at	---
1.93	2.20	0.27	4.95E-02	3.47E-01	DGKB	diacylglycerol kinase, beta 90kDa	chr7p21.2	1553524_at	NM_004080 /// NM_145695
2.67	3.00	0.34	4.96E-02	3.47E-01	NUP188	nucleoporin 188kDa	chr9q34.11	217601_at	NM_015354
2.46	2.71	0.25	4.96E-02	3.47E-01	---	---	---	241134_at	---

1.94	2.22	0.28	4.96E-02	3.47E-01	ABHD12B	abhydrolase domain containing 12B	chr14q22.1	237974_at	NM_181533 /// NM_181814
3.30	3.72	0.42	4.96E-02	3.48E-01	SARDH	sarcosine dehydrogenase	chr9q33-q34	210862_s_at	NM_001134707 /// NM_007101
4.26	4.88	0.62	4.97E-02	3.48E-01	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	chr1q24-q25	220342_x_at	NM_025191
2.67	2.97	0.30	4.97E-02	3.48E-01	---	---	---	241840_at	---
3.99	4.44	0.45	4.97E-02	3.48E-01	41336	membrane-associated ring finger (C3HC4) 3	chr5q23.2	230385_at	NM_178450
5.36	5.74	0.37	4.97E-02	3.48E-01	ERF	Ets2 repressor factor	chr19q13	230368_at	NM_006494
2.35	2.89	0.54	4.97E-02	3.48E-01	AKAP12	A kinase (PRKA) anchor protein 12	chr6q24-q25	227529_s_at	NM_005100 /// NM_144497
2.44	2.91	0.48	4.97E-02	3.48E-01	---	---	---	1559020_a_at	---
4.97	5.26	0.29	4.97E-02	3.48E-01	MAP6D1	MAP6 domain containing 1	chr3q27.1	239473_x_at	NM_024871
3.59	3.96	0.37	4.98E-02	3.48E-01	---	---	---	229984_at	---
3.84	4.17	0.34	4.98E-02	3.48E-01	---	---	---	224122_at	---
2.35	2.77	0.42	4.98E-02	3.48E-01	---	---	---	1563635_at	---
7.41	8.18	0.78	4.98E-02	3.48E-01	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	chr11q12	223343_at	NM_021201 /// NM_206938 /// NM_206939 /// NM_206940
6.44	7.02	0.58	4.98E-02	3.48E-01	LAMA2	laminin, alpha 2	chr6q22-q23	205116_at	NM_000426 /// NM_001079823
7.99	8.63	0.64	4.99E-02	3.48E-01	TCF4	transcription factor 4	chr18q21.1	203753_at	NM_001083962 /// NM_003199
10.50	10.94	0.45	4.99E-02	3.48E-01	DSTN	destrin (actin depolymerizing factor)	chr20p12.1	201022_s_at	NM_001011546 /// NM_006870
2.06	2.40	0.33	4.99E-02	3.48E-01	GCM1	glial cells missing homolog 1 (Drosophila)	chr6p21-p12	206269_at	NM_003643
2.67	2.94	0.27	4.99E-02	3.48E-01	---	---	---	210922_at	---
5.43	7.13	1.71	5.02E-02	3.48E-01	ZNF148	zinc finger protein 148	chr3q21	203319_s_at	NM_021964
2.97	3.87	0.90	5.02E-02	3.48E-01	JMJD2C	jumonji domain containing 2C	chr9p24.1	1556493_a_at	NM_015061
5.02	5.78	0.75	5.00E-02	3.48E-01	FNIP2	folliculin interacting protein 2	chr4q32.1	225924_at	NM_020840
6.73	7.45	0.72	5.00E-02	3.48E-01	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	chr1p13	201180_s_at	NM_006496
4.50	5.11	0.61	5.00E-02	3.48E-01	BTBD7	BTB (POZ) domain containing 7	chr14q32.12-q32.13	224943_at	NM_001002860 /// NM_018167
5.79	6.27	0.47	5.01E-02	3.48E-01	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16q22-q23	205315_s_at	NM_006750
2.52	2.97	0.45	5.02E-02	3.48E-01	KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	chr2p24	205968_at	NM_002252
4.20	4.63	0.43	5.00E-02	3.48E-01	RASAL1	RAS protein activator like 1 (GAP1 like)	chr12q23-q24	233144_s_at	NM_004658
3.00	3.40	0.40	5.01E-02	3.48E-01	---	---	---	232793_at	---
3.63	4.03	0.39	5.02E-02	3.48E-01	PCNX	pecanex homolog (Drosophila)	chr14q24.2	235082_at	NM_014982
2.45	2.83	0.38	5.00E-02	3.48E-01	---	---	---	240562_at	---
2.96	3.33	0.37	5.01E-02	3.48E-01	GHRL	Ghrelin/obestatin prepropeptide	chr3p26-p25	237647_at	NM_016362
2.88	3.24	0.36	5.00E-02	3.48E-01	DIAPH3	diaphanous homolog 3 (Drosophila)	chr13q21.2	229097_at	NM_001042517 /// NM_030932
2.39	2.75	0.36	4.99E-02	3.48E-01	---	---	---	240833_at	---
3.77	4.12	0.35	5.02E-02	3.48E-01	TMEM43	Transmembrane protein 43	chr3p25.1	233489_at	NM_024334
4.01	4.35	0.35	5.01E-02	3.48E-01	PQLC1	PQ loop repeat containing 1	chr18q23	230181_at	NM_025078
3.18	3.53	0.34	5.01E-02	3.48E-01	---	---	---	232227_at	---
2.57	2.91	0.34	5.01E-02	3.48E-01	---	---	---	236099_at	---
2.05	2.39	0.34	5.01E-02	3.48E-01	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	chr2q36.1	237159_x_at	NM_001039569
2.02	2.36	0.33	5.01E-02	3.48E-01	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	chr3q25	211379_x_at	NM_001038628 /// NM_003781 /// NM_033167 /// NM_033168 /// NM_033169
2.75	3.07	0.32	5.01E-02	3.48E-01	WDR76	WD repeat domain 76	chr15q15.3	205519_at	NM_024908
2.88	3.20	0.32	5.00E-02	3.48E-01	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	chr1q31	238450_at	NM_001018053 /// NM_006212
2.36	2.68	0.32	5.00E-02	3.48E-01	LOC728678	Similar to p40	chr3p22.3	234562_x_at	XR_015757 /// XR_039160 /// XR_039547
2.21	2.50	0.29	5.00E-02	3.48E-01	ZNF287	zinc finger protein 287	chr17p11.2	216453_at	NM_020653
2.51	2.80	0.28	5.02E-02	3.48E-01	---	---	---	1560725_at	---
2.56	2.84	0.28	5.01E-02	3.48E-01	---	---	---	240825_at	---
5.31	5.58	0.27	5.02E-02	3.48E-01	HPCA	hippocalcin	chr1p35-p34.2	205454_at	NM_002143

2.05	2.29	0.23	5.02E-02	3.48E-01	PTGR2	prostaglandin reductase 2	chr14q24.3	230774_at	NM_152444
13.20	13.42	0.22	5.01E-02	3.48E-01	COX1	cytochrome c oxidase I	---	1553538_s_at	---
5.16	6.24	1.08	5.02E-02	3.49E-01	SH3BGR	SH3 domain binding glutamic acid-rich protein	chr21q22.3	204979_s_at	NM_001001713 /// NM_007341
3.56	3.88	0.32	5.02E-02	3.49E-01	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	chr9p11.1	209646_x_at	NM_000692
2.41	2.67	0.26	5.02E-02	3.49E-01	TMEM156	transmembrane protein 156	chr4p14	220169_at	NM_024943
3.66	4.05	0.39	5.03E-02	3.49E-01	GCK	glucokinase (hexokinase 4)	chr7p15.3-p15.1	211167_s_at	NM_000162 /// NM_033507 /// NM_033508
6.08	6.42	0.34	5.03E-02	3.49E-01	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	chr19p13.11	232438_at	NM_021235
3.84	4.15	0.31	5.03E-02	3.49E-01	---	---	---	241434_at	---
2.88	3.59	0.71	5.03E-02	3.49E-01	COL1A1	collagen, type I, alpha 1	chr17q21.33	202311_s_at	NM_000088
5.07	5.75	0.67	5.04E-02	3.49E-01	SETX	senataxin	chr9q34.13	201965_s_at	NM_015046
3.02	3.37	0.35	5.03E-02	3.49E-01	---	---	---	235661_at	---
1.78	2.04	0.26	5.04E-02	3.49E-01	EXOC5	exocyst complex component 5	chr14q23.1	224253_at	NM_006544
5.14	5.86	0.71	5.04E-02	3.49E-01	LPAR1	lysophosphatidic acid receptor 1	chr9q31.3	204036_at	NM_001401 /// NM_057159
4.79	5.45	0.66	5.04E-02	3.49E-01	CADM1	cell adhesion molecule 1	chr11q23.2	209032_s_at	NM_001098517 /// NM_014333
4.34	4.79	0.45	5.04E-02	3.49E-01	FREQ	frequenin homolog (Drosophila)	chr9q34	230146_s_at	NM_001128826 /// NM_014286
5.20	5.55	0.35	5.04E-02	3.49E-01	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	chr2q23.3	225709_at	NM_152522
2.33	2.70	0.37	5.04E-02	3.49E-01	---	---	---	244473_at	---
4.11	4.67	0.56	5.05E-02	3.49E-01	SVIL	supervillin	chr10p11.2	202566_s_at	NM_003174 /// NM_021738
4.44	4.89	0.45	5.05E-02	3.49E-01	FAM69B	family with sequence similarity 69, member B	chr9q34.3	229002_at	NM_152421
3.58	4.03	0.45	5.05E-02	3.49E-01	---	---	---	243558_at	---
2.88	3.33	0.45	5.05E-02	3.49E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31 /// LOC100126583 /// LOC100133739 /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant gamma 4 (G4m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical LOC100126583 /// similar to hCG2038920 /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	211639_x_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001718220 /// XM_001724554 /// XM_941465
5.71	6.10	0.40	5.05E-02	3.49E-01	---	---	---	216982_x_at	---
2.45	2.75	0.29	5.05E-02	3.49E-01	PDPK1	3-phosphoinositide dependent protein kinase-1	chr16p13.3	221244_s_at	NM_002613 /// NM_031268
3.67	3.96	0.29	5.05E-02	3.49E-01	---	---	---	229869_at	---
3.14	3.42	0.28	5.05E-02	3.49E-01	---	---	---	236537_at	---
4.06	4.32	0.26	5.05E-02	3.49E-01	CCDC28B	coiled-coil domain containing 28B	chr1p35.1	219585_at	NM_024296
1.90	2.15	0.25	5.05E-02	3.49E-01	TRAP1	TNF receptor-associated protein 1	chr16p13.3	239622_at	NM_016292
4.58	5.00	0.42	5.06E-02	3.49E-01	PITX3	paired-like homeodomain 3	chr10q25	208277_at	NM_005029
2.07	2.37	0.30	5.06E-02	3.49E-01	SFTA2	surfactant associated 2	chr6p21.33	244056_at	NM_205854
2.09	2.35	0.26	5.06E-02	3.49E-01	PRO2266	hypothetical protein PRO2266	chr6q15	220530_at	NR_002767
4.46	4.91	0.44	5.07E-02	3.49E-01	SAMD9	sterile alpha motif domain containing 9	chr7q21.2	228531_at	NM_017654
2.63	3.01	0.38	5.07E-02	3.49E-01	---	---	---	235133_at	---
3.32	4.07	0.76	5.08E-02	3.49E-01	GDAP1	ganglioside-induced differentiation-associated protein 1	chr8q21.11	226269_at	NM_001040875 /// NM_018972
6.84	7.30	0.45	5.08E-02	3.49E-01	---	---	---	243267_x_at	---
2.73	3.15	0.42	5.07E-02	3.49E-01	HMP19	HMP19 protein	chr5q35.2	218623_at	NM_015980
3.45	3.85	0.39	5.07E-02	3.49E-01	OR13C4	olfactory receptor, family 13, subfamily C, member 4	chr9q31.1	1567297_at	NM_001001919
4.92	5.28	0.36	5.07E-02	3.49E-01	ACY1	Aminoacylase 1	chr3p21.1	238849_at	NM_000666
2.45	2.79	0.34	5.08E-02	3.49E-01	MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	chr1p12-p11.2	224307_x_at	NM_152900
2.09	2.33	0.24	5.07E-02	3.49E-01	---	---	---	1560888_x_at	---
3.28	3.70	0.42	5.08E-02	3.50E-01	ACRBP	acrosin binding protein	chr12p13.31	223718_at	NM_032489
2.44	2.72	0.28	5.08E-02	3.50E-01	---	---	---	1556916_a_at	---
2.81	3.10	0.29	5.09E-02	3.50E-01	WDR66	WD repeat domain 66	chr12q24.31	1555007_s_at	NM_144668
2.13	2.40	0.27	5.09E-02	3.50E-01	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	chr1q31	239002_at	NM_018136
2.16	2.37	0.21	5.09E-02	3.50E-01	---	---	---	1562459_at	---
1.82	2.08	0.26	5.09E-02	3.50E-01	SOS2	son of sevenless homolog 2 (Drosophila)	chr14q21	217575_s_at	NM_006939
3.43	3.96	0.52	5.09E-02	3.50E-01	PON2	paraoxonase 2	chr7q21.3	242700_at	NM_000305 /// NM_001018161
2.34	2.65	0.31	5.10E-02	3.50E-01	CCDC15	coiled-coil domain containing 15	chr11q24.2	220466_at	NM_025004
4.37	4.79	0.43	5.10E-02	3.50E-01	---	---	---	236362_at	---
1.81	2.11	0.30	5.10E-02	3.50E-01	---	---	---	222332_at	---

5.93	6.50	0.57	5.10E-02	3.50E-01	PSEN1	presenilin 1	chr14q24.3	203460_s_at	NM_000021 /// NM_007318
4.22	4.72	0.50	5.10E-02	3.50E-01	C14orf143	chromosome 14 open reading frame 143	chr14q32.11	214264_s_at	NM_145231
2.36	2.63	0.27	5.11E-02	3.50E-01	---	---	---	222340_at	---
1.89	2.23	0.34	5.11E-02	3.51E-01	---	---	---	1561575_at	---
5.85	6.21	0.36	5.11E-02	3.51E-01	---	---	---	232970_at	---
3.06	3.45	0.39	5.12E-02	3.51E-01	CPNE5	copine V	chr6p21.1	227189_at	NM_020939
3.39	3.90	0.51	5.12E-02	3.51E-01	---	---	---	240324_at	---
2.27	2.50	0.23	5.12E-02	3.51E-01	---	---	---	1563611_at	---
2.48	2.73	0.25	5.13E-02	3.51E-01	---	---	---	1554964_x_at	---
3.16	3.63	0.47	5.13E-02	3.51E-01	RSAD2	radical S-adenosyl methionine domain containing 2	chr2p25.2	213797_at	NM_080657
4.58	4.94	0.35	5.13E-02	3.52E-01	C17orf89 /// LOC100133328	chromosome 17 open reading frame 89 /// similar to hCG19906	chr17q25.3 /// chr1q42.12	225966_at	NM_001086521 /// XR_038581 /// XR_038620 /// XR_038656
3.25	3.64	0.39	5.13E-02	3.52E-01	---	---	---	241974_at	---
2.53	2.89	0.36	5.13E-02	3.52E-01	---	---	---	236881_at	---
4.18	4.57	0.39	5.13E-02	3.52E-01	---	---	---	243245_at	---
3.77	4.21	0.44	5.14E-02	3.52E-01	DRD2	dopamine receptor D2	chr11q23	216924_s_at	NM_000795 /// NM_016574
2.77	3.20	0.43	5.14E-02	3.52E-01	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	chr3q21.1	227741_at	NM_198402
2.83	3.15	0.32	5.14E-02	3.52E-01	KLHDC4	kelch domain containing 4	chr16q24.3	237900_at	NM_017566
2.08	2.32	0.24	5.14E-02	3.52E-01	MARK1	MAP/microtubule affinity-regulating kinase 1	chr1q41	1560407_at	NM_018650
3.88	4.15	0.28	5.14E-02	3.52E-01	---	---	---	240774_at	---
3.87	4.43	0.56	5.14E-02	3.52E-01	RARS2	arginyl-tRNA synthetase 2, mitochondrial	chr6q16.1	1561048_at	NM_020320
7.51	8.05	0.54	5.14E-02	3.52E-01	GMPS	guanine monphosphate synthetase	chr3q24	214431_at	NM_003875
2.17	2.44	0.27	5.14E-02	3.52E-01	PTPN12	protein tyrosine phosphatase, non-receptor type 12	chr7q11.23	216884_at	NM_001131008 /// NM_001131009 /// NM_002835
2.78	3.16	0.37	5.15E-02	3.52E-01	SLC39A8	solute carrier family 39 (zinc transporter), member 8	chr4q22-q24	222935_x_at	NM_022154
2.86	3.20	0.34	5.15E-02	3.52E-01	CNTNAP2	contactin associated protein-like 2	chr7q35-q36	219300_s_at	NM_014141
2.79	3.49	0.70	5.15E-02	3.52E-01	C18orf34	chromosome 18 open reading frame 34	chr18q12.1	1558820_a_at	NM_001105528 /// NM_198995
3.68	4.12	0.44	5.15E-02	3.52E-01	TSSK2	testis-specific serine kinase 2	chr22q11.21	217275_at	NM_053006
3.54	3.96	0.42	5.15E-02	3.52E-01	CSF2RA /// LOC100133516	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) /// hypothetical protein LOC100133516	chrXp22.32 and Yp11.3	210340_s_at	NM_006140 /// NM_172245 /// NM_172246 /// NM_172247 /// NM_172249 /// XM_001714505
3.56	3.93	0.37	5.15E-02	3.52E-01	GGN	gametogenetin	chr19q13.2	244305_at	NM_152657
5.54	5.98	0.44	5.15E-02	3.52E-01	LOC644215	hypothetical LOC644215	chr10q24.1	1559822_s_at	XM_927403 /// XM_938015
3.12	3.39	0.27	5.16E-02	3.52E-01	---	---	---	239888_at	---
4.18	4.61	0.43	5.16E-02	3.52E-01	TMC6	Transmembrane channel-like 6	chr17q25.3	236482_at	NM_001127198 /// NM_007267
2.86	3.45	0.58	5.17E-02	3.52E-01	---	---	---	243826_at	---
5.83	6.33	0.49	5.17E-02	3.52E-01	VANGL1	vang-like 1 (van gogh, Drosophila)	chr1p11-p13.1	229997_at	NM_138959
2.05	2.34	0.29	5.16E-02	3.52E-01	---	---	---	243071_at	---
2.33	2.61	0.29	5.17E-02	3.52E-01	---	---	---	215971_at	---
2.31	2.59	0.28	5.17E-02	3.52E-01	MOBP	myelin-associated oligodendrocyte basic protein	chr3p22.1	207659_s_at	NM_182935 /// NR_003090
2.26	3.20	0.95	5.17E-02	3.52E-01	---	---	---	1563719_a_at	---
2.12	2.49	0.37	5.17E-02	3.52E-01	---	---	---	1557707_at	---
2.18	2.50	0.31	5.17E-02	3.52E-01	ARSK	Arylsulfatase family, member K	chr5q15	1569133_x_at	NM_198150
2.80	3.09	0.29	5.17E-02	3.52E-01	LOC143381	hypothetical protein LOC143381	chr10q26.11	227550_at	---
2.02	2.30	0.28	5.17E-02	3.52E-01	SYDE2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	chr1p22.3	1560101_at	NM_032184
2.01	2.26	0.25	5.18E-02	3.52E-01	---	---	---	240848_at	---
2.12	2.40	0.28	5.18E-02	3.53E-01	---	---	---	241726_at	---
1.93	2.18	0.26	5.18E-02	3.53E-01	PIAS2	protein inhibitor of activated STAT, 2	chr18q21.1	214593_at	NM_004671 /// NM_173206
3.72	4.33	0.61	5.19E-02	3.53E-01	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	chr2q11.2-q12	218181_s_at	NM_004834 /// NM_145686 /// NM_145687
2.03	2.33	0.29	5.19E-02	3.53E-01	LOC221442	hypothetical LOC221442	chr6p21.1	236832_at	XR_039837 /// XR_039838 /// XR_039839
5.28	5.87	0.59	5.20E-02	3.53E-01	ZNF264	zinc finger protein 264	chr19q13.4	205917_at	NM_003417
3.99	4.50	0.50	5.20E-02	3.53E-01	---	---	---	230247_at	---
4.91	5.91	1.00	5.20E-02	3.53E-01	TAOK1	TAO kinase 1	chr17q11.2	227454_at	NM_020791
3.27	3.55	0.28	5.20E-02	3.53E-01	N4BP2L2	NEDD4 binding protein 2-like 2	chr13q13.1	242576_x_at	NM_014887 /// NM_033111

5.89	6.21	0.32	5.21E-02	3.54E-01	SPTBN4	spectrin, beta, non-erythrocytic 4	chr19q13.13	220185_at	NM_020971 /// NM_025213																				
4.17	4.82	0.65	5.21E-02	3.54E-01	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	chr15q14	1555310_a_at	NM_001128628 /// NM_001128629 /// NM_020168																				
4.22	4.64	0.43	5.22E-02	3.54E-01	---	---	---	240853_at	---																				
6.40	6.85	0.45	5.22E-02	3.54E-01	BAIAP2L2	BAI1-associated protein 2-like 2	chr22q13.1	228876_at	NM_025045																				
3.42	3.75	0.33	5.23E-02	3.54E-01	---	---	---	217278_x_at	---																				
5.93	6.24	0.31	5.22E-02	3.54E-01	PADI1	peptidyl arginine deiminase, type I	chr1p36.13	220962_s_at	NM_013358																				
3.56	4.32	0.76	5.23E-02	3.54E-01	---	---	---	215287_at	---																				
3.15	3.90	0.75	5.23E-02	3.54E-01	ACOT4	acyl-CoA thioesterase 4	chr14q24.3	229534_at	NM_152331																				
2.69	2.94	0.26	5.23E-02	3.54E-01	AMACR	alpha-methylacyl-CoA racemase	chr5p13	217111_at	NM_014324 /// NM_203382																				
6.55	7.29	0.74	5.23E-02	3.54E-01	TRAK2	trafficking protein, kinesin binding 2	chr2q33	202124_s_at	NM_015049																				
3.04	3.78	0.74	5.23E-02	3.54E-01	---	---	---	232773_at	---																				
5.65	6.01	0.36	5.23E-02	3.54E-01	NCOR2	nuclear receptor co-repressor 2	chr12q24	215205_x_at	NM_001077261 /// NM_006312																				
3.93	4.58	0.65	5.24E-02	3.55E-01	FPR3	formyl peptide receptor 3	chr19q13.3-q13.4	214560_at	NM_002030																				
3.73	4.25	0.52	5.24E-02	3.55E-01	FLJ11151	hypothetical protein FLJ11151	chr16p13.12	218610_s_at	NM_001099455 /// NM_018340																				
4.03	4.43	0.40	5.24E-02	3.55E-01	---	---	---	230279_at	---																				
3.02	3.36	0.34	5.24E-02	3.55E-01	GRK1	G protein-coupled receptor kinase 1	chr13q34	208041_at	NM_002929																				
1.84	2.11	0.28	5.24E-02	3.55E-01	GLS2	glutaminase 2 (liver, mitochondrial)	chr12q13	1564705_at	NM_013267																				
2.12	2.34	0.22	5.24E-02	3.55E-01	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	chr6q15	221234_s_at	NM_021813																				
5.08	5.96	0.88	5.25E-02	3.55E-01	KLHL28	kelch-like 28 (Drosophila)	chr14q21.3	235727_at	NM_017658																				
4.13	4.60	0.47	5.25E-02	3.55E-01	BCL7A	B-cell CLL/lymphoma 7A	chr12q24.13	203795_s_at	NM_001024808 /// NM_020993																				
3.70	4.16	0.45	5.25E-02	3.55E-01	---	---	---	232346_at	---																				
5.74	6.16	0.42	5.25E-02	3.55E-01	FIBCD1	fibrinogen C domain containing 1	chr9q34.12-q34.13	238943_at	NM_032843																				
2.53	2.85	0.32	5.25E-02	3.55E-01	---	---	---	1569181_x_at	---																				
2.80	3.09	0.29	5.25E-02	3.55E-01	---	---	---	239718_at	---																				
2.38	2.64	0.27	5.25E-02	3.55E-01	KCNH5	potassium voltage-gated channel, subfamily H (eag-related), member 5	chr14q23.1	1555074_a_at	NM_139318 /// NM_172375 /// NM_172376																				
8.46	10.16	1.70	5.27E-02	3.55E-01	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	chr14q32.33	211968_s_at	NM_001017963 /// NM_005348																				
6.12	7.16	1.04	5.27E-02	3.55E-01	BBX	bobby sox homolog (Drosophila)	chr3q13.1	232008_s_at	NM_020235																				
9.42	9.98	0.55	5.27E-02	3.55E-01	SEPP1	selenoprotein P, plasma, 1	chr5q31	201427_s_at	NM_001085486 /// NM_001093726 /// NM_005410																				
3.76	4.24	0.48	5.26E-02	3.55E-01	CYB561	cytochrome b-561	chr17q11-qter	210816_s_at	NM_001017916 /// NM_001017917 /// NM_001915																				
2.24	2.70	0.47	5.26E-02	3.55E-01	---	---	---	1557222_at	---																				
2.51	2.97	0.46	5.26E-02	3.55E-01	ZNF519	zinc finger protein 519	chr18p11.21	1564190_x_at	NM_145287																				
3.19	3.64	0.44	5.27E-02	3.55E-01	---	---	---	242192_at	---																				
2.61	3.00	0.38	5.27E-02	3.55E-01	PML	promyelocytic leukemia	chr15q22	211589_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250																				
3.74	4.11	0.37	5.27E-02	3.55E-01	---	---	---	244554_at	---																				
2.15	2.51	0.36	5.26E-02	3.55E-01	---	---	---	1559458_at	---																				
2.82	3.17	0.35	5.26E-02	3.55E-01	---	---	---	221186_at	---																				

4.92	5.27	0.35	5.27E-02	3.55E-01	LOC554235	hypothetical protein LOC554235	chr19q13.33	230912_at	NM_001024656 /// NM_001114598
5.39	5.71	0.33	5.27E-02	3.55E-01	---	---	---	235920_at	---
2.96	3.28	0.32	5.27E-02	3.55E-01	OR1Q1	olfactory receptor, family 1, subfamily Q, member 1	chr9q33.2	1567065_at	NM_012364
4.27	4.59	0.32	5.27E-02	3.55E-01	TRPM8	transient receptor potential cation channel, subfamily M, member 8	chr2q37.1	220226_at	NM_024080
2.64	2.95	0.31	5.27E-02	3.55E-01	FGB	fibrinogen beta chain	chr4q28	204988_at	NM_005141
2.60	2.89	0.29	5.25E-02	3.55E-01	LOC284475	hypothetical protein LOC284475	chr1p13.1	240661_at	---
1.88	2.17	0.29	5.26E-02	3.55E-01	PTPRR	protein tyrosine phosphatase, receptor type, R	chr12q15	206084_at	NM_002849 /// NM_130846
3.17	3.46	0.29	5.27E-02	3.55E-01	ZNF264	zinc finger protein 264	chr19q13.4	1558698_at	NM_003417
2.60	2.87	0.27	5.26E-02	3.55E-01	DSTN	Destrin (actin depolymerizing factor)	chr20p12.1	230933_at	NM_001011546 /// NM_006870
1.89	2.14	0.25	5.26E-02	3.55E-01	---	---	---	1561236_at	---
1.94	2.18	0.24	5.28E-02	3.55E-01	---	---	---	1568406_at	---
1.84	2.05	0.22	5.27E-02	3.55E-01	---	---	---	234150_at	---
1.93	2.14	0.21	5.27E-02	3.55E-01	SGOL1	Shugoshin-like 1 (S. pombe)	chr3p24.3	231938_at	NM_001012409 /// NM_001012410 /// NM_001012411 /// NM_001012412 /// NM_001012413 /// NM_138484
2.31	3.17	0.87	5.28E-02	3.55E-01	---	---	---	241506_at	---
4.83	5.66	0.83	5.29E-02	3.55E-01	---	---	---	244015_at	---
5.84	6.45	0.61	5.28E-02	3.55E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	211317_s_at	NM_001127183 /// NM_001127184 /// NM_003879
2.48	2.94	0.46	5.28E-02	3.55E-01	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	chr5p15.1-p14	210602_s_at	NM_004932
2.64	3.05	0.41	5.28E-02	3.55E-01	---	---	---	215914_at	---
6.63	7.00	0.37	5.28E-02	3.55E-01	---	---	---	234010_at	---
4.92	5.25	0.33	5.29E-02	3.55E-01	SARDH	Sarcosine dehydrogenase	chr9q33-q34	234586_at	NM_001134707 /// NM_007101
3.04	3.36	0.32	5.28E-02	3.55E-01	ARHGAP1	Rho GTPase activating protein 1	chr11p12-q12	217153_at	NM_004308
2.26	2.50	0.24	5.28E-02	3.55E-01	SERTAD4	SERTA domain containing 4	chr1q32.1-q41	230660_at	NM_019605
2.29	2.51	0.22	5.30E-02	3.55E-01	FABP7	fatty acid binding protein 7, brain	chr6q22-q23	205030_at	NM_001446
4.87	5.14	0.27	5.30E-02	3.55E-01	L3MBTL	l(3)mbt-like (Drosophila)	chr20q13.12	206823_at	NM_015478 /// NM_032107
5.74	6.65	0.91	5.30E-02	3.55E-01	ATM	ataxia telangiectasia mutated	chr11q22-q23	210858_x_at	NM_000051 /// NM_138292
2.33	2.60	0.27	5.30E-02	3.55E-01	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	chr11q12	217418_x_at	NM_021950 /// NM_152866
2.32	2.56	0.24	5.30E-02	3.55E-01	---	---	---	230227_at	---
2.76	3.55	0.79	5.30E-02	3.55E-01	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	chr9p24	213664_at	NM_004170
3.20	3.53	0.33	5.30E-02	3.55E-01	LOC100132369	hypothetical protein LOC100132369	chr12p13.33	228712_at	XM_001714404 /// XM_001715452 /// XM_001716240
5.86	6.14	0.28	5.31E-02	3.55E-01	---	---	---	240398_at	---
2.93	3.21	0.28	5.30E-02	3.55E-01	SPG11	spastic paraplegia 11 (autosomal recessive)	chr15q14	241920_x_at	NM_025137
1.89	2.15	0.27	5.30E-02	3.55E-01	---	---	---	1565565_at	---
2.11	2.34	0.23	5.31E-02	3.55E-01	TM4SF20	transmembrane 4 L six family member 20	chr2q36.3	220639_at	NM_024795
3.94	4.32	0.39	5.31E-02	3.56E-01	PAX8	paired box 8	chr2q12-q14	207921_x_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992
2.30	2.65	0.36	5.31E-02	3.56E-01	---	---	---	1560048_at	---
2.69	2.98	0.29	5.31E-02	3.56E-01	LRRTM1	leucine rich repeat transmembrane neuronal 1	chr2p12	238815_at	NM_178839
3.18	3.61	0.43	5.32E-02	3.56E-01	NF1	neurofibromin 1	chr17q11.2	204325_s_at	NM_000267 /// NM_001042492 /// NM_001128147
2.21	2.98	0.77	5.32E-02	3.56E-01	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	chr6p21.1-p11.2	227803_at	NM_021572
9.39	10.38	0.99	5.33E-02	3.56E-01	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	chr15q22.2	222404_x_at	NM_016395

6.73	7.38	0.65	5.33E-02	3.56E-01	GSK3B	glycogen synthase kinase 3 beta	chr3q13.3	209945_s_at	NM_002093
2.81	3.24	0.43	5.33E-02	3.56E-01	ANKRD13C	ankyrin repeat domain 13C	chr1p32.3-p31.3	238597_at	NM_030816
5.01	5.43	0.42	5.34E-02	3.56E-01	CXCR3	chemokine (C-X-C motif) receptor 3	chrXq13	217119_s_at	NM_001504
4.21	4.62	0.41	5.33E-02	3.56E-01	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	chr19q13.1	217069_at	NM_014727
1.90	2.26	0.36	5.34E-02	3.56E-01	PCDH15	protocadherin 15	chr10q21.1	1553344_at	NM_033056
4.53	4.88	0.34	5.33E-02	3.56E-01	PDZD3	PDZ domain containing 3	chr11q23.3	220303_at	NM_024791
1.94	2.27	0.33	5.33E-02	3.56E-01	---	---	---	241664_x_at	---
2.84	3.15	0.31	5.32E-02	3.56E-01	---	---	---	222319_at	---
2.54	2.78	0.24	5.34E-02	3.56E-01	---	---	---	1562106_at	---
2.33	2.55	0.22	5.33E-02	3.56E-01	D21S2089E	D21S2089E	chr21q21.1	1560633_a_at	---
1.84	2.05	0.21	5.33E-02	3.56E-01	GRIK2	Glutamate receptor, ionotropic, kainate 2	chr6q16.3-q21	215655_at	NM_021956 /// NM_175768
6.03	6.50	0.47	5.34E-02	3.56E-01	MAP2K7	mitogen-activated protein kinase kinase 7	chr19p13.3-p13.2	216206_x_at	NM_145185
4.68	5.10	0.43	5.34E-02	3.56E-01	SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	chr6p23	229112_at	NM_012241 /// NM_031244
2.83	3.23	0.40	5.35E-02	3.56E-01	KCTD15	potassium channel tetramerisation domain containing 15	chr19q13.11	228683_s_at	NM_001129994 /// NM_001129995 /// NM_024076
3.09	3.45	0.36	5.35E-02	3.56E-01	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	chr2p13.1	211157_at	NM_004263
4.04	4.39	0.35	5.34E-02	3.56E-01	LMBR1	limb region 1 homolog (mouse)	chr7q36	224036_s_at	NM_022458
2.59	2.90	0.30	5.34E-02	3.56E-01	C9orf167	Chromosome 9 open reading frame 167	chr9q34.3	229708_at	NM_017723
2.06	2.34	0.28	5.35E-02	3.56E-01	---	---	---	243743_at	---
12.45	12.68	0.23	5.35E-02	3.56E-01	RPS27A /// UBB /// UBC	ribosomal protein S27a /// ubiquitin B /// ubiquitin C	chr12q24.3 /// chr17p12-p11.2 /// chr2p16	200633_at	NM_002954 /// NM_018955 /// NM_021009
3.96	4.47	0.51	5.35E-02	3.56E-01	C10orf18	chromosome 10 open reading frame 18	chr10p15.1	244165_at	NM_017782
4.44	4.76	0.32	5.35E-02	3.56E-01	CRH	corticotropin releasing hormone	chr8q13	205629_s_at	NM_000756
5.04	5.48	0.44	5.35E-02	3.56E-01	HK2	hexokinase 2	chr2p13	202934_at	NM_000189
2.94	3.29	0.36	5.35E-02	3.56E-01	DCBLD1	discoidin, CUB and LCCL domain containing 1	chr6q22.2	1553768_a_at	NM_173674
2.31	2.60	0.28	5.36E-02	3.56E-01	---	---	---	241316_at	---
3.29	3.68	0.39	5.36E-02	3.56E-01	DNAJB13	DnaJ (Hsp40) related, subfamily B, member 13	chr11q13.4	230936_at	NM_153614
5.00	6.14	1.14	5.36E-02	3.56E-01	PPIG	peptidylprolyl isomerase G (cyclophilin G)	chr2q31.1	208993_s_at	NM_004792
4.44	4.96	0.52	5.36E-02	3.56E-01	KIAA1737	KIAA1737	chr14q24.3	225623_at	NM_033426
4.58	4.93	0.35	5.36E-02	3.56E-01	CHD5	chromodomain helicase DNA binding protein 5	chr1p36.31	213965_s_at	NM_015557
1.92	2.19	0.27	5.36E-02	3.56E-01	---	---	---	243856_at	---
4.43	4.77	0.34	5.36E-02	3.56E-01	---	---	---	236942_at	---
5.21	6.56	1.35	5.38E-02	3.57E-01	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	chr6p21	209055_s_at	NM_001253
3.84	4.56	0.72	5.38E-02	3.57E-01	MYO6	myosin VI	chr6q13	203215_s_at	NM_004999
3.08	3.52	0.44	5.38E-02	3.57E-01	---	---	---	243675_at	---
3.43	3.82	0.38	5.38E-02	3.57E-01	NUP50	nucleoporin 50kDa	chr22q13.31	218293_x_at	NM_007172 /// NM_153645
1.84	2.19	0.35	5.37E-02	3.57E-01	---	---	---	234154_at	---
2.56	2.90	0.35	5.37E-02	3.57E-01	---	---	---	242816_at	---
2.19	2.53	0.35	5.38E-02	3.57E-01	---	---	---	239588_s_at	---
2.70	3.01	0.31	5.37E-02	3.57E-01	---	---	---	238442_at	---
5.21	5.53	0.31	5.37E-02	3.57E-01	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide	chr1p36.3-p36.2	223518_at	NM_004401 /// NM_213566
2.15	2.45	0.30	5.37E-02	3.57E-01	SMC3	Structural maintenance of chromosomes 3	chr10q25	1556925_at	NM_005445
1.92	2.19	0.27	5.37E-02	3.57E-01	TMEM26	transmembrane protein 26	chr10q21.2	1555025_at	NM_178505
2.81	3.07	0.26	5.37E-02	3.57E-01	KATNAL1	katanin p60 subunit A-like 1	chr13q12.3	223790_at	NM_001014380 /// NM_032116
3.67	3.92	0.25	5.37E-02	3.57E-01	C6orf27	chromosome 6 open reading frame 27	chr6p21.33	221301_at	NM_025258
2.89	3.12	0.22	5.38E-02	3.57E-01	WDR38	WD repeat domain 38	chr9q33.3	244109_at	NM_001045476
2.58	3.23	0.66	5.38E-02	3.57E-01	SCARA5	Scavenger receptor class A, member 5 (putative)	chr8p21.1	229839_at	NM_173833
2.25	2.64	0.39	5.38E-02	3.57E-01	C9orf130	chromosome 9 open reading frame 130	chr9q22.32	1557788_a_at	NR_023389 /// NR_023390 /// XM_001722853 /// XM_001724349 /// XM_001732875
2.12	2.42	0.30	5.38E-02	3.57E-01	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	chr2q32	210665_at	NM_001032281 /// NM_006287
2.19	2.47	0.28	5.38E-02	3.57E-01	ANKRD12	ankyrin repeat domain 12	chr18p11.22	216550_x_at	NM_001083625 /// NM_015208
3.81	4.55	0.74	5.39E-02	3.57E-01	PHCA	phytoceramidase, alkaline	chr11q13.5	222687_s_at	NM_018367

2.98	3.71	0.73	5.39E-02	3.57E-01	---	---	---	240499_at	---
2.28	2.94	0.67	5.40E-02	3.57E-01	DCLK1	Doublecortin-like kinase 1	chr13q13	229800_at	NM_004734
3.37	3.78	0.40	5.39E-02	3.57E-01	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	chr9q32	207223_s_at	NM_005156
2.90	3.28	0.38	5.39E-02	3.57E-01	COBLL1	COBL-like 1	chr2q24.3	215393_s_at	NM_014900
4.16	4.48	0.33	5.40E-02	3.57E-01	SCYL1	SCY1-like 1 (S. cerevisiae)	chr11q13	229601_at	NM_001048218 /// NM_020680
2.03	2.30	0.27	5.39E-02	3.57E-01	ZNF197	zinc finger protein 197	chr3p21	233070_at	NM_001024855 /// NM_006991
3.16	3.40	0.24	5.39E-02	3.57E-01	BAAT	bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase)	chr9q22.3	206913_at	NM_001127610 /// NM_001701
2.30	2.52	0.22	5.40E-02	3.57E-01	---	---	---	243014_at	---
3.99	4.66	0.67	5.40E-02	3.57E-01	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	chr12q13.13	231862_at	NM_001127321 /// NM_001127322 /// NM_012117
3.60	3.99	0.39	5.40E-02	3.57E-01	---	---	---	230638_at	---
2.51	3.04	0.53	5.40E-02	3.57E-01	STAT4	signal transducer and activator of transcription 4	chr2q32.2-q32.3	206118_at	NM_003151
2.63	3.01	0.38	5.41E-02	3.57E-01	KLHDC10	kelch domain containing 10	chr7q32.2	242746_at	NM_014997
3.59	3.96	0.37	5.40E-02	3.57E-01	LOC100131419	hypothetical protein LOC100131419	chr17q25.3	1563228_x_at	XM_001717284 /// XM_001721800 /// XM_001726788
2.38	2.77	0.39	5.41E-02	3.57E-01	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	chr5q13-q14	210812_at	NM_001131022 /// NM_003401 /// NM_022406 /// NM_022550
2.65	2.91	0.26	5.41E-02	3.57E-01	---	---	---	234424_at	---
2.35	2.58	0.24	5.41E-02	3.57E-01	ACADL	acyl-Coenzyme A dehydrogenase, long chain	chr2q34-q35	206068_s_at	NM_001608
6.16	7.20	1.04	5.41E-02	3.57E-01	ZBTB20	zinc finger and BTB domain containing 20	chr3q13.2	222357_at	NM_015642
2.88	3.16	0.28	5.41E-02	3.57E-01	NXPH4	neurexophilin 4	chr12q13.3	221967_at	NM_007224
5.78	6.15	0.37	5.42E-02	3.57E-01	---	---	---	230345_at	---
3.64	3.96	0.31	5.42E-02	3.57E-01	EIF2C3 /// EIF2C4	eukaryotic translation initiation factor 2C, 3 /// eukaryotic translation initiation factor 2C, 4	chr1p34.3	222842_at	NM_017629 /// NM_024852 /// NM_177422
2.35	2.66	0.31	5.42E-02	3.57E-01	SEC24D	SEC24 related gene family, member D (S. cerevisiae)	chr4q26	215209_at	NM_014822
2.49	2.78	0.29	5.42E-02	3.57E-01	---	---	---	221930_at	---
2.89	3.62	0.74	5.42E-02	3.57E-01	STOX1	storkhead box 1	chr10q21.3	229378_at	NM_001130159 /// NM_001130160 /// NM_001130161 /// NM_001130162 /// NM_152709
2.30	2.79	0.48	5.42E-02	3.57E-01	ZNF788	zinc finger family member 788	chr19p13.2	244552_at	XR_015208 /// XR_015647 /// XR_041527
5.36	5.75	0.38	5.42E-02	3.57E-01	SULT2B1	sulfotransferase family, cytosolic, 2B, member 1	chr19q13.3	205759_s_at	NM_004605 /// NM_177973
3.60	3.85	0.25	5.42E-02	3.57E-01	---	---	---	226105_at	---
2.25	2.54	0.29	5.42E-02	3.57E-01	---	---	---	1559949_at	---
3.25	3.86	0.62	5.43E-02	3.57E-01	PTPRG	protein tyrosine phosphatase, receptor type, G	chr3p21-p14	1569323_at	NM_002841
5.67	6.10	0.43	5.43E-02	3.57E-01	---	---	---	234882_at	---
4.62	4.98	0.36	5.43E-02	3.57E-01	C16orf35	Chromosome 16 open reading frame 35	chr16p13.3	229122_x_at	NM_001039476 /// NM_001077350
3.17	3.53	0.36	5.43E-02	3.57E-01	CD5	CD5 molecule	chr11q13	230489_at	NM_014207
3.33	4.05	0.72	5.44E-02	3.57E-01	ATP8A2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	chr13q12	219659_at	NM_016529
3.25	3.59	0.34	5.44E-02	3.57E-01	---	---	---	241474_at	---
3.87	4.11	0.24	5.44E-02	3.57E-01	EFNA2	ephrin-A2	chr19p13.3	208256_at	NM_001405
6.10	7.27	1.17	5.44E-02	3.57E-01	LOC727820	hypothetical protein LOC727820	chr1q21.1	227384_s_at	XR_041980
2.48	2.74	0.26	5.44E-02	3.57E-01	---	---	---	240582_x_at	---
6.76	7.77	1.02	5.44E-02	3.58E-01	CFH /// CFHR1	complement factor H /// complement factor H-related 1	chr1q32	215388_s_at	NM_000186 /// NM_001014975 /// NM_002113
4.87	5.78	0.91	5.44E-02	3.58E-01	---	---	---	242695_at	---
6.16	6.58	0.42	5.45E-02	3.58E-01	TSHZ2	teashirt zinc finger homeobox 2	chr20q13.2	220213_at	NM_173485

4.82	5.17	0.35	5.45E-02	3.58E-01	UBOX5	U-box domain containing 5	chr20p13	215544_s_at	NM_014948 /// NM_199415
4.35	5.38	1.02	5.45E-02	3.58E-01	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	chr13q33	214927_at	NM_004791
6.58	7.06	0.48	5.45E-02	3.58E-01	---	---	---	243297_at	---
4.63	5.60	0.97	5.45E-02	3.58E-01	OPA1	optic atrophy 1 (autosomal dominant)	chr3q28-q29|3q28-q29	212214_at	NM_015560 /// NM_130831 /// NM_130832 /// NM_130833 /// NM_130834 /// NM_130835 /// NM_130836 /// NM_130837
2.35	2.78	0.42	5.46E-02	3.58E-01	---	---	---	215854_at	---
3.30	3.70	0.40	5.46E-02	3.58E-01	DEFB118	defensin, beta 118	chr20q11.1-q11.22	233221_at	NM_054112
3.44	3.78	0.34	5.46E-02	3.58E-01	LOC100129006	hypothetical protein LOC100129006	chr7q22.1	243757_at	XM_001716990 /// XM_001724688 /// XM_001725176
2.61	2.91	0.30	5.46E-02	3.58E-01	---	---	---	229277_at	---
4.99	5.26	0.28	5.46E-02	3.58E-01	---	---	---	214345_at	---
4.94	5.52	0.58	5.46E-02	3.58E-01	---	---	---	211973_at	---
3.35	3.70	0.35	5.46E-02	3.58E-01	LOC148189	Hypothetical protein LOC148189	chr19q12	235191_at	---
5.72	6.04	0.32	5.46E-02	3.58E-01	KIAA0859	KIAA0859	chr1q24-q25.3	212407_at	NM_001007239 /// NM_014955 /// NM_015935
2.24	2.54	0.30	5.46E-02	3.58E-01	NUDT4 /// NUDT4P1	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	chr12q21 /// chr1q21.1	212182_at	NM_019094 /// NM_199040 /// NR_002212
3.89	4.36	0.46	5.47E-02	3.58E-01	APOC2	Apolipoprotein C-II	chr19q13.2	231561_s_at	NM_000483
3.14	3.47	0.33	5.47E-02	3.58E-01	---	---	---	216754_at	---
3.69	4.20	0.50	5.47E-02	3.58E-01	LOC344595	hypothetical LOC344595	chr3q13.12	239466_at	XM_001128525 /// XM_943541
2.54	2.86	0.32	5.47E-02	3.58E-01	---	---	---	240220_at	---
2.05	2.39	0.34	5.47E-02	3.58E-01	---	---	---	1556935_at	---
4.83	5.46	0.63	5.47E-02	3.58E-01	IGHA1 /// IGHG1 /// IGHG3 /// IGHM /// IGHV4-31 /// IGHV@ /// LOC100133739	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable group /// similar to hCG2038920	chr14q32.33	211868_x_at	XM_001718220
2.63	2.96	0.33	5.47E-02	3.58E-01	SFRS12	Splicing factor, arginine/serine-rich 12	chr5q12.3	242184_s_at	NM_001077199 /// NM_139168
4.31	4.72	0.40	5.47E-02	3.58E-01	SLC39A5	solute carrier family 39 (metal ion transporter), member 5	chr12q13.2	231667_at	NM_173596
2.68	3.26	0.58	5.48E-02	3.58E-01	---	---	---	1556048_at	---
2.84	3.11	0.26	5.48E-02	3.58E-01	TP73	tumor protein p73	chr1p36.3	220804_s_at	NM_001126240 /// NM_001126241 /// NM_001126242 /// NM_005427
13.30	13.51	0.21	5.48E-02	3.58E-01	ND3 /// SH3KBP1	NADH dehydrogenase, subunit 3 (complex I) /// SH3-domain kinase binding protein 1	chrXp22.1-p21.3	1553588_at	NM_001024666 /// NM_031892
3.88	4.32	0.43	5.48E-02	3.58E-01	---	---	---	216584_at	---
6.71	7.32	0.62	5.49E-02	3.58E-01	RICTOR	rapamycin-insensitive companion of mTOR	chr5p13.1	228248_at	NM_152756
4.92	5.32	0.40	5.48E-02	3.58E-01	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4	chr17q24-q25	218063_s_at	NM_012121
4.66	5.06	0.41	5.49E-02	3.58E-01	RCP9	calcitonin gene-related peptide-receptor component protein	chr7q11.21	203899_s_at	NM_001040647 /// NM_001040648 /// NM_014478
2.88	3.26	0.37	5.49E-02	3.58E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	205962_at	NM_002577
2.36	2.71	0.36	5.49E-02	3.58E-01	RGS7	regulator of G-protein signaling 7	chr1q43|1q23.1	216970_at	NM_002924
2.55	3.29	0.74	5.49E-02	3.58E-01	C5orf17	chromosome 5 open reading frame 17	chr5p14.2	1552954_at	XR_000590 /// XR_000620
6.83	7.31	0.48	5.50E-02	3.58E-01	NSFL1C	NSFL1 (p97) cofactor (p47)	chr20p13	217830_s_at	NM_016143 /// NM_018839 /// NM_182483
4.46	4.81	0.35	5.49E-02	3.58E-01	KLK14	kallikrein-related peptidase 14	chr19q13.3-q13.4	220573_at	NM_022046
3.25	3.58	0.33	5.50E-02	3.58E-01	---	---	---	243017_at	---
6.11	6.50	0.39	5.51E-02	3.59E-01	DUOXA2	dual oxidase maturation factor 2	chr15q15.1	230615_at	NM_207581

4.66	5.00	0.34	5.51E-02	3.59E-01	PRDM8	PR domain containing 8	chr4q21	219835_at	NM_001099403 /// NM_020226
2.58	3.08	0.50	5.51E-02	3.59E-01	---	---	---	237733_at	---
2.37	2.63	0.25	5.51E-02	3.59E-01	---	---	---	231167_at	---
6.85	7.42	0.57	5.51E-02	3.59E-01	TCTA	T-cell leukemia translocation altered gene	chr3p21	203054_s_at	NM_022171
4.05	4.66	0.61	5.51E-02	3.59E-01	CCPG1	cell cycle progression 1	chr15q21.1	222156_x_at	NM_004748 /// NM_020739
3.50	4.31	0.81	5.52E-02	3.59E-01	LCOR	ligand dependent nuclear receptor corepressor	chr10q24	228454_at	NM_032440
4.66	5.19	0.53	5.52E-02	3.59E-01	MBP	myelin basic protein	chr18q23	225407_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385
2.95	3.41	0.46	5.52E-02	3.59E-01	RNF125	ring finger protein 125	chr18q12.1	207735_at	NM_017831
4.20	4.60	0.40	5.52E-02	3.59E-01	---	---	---	244086_at	---
3.06	3.45	0.39	5.52E-02	3.59E-01	ADRBK2	adrenergic, beta, receptor kinase 2	chr22q11|22q12.1	204184_s_at	NM_005160
4.80	5.14	0.34	5.52E-02	3.59E-01	RXRA	retinoid X receptor, alpha	chr9q34.3	202426_s_at	NM_002957
1.99	2.28	0.29	5.52E-02	3.59E-01	TIGD6	tigger transposable element derived 6	chr5q33.1	220986_s_at	NM_030953
4.91	5.25	0.35	5.53E-02	3.59E-01	MIER2	mesoderm induction early response 1, family member 2	chr19p13.3	221863_at	NM_017550
2.13	2.46	0.32	5.53E-02	3.59E-01	---	---	---	230898_at	---
2.30	2.57	0.26	5.53E-02	3.59E-01	PBRM1	polybromo 1	chr3p21	223900_s_at	NM_018165 /// NM_018313 /// NM_181042
3.15	4.26	1.11	5.53E-02	3.59E-01	KIAA1033	KIAA1033	chr12q24.11	215936_s_at	NM_015275
6.33	6.69	0.36	5.53E-02	3.59E-01	PDLIM4	PDZ and LIM domain 4	chr5q31.1	214174_s_at	NM_001131027 /// NM_003687
6.83	7.68	0.85	5.54E-02	3.59E-01	AFTPH	aftiphilin	chr2p14	217939_s_at	NM_001002243 /// NM_017657 /// NM_203437
3.36	3.65	0.29	5.53E-02	3.59E-01	DNAI1	dynein, axonemal, intermediate chain 1	chr9p21-p13	220125_at	NM_012144
2.31	2.58	0.27	5.53E-02	3.59E-01	ZNF818P	zinc finger protein 818 pseudogene	chr19q13.41	238149_at	XR_040818 /// XR_040819 /// XR_040820
2.77	3.05	0.29	5.54E-02	3.59E-01	---	---	---	236449_at	---
2.86	3.21	0.35	5.54E-02	3.60E-01	SCARF2	Scavenger receptor class F, member 2	chr22q11.21	241691_at	NM_153334 /// NM_182895
1.99	2.23	0.25	5.55E-02	3.60E-01	---	---	---	243307_at	---
2.49	3.69	1.20	5.55E-02	3.60E-01	SCG5	secretogranin V (7B2 protein)	chr15q13-q14	203889_at	NM_003020
4.36	5.54	1.18	5.55E-02	3.60E-01	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	chr8q13	216266_s_at	NM_006421
6.35	7.35	1.00	5.55E-02	3.60E-01	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	chr2p16.1	233759_s_at	NM_001122964 /// NM_020463
3.60	4.36	0.76	5.55E-02	3.60E-01	---	---	---	236934_at	---
5.70	6.08	0.38	5.55E-02	3.60E-01	---	---	---	1556442_x_at	---
3.55	3.90	0.35	5.55E-02	3.60E-01	LOC751071	hypothetical protein LOC751071	chr11q12.3	239316_at	NM_001043229
4.73	5.12	0.38	5.56E-02	3.60E-01	NR2F6	nuclear receptor subfamily 2, group F, member 6	chr19p13.1	209261_s_at	NM_005234
4.15	4.79	0.64	5.56E-02	3.60E-01	ARHGAP24	Rho GTPase activating protein 24	chr4q21.23-q21.3	223422_s_at	NM_001025616 /// NM_001042669 /// NM_031305
2.09	2.50	0.41	5.56E-02	3.60E-01	DBT	dihydrolipoamide branched chain transacylase E2	chr1p31	205371_s_at	NM_001918
4.49	5.29	0.80	5.56E-02	3.60E-01	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	chr14q24.1	225926_at	NM_006370
9.36	9.96	0.60	5.56E-02	3.60E-01	SET	SET nuclear oncogene	chr9q34	210231_x_at	NM_001122821 /// NM_003011
2.84	3.22	0.38	5.56E-02	3.60E-01	---	---	---	235193_at	---
3.10	3.42	0.32	5.56E-02	3.60E-01	SSX5	synovial sarcoma, X breakpoint 5	chrXp11.23	208528_x_at	NM_021015 /// NM_175723
5.77	6.43	0.66	5.57E-02	3.61E-01	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	chr8q13	202956_at	NM_006421
5.49	6.15	0.66	5.57E-02	3.61E-01	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	chr12q14.2	233888_s_at	NM_020762
3.50	3.87	0.37	5.57E-02	3.61E-01	---	---	---	1568997_at	---
2.76	3.20	0.44	5.57E-02	3.61E-01	---	---	---	1558418_at	---

4.81	5.24	0.43	5.57E-02	3.61E-01	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	chr3p14.1	225474_at	NM_001033057 /// NM_004742 /// NM_015520
6.88	7.27	0.39	5.58E-02	3.61E-01	C14orf166B	chromosome 14 open reading frame 166B	chr14q24.3	233941_at	NM_001081002 /// NM_194287
3.51	3.87	0.35	5.57E-02	3.61E-01	SH2D5	SH2 domain containing 5	chr1p36.12	230973_at	NM_001103160 /// NM_001103161
2.78	3.09	0.32	5.58E-02	3.61E-01	ACAT1	acetyl-Coenzyme A acetyltransferase 1	chr11q22.3-q23.1	1559239_s_at	NM_000019
5.88	6.52	0.64	5.58E-02	3.61E-01	TMED8	Transmembrane emp24 protein transport domain containing 8	chr14q24.3	242617_at	NM_213601
4.41	5.20	0.79	5.58E-02	3.61E-01	CCDC58	coiled-coil domain containing 58	chr3q21.1	235244_at	NM_001017928
3.23	3.65	0.41	5.58E-02	3.61E-01	PADI3	peptidyl arginine deiminase, type III	chr1p36.13	220779_at	NM_016233
5.68	6.43	0.75	5.58E-02	3.61E-01	NPDC1	neural proliferation, differentiation and control, 1	chr9q34.3	218086_at	NM_015392
3.77	4.73	0.97	5.59E-02	3.61E-01	CYB5R4	cytochrome b5 reductase 4	chr6pter-q22.33	219079_at	NM_016230
2.79	3.03	0.24	5.59E-02	3.61E-01	TFF2	trefoil factor 2	chr21q22.3	214476_at	NM_005423
3.96	4.34	0.38	5.60E-02	3.61E-01	---	---	---	234400_at	---
6.26	7.31	1.05	5.62E-02	3.61E-01	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	chr2q37.1	201198_s_at	NM_002807
7.18	8.18	0.99	5.61E-02	3.61E-01	CCDC47	coiled-coil domain containing 47	chr17q23.3	222432_s_at	NM_020198
5.06	5.94	0.88	5.61E-02	3.61E-01	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	chr2q32.2	203711_s_at	NM_014362 /// NM_198047
4.25	5.00	0.75	5.61E-02	3.61E-01	SWAP70	SWAP-70 protein	chr11p15	209307_at	NM_015055
3.53	4.24	0.71	5.61E-02	3.61E-01	---	---	---	243584_at	---
7.66	8.26	0.60	5.60E-02	3.61E-01	PLTP	phospholipid transfer protein	chr20q12-q13.1	202075_s_at	NM_006227 /// NM_182676
2.79	3.34	0.55	5.62E-02	3.61E-01	---	---	---	240960_at	---
4.84	5.26	0.42	5.62E-02	3.61E-01	LARP1	La ribonucleoprotein domain family, member 1	chr5q33.2	239663_x_at	NM_015315 /// NM_033551
3.90	4.32	0.42	5.62E-02	3.61E-01	CDH24	cadherin-like 24	chr14q11.2	1553166_at	NM_022478 /// NM_144985
3.52	3.94	0.41	5.61E-02	3.61E-01	PAGE5	P antigen family, member 5 (prostate associated)	chrXp11.21	236152_at	NM_001013435 /// NM_130467
2.99	3.38	0.39	5.61E-02	3.61E-01	---	---	---	228807_at	---
3.08	3.43	0.35	5.61E-02	3.61E-01	JPH2	junctophilin 2	chr20q13.12	220385_at	NM_020433 /// NM_175913
2.66	2.98	0.32	5.61E-02	3.61E-01	LOC389043	hypothetical gene supported by AK125982; BC042817	chr2q21.1	240546_at	XM_001724474 /// XM_374012 /// XM_943029
6.45	6.77	0.32	5.60E-02	3.61E-01	EVX1	even-skipped homeobox 1	chr7p15-p14	207914_x_at	NM_001989
2.46	2.78	0.32	5.62E-02	3.61E-01	CCDC120	coiled-coil domain containing 120	chrXp11.23	232996_at	NM_033626
4.06	4.36	0.29	5.61E-02	3.61E-01	SCARA5	scavenger receptor class A, member 5 (putative)	chr8p21.1	1554705_at	NM_173833
2.69	2.98	0.29	5.62E-02	3.61E-01	CCDC155	coiled-coil domain containing 155	chr19q13.33	240950_s_at	NM_144688
2.35	2.63	0.29	5.61E-02	3.61E-01	CALD1	caldesmon 1	chr7q33	231881_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
2.97	3.25	0.28	5.61E-02	3.61E-01	---	---	---	213777_s_at	---
1.94	2.20	0.26	5.62E-02	3.61E-01	---	---	---	1570226_at	---
1.92	2.15	0.23	5.60E-02	3.61E-01	C11orf87	chromosome 11 open reading frame 87	chr11q22.3	1557181_s_at	NM_207645
2.28	2.49	0.21	5.60E-02	3.61E-01	UMOD	Uromodulin	chr16p12.3	238248_at	NM_001008389 /// NM_003361
5.82	6.80	0.98	5.63E-02	3.61E-01	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	chr2p16.1	224474_x_at	NM_001122964 /// NM_020463
3.71	4.13	0.42	5.63E-02	3.61E-01	TRIM54	tripartite motif-containing 54	chr2p23.3	233669_s_at	NM_032546 /// NM_187841
2.32	2.59	0.26	5.63E-02	3.61E-01	41341	membrane-associated ring finger (C3HC4) 8	chr10q11.21	236056_s_at	NM_001002265 /// NM_001002266 /// NM_145021
5.25	6.38	1.13	5.63E-02	3.61E-01	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	chrXq13.1-q21.1	208860_s_at	NM_000489 /// NM_138270
4.74	5.16	0.42	5.63E-02	3.62E-01	CDAN1	Congenital dyserythropoietic anemia, type I	chr15q15.2	231080_at	NM_138477
3.65	4.20	0.56	5.64E-02	3.62E-01	---	---	---	229580_at	---
3.97	4.31	0.34	5.64E-02	3.62E-01	---	---	---	240157_at	---

7.33	8.54	1.21	5.64E-02	3.62E-01	FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	chr1q22	201275_at	NM_002004
2.66	3.12	0.46	5.64E-02	3.62E-01	---	---	---	1569538_at	---
2.67	3.09	0.42	5.64E-02	3.62E-01	---	---	---	233181_at	---
3.54	4.13	0.59	5.64E-02	3.62E-01	DDHD1	DDHD domain containing 1	chr14q21	225965_at	NM_030637
2.71	3.42	0.70	5.65E-02	3.62E-01	---	---	---	242881_x_at	---
3.32	3.67	0.35	5.65E-02	3.62E-01	FSCN2	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	chr17q25	207204_at	NM_001077182 /// NM_012418
2.29	2.59	0.30	5.65E-02	3.62E-01	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	chr11q21	211334_at	NM_005590 /// NM_005591
4.71	5.09	0.38	5.65E-02	3.62E-01	CYP2C9	Cytochrome P450, family 2, subfamily C, polypeptide 9	chr10q24	214419_s_at	NM_000771
2.57	2.95	0.38	5.65E-02	3.62E-01	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	chr17q24.3	217504_at	NM_080284
4.31	4.63	0.32	5.65E-02	3.62E-01	SYT7	synaptotagmin VII	chr11q12-q13.1	232025_at	NM_004200
2.00	2.32	0.31	5.66E-02	3.62E-01	TDRD1	tudor domain containing 1	chr10q25.3	221018_s_at	NM_198795
2.38	2.67	0.30	5.66E-02	3.62E-01	C16orf84	Chromosome 16 open reading frame 84	chr16q24.3	1561501_s_at	NM_001012759 /// NM_001012762
2.72	2.98	0.26	5.66E-02	3.62E-01	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	chr12q24.22	206864_s_at	NM_003806
2.91	3.55	0.64	5.66E-02	3.62E-01	---	---	---	239611_at	---
4.28	4.84	0.56	5.66E-02	3.62E-01	STAC	SH3 and cysteine rich domain	chr3p22.3	205743_at	NM_003149
2.97	3.37	0.40	5.66E-02	3.62E-01	FAM120AOS	family with sequence similarity 120A opposite strand	chr9q22.31	230308_at	NM_198841
3.62	4.80	1.18	5.67E-02	3.62E-01	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	chr9q34	206450_at	NM_000787
2.08	2.32	0.24	5.67E-02	3.62E-01	---	---	---	215986_at	---
5.56	6.98	1.42	5.67E-02	3.62E-01	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	chr5p14-p13	221750_at	NM_001098272 /// NM_002130
3.91	4.39	0.48	5.67E-02	3.62E-01	DKFZP434K028	hypothetical LOC26070	chr11q12.3	234356_at	---
3.75	4.06	0.31	5.67E-02	3.62E-01	ZNF318	Zinc finger protein 318	chr6pter-p12.1	231388_at	NM_014345
2.90	3.57	0.66	5.67E-02	3.62E-01	IGHM	immunoglobulin heavy constant mu	chr14q32.33	216491_x_at	---
2.72	3.28	0.55	5.67E-02	3.62E-01	TMEM56	Transmembrane protein 56	chr1p21.3	237515_at	NM_152487
2.90	3.21	0.31	5.67E-02	3.62E-01	SLC31A1	solute carrier family 31 (copper transporters), member 1	chr9q31-q32	236217_at	NM_001859
2.25	2.49	0.24	5.67E-02	3.62E-01	BNC2	basonuclin 2	chr9p22.3-p22.2	235723_at	NM_017637
2.60	2.92	0.32	5.68E-02	3.62E-01	SOX4	SRY (sex determining region Y)-box 4	chr6p22.3	213665_at	NM_003107
7.62	8.19	0.57	5.68E-02	3.62E-01	MRC1 /// MRC1L1	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1	chr10p12.33	204438_at	NM_001009567 /// NM_002438
3.19	3.69	0.50	5.68E-02	3.62E-01	---	---	---	236167_at	---
3.82	4.25	0.43	5.68E-02	3.62E-01	CPNE9	copine family member IX	chr3p25.3	239139_at	NM_153635
2.42	2.74	0.32	5.68E-02	3.62E-01	---	---	---	232363_at	---
5.12	5.44	0.32	5.68E-02	3.62E-01	LOC388588	hypothetical LOC388588	chr1p36.32	230840_at	XR_039846 /// XR_039847 /// XR_039848
2.09	2.38	0.29	5.68E-02	3.62E-01	---	---	---	1562472_at	---
1.99	2.22	0.22	5.68E-02	3.62E-01	LOC440900	hypothetical LOC440900	chr2q14.1	230797_s_at	XR_041709 /// XR_041710 /// XR_041711
1.92	2.13	0.21	5.68E-02	3.62E-01	---	---	---	1561239_at	---
2.02	2.36	0.34	5.68E-02	3.62E-01	---	---	---	237369_at	---
2.01	2.28	0.27	5.68E-02	3.62E-01	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	chr15q22	240703_s_at	NM_003922
2.63	3.10	0.48	5.69E-02	3.63E-01	---	---	---	244290_at	---
2.15	2.45	0.31	5.69E-02	3.63E-01	---	---	---	240635_at	---
10.62	11.30	0.68	5.70E-02	3.63E-01	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	chr14q32.33	214328_s_at	NM_001017963 /// NM_005348
4.43	4.84	0.41	5.69E-02	3.63E-01	LRCH1	leucine-rich repeats and calponin homology (CH) domain containing 1	chr13q14.13-q14.2	235012_at	NM_015116
2.12	2.44	0.32	5.70E-02	3.63E-01	MUC19	mucin 19, oligomeric	chr12q12	1553436_at	XM_001714368 /// XM_497341 /// XM_936590
2.93	3.18	0.25	5.70E-02	3.63E-01	PCDHGA3	protocadherin gamma subfamily A, 3	chr5q31	216343_at	NM_018916 /// NM_032011
4.67	5.64	0.97	5.70E-02	3.63E-01	CHD9	chromodomain helicase DNA binding protein 9	chr16q12.2	229586_at	NM_025134
3.12	3.62	0.49	5.70E-02	3.63E-01	---	---	---	1570177_at	---
2.60	3.22	0.62	5.71E-02	3.63E-01	TNRC6B	trinucleotide repeat containing 6B	chr22q13.1	230779_at	NM_001024843 /// NM_015088
6.47	6.74	0.26	5.71E-02	3.63E-01	C6orf35 /// LOC730074	chromosome 6 open reading frame 35 /// hypothetical LOC730074	chr6q25.3	222638_s_at	NM_018452 /// XM_001133047 /// XM_001713717

4.18	4.56	0.37	5.71E-02	3.63E-01	ZG16	zymogen granule protein 16	chr16p13.3	214142_at	NM_152338
8.15	8.67	0.52	5.72E-02	3.63E-01	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	chr9q31.1	208959_s_at	NM_015051
7.67	8.12	0.46	5.71E-02	3.63E-01	LOC440836	Similar to MGC52679 protein	chr22q13.33	238326_at	NM_001014440
2.19	2.60	0.42	5.71E-02	3.63E-01	---	---	---	216683_at	---
4.85	5.23	0.39	5.72E-02	3.63E-01	SFRP5	secreted frizzled-related protein 5	chr10q24.1	207468_s_at	NM_003015
3.19	3.47	0.29	5.71E-02	3.63E-01	NGB	neuroglobin	chr14q24.3	236677_at	NM_021257
2.20	2.49	0.28	5.72E-02	3.63E-01	DUSP21	dual specificity phosphatase 21	chrXp11.4-p11.23	220515_at	NM_022076
2.26	2.50	0.24	5.72E-02	3.63E-01	P53AIP1	p53-regulated apoptosis-inducing protein 1	chr11q24	220403_s_at	NM_022112
3.73	4.14	0.40	5.72E-02	3.63E-01	---	---	---	1565903_at	---
2.81	3.09	0.28	5.72E-02	3.63E-01	FAM163A	Family with sequence similarity 163, member A	chr1q25.2	231267_at	NM_173509
3.00	3.46	0.46	5.72E-02	3.63E-01	ZFP28	zinc finger protein 28 homolog (mouse)	---	231943_at	NM_020828
3.37	3.69	0.31	5.72E-02	3.63E-01	SIGLEC15	sialic acid binding Ig-like lectin 15	chr18q12.3	215856_at	NM_213602
4.83	5.66	0.83	5.73E-02	3.64E-01	SDCCAG10	serologically defined colon cancer antigen 10	chr5q12.3	1555495_a_at	NM_005869
7.93	8.49	0.56	5.73E-02	3.64E-01	OPTN	optineurin	chr10p13	202074_s_at	NM_001008211 /// NM_001008212 /// NM_001008213 /// NM_021980
2.57	3.07	0.50	5.73E-02	3.64E-01	PION	Pigeon homolog (Drosophila)	chr7q11.23	240061_at	NM_017439
3.30	3.67	0.37	5.73E-02	3.64E-01	ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	chr9q34	223844_at	NM_139025 /// NM_139026 /// NM_139027
3.03	3.32	0.29	5.73E-02	3.64E-01	CCBL1	cysteine conjugate-beta lyase, cytoplasmic	chr9q34.11	1570650_at	NM_001122671 /// NM_001122672 /// NM_004059
2.06	2.36	0.29	5.73E-02	3.64E-01	ANO2	anoctamin 2	chr12p13.3	220111_s_at	NM_020373
2.05	2.32	0.28	5.73E-02	3.64E-01	---	---	---	243220_at	---
3.30	3.69	0.39	5.74E-02	3.64E-01	PAX5	paired box 5	chr9p13	206802_at	NM_016734
4.88	5.26	0.37	5.74E-02	3.64E-01	---	---	---	231189_at	---
3.02	3.28	0.26	5.74E-02	3.64E-01	TOP3A	topoisomerase (DNA) III alpha	chr17p12-p11.2	214300_s_at	NM_004618
2.28	2.55	0.26	5.74E-02	3.64E-01	HIST1H1E	histone cluster 1, H1e	chr6p21.3	208553_at	NM_005321
2.34	2.58	0.24	5.74E-02	3.64E-01	HIST1H2BC	histone cluster 1, H2bc	chr6p21.3	236193_at	NM_003526
3.37	3.75	0.38	5.74E-02	3.64E-01	---	---	---	1566821_at	---
1.81	2.12	0.31	5.75E-02	3.64E-01	LOC653284	zinc finger protein LOC653284	chr19q13.12	1560779_a_at	XM_058997 /// XM_932948
6.18	6.93	0.74	5.75E-02	3.64E-01	TRIM24	tripartite motif-containing 24	chr7q32-q34	204391_x_at	NM_003852 /// NM_015905
3.87	4.14	0.27	5.75E-02	3.64E-01	ALPPL2	alkaline phosphatase, placental-like 2	chr2q37	216377_x_at	NM_031313
2.21	2.49	0.28	5.75E-02	3.64E-01	---	---	---	231574_at	---
3.89	4.25	0.36	5.75E-02	3.64E-01	C1orf64	chromosome 1 open reading frame 64	chr1p36.13	229381_at	NM_178840
2.78	3.17	0.39	5.75E-02	3.64E-01	---	---	---	1562045_at	---
3.06	3.41	0.35	5.75E-02	3.64E-01	ESR2	estrogen receptor 2 (ER beta)	chr14q23.2	211118_x_at	NM_001040275 /// NM_001040276 /// NM_001437
4.62	5.00	0.38	5.76E-02	3.64E-01	---	---	---	232731_x_at	---
3.60	3.90	0.30	5.76E-02	3.64E-01	NEU3	sialidase 3 (membrane sialidase)	chr11q13.5	216082_at	NM_006656
4.48	4.98	0.49	5.76E-02	3.64E-01	MAP3K6	mitogen-activated protein kinase kinase kinase 6	chr1p36.11	219278_at	NM_004672
2.96	3.27	0.31	5.76E-02	3.64E-01	C1orf95	Chromosome 1 open reading frame 95	chr1q42.12	213925_at	NM_001003665
5.54	6.47	0.93	5.76E-02	3.64E-01	PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	chr14q23.1	203338_at	NM_006246
2.41	2.79	0.39	5.76E-02	3.64E-01	CDH7	cadherin 7, type 2	chr18q22-q23	220679_s_at	NM_004361 /// NM_033646
4.99	5.28	0.30	5.77E-02	3.65E-01	POU5F1 /// POU5F1P1 /// POU5F1P3 /// POU5F1P4	POU class 5 homeobox 1 /// POU class 5 homeobox 1 pseudogene 1 /// POU class 5 homeobox 1 pseudogene 3 /// POU class 5 homeobox 1 pseudogene 4	chr12p13.31 /// chr1q22 /// chr6p21.31 /// chr8q24.21	208286_x_at	NM_002701 /// NM_203289 /// NR_002304
2.35	2.74	0.39	5.77E-02	3.65E-01	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	chrXq22.3	1553219_a_at	NM_001025580 /// NM_015365
3.41	3.94	0.53	5.78E-02	3.65E-01	MED28	Mediator complex subunit 28	chr4p16	214831_at	NM_025205
4.84	5.28	0.44	5.78E-02	3.65E-01	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	chr16p13.3	232085_at	NM_001040439 /// NM_015133
6.50	7.62	1.12	5.78E-02	3.65E-01	ZNF292	zinc finger protein 292	chr6q15	212368_at	NM_015021
4.75	5.14	0.39	5.78E-02	3.65E-01	GPR162	G protein-coupled receptor 162	chr12p13	205056_s_at	NM_014449 /// NM_019858
3.87	4.43	0.56	5.78E-02	3.65E-01	POLK	polymerase (DNA directed) kappa	chr5q13	223261_at	NM_016218
3.00	3.41	0.41	5.79E-02	3.65E-01	---	---	---	243120_at	---

2.43	2.75	0.33	5.78E-02	3.65E-01	KCNA7	potassium voltage-gated channel, shaker-related subfamily, member 7	chr19q13.3	232936_at	NM_031886
2.67	2.94	0.27	5.79E-02	3.65E-01	LCAT	Lecithin-cholesterol acyltransferase	chr16q22.1	216390_at	NM_000229
2.38	2.64	0.26	5.78E-02	3.65E-01	---	---	---	234164_at	---
2.24	2.46	0.23	5.79E-02	3.65E-01	ARHGAP25	Rho GTPase activating protein 25	chr2p14	1555076_at	NM_001007231 /// NM_014882
7.33	8.74	1.41	5.79E-02	3.65E-01	COL3A1	collagen, type III, alpha 1	chr2q31	201852_x_at	NM_000090
5.23	6.36	1.13	5.79E-02	3.65E-01	KIAA1033	KIAA1033	chr12q24.11	212794_s_at	NM_015275
2.94	3.44	0.50	5.79E-02	3.65E-01	---	---	---	1556658_a_at	---
5.76	6.20	0.44	5.79E-02	3.65E-01	SAA1 /// SAA2	serum amyloid A1 /// serum amyloid A2	chr11p15.1 /// chr11p15.1-p14	208607_s_at	NM_000331 /// NM_001127380 /// NM_030754 /// NM_199161
2.06	2.35	0.30	5.79E-02	3.65E-01	CLDN20	claudin 20	chr6q25	1554812_at	NM_001001346
2.13	2.41	0.28	5.79E-02	3.65E-01	---	---	---	234447_at	---
6.84	7.79	0.95	5.80E-02	3.65E-01	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	chr17p11.2	210544_s_at	NM_000382 /// NM_001031806
3.90	4.41	0.52	5.80E-02	3.65E-01	---	---	---	230411_at	---
2.52	2.88	0.36	5.80E-02	3.65E-01	LEPR	leptin receptor	chr1p31	211354_s_at	NM_001003679 /// NM_001003680 /// NM_002303
2.57	2.91	0.34	5.80E-02	3.65E-01	DKFZp566H0824	hypothetical LOC54744	chr1p36.23	207470_at	XR_041382 /// XR_041383 /// XR_041384
5.07	5.80	0.73	5.81E-02	3.65E-01	LYRM7	Lyrm7 homolog (mouse)	chr5q31.1	240344_x_at	NM_181705
3.47	4.18	0.71	5.81E-02	3.65E-01	AK3	adenylate kinase 3	chr9p24.1-p24.3	224151_s_at	NM_016282
2.04	2.35	0.30	5.81E-02	3.65E-01	---	---	---	236287_at	---
2.20	2.43	0.23	5.81E-02	3.66E-01	DYX1C1	dyslexia susceptibility 1 candidate 1	chr15q21.3	235273_at	NM_001033559 /// NM_001033560 /// NM_130810
4.40	4.66	0.26	5.81E-02	3.66E-01	DDN	dendrin	chr12q13.12	214788_x_at	NM_015086
4.99	5.87	0.88	5.82E-02	3.66E-01	---	---	---	234224_at	---
5.58	5.95	0.37	5.81E-02	3.66E-01	MTF1	metal-regulatory transcription factor 1	chr1p33	205323_s_at	NM_005955
6.22	6.81	0.58	5.82E-02	3.66E-01	ZNF420	zinc finger protein 420	chr19q13.12	242761_s_at	NM_144689
2.28	2.51	0.23	5.82E-02	3.66E-01	FLJ34047	hypothetical protein FLJ34047	chr5p15.1	1553335_x_at	XR_017758 /// XR_017902 /// XR_039992
3.29	3.71	0.42	5.83E-02	3.66E-01	MTMR9	myotubularin related protein 9	chr8p23-p22	204837_at	NM_015458
2.69	3.02	0.33	5.83E-02	3.66E-01	---	---	---	1557697_at	---
4.23	4.52	0.30	5.83E-02	3.66E-01	SPTBN1	Spectrin, beta, non-erythrocytic 1	chr2p21	213914_s_at	NM_003128 /// NM_178313
3.42	3.68	0.26	5.84E-02	3.66E-01	---	---	---	236441_at	---
2.89	3.12	0.23	5.84E-02	3.67E-01	---	---	---	221116_at	---
2.60	3.02	0.42	5.84E-02	3.67E-01	---	---	---	237292_at	---
2.23	2.57	0.34	5.84E-02	3.67E-01	MPHOSPH9	M-phase phosphoprotein 9	chr12q24.31	215731_s_at	NM_022782
4.30	4.63	0.33	5.84E-02	3.67E-01	TMPRSS5	transmembrane protease, serine 5	chr11q	221032_s_at	NM_030770
3.69	3.92	0.23	5.84E-02	3.67E-01	C6orf165	chromosome 6 open reading frame 165	chr6q15	230273_at	NM_001031743 /// NM_178823
6.51	7.09	0.58	5.85E-02	3.67E-01	TNPO3	transportin 3	chr7q32.1	212318_at	NM_012470
3.82	4.18	0.36	5.85E-02	3.67E-01	---	---	---	236093_at	---
2.60	2.95	0.34	5.85E-02	3.67E-01	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	chr11q23.3	215064_at	NM_001024956 /// NM_006918
2.65	2.99	0.34	5.85E-02	3.67E-01	CXorf41	chromosome X open reading frame 41	chrXq22.3	231389_at	NM_173494
5.44	5.85	0.41	5.85E-02	3.67E-01	RNF141	ring finger protein 141	chr11p15.4	219104_at	NM_016422
2.89	3.13	0.24	5.86E-02	3.67E-01	---	---	---	237826_at	---
3.16	3.57	0.41	5.86E-02	3.67E-01	---	---	---	236446_at	---
2.49	2.78	0.29	5.86E-02	3.67E-01	TPPP2	tubulin polymerization-promoting protein family member 2	chr14q11.2	231140_at	NM_173846
2.83	3.59	0.76	5.86E-02	3.67E-01	BHLHB5	basic helix-loop-helix domain containing, class B, 5	chr8q13	228636_at	NM_152414
5.12	5.48	0.37	5.86E-02	3.67E-01	ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	chr16q22.1	228784_at	NM_006927
2.27	2.63	0.36	5.87E-02	3.67E-01	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	chr18p11.32	1558747_at	NM_015295
5.20	5.60	0.39	5.87E-02	3.67E-01	SSTR3	somatostatin receptor 3	chr22q13.1	214491_at	NM_001051
7.87	8.29	0.42	5.87E-02	3.68E-01	SOX15	SRY (sex determining region Y)-box 15	chr17p13	217040_x_at	NM_006942
2.79	3.11	0.32	5.87E-02	3.68E-01	---	---	---	237796_at	---
2.06	2.28	0.22	5.87E-02	3.68E-01	LACE1	lactation elevated 1	chr6q22.1	1563671_at	NM_145315

5.09	6.26	1.17	5.88E-02	3.68E-01	---	---	---	244457_at	---
3.23	3.63	0.40	5.87E-02	3.68E-01	PCDH18	protocadherin 18	chr4q31	225977_at	NM_019035
3.61	3.96	0.35	5.87E-02	3.68E-01	LOC100130494 /// LOC728448	hypothetical protein LOC100130494 /// peptidylprolyl isomerase E pseudogene	chr1p34.2	237473_at	NR_003929 /// XM_001723297 /// XM_001725351 /// XM_001725544
4.34	4.80	0.46	5.88E-02	3.68E-01	KLF7	Kruppel-like factor 7 (ubiquitous)	chr2q32	204334_at	NM_003709
3.89	4.23	0.35	5.88E-02	3.68E-01	---	---	---	243119_at	---
3.85	4.20	0.35	5.89E-02	3.68E-01	HOXA3	homeobox A3	chr7p15-p14	208604_s_at	NM_030661 /// NM_153631 /// NM_153632
4.24	4.57	0.33	5.89E-02	3.68E-01	---	---	---	229988_at	---
2.17	2.48	0.31	5.89E-02	3.68E-01	---	---	---	1556262_at	---
1.95	2.21	0.26	5.89E-02	3.68E-01	ZDHHC21	zinc finger, DHHC-type containing 21	chr9p22.3	233247_x_at	NM_178566
4.56	5.39	0.83	5.89E-02	3.68E-01	SHH	Sonic hedgehog homolog (Drosophila)	chr7q36	236263_at	NM_000193
5.68	6.10	0.42	5.89E-02	3.68E-01	PYCR1	pyrroline-5-carboxylate reductase 1	chr17q25.3	202148_s_at	NM_006907 /// NM_153824
3.89	4.62	0.72	5.90E-02	3.68E-01	FAM129A	family with sequence similarity 129, member A	chr1q25	217966_s_at	NM_052966
2.98	3.35	0.37	5.90E-02	3.68E-01	MYT1	myelin transcription factor 1	chr20q13.33	1556269_at	NM_004535
2.93	3.27	0.35	5.90E-02	3.68E-01	---	---	---	1566113_at	---
2.71	2.95	0.25	5.90E-02	3.68E-01	---	---	---	1559169_at	---
2.85	3.21	0.37	5.90E-02	3.68E-01	---	---	---	232236_at	---
2.65	2.94	0.29	5.90E-02	3.68E-01	SCN3A	sodium channel, voltage-gated, type III, alpha subunit	chr2q24	232512_at	NM_001081676 /// NM_001081677 /// NM_006922
4.64	5.38	0.74	5.91E-02	3.68E-01	NID2	nidogen 2 (osteonidogen)	chr14q21-q22	204114_at	NM_007361
3.62	4.06	0.44	5.91E-02	3.68E-01	RAI1	retinoic acid induced 1	chr17p11.2	219830_at	NM_030665
1.88	2.23	0.35	5.91E-02	3.68E-01	---	---	---	1566644_at	---
2.01	2.35	0.35	5.91E-02	3.68E-01	---	---	---	230230_at	---
1.96	2.23	0.27	5.91E-02	3.68E-01	ACSL6	acyl-CoA synthetase long-chain family member 6	chr5q31	211207_s_at	NM_001009185 /// NM_015256
1.88	2.13	0.25	5.91E-02	3.68E-01	---	---	---	215405_at	---
8.48	8.90	0.43	5.91E-02	3.69E-01	---	---	---	AFFX-BioDn-5_at	---
3.23	3.63	0.40	5.91E-02	3.69E-01	TPM1	tropomyosin 1 (alpha)	chr15q22.1	206117_at	NM_000366 /// NM_001018004 /// NM_001018005 /// NM_001018006 /// NM_001018007 /// NM_001018008 /// NM_001018020
6.43	7.59	1.17	5.93E-02	3.69E-01	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	chr21q22.3	202245_at	NM_001001438 /// NM_002340
4.34	4.73	0.39	5.93E-02	3.69E-01	ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif, 14	chr10q21	230167_at	NM_080722 /// NM_139155
4.16	4.54	0.38	5.93E-02	3.69E-01	JMJD1C	jumonji domain containing 1C	chr10q21.2-q21.3	230007_at	NM_004241 /// NM_032776
2.73	3.11	0.38	5.93E-02	3.69E-01	---	---	---	237031_at	---
2.65	3.03	0.38	5.92E-02	3.69E-01	---	---	---	237803_x_at	---
2.88	3.23	0.36	5.93E-02	3.69E-01	LOC728475	hypothetical LOC728475	chr10q23.32	242010_at	XM_001127438 /// XM_001127527 /// XM_001714506
3.12	3.47	0.35	5.93E-02	3.69E-01	---	---	---	236018_at	---
4.73	5.07	0.34	5.92E-02	3.69E-01	PDZD4	PDZ domain containing 4	chrXq28	223543_at	NM_032512
4.28	4.61	0.33	5.93E-02	3.69E-01	LOC399884	hypothetical LOC399884	chr11p11.2	244252_at	---
4.74	5.06	0.32	5.93E-02	3.69E-01	FBXL6	F-box and leucine-rich repeat protein 6	chr8q24.3	239416_at	NM_012162 /// NM_024555
3.10	3.41	0.32	5.93E-02	3.69E-01	---	---	---	240003_at	---

2.25	2.56	0.31	5.93E-02	3.69E-01	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	chr6p24	210669_at	NM_001032280 /// NM_001042425 /// NM_003220
2.22	2.50	0.27	5.92E-02	3.69E-01	---	---	---	1561700_at	---
2.53	2.80	0.27	5.93E-02	3.69E-01	---	---	---	1562862_at	---
2.66	2.88	0.22	5.92E-02	3.69E-01	HIST1H3I	histone cluster 1, H3i	chr6p22-p21.3	214509_at	NM_003533
5.21	6.16	0.95	5.94E-02	3.69E-01	LNPEP	leucyl/cystinyl aminopeptidase	chr5q15	231866_at	NM_005575 /// NM_175920
6.17	6.90	0.74	5.94E-02	3.69E-01	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	chr18q12.2	225953_at	NM_018170
4.27	4.62	0.36	5.94E-02	3.69E-01	SCGB3A1	secretoglobin, family 3A, member 1	chr5q35-qter	230378_at	NM_052863
2.67	3.22	0.55	5.94E-02	3.69E-01	PRSS23	Protease, serine, 23	chr11q14.1	229441_at	NM_007173
2.83	3.37	0.54	5.95E-02	3.69E-01	---	---	---	220870_at	---
2.60	3.04	0.45	5.94E-02	3.69E-01	HERV-FRD	HERV-FRD provirus ancestral Env polyprotein	chr6p24.1	1555880_at	NM_207582
6.40	6.81	0.41	5.94E-02	3.69E-01	MYOG	myogenin (myogenic factor 4)	chr1q31-q41	207282_s_at	NM_002479
6.31	6.63	0.33	5.95E-02	3.69E-01	CCDC71	coiled-coil domain containing 71	chr3p21.31	219893_at	NM_022903
7.63	8.77	1.14	5.95E-02	3.69E-01	MAP3K2	mitogen-activated protein kinase kinase kinase 2	chr2q14.3	226979_at	NM_006609
5.01	5.58	0.58	5.95E-02	3.69E-01	TMLHE	trimethyllysine hydroxylase, epsilon	chrXq28	222744_s_at	NM_018196
2.10	2.40	0.30	5.95E-02	3.69E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1564805_a_at	NM_153003
2.29	2.57	0.28	5.95E-02	3.69E-01	CXorf27	chromosome X open reading frame 27	chrXp21.1	215142_at	NM_012274
1.82	2.06	0.24	5.95E-02	3.69E-01	KLHL14	kelch-like 14 (Drosophila)	chr18q12.1	1554941_at	NM_020805
2.75	3.02	0.27	5.96E-02	3.69E-01	TMEM130	transmembrane protein 130	chr7q22.1	238426_at	NM_001134450 /// NM_001134451 /// NM_152913
2.71	3.07	0.35	5.96E-02	3.69E-01	FANCI	Fanconi anemia, complementation group I	chr15q26.1	213007_at	NM_001113378 /// NM_018193
2.93	3.18	0.25	5.96E-02	3.69E-01	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	chr17q23.3	211045_s_at	NM_030779 /// NM_173092
2.97	3.30	0.33	5.97E-02	3.69E-01	---	---	---	229373_at	---
3.71	4.17	0.46	5.97E-02	3.70E-01	ZNF75D	zinc finger protein 75D	chrXq26.3	213659_at	NM_007131
2.11	2.41	0.30	5.97E-02	3.70E-01	C4orf6	chromosome 4 open reading frame 6	chr4p16.1	207241_at	NM_005750
4.03	5.59	1.56	5.97E-02	3.70E-01	FATE1	fetal and adult testis expressed 1	chrXq28	231573_at	NM_033085
8.01	9.01	1.00	5.97E-02	3.70E-01	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	chr15q21.2	202467_s_at	NM_004236
6.31	7.11	0.80	5.98E-02	3.70E-01	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	chr7q22.1	223190_s_at	NM_018682 /// NM_182931
4.25	4.65	0.40	5.98E-02	3.70E-01	FRG1B	Hypothetical protein LOC283788	chr20q11.1	234949_at	NR_003579
3.85	4.23	0.38	5.98E-02	3.70E-01	FBXL2	F-box and leucine-rich repeat protein 2	chr3p22.3	214436_at	NM_012157
2.25	2.53	0.29	5.98E-02	3.70E-01	---	---	---	233370_at	---
2.67	2.95	0.28	5.98E-02	3.70E-01	---	---	---	221380_at	---
2.42	2.67	0.25	5.98E-02	3.70E-01	RCOR3	REST corepressor 3	chr1q32.2-q32.3	241433_at	NM_018254
2.09	2.30	0.20	5.98E-02	3.70E-01	LMO3	LIM domain only 3 (rhombotin-like 2)	chr12p12.3	1565936_a_at	NM_001001395 /// NM_018640
3.32	3.87	0.54	5.98E-02	3.70E-01	CES3	carboxylesterase 3	chr16q22.1	234008_s_at	NM_024922
2.38	2.69	0.31	5.98E-02	3.70E-01	TRIM66	tripartite motif-containing 66	chr11p15.4	237679_at	XM_001716253 /// XM_001716830 /// XM_001717903
2.35	2.75	0.40	5.99E-02	3.70E-01	HPR	haptoglobin-related protein	chr16q22.1	208471_at	NM_020995
2.73	3.11	0.38	5.99E-02	3.70E-01	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	chr18p11.32	204162_at	NM_006101
2.49	2.86	0.37	5.99E-02	3.70E-01	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	chr17q21.32	216261_at	NM_000212
2.17	2.51	0.34	5.99E-02	3.70E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	1558608_a_at	NM_002581
4.04	4.25	0.21	6.00E-02	3.70E-01	CCDC123	coiled-coil domain containing 123	chr19q13.11	1563919_a_at	NM_032816
6.30	6.93	0.63	6.00E-02	3.70E-01	CADPS2	Ca++-dependent secretion activator 2	chr7q31.3	219572_at	NM_001009571 /// NM_017954
2.42	2.76	0.35	6.00E-02	3.70E-01	MED31	mediator complex subunit 31	chr17p13.2	236241_at	NM_016060
6.83	8.37	1.54	6.01E-02	3.70E-01	C9orf5	chromosome 9 open reading frame 5	chr9q31	223007_s_at	NM_001099734 /// NM_032012
3.30	3.59	0.29	6.01E-02	3.70E-01	VWA5B1	von Willebrand factor A domain containing 5B1	chr1p36.12	1552854_a_at	XM_001720309 /// XM_001722222 /// XM_001722706
5.02	5.64	0.62	6.01E-02	3.70E-01	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	chr2q33	225189_s_at	NM_203365 /// NM_213589
4.72	5.75	1.02	6.02E-02	3.71E-01	KRCC1	lysine-rich coiled-coil 1	chr2p11.2	222585_x_at	NM_016618
2.24	2.49	0.25	6.01E-02	3.71E-01	DSC2	desmocollin 2	chr18q12.1	204751_x_at	NM_004949 /// NM_024422

2.60	3.03	0.44	6.02E-02	3.71E-01	---	---	---	229504_at	---
6.65	7.05	0.39	6.03E-02	3.71E-01	CDC16	cell division cycle 16 homolog (S. cerevisiae)	chr13q34	209658_at	NM_001078645 /// NM_003903
2.76	3.10	0.34	6.02E-02	3.71E-01	---	---	---	239339_at	---
4.11	4.44	0.33	6.02E-02	3.71E-01	---	---	---	1561270_at	---
5.61	6.47	0.86	6.03E-02	3.71E-01	RASA2	RAS p21 protein activator 2	chr3q22-q23	230669_at	NM_006506
5.40	5.79	0.39	6.04E-02	3.71E-01	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	chr17q21.32	206493_at	NM_000419
1.88	2.23	0.35	6.03E-02	3.71E-01	BPA-1	brain peptide A1	chr1p31.3	1555547_at	XM_001726020 /// XM_001726623 /// XM_001726673
3.24	3.56	0.32	6.04E-02	3.71E-01	B4GALNT4	beta-1,4-N-acetyl-galactosaminyl transferase 4	chr11p15.5	238080_at	NM_178537
3.39	3.69	0.30	6.03E-02	3.71E-01	---	---	---	228797_at	---
2.15	2.44	0.30	6.03E-02	3.71E-01	---	---	---	239614_x_at	---
1.89	2.18	0.29	6.03E-02	3.71E-01	---	---	---	241094_at	---
4.35	4.63	0.28	6.03E-02	3.71E-01	ZNF800	zinc finger protein 800	chr7q31.33	227104_x_at	NM_176814
2.92	3.18	0.26	6.03E-02	3.71E-01	---	---	---	237059_at	---
2.07	2.30	0.23	6.04E-02	3.71E-01	SLC34A2	solute carrier family 34 (sodium phosphate), member 2	chr4p15.3-p15.1	204124_at	NM_006424
2.67	2.99	0.33	6.04E-02	3.71E-01	---	---	---	239574_at	---
3.48	3.71	0.23	6.04E-02	3.71E-01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	215260_s_at	NM_003200
5.16	5.75	0.59	6.04E-02	3.71E-01	HSPB2	heat shock 27kDa protein 2	chr11q22-q23	205824_at	NM_001541
2.88	3.27	0.39	6.04E-02	3.71E-01	TREX2	three prime repair exonuclease 2	chrXq28	211788_s_at	NM_080701
5.98	6.97	0.98	6.04E-02	3.71E-01	THUMPD1	THUMP domain containing 1	chr16p12.2	206555_s_at	NM_017736
5.31	5.58	0.27	6.05E-02	3.71E-01	RAP1GAP	RAP1 GTPase activating protein	chr1p36.1-p35	210618_at	NM_002885
2.10	2.33	0.24	6.05E-02	3.71E-01	FAM20A	family with sequence similarity 20, member A	chr17q24.2	241981_at	NM_017565
2.31	2.59	0.29	6.05E-02	3.71E-01	COL14A1	collagen, type XIV, alpha 1	chr8q23	216865_at	NM_021110
5.71	6.65	0.94	6.05E-02	3.72E-01	CHMP2B	chromatin modifying protein 2B	chr3p11.2	202537_s_at	NM_014043
3.36	3.74	0.38	6.05E-02	3.72E-01	---	---	---	234239_at	---
2.71	3.02	0.31	6.06E-02	3.72E-01	LOC339483	Hypothetical LOC339483	chr1p35.1	244718_at	XR_040224 /// XR_040225 /// XR_040226
2.14	2.44	0.30	6.05E-02	3.72E-01	---	---	---	234889_at	---
2.10	2.32	0.22	6.06E-02	3.72E-01	OK/SW-CL.58	OK/SW-CL.58	chr13q12.3	1554971_at	XM_001720283 /// XM_001722964 /// XM_001724245
2.07	2.29	0.22	6.06E-02	3.72E-01	PKD1L1	polycystic kidney disease 1 like 1	chr7p12.3	1553004_at	NM_138295
2.55	2.83	0.28	6.06E-02	3.72E-01	---	---	---	233553_at	---
2.38	2.65	0.27	6.06E-02	3.72E-01	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	chr4q28-q32	209921_at	NM_014331
1.89	2.11	0.22	6.06E-02	3.72E-01	---	---	---	240922_at	---
8.13	8.47	0.34	6.07E-02	3.72E-01	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	chr19p13.11	206792_x_at	NM_000923 /// NM_001098818 /// NM_001098819
2.26	2.68	0.41	6.07E-02	3.72E-01	C14orf86	chromosome 14 open reading frame 86	chr14q32.13	1557211_a_at	---
5.73	6.76	1.04	6.07E-02	3.72E-01	RC3H2	ring finger and CCCH-type zinc finger domains 2	chr9q34	220202_s_at	NM_001100588 /// NM_018835
4.50	5.40	0.91	6.08E-02	3.72E-01	TPSAB1	tryptase alpha/beta 1	chr16p13.3	207741_x_at	NM_003294 /// XM_001720738 /// XM_001720740
2.69	2.95	0.26	6.08E-02	3.72E-01	CD53	CD53 molecule	chr1p13	237606_at	NM_000560 /// NM_001040033
4.70	4.93	0.24	6.08E-02	3.72E-01	---	---	---	243138_at	---
3.44	3.83	0.39	6.08E-02	3.72E-01	C8orf38	chromosome 8 open reading frame 38	chr8q22.1	230016_at	NM_152416
4.46	4.93	0.47	6.08E-02	3.72E-01	NRXN2	neurexin 2	chr11q13	209983_s_at	NM_015080 /// NM_138732 /// NM_138734
3.30	3.61	0.31	6.08E-02	3.72E-01	---	---	---	230390_at	---
6.57	7.39	0.82	6.09E-02	3.72E-01	UFSP2	UFM1-specific peptidase 2	chr4q35.1	218449_at	NM_018359
3.07	3.75	0.68	6.08E-02	3.72E-01	ARID2	AT rich interactive domain 2 (ARID, RFX-like)	chr12q12	1553349_at	NM_152641
4.11	4.66	0.54	6.09E-02	3.72E-01	---	---	---	244019_at	---

2.59	3.04	0.45	6.08E-02	3.72E-01	HSF2	heat shock transcription factor 2	chr6q22.31	211220_s_at	NM_004506
3.08	3.52	0.43	6.09E-02	3.72E-01	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	chr2q11.2-q12	222548_s_at	NM_004834 /// NM_145686 /// NM_145687
2.79	3.11	0.32	6.09E-02	3.72E-01	SAE1	SUMO1 activating enzyme subunit 1	chr19q13.32	241185_at	NM_005500
3.68	3.99	0.31	6.08E-02	3.72E-01	ZFYVE20	zinc finger, FYVE domain containing 20	chr3p24.3	231765_at	NM_022340
4.45	4.73	0.28	6.08E-02	3.72E-01	C1orf89	chromosome 1 open reading frame 89	chr1p36.13	220963_s_at	NM_030907
1.90	2.15	0.25	6.09E-02	3.72E-01	VSTM2A	V-set and transmembrane domain containing 2A	chr7p11.2	236308_at	NM_182546
3.75	4.37	0.62	6.09E-02	3.72E-01	---	---	---	230744_at	---
2.83	3.18	0.36	6.09E-02	3.72E-01	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	chr17q11.2	32128_at	NM_002988
2.43	2.82	0.39	6.09E-02	3.72E-01	LOC100132409	similar to PRO1082	chr3q13.31	223890_at	XM_001721470 /// XM_001721636 /// XM_001722471
5.60	5.91	0.31	6.10E-02	3.72E-01	KIAA0562	KIAA0562	chr1p36.32	204074_s_at	NM_014704
3.34	3.76	0.42	6.10E-02	3.72E-01	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	chr5q12.3	228745_at	NM_019072
2.38	2.67	0.29	6.10E-02	3.73E-01	---	---	---	239934_x_at	---
5.02	5.33	0.31	6.10E-02	3.73E-01	PQLC2	PQ loop repeat containing 2	chr1p36.13	220453_at	NM_001040125 /// NM_001040126 /// NM_017765
2.28	2.58	0.30	6.10E-02	3.73E-01	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	chr2q35	236684_at	NM_005444
4.69	5.07	0.38	6.11E-02	3.73E-01	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	chr5p15.33	231480_at	NM_001003841 /// XM_001716583 /// XM_001720416 /// XM_001722996
4.39	4.68	0.29	6.11E-02	3.73E-01	---	---	---	243058_at	---
2.35	2.60	0.25	6.11E-02	3.73E-01	---	---	---	1566046_at	---
5.95	7.15	1.19	6.12E-02	3.73E-01	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	chr18q12.2	222559_s_at	NM_018170
7.01	8.04	1.03	6.12E-02	3.73E-01	---	---	---	213015_at	---
6.98	7.40	0.42	6.12E-02	3.73E-01	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	chr19p13.2	206338_at	NM_001420 /// NM_032281
3.44	3.78	0.34	6.12E-02	3.73E-01	SYT5	synaptotagmin V	chr19q|11p	206161_s_at	NM_003180
3.05	3.33	0.28	6.12E-02	3.73E-01	---	---	---	240012_at	---
2.24	2.60	0.36	6.13E-02	3.73E-01	NUDT10	Nudix (nucleoside diphosphate linked moiety X)-type motif 10	chrXp11.23	241598_at	NM_153183
5.70	6.24	0.54	6.13E-02	3.73E-01	RRAGD	Ras-related GTP binding D	chr6q15-q16	221523_s_at	NM_021244
2.71	2.90	0.20	6.13E-02	3.73E-01	---	---	---	1555580_at	---
5.02	5.95	0.93	6.14E-02	3.73E-01	ZNF430	zinc finger protein 430	chr19p12	206829_x_at	NM_025189
4.18	4.44	0.27	6.14E-02	3.73E-01	RPRML	reprimo-like	chr17q21.32	1554655_a_at	NM_203400
2.78	3.02	0.24	6.14E-02	3.73E-01	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	chr2q33.2	1555099_at	NM_033066
2.70	3.03	0.32	6.14E-02	3.73E-01	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	chr3p14.3-p14.2	1554697_at	NM_182920
2.86	3.19	0.33	6.14E-02	3.74E-01	---	---	---	242299_at	---
5.40	5.77	0.37	6.14E-02	3.74E-01	CUX1	cut-like homeobox 1	chr7q22.1	202367_at	NM_001913 /// NM_181500 /// NM_181552
3.11	3.41	0.30	6.14E-02	3.74E-01	FBLN1	fibulin 1	chr22q13.31	207835_at	NM_001996 /// NM_006485 /// NM_006486 /// NM_006487
5.34	6.41	1.07	6.15E-02	3.74E-01	PIAS1	protein inhibitor of activated STAT, 1	chr15q	217862_at	NM_016166
4.81	5.20	0.39	6.15E-02	3.74E-01	SAMD14	sterile alpha motif domain containing 14	chr17q21.33	213866_at	NM_174920
5.42	6.53	1.11	6.15E-02	3.74E-01	LOC727820	hypothetical protein LOC727820	chr1q21.1	227383_at	XR_041980
5.19	5.81	0.61	6.15E-02	3.74E-01	DPY19L4	dpy-19-like 4 (C. elegans)	chr8q22.1	213391_at	NM_181787
1.99	2.32	0.33	6.15E-02	3.74E-01	---	---	---	1569921_at	---
2.24	2.56	0.32	6.16E-02	3.74E-01	---	---	---	1562865_at	---
2.51	2.78	0.27	6.16E-02	3.74E-01	PCDHGA8	protocadherin gamma subfamily A, 8	chr5q31	210368_at	NM_014004 /// NM_032088
2.09	2.36	0.27	6.15E-02	3.74E-01	---	---	---	235651_at	---
1.86	2.06	0.20	6.15E-02	3.74E-01	ZC3HAV1L	zinc finger CCCH-type, antiviral 1-like	chr7q34	1553781_at	NM_080660
5.13	5.71	0.59	6.16E-02	3.74E-01	CREB1	cAMP responsive element binding protein 1	chr2q34	204314_s_at	NM_004379 /// NM_134442

5.83	6.30	0.47	6.16E-02	3.74E-01	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	chr12q24.13	226540_at	NM_001111322 /// NM_024072																					
2.56	2.87	0.31	6.17E-02	3.74E-01	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	chr12p13.3	208020_s_at	NM_000719 /// NM_001129827 /// NM_001129829 /// NM_001129830 /// NM_001129831 /// NM_001129832 /// NM_001129833 /// NM_001129834 /// NM_001129835 /// NM_001129836 /// NM_001129837 /// NM_001129838 /// NM_001129839 /// NM_001129840 /// NM_001129841 /// NM_001129842 /// NM_001129843 /// NM_001129844 /// NM_001129846 /// NM_199460																			
4.16	4.50	0.34	6.17E-02	3.74E-01	---	---	---	244332_at	---																					
5.72	6.07	0.35	6.17E-02	3.74E-01	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	chr18q23	208196_x_at	NM_006162 /// NM_172387 /// NM_172388 /// NM_172389 /// NM_172390																					
3.18	3.57	0.39	6.17E-02	3.74E-01	ZBTB38	zinc finger and BTB domain containing 38	chr3q23	230754_at	NM_001080412																					
4.95	5.32	0.37	6.18E-02	3.74E-01	PIGQ	phosphatidylinositol glycan anchor biosynthesis, class Q	chr16p13.3	204144_s_at	NM_004204 /// NM_148920																					
5.72	6.21	0.49	6.18E-02	3.75E-01	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	chrXq13.1-q21.1	208861_s_at	NM_000489 /// NM_138270																					
6.76	7.17	0.41	6.18E-02	3.75E-01	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	chr22q13.33	205050_s_at	NM_012324 /// NM_016431																					
2.72	3.16	0.44	6.19E-02	3.75E-01	SMA4	Glucuronidase, beta pseudogene	chr5q13	214850_at	---																					
6.59	7.02	0.43	6.19E-02	3.75E-01	LOC283335	hypothetical protein LOC283335	chr12q13.13	243285_at	---																					
1.94	2.20	0.25	6.19E-02	3.75E-01	RBAK	RB-associated KRAB zinc finger	chr7p22.1	1553122_s_at	NM_021163																					
2.22	2.46	0.25	6.19E-02	3.75E-01	---	---	---	237707_at	---																					
4.79	5.94	1.14	6.19E-02	3.75E-01	FILIP1L	filamin A interacting protein 1-like	chr3q12.1	1554966_a_at	NM_001042459 /// NM_014890 /// NM_182909																					
1.86	2.16	0.30	6.19E-02	3.75E-01	---	---	---	1556541_s_at	---																					
4.06	4.44	0.38	6.19E-02	3.75E-01	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	chr1p36.3	206800_at	NM_005957																					
2.20	2.55	0.35	6.19E-02	3.75E-01	LOC388564	Hypothetical gene supported by BC052596	chr19q13.42	229938_at	XM_498725 /// XM_938054																					
3.52	4.01	0.49	6.20E-02	3.75E-01	CASP10	caspase 10, apoptosis-related cysteine peptidase	chr2q33-q34	211888_x_at	NM_001230 /// NM_032974 /// NM_032977																					
2.16	2.47	0.31	6.20E-02	3.75E-01	IGF2BP1	Insulin-like growth factor 2 mRNA binding protein 1	chr17q21.32	241574_s_at	NM_006546																					
5.57	7.10	1.52	6.20E-02	3.75E-01	PDK4	pyruvate dehydrogenase kinase, isozyme 4	chr7q21.3	205960_at	NM_002612																					
2.95	3.38	0.43	6.21E-02	3.76E-01	---	---	---	1561056_a_at	---																					
3.78	4.35	0.58	6.21E-02	3.76E-01	---	---	---	1556527_a_at	---																					
4.18	4.51	0.33	6.21E-02	3.76E-01	---	---	---	234435_at	---																					
7.77	8.15	0.39	6.22E-02	3.76E-01	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	chr3q21-q22	212694_s_at	NM_000532																					
3.49	3.88	0.39	6.22E-02	3.76E-01	SBNO1	strawberry notch homolog 1 (Drosophila)	chr12q24.31	218737_at	NM_018183																					

1.75	2.00	0.26	6.22E-02	3.76E-01	TRPM1	transient receptor potential cation channel, subfamily M, member 1	chr15q13-q14	237070_at	NM_002420
1.69	1.91	0.22	6.22E-02	3.76E-01	MYLK3	myosin light chain kinase 3	chr16q11.2	1568926_x_at	NM_182493
5.51	5.86	0.35	6.22E-02	3.76E-01	DUX1	double homeobox, 1	chr10q26.3	208176_at	NM_012146
2.95	3.23	0.28	6.22E-02	3.76E-01	LOC100147773	hypothetical LOC100147773	---	240185_at	---
3.86	4.32	0.46	6.22E-02	3.76E-01	ZNF221	zinc finger protein 221	chr19q13.2	233848_x_at	NM_013359
2.43	2.80	0.37	6.22E-02	3.76E-01	---	---	---	243242_at	---
2.65	3.26	0.61	6.22E-02	3.76E-01	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	chr12q12	234268_at	NM_052885
4.40	5.21	0.81	6.23E-02	3.76E-01	AQR	aquarius homolog (mouse)	chr15q14	212583_at	NM_014691
5.55	5.89	0.34	6.23E-02	3.76E-01	EPHB2	EPH receptor B2	chr1p36.1-p35	210651_s_at	NM_004442 /// NM_017449
4.27	5.13	0.86	6.24E-02	3.76E-01	---	---	---	231281_at	---
3.96	4.80	0.84	6.24E-02	3.76E-01	SORBS2	sorbin and SH3 domain containing 2	chr4q35.1	220858_at	NM_003603 /// NM_021069
3.37	4.05	0.68	6.23E-02	3.76E-01	---	---	---	1559425_at	---
4.19	4.78	0.59	6.24E-02	3.76E-01	---	---	---	244358_at	---
2.96	3.45	0.49	6.25E-02	3.76E-01	ZNF85	zinc finger protein 85	chr19p13.1-p12	1554445_at	NM_003429
3.53	4.01	0.49	6.24E-02	3.76E-01	PCDHGA10	protocadherin gamma subfamily A, 10	chr5q31	211875_x_at	NM_018913 /// NM_032090
2.17	2.66	0.48	6.25E-02	3.76E-01	LOC100129762 /// PRUNE2	similar to KIAA0367 /// prune homolog 2 (Drosophila)	chr9q21.13	212806_at	NM_015225 /// NM_138818 /// XM_001715010 /// XM_001719626 /// XM_001719633 /// XM_001722398 /// XM_001722406
7.19	7.60	0.41	6.24E-02	3.76E-01	RABGAP1	RAB GTPase activating protein 1	chr9q33.2	204028_s_at	NM_012197
2.54	2.91	0.38	6.23E-02	3.76E-01	C11orf76	chromosome 11 open reading frame 76	chr11q13.3	224139_at	XR_041798 /// XR_041799 /// XR_041800
3.81	4.19	0.37	6.25E-02	3.76E-01	S100A5	S100 calcium binding protein A5	chr1q21	207763_at	NM_002962
2.69	3.06	0.37	6.23E-02	3.76E-01	---	---	---	234211_at	---
3.65	4.01	0.36	6.24E-02	3.76E-01	GPRIN1	G protein regulated inducer of neurite outgrowth 1	chr5q35.2	227975_at	NM_052899
3.57	3.91	0.34	6.24E-02	3.76E-01	FBLIM1	filamin binding LIM protein 1	chr1p36.21	1554795_a_at	NM_001024215 /// NM_001024216 /// NM_017556
5.44	5.77	0.34	6.24E-02	3.76E-01	LIN37	lin-37 homolog (C. elegans)	chr19q13.1	232534_at	NM_019104
5.43	5.76	0.33	6.23E-02	3.76E-01	PRB4 /// PRH1 /// PRH2	proline-rich protein BstNI subfamily 4 /// proline-rich protein HaeIII subfamily 1 /// proline-rich protein HaeIII subfamily 2	chr12p13.2	205272_s_at	NM_001110213 /// NM_002723 /// NM_005042 /// NM_006250
2.83	3.10	0.27	6.25E-02	3.76E-01	ITSN2	Intersectin 2	chr2pter-p25.1	240941_at	NM_006277 /// NM_019595 /// NM_147152
1.85	2.10	0.25	6.24E-02	3.76E-01	---	---	---	215643_at	---
3.36	3.70	0.34	6.25E-02	3.76E-01	ICAM5	intercellular adhesion molecule 5, telencephalin	chr19p13.2	206906_at	NM_003259
2.95	3.26	0.30	6.25E-02	3.76E-01	---	---	---	239152_at	---
4.82	5.25	0.44	6.25E-02	3.76E-01	ZNF273 /// ZNF493 /// ZNF738	zinc finger protein 273 /// zinc finger protein 493 /// zinc finger protein 738	chr19p12 /// chr7q11.21	240155_x_at	NM_001076678 /// NM_021148 /// NM_175910 /// NR_003099 /// XR_040185 /// XR_040186 /// XR_040187
2.26	2.56	0.30	6.25E-02	3.76E-01	COPB1	Coatomer protein complex, subunit beta 1	chr11p15.2	233308_at	NM_016451
2.45	2.74	0.29	6.25E-02	3.76E-01	C2orf73	chromosome 2 open reading frame 73	chr2p16.2	231081_at	NM_001100396
1.93	2.24	0.31	6.25E-02	3.76E-01	---	---	---	1569656_at	---
3.91	4.28	0.37	6.25E-02	3.76E-01	CCNB2	Cyclin B2	chr15q22.2	232764_at	NM_004701
2.38	2.71	0.32	6.26E-02	3.76E-01	KRT71	keratin 71	chr12q13.13	231461_at	NM_033448
3.09	3.41	0.32	6.26E-02	3.76E-01	METTL6	methyltransferase like 6	chr3p24.3	1553688_at	NM_152396
3.36	3.67	0.31	6.26E-02	3.76E-01	ZFHX3	Zinc finger homeobox 3	chr16q22.3-q23.1	243323_s_at	NM_006885
2.95	3.25	0.30	6.26E-02	3.76E-01	---	---	---	237782_at	---

2.20	2.52	0.31	6.27E-02	3.76E-01	HYDIN /// HYDIN2	hydrocephalus inducing homolog (mouse) /// hydrocephalus inducing homolog 2 (mouse)	chr16q22.1-q22.3 /// chr1q21.1	1554907_a_at	NM_017558 /// NM_032821 /// XM_001717859
3.43	3.92	0.50	6.27E-02	3.76E-01	LOC644450	hypothetical protein LOC644450	chr1q12	222347_at	XM_927590
2.14	2.43	0.30	6.27E-02	3.76E-01	SUGT1L1	SGT1, suppressor of G2 allele of SKP1 like 1 (S. cerevisiae)	chr13q14.11	240409_at	NR_003365
3.04	3.31	0.27	6.27E-02	3.76E-01	---	---	---	216567_at	---
5.35	5.94	0.59	6.27E-02	3.77E-01	PGR	progesterone receptor	chr11q22-q23	228554_at	NM_000926
3.66	3.96	0.30	6.27E-02	3.77E-01	CFC1	cripto, FRL-1, cryptic family 1	chr2q21.1	236724_at	NM_032545
6.45	6.88	0.43	6.28E-02	3.77E-01	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	chr14q24	202309_at	NM_005956
1.82	2.17	0.35	6.27E-02	3.77E-01	---	---	---	1558854_a_at	---
3.36	3.78	0.42	6.28E-02	3.77E-01	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	chr7p11	1569033_at	NM_006547
6.88	7.27	0.39	6.28E-02	3.77E-01	MEX3A	mex-3 homolog A (C. elegans)	chr1q22	236885_at	NM_001093725
3.18	3.44	0.26	6.28E-02	3.77E-01	---	---	---	234842_at	---
8.05	8.97	0.92	6.28E-02	3.77E-01	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	chr11p11.2	217869_at	NM_016142
5.91	6.33	0.42	6.28E-02	3.77E-01	FBXL5	F-box and leucine-rich repeat protein 5	chr4p15.33	209005_at	NM_012161 /// NM_033535
3.65	4.58	0.93	6.28E-02	3.77E-01	---	---	---	243908_at	---
2.10	2.44	0.34	6.28E-02	3.77E-01	---	---	---	231608_at	---
2.41	2.71	0.30	6.28E-02	3.77E-01	---	---	---	233450_at	---
6.74	7.46	0.72	6.29E-02	3.77E-01	BTN3A2	butyrophilin, subfamily 3, member A2	chr6p22.1	209846_s_at	NM_007047
2.87	3.17	0.30	6.29E-02	3.77E-01	NAV2	neuron navigator 2	chr11p15.1	218330_s_at	NM_001111018 /// NM_001111019 /// NM_145117 /// NM_182964
2.23	2.58	0.35	6.29E-02	3.77E-01	---	---	---	242094_at	---
3.23	3.67	0.44	6.29E-02	3.77E-01	---	---	---	1570335_at	---
1.95	2.20	0.26	6.29E-02	3.77E-01	TMCO5A	transmembrane and coiled-coil domains 5A	chr15q14	1553636_at	NM_152453
2.40	2.66	0.26	6.29E-02	3.77E-01	GYPE	glycophorin E	chr4q31.1	207854_at	NM_002102 /// NM_198682
3.11	3.51	0.40	6.30E-02	3.77E-01	C17orf80	chromosome 17 open reading frame 80	chr17q25.1	223352_s_at	NM_001100621 /// NM_001100622 /// NM_017941
2.02	2.28	0.26	6.29E-02	3.77E-01	KLHL9	kelch-like 9 (Drosophila)	chr9p22	237123_x_at	NM_018847
2.17	2.38	0.21	6.30E-02	3.77E-01	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	chr2q14.3	234167_at	NM_032390
9.04	9.73	0.68	6.30E-02	3.77E-01	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	chr15q22.2	222405_at	NM_016395
6.33	6.75	0.42	6.30E-02	3.77E-01	AMN	amnionless homolog (mouse)	chr14q32.3	220989_s_at	NM_030943
4.42	4.91	0.49	6.30E-02	3.77E-01	RBP5	retinol binding protein 5, cellular	chr12p13.31	223820_at	NM_031491
3.79	4.26	0.48	6.30E-02	3.77E-01	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	chr11q13	230374_at	NM_138689
1.84	2.07	0.23	6.31E-02	3.77E-01	---	---	---	1565742_at	---
2.66	3.53	0.87	6.31E-02	3.77E-01	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	chr17q24.2	207038_at	NM_004694
4.87	5.53	0.66	6.31E-02	3.77E-01	GSPT2	G1 to S phase transition 2	chrXp11.22	205541_s_at	NM_018094
2.24	2.87	0.63	6.31E-02	3.77E-01	PRUNE2	prune homolog 2 (Drosophila)	chr9q21.13	1552455_at	NM_015225 /// NM_138818
4.73	5.33	0.60	6.31E-02	3.77E-01	RHOQ	ras homolog gene family, member Q	chr2p21	214449_s_at	NM_012249
3.10	3.41	0.31	6.31E-02	3.77E-01	SOAT2	sterol O-acyltransferase 2	chr12q13.13	210677_at	NM_003578
2.59	2.88	0.28	6.31E-02	3.77E-01	STXBP4	Syntaxin binding protein 4	chr17q22	237706_at	NM_178509
4.15	4.56	0.41	6.32E-02	3.78E-01	CHST13	Carbohydrate (chondroitin 4) sulfotransferase 13	chr3q21.3	242503_at	NM_152889
2.43	2.84	0.41	6.32E-02	3.78E-01	TTC30B	tetratricopeptide repeat domain 30B	chr2q31.2	1554588_a_at	NM_152517
2.04	2.25	0.21	6.32E-02	3.78E-01	LOC100129335 /// LOC100134495	hypothetical protein LOC100129335 /// hypothetical protein LOC100134495	chr7p21.1	244079_at	XM_001715578 /// XM_001716919 /// XM_001717229 /// XM_001718009
4.78	5.67	0.89	6.32E-02	3.78E-01	PHKB	phosphorylase kinase, beta	chr16q12-q13	202739_s_at	NM_000293 /// NM_001031835
2.30	2.53	0.23	6.33E-02	3.78E-01	---	---	---	236919_at	---
3.94	4.32	0.38	6.33E-02	3.78E-01	CNIH4	cornichon homolog 4 (Drosophila)	chr1q42.11	228437_at	NM_014184
4.07	4.38	0.30	6.33E-02	3.78E-01	ZNF323	zinc finger protein 323	chr6p21.31|6p22.3 p22.1	222016_s_at	NM_030899 /// NM_145909
2.35	2.58	0.22	6.33E-02	3.78E-01	ONECUT1	one cut homeobox 1	chr15q21.1-q21.2	210745_at	NM_004498
2.35	3.01	0.65	6.34E-02	3.78E-01	TDO2	tryptophan 2,3-dioxygenase	chr4q31-q32	205943_at	NM_005651
1.98	2.23	0.25	6.34E-02	3.78E-01	C6orf112	chromosome 6 open reading frame 112	chr6q21	232492_at	---
6.46	6.82	0.37	6.34E-02	3.78E-01	TBKBP1	TBK1 binding protein 1	chr17q21.32	205424_at	NM_014726

11.83	12.14	0.32	6.34E-02	3.78E-01	---	---	---	AFFX-r2-P1-cre-5_at	---
1.96	2.24	0.27	6.34E-02	3.78E-01	---	---	---	241287_x_at	---
2.20	2.45	0.25	6.34E-02	3.78E-01	---	---	---	1561786_at	---
1.95	2.16	0.21	6.34E-02	3.78E-01	---	---	---	236733_at	---
3.68	4.24	0.56	6.34E-02	3.78E-01	SVIP	small VCP/p97-interacting protein	chr11p14.2	230285_at	NM_148893
4.28	5.12	0.84	6.35E-02	3.78E-01	TRIM2	tripartite motif-containing 2	chr4q31.3	202341_s_at	NM_001130067 /// NM_015271
2.84	3.25	0.41	6.35E-02	3.78E-01	---	---	---	1562885_at	---
5.52	5.99	0.47	6.36E-02	3.79E-01	---	---	---	237534_at	---
4.91	5.29	0.39	6.36E-02	3.79E-01	---	---	---	230853_at	---
2.85	3.09	0.23	6.36E-02	3.79E-01	---	---	---	228682_at	---
3.67	4.02	0.35	6.36E-02	3.79E-01	CDX2	caudal type homeobox 2	chr13q12.3	206387_at	NM_001265
2.55	2.87	0.32	6.37E-02	3.79E-01	LOC389328	hypothetical LOC389328	chr5q31.1	236444_x_at	XM_374137 /// XM_943867
2.21	2.50	0.28	6.37E-02	3.79E-01	---	---	---	234184_at	---
3.10	3.37	0.27	6.36E-02	3.79E-01	---	---	---	239215_at	---
10.20	10.58	0.38	6.37E-02	3.79E-01	CST2 /// CST3	cystatin SA /// cystatin C	chr20p11.21	201360_at	NM_000099 /// NM_001322
7.35	8.37	1.03	6.37E-02	3.79E-01	GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide	chr9q21	202615_at	NM_002072
4.34	4.80	0.46	6.37E-02	3.79E-01	RBPMS2	RNA binding protein with multiple splicing 2	chr15q22.31	228802_at	NM_194272
3.87	4.24	0.37	6.38E-02	3.79E-01	RGS14	regulator of G-protein signaling 14	chr5q35.3	211021_s_at	NM_006480
7.19	8.56	1.37	6.38E-02	3.79E-01	TTC3	tetratricopeptide repeat domain 3	chr21q22.2	208662_s_at	NM_001001894 /// NM_003316
2.41	2.75	0.34	6.38E-02	3.79E-01	---	---	---	242132_x_at	---
3.03	3.34	0.31	6.38E-02	3.79E-01	LOC259308	hypothetical LOC259308	chr9p12	243270_at	XR_041842 /// XR_041843
4.08	4.71	0.63	6.39E-02	3.79E-01	RTN4IP1	reticulon 4 interacting protein 1	chr6q21	224509_s_at	NM_032730
1.78	2.00	0.22	6.39E-02	3.79E-01	---	---	---	234358_at	---
2.07	2.30	0.23	6.39E-02	3.79E-01	---	---	---	1561431_at	---
6.56	7.30	0.74	6.39E-02	3.79E-01	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	chr13q14.3	208885_at	NM_002298
9.78	10.40	0.62	6.39E-02	3.79E-01	SCARB1	scavenger receptor class B, member 1	chr12q24.31	201819_at	NM_001082959 /// NM_005505
5.97	6.44	0.47	6.39E-02	3.79E-01	MED7	mediator complex subunit 7	chr5q33.3	204350_s_at	NM_001100816 /// NM_004270
2.18	2.56	0.38	6.40E-02	3.80E-01	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	chr1p13.3	215014_at	NM_004980 /// NM_172198
2.86	3.18	0.32	6.40E-02	3.80E-01	---	---	---	215360_at	---
6.58	7.84	1.25	6.40E-02	3.80E-01	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	chr7q21.2-q21.3|7q21.2	202314_at	NM_000786
2.89	3.15	0.26	6.40E-02	3.80E-01	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16q22-q23	238925_at	NM_006750
4.96	5.29	0.33	6.40E-02	3.80E-01	SMO	smoothened homolog (Drosophila)	chr7q32.3	218629_at	NM_005631
3.97	4.69	0.72	6.41E-02	3.80E-01	LPGAT1	lysophosphatidylglycerol acyltransferase 1	chr1q32	1555058_a_at	NM_014873
6.03	6.39	0.35	6.41E-02	3.80E-01	---	---	---	233296_x_at	---
6.45	7.53	1.08	6.42E-02	3.80E-01	RC3H2	ring finger and CCCH-type zinc finger domains 2	chr9q34	231716_at	NM_001100588 /// NM_018835
8.03	9.00	0.96	6.42E-02	3.80E-01	TROVE2	TROVE domain family, member 2	chr1q31	212852_s_at	NM_001042369 /// NM_001042370 /// NM_004600
3.21	3.70	0.50	6.42E-02	3.80E-01	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)	chr6q21-q22	219915_s_at	NM_018593
2.62	2.97	0.35	6.42E-02	3.80E-01	LOC100129386	hypothetical protein LOC100129386	chr11p15.4	238216_at	XM_001715291 /// XM_001716175 /// XM_001716751
1.88	2.09	0.21	6.41E-02	3.80E-01	---	---	---	224214_at	---
6.94	7.78	0.85	6.42E-02	3.80E-01	MED13	mediator complex subunit 13	chr17q22-q23	201986_at	NM_005121
9.64	10.14	0.49	6.42E-02	3.80E-01	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	chr20q13.1	217718_s_at	NM_003404 /// NM_139323
3.78	4.01	0.23	6.42E-02	3.80E-01	---	---	---	243763_x_at	---
2.69	2.97	0.28	6.43E-02	3.80E-01	FBN1	fibrillin 1	chr15q21.1	235318_at	NM_000138
2.64	2.93	0.30	6.43E-02	3.80E-01	---	---	---	243590_at	---
2.90	3.47	0.57	6.43E-02	3.80E-01	---	---	---	236237_at	---
3.33	3.72	0.38	6.44E-02	3.81E-01	---	---	---	234095_at	---
2.02	2.23	0.21	6.44E-02	3.81E-01	---	---	---	1569231_x_at	---
2.63	3.03	0.40	6.44E-02	3.81E-01	SLC9A2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	chr2q11.2	211116_at	NM_003048

2.68	3.00	0.32	6.44E-02	3.81E-01	---	---	---	244100_at	---
2.03	2.27	0.24	6.44E-02	3.81E-01	KIAA0506	hypothetical LOC57239	---	214897_at	---
7.22	7.67	0.45	6.45E-02	3.81E-01	RPP25	ribonuclease P/MRP 25kDa subunit	chr15q24.1	223415_at	NM_017793
2.69	3.13	0.44	6.45E-02	3.81E-01	---	---	---	228732_at	---
6.08	6.41	0.33	6.45E-02	3.81E-01	GRRP1	glycine/arginine rich protein 1	chr1p36.11	220430_at	NM_024869
2.59	2.88	0.29	6.45E-02	3.81E-01	TMEM182	transmembrane protein 182	chr2q12.1	238578_at	NM_144632
4.93	5.26	0.33	6.45E-02	3.81E-01	HRH2	histamine receptor H2	chr5q35.2	220805_at	NM_001131055 /// NM_022304
4.11	4.88	0.77	6.46E-02	3.81E-01	AQP2	aquaporin 2 (collecting duct)	chr12q12-q13	206672_at	NM_000486
4.19	4.61	0.42	6.46E-02	3.81E-01	---	---	---	233596_at	---
8.14	8.80	0.66	6.46E-02	3.81E-01	ATL3	atlastin 3	chr11q13.1	224893_at	NM_015459
3.96	4.36	0.40	6.46E-02	3.81E-01	ACSM5	acyl-CoA synthetase medium-chain family member 5	chr16p12.3	89977_at	NM_017888
5.74	6.52	0.78	6.46E-02	3.81E-01	FEM1B	fem-1 homolog b (C. elegans)	chr15q22	212367_at	NM_015322
3.62	4.10	0.48	6.47E-02	3.81E-01	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	chr19p13.3	220182_at	NM_024103
3.58	4.29	0.71	6.48E-02	3.81E-01	CEP63	centrosomal protein 63kDa	chr3q22.1-q22.2	222151_s_at	NM_001042383 /// NM_001042384 /// NM_001042400 /// NM_025180
6.59	7.28	0.68	6.48E-02	3.81E-01	PLSCR4	phospholipid scramblase 4	chr3q24	218901_at	NM_001128304 /// NM_001128305 /// NM_001128306 /// NM_020353
3.73	4.23	0.50	6.49E-02	3.81E-01	---	---	---	238761_at	---
2.49	2.97	0.48	6.48E-02	3.81E-01	---	---	---	231502_at	---
2.84	3.30	0.46	6.48E-02	3.81E-01	C1orf135	chromosome 1 open reading frame 135	chr1p36.11	220011_at	NM_024037
6.37	6.82	0.45	6.47E-02	3.81E-01	UBTF	Upstream binding transcription factor, RNA polymerase I	chr17q21.3	239920_at	NM_001076683 /// NM_001076684 /// NM_014233
6.26	6.69	0.42	6.48E-02	3.81E-01	PIAS1	protein inhibitor of activated STAT, 1	chr15q	217864_s_at	NM_016166
3.28	3.69	0.41	6.48E-02	3.81E-01	---	---	---	237464_at	---
3.76	4.16	0.39	6.48E-02	3.81E-01	GPRC5B	G protein-coupled receptor, family C, group 5, member B	chr16p12	203631_s_at	NM_016235
3.93	4.31	0.38	6.47E-02	3.81E-01	ZEB1	zinc finger E-box binding homeobox 1	chr10p11.2	212758_s_at	NM_001128128 /// NM_030751
5.97	6.35	0.38	6.48E-02	3.81E-01	RIN1	Ras and Rab interactor 1	chr11q13.1	205211_s_at	NM_004292
4.74	5.11	0.37	6.48E-02	3.81E-01	---	---	---	240849_at	---
2.37	2.71	0.34	6.48E-02	3.81E-01	LOC100131813	similar to hCG2041218	chr8q22.3	230939_at	XM_001717557 /// XM_001717574 /// XM_001717690
2.81	3.14	0.33	6.47E-02	3.81E-01	SCN4A	sodium channel, voltage-gated, type IV, alpha subunit	chr17q23-q25.3	206981_at	NM_000334
4.01	4.33	0.31	6.48E-02	3.81E-01	---	---	---	238643_at	---
3.12	3.38	0.26	6.47E-02	3.81E-01	LOC541469	hypothetical protein LOC541469	chr19q13.2	220207_at	XR_039882 /// XR_039883 /// XR_039884
2.34	2.59	0.25	6.48E-02	3.81E-01	LOC339316	hypothetical protein LOC339316	chr19q12	242084_at	---
2.39	2.63	0.24	6.48E-02	3.81E-01	NRG2	neuregulin 2	chr5q23-q33	208062_s_at	NM_004883 /// NM_013981 /// NM_013982 /// NM_013983
1.77	1.98	0.21	6.47E-02	3.81E-01	---	---	---	1569661_at	---
2.82	3.12	0.30	6.49E-02	3.81E-01	G6PC2	glucose-6-phosphatase, catalytic, 2	chr2q24.3	221453_at	NM_001081686 /// NM_021176
5.01	5.97	0.95	6.49E-02	3.82E-01	MBNL1	Muscleblind-like (Drosophila)	chr3q25	235879_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297
2.81	3.17	0.35	6.49E-02	3.82E-01	---	---	---	215149_at	---
2.15	2.48	0.32	6.49E-02	3.82E-01	---	---	---	237050_at	---
2.42	2.67	0.25	6.50E-02	3.82E-01	CD244	CD244 molecule, natural killer cell receptor 2B4	chr1q23.3	234320_at	NM_016382

1.79	2.05	0.26	6.50E-02	3.82E-01	---	---	---	1561123_at	---
3.27	3.86	0.58	6.50E-02	3.82E-01	SMC2	structural maintenance of chromosomes 2	chr9q31.1	204240_s_at	NM_001042550 /// NM_001042551 /// NM_006444
3.46	3.80	0.35	6.50E-02	3.82E-01	---	---	---	1560680_at	---
3.52	4.34	0.82	6.51E-02	3.82E-01	---	---	---	242008_at	---
2.62	2.96	0.34	6.51E-02	3.82E-01	PSG5	pregnancy specific beta-1-glycoprotein 5	chr19q13.2	204830_x_at	NM_001130014 /// NM_002781
1.97	2.25	0.28	6.51E-02	3.82E-01	NKX2-3	NK2 transcription factor related, locus 3 (Drosophila)	chr10q24.2	1553808_a_at	NM_145285
8.66	9.29	0.63	6.51E-02	3.82E-01	FTH1	ferritin, heavy polypeptide 1	chr11q13	214211_at	NM_002032
2.03	2.31	0.28	6.51E-02	3.82E-01	---	---	---	215473_at	---
4.84	5.87	1.03	6.52E-02	3.82E-01	THOC2	THO complex 2	chrXq25-q26.3	222122_s_at	NM_001081550 /// NM_020449
3.73	4.19	0.46	6.51E-02	3.82E-01	LOC100134361	similar to hCG1811002	---	229930_at	XM_001726827
1.95	2.28	0.32	6.52E-02	3.82E-01	ALOX15	arachidonate 15-lipoxygenase	chr17p13.3	207328_at	NM_001140
2.36	2.65	0.30	6.52E-02	3.82E-01	---	---	---	242076_at	---
2.41	2.63	0.21	6.52E-02	3.82E-01	DOK7	docking protein 7	chr4p16.2	240633_at	NM_173660
8.85	9.23	0.38	6.52E-02	3.82E-01	PDIA3	protein disulfide isomerase family A, member 3	chr15q15	208612_at	NM_005313
4.77	6.10	1.33	6.52E-02	3.82E-01	ZNF271	zinc finger protein 271	chr18q12	211009_s_at	NM_001112663 /// NM_006629
3.51	4.61	1.10	6.53E-02	3.82E-01	SLC16A14	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	chr2q36.3	238029_s_at	NM_152527
4.84	5.58	0.74	6.53E-02	3.82E-01	CYFIP2	cytoplasmic FMR1 interacting protein 2	chr5q33.3	220999_s_at	NM_001037332 /// NM_001037333 /// NM_014376
4.77	5.13	0.36	6.52E-02	3.82E-01	DIAPH1	diaphanous homolog 1 (Drosophila)	chr5q31	215541_s_at	NM_001079812 /// NM_005219
2.07	2.36	0.29	6.53E-02	3.82E-01	SCLT1	sodium channel and clathrin linker 1	chr4q28.2	236487_at	NM_144643
2.43	2.67	0.25	6.53E-02	3.82E-01	C9orf27	Chromosome 9 open reading frame 27	chr9q31.3	1570345_at	NM_021208 /// NR_024032
6.43	7.26	0.83	6.53E-02	3.82E-01	FOXP1	forkhead box P1	chr3p14.1	224837_at	NM_001012505 /// NM_032682
9.55	10.21	0.66	6.54E-02	3.82E-01	TM7SF2	transmembrane 7 superfamily member 2	chr11q13	210130_s_at	NM_003273
3.22	3.65	0.42	6.54E-02	3.82E-01	KIAA1324L	KIAA1324-like	chr7q21.12	235301_at	NM_152748
4.87	5.21	0.35	6.54E-02	3.82E-01	CES4	carboxylesterase 4-like	chr16q12.2	206824_at	NR_003276
2.69	3.01	0.31	6.54E-02	3.82E-01	IL5RA	interleukin 5 receptor, alpha	chr3p26-p24	207902_at	NM_000564 /// NM_175724 /// NM_175725 /// NM_175726 /// NM_175727 /// NM_175728
2.54	2.83	0.29	6.54E-02	3.82E-01	DUOXA1	dual oxidase maturation factor 1	chr15q21.1	1554648_a_at	NM_144565
1.74	2.02	0.28	6.54E-02	3.82E-01	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	chr10p11.23	238778_at	NM_173496
2.32	2.57	0.25	6.54E-02	3.82E-01	---	---	---	237429_at	---
4.60	5.04	0.44	6.55E-02	3.82E-01	HEATR5A	HEAT repeat containing 5A	chr14q12	226510_at	NM_015473
7.09	7.40	0.30	6.55E-02	3.83E-01	PPP2R5B	protein phosphatase 2, regulatory subunit B', beta isoform	chr11q12-q13	204611_s_at	NM_006244
3.60	3.85	0.26	6.55E-02	3.83E-01	ARHGDIG	Rho GDP dissociation inhibitor (GDI) gamma	chr16p13.3	206888_s_at	NM_001176
2.53	2.96	0.44	6.56E-02	3.83E-01	---	---	---	1567997_x_at	---
2.45	2.73	0.29	6.56E-02	3.83E-01	---	---	---	231217_at	---
3.93	4.31	0.38	6.56E-02	3.83E-01	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	chrXq28	215911_x_at	NM_001001344 /// NM_021949
2.25	2.68	0.43	6.57E-02	3.83E-01	---	---	---	1569180_at	---
3.05	3.45	0.40	6.56E-02	3.83E-01	---	---	---	214309_s_at	---
3.69	3.98	0.29	6.57E-02	3.83E-01	---	---	---	235448_at	---
2.60	2.92	0.31	6.58E-02	3.84E-01	---	---	---	1562187_at	---
3.57	4.11	0.54	6.58E-02	3.84E-01	EWSR1 /// FLI1	Ewing sarcoma breakpoint region 1 /// Friend leukemia virus integration 1	chr11q24.1-q24.3 /// chr22q12.2	211825_s_at	NM_002017 /// NM_005243 /// NM_013986
7.80	8.20	0.40	6.58E-02	3.84E-01	OAF	OAF homolog (Drosophila)	chr11q23.3	225510_at	NM_178507
4.12	4.53	0.41	6.58E-02	3.84E-01	---	---	---	241561_at	---
4.47	5.50	1.03	6.59E-02	3.84E-01	---	---	---	232095_at	---
4.35	4.94	0.60	6.58E-02	3.84E-01	---	---	---	241472_at	---
3.07	3.45	0.38	6.58E-02	3.84E-01	FLJ13197	hypothetical FLJ13197	chr4p14	1570414_x_at	XR_040784 /// XR_040785 /// XR_040786
2.63	3.00	0.37	6.59E-02	3.84E-01	TNNI3	troponin I type 3 (cardiac)	chr19q13.4	205742_at	NM_000363

2.43	2.81	0.38	6.59E-02	3.84E-01	LOC254559	hypothetical LOC254559	chr15q26.1	238603_at	XM_943723
4.98	5.71	0.74	6.59E-02	3.84E-01	PUS3	pseudouridylate synthase 3	chr11q24.2	221277_s_at	NM_031307
5.83	6.97	1.14	6.59E-02	3.84E-01	BAT2D1	BAT2 domain containing 1	chr1q23.3	214055_x_at	NM_015172
1.95	2.17	0.22	6.59E-02	3.84E-01	RBAK	RB-associated KRAB zinc finger	chr7p22.1	241366_at	NM_021163
4.15	4.66	0.51	6.60E-02	3.84E-01	FBXO10	F-box protein 10	chr9p13.2	227222_at	NM_012166
4.37	4.76	0.39	6.60E-02	3.84E-01	---	---	---	241114_s_at	---
2.90	3.25	0.36	6.61E-02	3.84E-01	MDM2	Mdm2 p53 binding protein homolog (mouse)	chr12q14.3-q15	205385_at	NM_002392 /// NM_006878 /// NM_006879 /// NM_006881 /// NM_006882
4.11	4.45	0.34	6.61E-02	3.84E-01	CSNK1G1	casein kinase 1, gamma 1	chr15q22.1-q22.31	231920_s_at	NM_022048
2.92	3.25	0.33	6.60E-02	3.84E-01	MAP3K2	mitogen-activated protein kinase kinase kinase 2	chr2q14.3	235254_at	NM_006609
3.56	3.89	0.33	6.60E-02	3.84E-01	---	---	---	236567_at	---
2.82	3.15	0.32	6.61E-02	3.84E-01	ZNF681	zinc finger protein 681	chr19p12	236672_at	NM_138286
2.37	2.69	0.32	6.61E-02	3.84E-01	NANOS2	nanos homolog 2 (Drosophila)	chr19q13.32	1557767_at	NM_001029861
4.07	4.39	0.32	6.60E-02	3.84E-01	TMEM92	Transmembrane protein 92	chr17q21.33	216791_at	NM_153229
4.32	4.63	0.31	6.60E-02	3.84E-01	LOC138652	similar to hCG31140	chr9q22.31	234696_at	XM_001721508 /// XM_001722265 /// XM_001723775
2.14	2.37	0.23	6.60E-02	3.84E-01	---	---	---	243578_at	---
2.91	3.15	0.25	6.61E-02	3.84E-01	---	---	---	243101_x_at	---
3.11	3.47	0.36	6.62E-02	3.84E-01	LDHC	lactate dehydrogenase C	chr11p15.5-p15.3	207022_s_at	NM_002301 /// NM_017448
6.29	6.62	0.34	6.62E-02	3.84E-01	NOTUM	notum pectinacetylesterase homolog (Drosophila)	chr17q25.3	228649_at	NM_178493
4.78	5.08	0.30	6.62E-02	3.84E-01	ALX3	aristaless-like homeobox 3	chr1p13.3	207690_at	NM_006492
2.18	2.42	0.24	6.62E-02	3.84E-01	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	chr3q28-q29	220043_s_at	NM_005929 /// NM_033316
4.45	4.75	0.30	6.63E-02	3.84E-01	TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)	chr16p13	205688_at	NM_003223
5.44	5.81	0.37	6.63E-02	3.84E-01	---	---	---	229583_at	---
3.34	3.58	0.24	6.63E-02	3.84E-01	---	---	---	244156_at	---
6.39	7.06	0.66	6.63E-02	3.85E-01	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	chr11p15.5	211217_s_at	NM_000218 /// NM_181798
3.63	3.94	0.31	6.63E-02	3.85E-01	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	chr16p13.3	216139_s_at	NM_001040439 /// NM_015133
1.97	2.17	0.20	6.63E-02	3.85E-01	---	---	---	234566_at	---
10.62	11.36	0.74	6.64E-02	3.85E-01	HSPA8	heat shock 70kDa protein 8	chr11q24.1	224187_x_at	NM_006597 /// NM_153201
6.82	7.55	0.73	6.64E-02	3.85E-01	DNER	delta/notch-like EGF repeat containing	chr2q36.3	226281_at	NM_139072
2.36	2.96	0.60	6.64E-02	3.85E-01	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	chr21q21.3	219935_at	NM_007038
4.48	4.91	0.43	6.64E-02	3.85E-01	NFASC	neurofascin homolog (chicken)	chr1q32.1	230242_at	NM_015090
3.54	3.94	0.40	6.64E-02	3.85E-01	ONECUT2	one cut homeobox 2	chr18q21.1-q21.2	230271_at	NM_004852
6.92	7.32	0.39	6.64E-02	3.85E-01	PI16	peptidase inhibitor 16	chr6p21.2	228312_at	NM_153370
2.71	3.09	0.38	6.64E-02	3.85E-01	DYNC1LI2	Dynein, cytoplasmic 1, light intermediate chain 2	chr16q22.1	213162_at	NM_006141
5.37	5.73	0.36	6.64E-02	3.85E-01	PNMA3	paraneoplastic antigen MA3	chrXq28	220923_s_at	NM_013364
2.91	3.18	0.28	6.64E-02	3.85E-01	---	---	---	1566210_at	---
2.05	2.27	0.21	6.64E-02	3.85E-01	---	---	---	1559434_at	---
6.22	6.77	0.55	6.65E-02	3.85E-01	---	---	---	241359_at	---
3.73	4.15	0.42	6.65E-02	3.85E-01	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	chr17q23-q24	242482_at	NM_002734 /// NM_212471 /// NM_212472
2.69	3.10	0.41	6.65E-02	3.85E-01	---	---	---	238151_at	---
3.85	4.25	0.40	6.65E-02	3.85E-01	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	chr12q12-q13	213706_at	NM_005276
6.87	7.25	0.38	6.65E-02	3.85E-01	UBE2J2	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	chr1p36.33	226704_at	NM_058167 /// NM_194315 /// NM_194457 /// NM_194458
2.59	2.88	0.29	6.65E-02	3.85E-01	PLA2G3	phospholipase A2, group III	chr22q11.2-q13.2	220780_at	NM_015715
2.44	2.73	0.28	6.65E-02	3.85E-01	VSTM3	V-set and transmembrane domain containing 3	chr3q13.31	240070_at	NM_173799
3.02	3.32	0.30	6.65E-02	3.85E-01	---	---	---	229788_s_at	---
6.21	7.36	1.15	6.66E-02	3.85E-01	BBX	bobby sox homolog (Drosophila)	chr3q13.1	223135_s_at	NM_020235
6.54	6.80	0.26	6.66E-02	3.85E-01	NOL5A	nucleolar protein 5A (56kDa with KKE/D repeat)	chr20p13	200874_s_at	NM_006392
2.11	2.46	0.35	6.66E-02	3.85E-01	MYLK3	myosin light chain kinase 3	chr16q11.2	238834_at	NM_182493
3.60	3.89	0.28	6.67E-02	3.85E-01	INTS4	integrator complex subunit 4	chr11q14.1	233193_x_at	NM_033547

2.95	3.25	0.31	6.69E-02	3.86E-01	ATP2A3	ATPase, Ca++ transporting, ubiquitous	chr17p13.3	230453_s_at	NM_005173 /// NM_174953 /// NM_174954 /// NM_174955 /// NM_174956 /// NM_174957 /// NM_174958																					
3.23	3.53	0.30	6.69E-02	3.86E-01	41337	membrane-associated ring finger (C3HC4) 4	chr2q35	230112_at	NM_020814																					
2.07	2.32	0.26	6.69E-02	3.86E-01	---	---	---	1568897_at	---																					
6.64	7.88	1.25	6.69E-02	3.86E-01	COL6A2	collagen, type VI, alpha 2	chr21q22.3	209156_s_at	NM_001849 /// NM_058174 /// NM_058175																					
4.81	5.18	0.37	6.70E-02	3.86E-01	UNQ6487	LMNE6487	chr3p25.1	243523_at	XM_001721106 /// XM_001722119 /// XM_001726329																					
9.80	10.01	0.21	6.70E-02	3.86E-01	TEGT	testis enhanced gene transcript	chr12q12-q13	200804_at	NM_001098576 /// NM_003217																					
5.13	5.83	0.70	6.71E-02	3.86E-01	MOCS1	molybdenum cofactor synthesis 1	chr6p21.3	213181_s_at	NM_001075098 /// NM_005942 /// NM_005943 /// NM_138928																					
3.56	3.95	0.39	6.71E-02	3.86E-01	MAST2	microtubule associated serine/threonine kinase 2	chr1p34.1	215660_s_at	NM_015112																					
4.03	4.44	0.41	6.71E-02	3.86E-01	EFNB3	ephrin-B3	chr17p13.1-p11.2	210883_x_at	NM_001406																					
2.84	3.23	0.39	6.71E-02	3.86E-01	LOC727869	hypothetical LOC727869	chr11q22.2	239241_at	XM_001126620 /// XM_001128267 /// XM_001726061																					
2.46	2.65	0.19	6.71E-02	3.86E-01	---	---	---	1562098_at	---																					
3.33	3.73	0.40	6.72E-02	3.86E-01	SLC22A12	solute carrier family 22 (organic anion/urate transporter), member 12	chr11q13.1	237799_at	NM_144585 /// NM_153378																					
3.81	5.11	1.30	6.73E-02	3.87E-01	BEX1	brain expressed, X-linked 1	chrXq21-q23|Xq22	218332_at	NM_018476																					
5.44	5.84	0.40	6.73E-02	3.87E-01	TRPS1	trichorhinophalangeal syndrome I	chr8q24.12	218502_s_at	NM_014112																					
5.02	5.39	0.37	6.73E-02	3.87E-01	MYH14	myosin, heavy chain 14	chr19q13.33	217545_at	NM_001077186 /// NM_024729																					
2.92	3.18	0.26	6.73E-02	3.87E-01	WNT2	wingless-type MMTV integration site family member 2	chr7q31.2	205648_at	NM_003391 /// NR_024047																					
2.15	2.40	0.25	6.72E-02	3.87E-01	LOC646241	Hypothetical protein LOC646241	chr5p15.1	1561027_at	XM_933487																					
9.86	10.39	0.53	6.74E-02	3.87E-01	CANX	calnexin	chr5q35	200068_s_at	NM_001024649 /// NM_001746																					
2.59	3.01	0.42	6.74E-02	3.87E-01	---	---	---	232589_at	---																					
4.15	4.53	0.38	6.73E-02	3.87E-01	---	---	---	236516_at	---																					
2.74	3.08	0.33	6.74E-02	3.87E-01	FOXH1	forkhead box H1	chr8q24.3	207644_at	NM_003923																					
4.06	4.39	0.32	6.74E-02	3.87E-01	THRAP3	thyroid hormone receptor associated protein 3	chr1p34.3	222439_s_at	NM_005119																					
2.50	2.78	0.28	6.74E-02	3.87E-01	---	---	---	219721_at	---																					
2.10	2.37	0.27	6.74E-02	3.87E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	234390_x_at	---																					
2.02	2.25	0.24	6.73E-02	3.87E-01	DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	chr22q13.1	208382_s_at	NM_007068																					
3.85	4.25	0.40	6.75E-02	3.87E-01	---	---	---	237154_at	---																					
2.28	2.57	0.29	6.74E-02	3.87E-01	---	---	---	216147_at	---																					
1.83	2.05	0.22	6.75E-02	3.87E-01	---	---	---	240548_at	---																					
3.46	4.47	1.01	6.75E-02	3.87E-01	---	---	---	217179_x_at	---																					
4.81	5.67	0.86	6.76E-02	3.87E-01	---	---	---	239597_at	---																					
5.11	5.78	0.68	6.75E-02	3.87E-01	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	chr5q11	204863_s_at	NM_002184 /// NM_175767																					
6.29	6.72	0.43	6.76E-02	3.87E-01	ZDHHC24	zinc finger, DHHC-type containing 24	chr11q13.1	227549_x_at	NM_207340																					
3.94	4.35	0.41	6.76E-02	3.87E-01	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2	chr9q34	230430_at	NM_001246 /// NM_203468																					
3.73	4.07	0.34	6.76E-02	3.87E-01	---	---	---	243944_at	---																					
4.39	4.71	0.32	6.76E-02	3.87E-01	PLAC9	placenta-specific 9	chr10q22.3	230246_at	NM_001012973																					
7.16	7.44	0.27	6.76E-02	3.87E-01	MRPL51 /// SPTLC1	mitochondrial ribosomal protein L51 /// serine palmitoyltransferase, long chain base subunit 1	chr12p13.3-p13.1 /// chr9q22.2	224334_s_at	NM_006415 /// NM_016497 /// NM_178324																					
2.77	3.04	0.27	6.76E-02	3.87E-01	ZNF229	zinc finger protein 229	chr19q13.31	235717_at	NM_014518																					
2.13	2.39	0.26	6.75E-02	3.87E-01	---	---	---	AFFX-r2-Bs-lys-M_at	---																					

2.12	2.36	0.24	6.76E-02	3.87E-01	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	chr9q22.33	238626_at	NM_173551
1.80	2.01	0.21	6.75E-02	3.87E-01	---	---	---	1561870_at	---
4.15	4.93	0.78	6.77E-02	3.87E-01	PDGFA	platelet-derived growth factor alpha polypeptide	chr7p22	205463_s_at	NM_002607 /// NM_033023
5.91	6.42	0.52	6.77E-02	3.87E-01	CCDC25	coiled-coil domain containing 25	chr8p21.1	218125_s_at	NM_018246
4.23	4.78	0.54	6.77E-02	3.87E-01	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	chr15q14	219461_at	NM_001128628 /// NM_001128629 /// NM_020168
2.12	2.39	0.26	6.77E-02	3.87E-01	LOC100130212	hypothetical protein LOC100130212	chr2p22.2	244549_at	XM_001723180 /// XM_001724514 /// XM_001726873
2.24	2.54	0.30	6.77E-02	3.87E-01	---	---	---	244537_at	---
3.91	4.18	0.26	6.78E-02	3.88E-01	HR	hairless homolog (mouse)	chr8p21.2	210086_at	NM_005144 /// NM_018411
4.68	5.45	0.76	6.78E-02	3.88E-01	---	---	---	244383_at	---
2.89	3.26	0.37	6.78E-02	3.88E-01	OAZ3	ornithine decarboxylase antizyme 3	chr1q21.3	213863_s_at	NM_016178
2.27	2.53	0.26	6.79E-02	3.88E-01	---	---	---	1569782_at	---
2.97	4.78	1.81	6.79E-02	3.88E-01	CHGA	chromogranin A (parathyroid secretory protein 1)	chr14q32	204697_s_at	NM_001275
5.69	6.87	1.18	6.79E-02	3.88E-01	THY1	Thy-1 cell surface antigen	chr11q22.3-q23	213869_x_at	NM_006288
5.22	5.95	0.72	6.79E-02	3.88E-01	---	---	---	230886_at	---
2.78	3.04	0.26	6.80E-02	3.88E-01	C1orf21	Chromosome 1 open reading frame 21	chr1q25	237098_at	NM_030806
8.62	9.65	1.03	6.80E-02	3.88E-01	SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	chr19q13.3	206292_s_at	NM_003167
3.74	4.09	0.35	6.80E-02	3.88E-01	---	---	---	240434_at	---
3.28	3.74	0.47	6.81E-02	3.88E-01	THRSP	thyroid hormone responsive (SPOT14 homolog, rat)	chr11q13.5	229477_at	NM_003251
5.33	5.74	0.42	6.81E-02	3.88E-01	---	---	---	230107_at	---
4.69	5.05	0.36	6.81E-02	3.88E-01	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	chr18q22.3	227977_at	NM_175907
3.57	3.92	0.35	6.81E-02	3.88E-01	NRIP2	nuclear receptor interacting protein 2	chr12p13.33	215104_at	NM_031474
2.71	3.02	0.31	6.81E-02	3.88E-01	ZNF287	zinc finger protein 287	chr17p11.2	220055_at	NM_020653
5.21	5.51	0.30	6.81E-02	3.88E-01	E2F1	E2F transcription factor 1	chr20q11.2	204947_at	NM_005225
2.14	2.39	0.24	6.81E-02	3.88E-01	PNLIP	pancreatic lipase	chr10q26.1	205912_at	NM_000936
2.12	2.33	0.21	6.81E-02	3.88E-01	BHMT2	Betaine-homocysteine methyltransferase 2	chr5q13	242169_at	NM_017614
2.64	3.00	0.36	6.81E-02	3.88E-01	---	---	---	237680_at	---
8.91	9.41	0.49	6.82E-02	3.88E-01	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	chr17p11.2	202053_s_at	NM_000382 /// NM_001031806
3.56	3.97	0.41	6.82E-02	3.88E-01	SLC44A3	solute carrier family 44, member 3	chr1p21.3	228221_at	NM_001114106 /// NM_152369
5.32	5.69	0.37	6.82E-02	3.88E-01	---	---	---	236736_at	---
2.98	3.27	0.28	6.82E-02	3.88E-01	LOC142937	hypothetical protein BC008131	chr10p15.1	1552986_at	XM_495796 /// XM_938400
2.19	2.43	0.24	6.82E-02	3.88E-01	VN1R1	vomeronasal 1 receptor 1	chr19q13.4	221412_at	NM_020633
2.83	3.14	0.30	6.82E-02	3.88E-01	GDAP2	ganglioside induced differentiation associated protein 2	chr1p12	219473_at	NM_017686
3.41	3.84	0.43	6.83E-02	3.88E-01	---	---	---	236615_at	---
3.57	3.98	0.41	6.83E-02	3.88E-01	F2	coagulation factor II (thrombin)	chr11p11	205754_at	NM_000506
2.63	3.02	0.39	6.83E-02	3.88E-01	SLC28A2	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	chr15q15	216432_at	NM_004212
3.07	3.44	0.37	6.83E-02	3.88E-01	PEBP4	phosphatidylethanolamine-binding protein 4	chr8p21.3	227848_at	NM_144962
2.48	2.74	0.26	6.83E-02	3.88E-01	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	chr1p13-p12	204607_at	NM_005518
2.87	3.12	0.25	6.83E-02	3.88E-01	ZC3H7B	zinc finger CCCH-type containing 7B	chr22q13.2	206168_at	NM_017590
2.30	2.61	0.31	6.83E-02	3.88E-01	ST6GALNAC1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1	chr17q25.1	227725_at	NM_018414
3.30	4.68	1.38	6.84E-02	3.88E-01	DUOX1	dual oxidase 1	chr15q15.3	219597_s_at	NM_017434 /// NM_175940
5.02	5.73	0.72	6.84E-02	3.88E-01	USP31	ubiquitin specific peptidase 31	chr16p12.1	226035_at	NM_020718
4.14	4.80	0.66	6.84E-02	3.88E-01	---	---	---	238558_at	---
2.82	3.17	0.35	6.84E-02	3.88E-01	---	---	---	243599_at	---
4.21	4.53	0.33	6.84E-02	3.88E-01	ROBO4	roundabout homolog 4, magic roundabout (Drosophila)	chr11q24.2	220758_s_at	NM_019055
8.39	8.72	0.32	6.84E-02	3.88E-01	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	chr5p15.2	234981_x_at	NM_138809
2.49	2.76	0.27	6.84E-02	3.88E-01	---	---	---	216743_at	---

3.31	3.69	0.38	6.84E-02	3.88E-01	FLJ37078	hypothetical protein FLJ37078	chr7q11.23	1569074_at	NM_001110199 /// XM_001713635 /// XM_001713636 /// XM_001713637 /// XM_001713638
3.47	3.76	0.30	6.84E-02	3.88E-01	---	---	---	231526_at	---
2.66	3.07	0.41	6.85E-02	3.88E-01	MPPED2	metallophosphoesterase domain containing 2	chr11p13	215692_s_at	NM_001584
6.61	6.95	0.35	6.86E-02	3.89E-01	OBFC1	oligonucleotide/oligosaccharide-binding fold containing 1	chr10q24.33	219100_at	NM_024928
5.53	6.25	0.72	6.86E-02	3.89E-01	---	---	---	227576_at	---
2.28	2.52	0.25	6.86E-02	3.89E-01	LOC284244	hypothetical protein LOC284244	chr18q12.1	214162_at	---
7.37	8.14	0.76	6.86E-02	3.89E-01	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	chr16q22.1	203590_at	NM_006141
5.04	5.37	0.33	6.86E-02	3.89E-01	CNIH2	cornichon homolog 2 (Drosophila)	chr11q13.1	230070_at	NM_182553
2.30	2.52	0.22	6.86E-02	3.89E-01	---	---	---	215197_at	---
7.95	8.49	0.54	6.87E-02	3.89E-01	FADS1 /// FADS3	fatty acid desaturase 1 /// fatty acid desaturase 3	chr11q12-q13.1 /// chr11q12.2-q13.1	208963_x_at	NM_013402 /// NM_021727
3.83	4.29	0.47	6.87E-02	3.89E-01	---	---	---	242416_at	---
2.42	2.80	0.38	6.87E-02	3.89E-01	---	---	---	243848_at	---
4.75	5.09	0.33	6.87E-02	3.89E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	211180_x_at	NM_001001890 /// NM_001122607 /// NM_001754
2.33	2.63	0.30	6.87E-02	3.89E-01	---	---	---	237402_at	---
2.10	2.36	0.26	6.87E-02	3.89E-01	ADAM12	ADAM metallopeptidase domain 12	chr10q26.3	202952_s_at	NM_003474 /// NM_021641
5.53	6.09	0.56	6.88E-02	3.89E-01	LTB	lymphotoxin beta (TNF superfamily, member 3)	chr6p21.3	207339_s_at	NM_002341 /// NM_009588
3.50	3.98	0.48	6.88E-02	3.89E-01	KIAA0241	KIAA0241	chr7p14.3	212471_at	NM_015060
4.65	5.16	0.51	6.88E-02	3.89E-01	---	---	---	230733_at	---
3.69	4.00	0.31	6.88E-02	3.89E-01	CSAG2 /// CSAG3	CSAG family, member 2 /// CSAG family, member 3	chrXq28	220445_s_at	NM_001080848 /// NM_001129826 /// NM_001129828 /// NM_004909 /// NM_203311
2.47	2.80	0.34	6.89E-02	3.90E-01	---	---	---	1568807_a_at	---
5.20	5.47	0.26	6.89E-02	3.90E-01	---	---	---	215507_x_at	---
3.27	3.62	0.35	6.89E-02	3.90E-01	LOC388882	hypothetical LOC388882	chr22q11.23	1554940_a_at	XR_042117 /// XR_042118 /// XR_042119
3.08	3.41	0.33	6.89E-02	3.90E-01	---	---	---	1556247_a_at	---
2.04	2.39	0.35	6.89E-02	3.90E-01	BCHE	butyrylcholinesterase	chr3q26.1-q26.2	205433_at	NM_000055
2.17	2.43	0.26	6.89E-02	3.90E-01	---	---	---	1569167_at	---
7.05	7.55	0.50	6.89E-02	3.90E-01	CYP11B2	cytochrome P450, family 11, subfamily B, polypeptide 2	chr8q21-q22	214630_at	NM_000498
3.56	3.97	0.42	6.90E-02	3.90E-01	C20orf46	chromosome 20 open reading frame 46	chr20p13	219958_at	NM_018354
5.52	5.88	0.37	6.90E-02	3.90E-01	ELP2	Elongation protein 2 homolog (S. cerevisiae)	chr18q12.2	235623_at	NM_018255
3.82	4.03	0.21	6.90E-02	3.90E-01	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	chr5q12	204491_at	NM_001104631 /// NM_006203
4.28	4.85	0.57	6.90E-02	3.90E-01	---	---	---	239561_at	---
9.88	10.36	0.48	6.90E-02	3.90E-01	MORF4L1	mortality factor 4 like 1	chr15q24	217982_s_at	NM_006791 /// NM_206839
4.20	4.46	0.26	6.90E-02	3.90E-01	TRIM15	tripartite motif-containing 15	chr6p21.3	210177_at	NM_033229
3.89	4.56	0.66	6.91E-02	3.90E-01	ANKRD12	ankyrin repeat domain 12	chr18p11.22	212286_at	NM_001083625 /// NM_015208
3.88	4.24	0.36	6.91E-02	3.90E-01	ECE2	endothelin converting enzyme 2	chr3q27.1|.	206728_at	NM_001037324 /// NM_001100120 /// NM_001100121 /// NM_014693 /// NM_032331
3.77	4.30	0.53	6.92E-02	3.90E-01	FYB	FYN binding protein (FYB-120/130)	chr5p13.1	211795_s_at	NM_001465 /// NM_199335
2.88	3.26	0.38	6.92E-02	3.90E-01	---	---	---	1570107_at	---
2.14	2.43	0.30	6.91E-02	3.90E-01	ZC3H6	zinc finger CCCH-type containing 6	chr2q13	241372_at	NM_198581

5.52	6.13	0.60	6.92E-02	3.90E-01	FOXO3	forkhead box O3	chr6q21	204132_s_at	NM_001455 /// NM_201559
4.82	5.18	0.36	6.92E-02	3.90E-01	STAG3	stromal antigen 3	chr7q22.1	219753_at	NM_012447
3.56	3.84	0.28	6.92E-02	3.90E-01	---	---	---	216691_at	---
2.62	2.92	0.31	6.92E-02	3.90E-01	TEKT5	tektin 5	chr16p13.13	1553488_at	NM_144674
2.87	3.42	0.55	6.93E-02	3.90E-01	ATP5SL	ATP5S-like	chr19q13.2	1557759_at	NM_018035
7.06	7.50	0.44	6.93E-02	3.90E-01	---	---	---	238267_s_at	---
4.97	5.54	0.58	6.93E-02	3.90E-01	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	201861_s_at	NM_004735
2.78	3.07	0.29	6.93E-02	3.90E-01	PTPN21	Protein tyrosine phosphatase, non-receptor type 21	chr14q31.3	222092_at	NM_007039
4.41	4.73	0.32	6.93E-02	3.90E-01	LOC284600	hypothetical protein LOC284600	chr1p36.33	1559083_x_at	---
3.15	3.53	0.38	6.93E-02	3.90E-01	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	chr5q13-q14	210813_s_at	NM_001131022 /// NM_003401 /// NM_022406 /// NM_022550
6.41	6.72	0.31	6.94E-02	3.91E-01	NCOR2	nuclear receptor co-repressor 2	chr12q24	208889_s_at	NM_001077261 /// NM_006312
5.76	6.86	1.10	6.94E-02	3.91E-01	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	chr2q23.3	213729_at	NM_017892
2.27	2.60	0.33	6.94E-02	3.91E-01	---	---	---	238968_at	---
6.14	7.42	1.27	6.95E-02	3.91E-01	---	---	---	232615_at	---
2.99	3.23	0.24	6.95E-02	3.91E-01	---	---	---	230641_at	---
2.26	2.55	0.29	6.95E-02	3.91E-01	NRXN1	neurexin 1	chr2p16.3	209915_s_at	NM_004801 /// NM_138735
2.23	2.48	0.25	6.95E-02	3.91E-01	---	---	---	242969_at	---
6.59	6.99	0.41	6.96E-02	3.91E-01	SNX26	sorting nexin 26	chr19q13.12	215256_x_at	NM_052948
5.73	6.04	0.31	6.96E-02	3.91E-01	---	---	---	234881_at	---
1.92	2.16	0.24	6.95E-02	3.91E-01	---	---	---	221076_at	---
2.10	2.31	0.22	6.95E-02	3.91E-01	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	chr12q23.3	1556803_at	NM_018082
2.52	2.71	0.19	6.96E-02	3.91E-01	---	---	---	232590_at	---
2.90	3.14	0.24	6.96E-02	3.91E-01	DKFZP434P211 /// LOC100133536 /// LOC440821 /// LOC646074 /// LOC728093 /// LOC729915 /// POM121L1 /// POM121L3	POM121-like protein /// similar to hCG2002956 /// similar to POM121 membrane glycoprotein-like 1 /// similar to POM121-like 1 /// hypothetical LOC728093 /// hypothetical LOC729915 /// POM121 membrane glycoprotein-like 1 (rat) /// POM121 membrane glycoprotein-like 3 (rat)	chr20p11.21 /// chr22q11.22 /// chr22q11.23 /// chr5p13.3 /// chr5q21.1	1553818_x_at	NR_003714 /// XM_001719304 /// XM_001722873 /// XM_001724140 /// XM_929034 /// XR_019113 /// XR_036930 /// XR_038038 /// XR_042337 /// XR_042405
3.78	4.66	0.89	6.97E-02	3.91E-01	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	chr11q12	224358_s_at	NM_021201 /// NM_206938 /// NM_206939 /// NM_206940
3.38	3.66	0.28	6.97E-02	3.92E-01	LOC388553	similar to hCG1645909	chr19q13.32	241822_at	XM_001717914 /// XM_373809 /// XM_944980
2.84	3.32	0.48	6.97E-02	3.92E-01	ZNF75D	zinc finger protein 75D	chrXq26.3	1553225_s_at	NM_007131
3.14	3.45	0.31	6.98E-02	3.92E-01	---	---	---	241062_at	---
2.34	2.55	0.22	6.98E-02	3.92E-01	---	---	---	243251_at	---
4.06	4.73	0.67	6.98E-02	3.92E-01	TTBK2	Tau tubulin kinase 2	chr15q15.2	1557073_s_at	NM_173500
3.69	4.09	0.40	6.98E-02	3.92E-01	HRBL	HIV-1 Rev binding protein-like	chr7q22.1	206820_at	NM_006076
3.65	4.34	0.69	6.98E-02	3.92E-01	SP100	SP100 nuclear antigen	chr2q37.1	210218_s_at	NM_001080391 /// NM_003113
3.33	3.80	0.46	6.99E-02	3.92E-01	ERC1	ELKS/RAB6-interacting/CAST family member 1	chr12p13.3	1555294_a_at	NM_015064 /// NM_178037 /// NM_178038 /// NM_178039 /// NM_178040
2.62	2.84	0.23	6.99E-02	3.92E-01	SFTA1P	surfactant associated 1 (pseudogene)	chr10p14	243818_at	---
8.07	8.76	0.69	6.99E-02	3.92E-01	PTRF	polymerase I and transcript release factor	chr17q21.31	208789_at	NM_012232
2.48	2.76	0.28	6.99E-02	3.92E-01	TFG	TRK-fused gene	chr3q12.2	239385_at	NM_001007565 /// NM_006070
7.06	7.61	0.55	6.99E-02	3.92E-01	HDHD2	haloacid dehalogenase-like hydrolase domain containing 2	chr18q21.1	223155_at	NM_032124
2.28	2.78	0.50	7.00E-02	3.92E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	232748_at	NM_002581
3.92	4.20	0.28	7.00E-02	3.92E-01	MR1	major histocompatibility complex, class I-related	chr1q25.3	207566_at	NM_001531
2.16	2.36	0.20	7.00E-02	3.92E-01	---	---	---	1563958_at	---

6.12	6.82	0.70	7.00E-02	3.92E-01	SFRS18	splicing factor, arginine/serine-rich 18	chr6q16.3	225507_at	NM_015491 /// NM_032870
6.00	6.42	0.42	7.00E-02	3.92E-01	CAPS	calcyphosine	chr19p13.3	231710_at	NM_004058 /// NM_080590
4.73	5.08	0.35	7.00E-02	3.92E-01	MNX1	motor neuron and pancreas homeobox 1	chr7q36	214614_at	NM_005515
1.84	2.08	0.24	7.00E-02	3.92E-01	---	---	---	243925_at	---
4.70	5.00	0.30	7.01E-02	3.92E-01	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	chr16p13.3	222032_s_at	NM_003470
3.27	3.64	0.37	7.01E-02	3.92E-01	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	chr1q32.3	222906_at	NM_014053
2.45	2.75	0.30	7.01E-02	3.92E-01	ZFP36L1	zinc finger protein 36, C3H type-like 1	chr14q22-q24	213284_at	NM_004926
6.76	8.32	1.55	7.02E-02	3.92E-01	COL15A1	collagen, type XV, alpha 1	chr9q21-q22	203477_at	NM_001855
3.82	4.48	0.66	7.02E-02	3.92E-01	TSHZ2	teashirt zinc finger homeobox 2	chr20q13.2	243940_at	NM_173485
2.78	3.29	0.51	7.02E-02	3.92E-01	PSMC2	Proteasome (prosome, macropain) 26S subunit, ATPase, 2	chr7q22.1-q22.3	238020_at	NM_002803
4.34	4.79	0.46	7.02E-02	3.92E-01	RFC4	replication factor C (activator 1) 4, 37kDa	chr3q27	204023_at	NM_002916 /// NM_181573
2.33	2.73	0.40	7.02E-02	3.92E-01	LOC26010	viral DNA polymerase-transactivated protein 6	chr2q33.1	241812_at	NM_001100422 /// NM_001100423 /// NM_001100424 /// NM_015535
3.89	4.24	0.35	7.02E-02	3.92E-01	---	---	---	230096_at	---
2.01	2.35	0.34	7.02E-02	3.92E-01	---	---	---	242568_s_at	---
3.13	3.44	0.31	7.02E-02	3.92E-01	LOC441005	hypothetical gene supported by BC010180	chr4p16.3	1569172_a_at	XR_041317 /// XR_041318 /// XR_041319
1.84	2.13	0.29	7.02E-02	3.92E-01	TXLNB	taxilin beta	chr6q24.1	227834_at	NM_153235
4.27	4.55	0.29	7.02E-02	3.92E-01	---	---	---	238180_at	---
3.52	3.78	0.26	7.02E-02	3.92E-01	---	---	---	243955_at	---
2.17	2.40	0.23	7.02E-02	3.92E-01	CCDC14	coiled-coil domain containing 14	chr3q21.1	1561054_a_at	NM_022757
1.99	2.23	0.25	7.03E-02	3.92E-01	---	---	---	1566169_at	---
8.82	10.04	1.22	7.03E-02	3.93E-01	C9orf5	chromosome 9 open reading frame 5	chr9q31	223006_s_at	NM_001099734 /// NM_032012
6.14	7.25	1.10	7.03E-02	3.93E-01	ANKIB1	ankyrin repeat and IBR domain containing 1	chr7q21.2	224687_at	NM_019004
2.40	3.12	0.72	7.03E-02	3.93E-01	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2	chr5q34	242344_at	NM_000813 /// NM_021911
1.95	2.21	0.25	7.03E-02	3.93E-01	CDH9	cadherin 9, type 2 (T1-cadherin)	chr5p14	207729_at	NM_016279
6.95	7.66	0.71	7.03E-02	3.93E-01	GGPS1	geranylgeranyl diphosphate synthase 1	chr1q43	202322_s_at	NM_001037277 /// NM_001037278 /// NM_004837
4.33	4.70	0.36	7.04E-02	3.93E-01	PUNC	putative neuronal cell adhesion molecule	chr15q22.3-q23	232037_at	NM_004884
2.05	2.40	0.34	7.04E-02	3.93E-01	---	---	---	235761_at	---
3.92	4.26	0.34	7.04E-02	3.93E-01	CDC25A	cell division cycle 25 homolog A (S. pombe)	chr3p21	204695_at	NM_001789 /// NM_201567
2.56	2.86	0.30	7.04E-02	3.93E-01	LOC149703	hypothetical protein LOC149703	chr20q13.12	236652_at	---
3.04	3.30	0.26	7.04E-02	3.93E-01	KCNIP4	Kv channel interacting protein 4	chr4p15.31	224530_s_at	NM_001035003 /// NM_001035004 /// NM_025221 /// NM_147181 /// NM_147182 /// NM_147183
6.81	7.85	1.04	7.05E-02	3.93E-01	DHCR7	7-dehydrocholesterol reductase	chr11q13.2-q13.5	201790_s_at	NM_001360
2.03	2.28	0.25	7.05E-02	3.93E-01	C2orf52	chromosome 2 open reading frame 52	chr2q37.1	1552979_at	NM_173513 /// NR_024079
3.60	3.93	0.33	7.05E-02	3.93E-01	HIF3A	hypoxia inducible factor 3, alpha subunit	chr19q13.32	233517_s_at	NM_022462 /// NM_152794 /// NM_152795
4.65	5.27	0.62	7.06E-02	3.93E-01	FAM82B	family with sequence similarity 82, member B	chr8q21.3	222665_at	NM_016033
4.42	5.61	1.19	7.06E-02	3.93E-01	FAM129A	family with sequence similarity 129, member A	chr1q25	217967_s_at	NM_052966
2.96	3.29	0.33	7.06E-02	3.93E-01	---	---	---	244683_at	---
2.13	2.40	0.27	7.06E-02	3.93E-01	---	---	---	216769_x_at	---
3.20	3.80	0.60	7.07E-02	3.93E-01	---	---	---	1560342_at	---
2.96	3.34	0.38	7.07E-02	3.93E-01	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	chr2q37.1	1552965_a_at	NM_145236
5.32	5.64	0.33	7.07E-02	3.93E-01	---	---	---	238265_x_at	---
1.92	2.21	0.29	7.07E-02	3.93E-01	HMGA2	High mobility group AT-hook 2	chr12q15	1568286_at	NM_003483 /// NM_003484
1.86	2.05	0.20	7.07E-02	3.93E-01	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	chr17q21.32	215240_at	NM_000212

2.37	2.61	0.24	7.07E-02	3.94E-01	KANK4	KN motif and ankyrin repeat domains 4	chr1p31.3	229125_at	NM_181712
3.63	4.31	0.68	7.08E-02	3.94E-01	---	---	---	236395_at	---
2.83	3.15	0.32	7.07E-02	3.94E-01	---	---	---	1562289_at	---
2.11	2.35	0.24	7.08E-02	3.94E-01	---	---	---	1558802_at	---
5.49	6.40	0.91	7.08E-02	3.94E-01	FILIP1L	filamin A interacting protein 1-like	chr3q12.1	204135_at	NM_001042459 /// NM_014890 /// NM_182909
5.29	5.90	0.62	7.08E-02	3.94E-01	RABGAP1L	RAB GTPase activating protein 1-like	chr1q24	203020_at	NM_001035230 /// NM_014857
6.06	6.80	0.74	7.08E-02	3.94E-01	BBX	bobby sox homolog (Drosophila)	chr3q13.1	223134_at	NM_020235
2.26	2.57	0.30	7.08E-02	3.94E-01	---	---	---	236364_at	---
3.59	4.06	0.47	7.08E-02	3.94E-01	GPRC5B	G protein-coupled receptor, family C, group 5, member B	chr16p12	225511_at	NM_016235
2.73	3.05	0.32	7.09E-02	3.94E-01	---	---	---	233466_at	---
3.84	4.45	0.62	7.09E-02	3.94E-01	BAG5	BCL2-associated athanogene 5	chr14q32.33	202984_s_at	NM_001015048 /// NM_001015049 /// NM_004873
3.09	3.56	0.47	7.09E-02	3.94E-01	PLXNC1	plexin C1	chr12q23.3	206471_s_at	NM_005761
2.84	3.27	0.43	7.09E-02	3.94E-01	TTC25	tetratricopeptide repeat domain 25	chr17q21.2	223924_at	NM_031421
3.99	4.39	0.41	7.10E-02	3.94E-01	ACSL5	acyl-CoA synthetase long-chain family member 5	chr10q25.1-q25.2	218322_s_at	NM_016234 /// NM_203379 /// NM_203380
4.83	5.22	0.39	7.09E-02	3.94E-01	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	chr17q25	217573_at	NM_000835
2.69	3.07	0.39	7.09E-02	3.94E-01	FLJ33996 /// LOC100127971	hypothetical protein FLJ33996 /// hypothetical protein LOC100127971	chr12q13.13	236329_at	XM_001720872 /// XM_001720877 /// XM_001725504 /// XR_000901 /// XR_001317
6.94	7.30	0.36	7.09E-02	3.94E-01	ARVCF	armadillo repeat gene deletes in velocardiofacial syndrome	chr22q11.21	217516_x_at	NM_001670
2.90	3.25	0.35	7.09E-02	3.94E-01	SWAP70	SWAP-70 protein	chr11p15	210369_at	NM_015055
2.60	4.13	1.53	7.10E-02	3.94E-01	CD24	CD24 molecule	chr6q21	216379_x_at	NM_013230 /// XM_001725629
2.92	3.70	0.78	7.10E-02	3.94E-01	---	---	---	231484_at	---
4.92	5.36	0.43	7.10E-02	3.94E-01	TMED9	Transmembrane emp24 protein transport domain containing 9	chr5q35.3	239627_at	NM_017510
6.22	6.59	0.37	7.10E-02	3.94E-01	SELPLG	selectin P ligand	chr12q24	209880_s_at	NM_003006
2.10	2.41	0.31	7.10E-02	3.94E-01	WDR19	WD repeat domain 19	chr4p14	1555314_at	NM_025132
4.63	5.27	0.64	7.11E-02	3.94E-01	RIPK5	receptor interacting protein kinase 5	chr1q32.1	214663_at	NM_015375 /// NM_199462
1.97	2.27	0.30	7.11E-02	3.94E-01	OR2A20P /// OR2A9P	olfactory receptor, family 2, subfamily A, member 20 pseudogene /// olfactory receptor, family 2, subfamily A, member 9 pseudogene	chr7q35	1555890_at	NR_002157 /// NR_002158
2.20	2.43	0.23	7.11E-02	3.94E-01	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	chr2q23.3-q24.1	243779_at	NM_052917
3.21	3.76	0.55	7.11E-02	3.94E-01	---	---	---	238970_at	---
1.91	2.15	0.25	7.11E-02	3.94E-01	---	---	---	238309_x_at	---
2.96	3.39	0.43	7.11E-02	3.94E-01	---	---	---	233554_at	---
2.55	2.88	0.33	7.11E-02	3.94E-01	LOC286359	hypothetical protein LOC286359	chr9q22.33	1563606_a_at	XR_040737 /// XR_040738 /// XR_040739
6.71	7.89	1.18	7.12E-02	3.94E-01	PKN2	protein kinase N2	chr1p22.2	212629_s_at	NM_006256
6.08	6.59	0.50	7.12E-02	3.94E-01	NOL10	nucleolar protein 10	chr2p25.1	222684_s_at	NM_024894
2.31	2.56	0.25	7.12E-02	3.94E-01	---	---	---	236238_at	---
1.86	2.09	0.23	7.12E-02	3.94E-01	---	---	---	233407_at	---
5.89	7.00	1.11	7.12E-02	3.94E-01	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	chr2q36.3-q37.1	206638_at	NM_000867
4.38	4.70	0.32	7.12E-02	3.94E-01	---	---	---	214126_at	---
2.54	2.96	0.42	7.12E-02	3.94E-01	LOC253044	hypothetical protein LOC253044	chr15q24.1	1562748_at	---
2.30	2.55	0.24	7.13E-02	3.94E-01	---	---	---	238310_at	---
6.37	6.98	0.61	7.13E-02	3.94E-01	---	---	---	225923_at	---
3.44	4.03	0.59	7.13E-02	3.94E-01	---	---	---	241925_x_at	---
2.91	3.30	0.39	7.13E-02	3.94E-01	---	---	---	241211_at	---
2.20	2.58	0.38	7.13E-02	3.94E-01	DGUOK	deoxyguanosine kinase	chr2p13	241995_at	NM_080916 /// NM_080918
3.73	4.15	0.42	7.14E-02	3.95E-01	---	---	---	239592_at	---
5.30	5.70	0.40	7.14E-02	3.95E-01	---	---	---	1556646_at	---
2.79	3.20	0.41	7.14E-02	3.95E-01	JMJD1C	jumonji domain containing 1C	chr10q21.2-q21.3	241661_at	NM_004241 /// NM_032776
6.65	7.57	0.92	7.14E-02	3.95E-01	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	202379_s_at	NM_005385

5.13	5.67	0.55	7.15E-02	3.95E-01	SFRS12IP1	SFRS12-interacting protein 1	chr5q12.3	1553581_s_at	NM_173829
2.77	3.04	0.27	7.15E-02	3.95E-01	ZNRD1	zinc ribbon domain containing 1	chr6p21.3	234530_s_at	NM_014596 /// NM_170783
2.75	4.13	1.38	7.16E-02	3.95E-01	---	---	---	214768_x_at	---
5.79	6.73	0.94	7.16E-02	3.95E-01	PTGDS	prostaglandin D2 synthase 21kDa (brain)	chr9q34.2-q34.3	211663_x_at	NM_000954
3.56	3.87	0.31	7.16E-02	3.95E-01	BARX1	BARX homeobox 1	chr9q12	219845_at	NM_021570
1.91	2.17	0.25	7.16E-02	3.95E-01	SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	chr9p22.3	229712_at	NM_001039697
6.99	7.55	0.56	7.16E-02	3.95E-01	---	---	---	229803_s_at	---
4.62	4.97	0.34	7.16E-02	3.95E-01	C19orf47	chromosome 19 open reading frame 47	chr19q13.2	1554475_a_at	NM_178830
3.55	3.74	0.20	7.17E-02	3.95E-01	---	---	---	215956_at	---
4.48	4.88	0.40	7.17E-02	3.95E-01	HKDC1	hexokinase domain containing 1	chr10q21.3	237324_s_at	NM_025130
2.60	2.95	0.34	7.17E-02	3.95E-01	LOC100129448 /// WSCD2	hypothetical protein LOC100129448 /// WSC domain containing 2	chr12q23.3	207637_at	NM_014653 /// XM_001715530 /// XM_001717667 /// XM_001718795
2.03	2.31	0.28	7.17E-02	3.95E-01	ZNF135	zinc finger protein 135	chr19q13.4	206142_at	NM_003436
3.65	3.92	0.27	7.17E-02	3.95E-01	HAS1	hyaluronan synthase 1	chr19q13.4	207316_at	NM_001523
5.68	7.28	1.60	7.18E-02	3.96E-01	---	---	---	242856_at	---
5.72	6.22	0.50	7.18E-02	3.96E-01	GTPBP8	GTP-binding protein 8 (putative)	chr3q13.2	221046_s_at	NM_014170 /// NM_138485
3.29	3.65	0.36	7.18E-02	3.96E-01	---	---	---	237087_at	---
2.69	2.98	0.29	7.18E-02	3.96E-01	---	---	---	216372_at	---
2.45	2.73	0.28	7.18E-02	3.96E-01	---	---	---	236929_at	---
6.32	6.69	0.37	7.18E-02	3.96E-01	S1PR2	sphingosine-1-phosphate receptor 2	chr19p13.2	227684_at	NM_004230
2.01	2.24	0.23	7.18E-02	3.96E-01	FTHL17	ferritin, heavy polypeptide-like 17	chrXp21	224379_at	NM_031894
3.09	3.46	0.37	7.19E-02	3.96E-01	---	---	---	232757_at	---
4.66	5.39	0.73	7.19E-02	3.96E-01	LOC730057	Hypothetical LOC730057	chr3p14.1	1556364_at	XM_001132251 /// XM_001132871 /// XM_001716450
2.76	3.02	0.26	7.19E-02	3.96E-01	DUOX1	dual oxidase 1	chr15q15.3	1565795_at	NM_017434 /// NM_175940
3.16	3.56	0.40	7.19E-02	3.96E-01	hCG_1818231	hCG1818231	chr10q22.1	239136_at	XR_042007 /// XR_042008 /// XR_042009
5.10	5.48	0.38	7.19E-02	3.96E-01	NGF	nerve growth factor (beta polypeptide)	chr1p13.1	206814_at	NM_002506
5.44	5.78	0.33	7.19E-02	3.96E-01	SLC25A42	solute carrier family 25, member 42	chr19p13.11	226737_at	NM_178526
2.55	2.92	0.37	7.20E-02	3.96E-01	C3orf17	chromosome 3 open reading frame 17	chr3q13.2	225279_s_at	NM_001025072 /// NM_001025073 /// NM_015412
1.84	2.13	0.28	7.20E-02	3.96E-01	---	---	---	243734_x_at	---
2.50	2.75	0.25	7.20E-02	3.96E-01	KANK1	KN motif and ankyrin repeat domains 1	chr9p24.3	216762_at	NM_015158 /// NM_153186
2.21	2.53	0.31	7.21E-02	3.96E-01	---	---	---	236373_at	---
4.63	5.13	0.50	7.21E-02	3.96E-01	ALDOB	aldolase B, fructose-bisphosphate	chr9q21.3-q22.2	211357_s_at	NM_000035
2.67	3.03	0.36	7.21E-02	3.96E-01	---	---	---	224547_at	---
2.67	3.00	0.33	7.22E-02	3.96E-01	---	---	---	236687_at	---
4.34	4.61	0.26	7.22E-02	3.96E-01	---	---	---	235487_at	---
2.94	3.20	0.26	7.22E-02	3.96E-01	---	---	---	1560986_a_at	---
3.13	3.38	0.25	7.22E-02	3.96E-01	INSM2	insulinoma-associated 2	chr14q13.2	240841_at	NM_032594
1.54	1.73	0.19	7.22E-02	3.96E-01	---	---	---	202015_x_at	---
5.33	6.26	0.93	7.22E-02	3.97E-01	PTPRK	protein tyrosine phosphatase, receptor type, K	chr6q22.2-q22.3	203038_at	NM_002844
2.20	4.08	1.88	7.23E-02	3.97E-01	SCG2	secretogranin II (chromogranin C)	chr2q35-q36	204035_at	NM_003469
5.90	6.86	0.95	7.23E-02	3.97E-01	COBLL1	COBL-like 1	chr2q24.3	203642_s_at	NM_014900
7.91	8.42	0.51	7.23E-02	3.97E-01	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	chr20q13.1	208743_s_at	NM_003404 /// NM_139323
3.20	3.57	0.38	7.23E-02	3.97E-01	---	---	---	236340_at	---
2.80	3.15	0.35	7.23E-02	3.97E-01	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	chr14q24.3	238886_at	NM_006827
3.52	3.84	0.33	7.23E-02	3.97E-01	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	chr10p12	1559419_at	NM_000724 /// NM_201570 /// NM_201571 /// NM_201572 /// NM_201590 /// NM_201593 /// NM_201596 /// NM_201597
2.40	2.66	0.27	7.23E-02	3.97E-01	---	---	---	216527_at	---
3.96	4.21	0.24	7.23E-02	3.97E-01	LOC646762	hypothetical protein LOC646762	chr7p15.1	1560006_a_at	XR_041099

3.11	4.12	1.02	7.23E-02	3.97E-01	STEAP4	STEAP family member 4	chr7q21.12	220187_at	NM_024636
2.24	2.48	0.24	7.23E-02	3.97E-01	MAOB	monoamine oxidase B	chrXp11.23	1561010_a_at	NM_000898
5.27	5.94	0.67	7.24E-02	3.97E-01	CCND2	cyclin D2	chr12p13	200952_s_at	NM_001759
2.32	2.65	0.33	7.24E-02	3.97E-01	ARX	aristaless related homeobox	chrXp21	238878_at	NM_139058
2.76	3.06	0.29	7.24E-02	3.97E-01	SSBP1	single-stranded DNA binding protein 1	chr7q34	1562442_a_at	NM_003143
4.86	5.30	0.44	7.25E-02	3.97E-01	ZNF416	zinc finger protein 416	chr19q13.4	223589_at	NM_017879
3.07	3.42	0.36	7.25E-02	3.97E-01	---	---	---	242004_x_at	---
6.00	6.35	0.35	7.25E-02	3.97E-01	WDR33	WD repeat domain 33	chr2q14.3	223147_s_at	NM_001006622 /// NM_001006623 /// NM_018383
7.24	7.58	0.34	7.25E-02	3.97E-01	GABARAPL1	GABA(A) receptor-associated protein like 1	chr12p13.2	208868_s_at	NM_031412
3.09	3.38	0.29	7.25E-02	3.97E-01	HNT	neurotrimin	chr11q25	222020_s_at	NM_001048209 /// NM_016522
5.20	6.01	0.80	7.26E-02	3.97E-01	GLS	glutaminase	chr2q32-q34	203157_s_at	NM_014905
2.91	3.29	0.38	7.26E-02	3.97E-01	CHSY3	chondroitin sulfate synthase 3	chr5q23.3	242100_at	NM_175856
3.53	3.90	0.37	7.26E-02	3.97E-01	LOC148189	Hypothetical protein LOC148189	chr19q12	232281_at	---
2.96	3.19	0.23	7.26E-02	3.97E-01	---	---	---	244824_at	---
2.78	2.99	0.21	7.26E-02	3.97E-01	---	---	---	240588_at	---
4.95	5.47	0.52	7.26E-02	3.97E-01	UNKL	unkempt homolog (Drosophila)-like	chr16p13.3	221064_s_at	NM_001037125 /// NM_023076
3.59	4.17	0.58	7.27E-02	3.97E-01	AGTPBP1	ATP/GTP binding protein 1	chr9q21.33	204500_s_at	NM_015239
2.11	2.39	0.28	7.26E-02	3.97E-01	---	---	---	1565107_x_at	---
2.27	2.50	0.23	7.26E-02	3.97E-01	NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	chr16q23.1	215824_at	NM_001105663
1.96	2.18	0.22	7.26E-02	3.97E-01	C12orf39	chromosome 12 open reading frame 39	chr12p12.1	229778_at	NM_030572
2.12	2.50	0.38	7.27E-02	3.97E-01	ACVR1C	activin A receptor, type IC	chr2q24.1	1552519_at	NM_001111031 /// NM_001111032 /// NM_001111033 /// NM_145259
2.25	2.59	0.34	7.27E-02	3.97E-01	LOC196993	hypothetical protein LOC196993	chr15q23	214418_at	NM_001102658
7.21	8.40	1.19	7.27E-02	3.97E-01	ZC3H15	zinc finger CCCH-type containing 15	chr2q32.1	201593_s_at	NM_018471
5.58	5.87	0.29	7.27E-02	3.97E-01	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	chr19q13.43	234948_at	NM_012254
2.22	2.59	0.36	7.27E-02	3.97E-01	FOXP2	forkhead box P2	chr7q31	1555352_at	NM_014491 /// NM_148898 /// NM_148899
2.64	3.03	0.39	7.28E-02	3.98E-01	FLJ14082	hypothetical protein FLJ14082	chr2q11.1	206659_at	XR_041868 /// XR_041869 /// XR_041870
2.09	2.40	0.30	7.28E-02	3.98E-01	ZNF224	Zinc finger protein 224	chr19q13.2	222947_at	NM_013398
2.16	2.47	0.32	7.29E-02	3.98E-01	---	---	---	1559455_at	---
2.38	2.59	0.22	7.29E-02	3.98E-01	LOC440173	LOC440173	chr14q12	229761_at	---
4.21	4.57	0.35	7.29E-02	3.98E-01	ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)	chr3p25.3-p25.2	222709_at	NM_006395
7.69	8.34	0.65	7.29E-02	3.98E-01	KTN1	kinectin 1 (kinesin receptor)	chr14q22.1	200915_x_at	NM_001079521 /// NM_001079522 /// NM_004986 /// NM_182926
3.57	3.92	0.35	7.30E-02	3.98E-01	TES	testis derived transcript (3 LIM domains)	chr7q31.2	202720_at	NM_015641 /// NM_152829
3.04	3.40	0.36	7.30E-02	3.98E-01	HTR6	5-hydroxytryptamine (serotonin) receptor 6	chr1p36-p35	206944_at	NM_000871
3.81	4.43	0.62	7.30E-02	3.98E-01	CLIP1	CAP-GLY domain containing linker protein 1	chr12q24.3	1558924_s_at	NM_002956 /// NM_198240
2.28	2.59	0.31	7.30E-02	3.99E-01	FAM119A	family with sequence similarity 119, member A	chr2q33.3	1553743_at	NM_001127395 /// NM_145280
4.65	5.46	0.82	7.31E-02	3.99E-01	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	chr2p21	202437_s_at	NM_000104
4.86	5.29	0.43	7.31E-02	3.99E-01	---	---	---	208278_s_at	---
2.48	2.84	0.35	7.31E-02	3.99E-01	GLI2	GLI-Kruppel family member GLI2	chr2q14	207034_s_at	NM_005270
3.15	3.48	0.33	7.31E-02	3.99E-01	LOC100131733	hypothetical protein LOC100131733	chr12q24.11	228675_at	XM_001714181 /// XM_001722340 /// XM_001726102
1.95	2.22	0.26	7.31E-02	3.99E-01	---	---	---	237597_at	---

9.23	9.91	0.68	7.32E-02	3.99E-01	CSDE1	cold shock domain containing E1, RNA-binding	chr1p22	219939_s_at	NM_001007553 /// NM_001130523 /// NM_007158																				
2.50	2.80	0.29	7.32E-02	3.99E-01	---	---	---	1560286_s_at	---																				
3.70	3.95	0.25	7.32E-02	3.99E-01	LOC728073	hypothetical protein LOC728073	chr17q25.1	1564559_at	XR_040683 /// XR_040684 /// XR_040685																				
2.00	2.20	0.20	7.32E-02	3.99E-01	---	---	---	234126_at	---																				
1.92	2.14	0.22	7.32E-02	3.99E-01	---	---	---	243204_at	---																				
3.46	3.84	0.38	7.32E-02	3.99E-01	LOC644844	hypothetical LOC644844	chr15q15.1	230485_at	XR_040288 /// XR_040289 /// XR_040290																				
2.15	2.54	0.39	7.33E-02	3.99E-01	STRBP	Chromosome 9 open reading frame 45	chr9q33.3	229513_at	NM_018387																				
2.25	2.48	0.23	7.33E-02	3.99E-01	C10orf55	chromosome 10 open reading frame 55	chr10q22.2	1557531_a_at	NM_001001791																				
3.90	4.28	0.38	7.33E-02	3.99E-01	FLJ44451 /// IDS	hypothetical protein FLJ44451 /// iduronate 2-sulfatase	chrXq28	1559136_s_at	NM_000202 /// NM_006123 /// XM_001714058																				
2.64	3.12	0.48	7.33E-02	3.99E-01	FGF13	fibroblast growth factor 13	chrXq26.3	205110_s_at	NM_004114 /// NM_033642																				
3.48	3.75	0.27	7.33E-02	3.99E-01	GAPVD1	GTPase activating protein and VPS9 domains 1	chr9q33.3	235553_at	NM_015635																				
4.70	5.03	0.32	7.34E-02	3.99E-01	---	---	---	220616_at	---																				
2.59	2.82	0.24	7.34E-02	3.99E-01	ALX1	ALX homeobox 1	chr12q21.3-q22	206837_at	NM_006982																				
2.36	2.59	0.24	7.34E-02	3.99E-01	NAT12	N-acetyltransferase 12	chr14q23.1	228322_at	NM_001011713																				
2.40	2.73	0.33	7.34E-02	3.99E-01	SEZ6	seizure related 6 homolog (mouse)	chr17q11.2	229651_at	NM_001098635 /// NM_178860																				
2.52	2.76	0.24	7.34E-02	3.99E-01	FLJ10232	hypothetical protein FLJ10232	chr9q34.11	208162_s_at	XR_041437 /// XR_041438 /// XR_041439																				
3.04	3.43	0.40	7.35E-02	3.99E-01	ROR1	receptor tyrosine kinase-like orphan receptor 1	chr1p32-p31	211057_at	NM_001083592 /// NM_005012																				
3.53	3.83	0.30	7.35E-02	3.99E-01	TMEM114	Similar to hCG15406	chr16p13	231462_at	---																				
2.07	2.35	0.28	7.35E-02	3.99E-01	---	---	---	1561678_at	---																				
2.07	2.34	0.27	7.35E-02	3.99E-01	FAM12A	family with sequence similarity 12, member A	chr14q11.2	208142_at	NM_006683																				
4.08	4.50	0.41	7.35E-02	3.99E-01	GKN1	gastrokine 1	chr2p14	220191_at	NM_019617																				
4.89	5.25	0.36	7.35E-02	3.99E-01	---	---	---	234746_at	---																				
2.67	2.94	0.27	7.35E-02	3.99E-01	HS6ST3 /// LOC100134314	heparan sulfate 6-O-sulfotransferase 3 /// similar to heparan sulfate 6-O-sulfotransferase 3	chr13q32.1	1552842_at	NM_153456 /// XM_001720419																				
3.71	4.04	0.33	7.35E-02	3.99E-01	FZD4	frizzled homolog 4 (Drosophila)	chr11q14.2	224337_s_at	NM_012193																				
3.21	3.62	0.41	7.35E-02	4.00E-01	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	chr5q14.2	1570523_s_at	NM_001131028 /// NM_031482																				
5.46	5.87	0.41	7.35E-02	4.00E-01	RIC8B	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	chr12q23.3	219446_at	NM_018157																				
2.38	2.67	0.29	7.36E-02	4.00E-01	MAG	myelin associated glycoprotein	chr19q13.1	217447_at	NM_002361 /// NM_080600																				
2.76	3.09	0.33	7.36E-02	4.00E-01	TPO	thyroid peroxidase	chr2p25	210342_s_at	NM_000547 /// NM_175719 /// NM_175721 /// NM_175722																				
2.74	3.11	0.38	7.36E-02	4.00E-01	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	chr1q42.11	214464_at	NM_003607 /// NM_014826																				
7.81	8.17	0.37	7.36E-02	4.00E-01	MED13	mediator complex subunit 13	chr17q22-q23	201987_at	NM_005121																				
3.08	3.38	0.30	7.36E-02	4.00E-01	---	---	---	236062_at	---																				
3.74	4.12	0.37	7.37E-02	4.00E-01	---	---	---	230330_at	---																				
2.60	2.96	0.36	7.37E-02	4.00E-01	FLJ44606	hypothetical gene supported by AK126569	chr5q23.2	230404_at	XM_001722994 /// XM_932789 /// XM_943643																				
2.77	2.99	0.22	7.37E-02	4.00E-01	chromosome 1 open reading frame 191	CDNA FLJ13821 fis, clone THYRO1000484	---	232469_x_at	---																				
5.18	5.80	0.63	7.38E-02	4.00E-01	IFIH1	interferon induced with helicase C domain 1	chr2q24	219209_at	NM_022168																				
7.98	8.51	0.53	7.38E-02	4.00E-01	CD151	CD151 molecule (Raph blood group)	chr11p15.5	204306_s_at	NM_001039490 /// NM_004357 /// NM_139029 /// NM_139030																				
2.94	3.40	0.46	7.38E-02	4.00E-01	RHOJ	ras homolog gene family, member J	chr14q23.2	235131_at	NM_020663																				
3.24	3.63	0.40	7.38E-02	4.00E-01	---	---	---	240016_at	---																				
5.79	6.17	0.37	7.38E-02	4.00E-01	GNG7	guanine nucleotide binding protein (G protein), gamma 7	chr19p13.3	206896_s_at	NM_052847																				
3.01	3.38	0.37	7.38E-02	4.00E-01	---	---	---	242436_at	---																				

2.00	2.30	0.29	7.38E-02	4.00E-01	KRT222P	keratin 222 pseudogene	chr17q21.2	243998_at	NM_152349
5.35	5.64	0.29	7.38E-02	4.00E-01	C19orf57	chromosome 19 open reading frame 57	chr19p13.12	206901_at	NM_024323
2.72	3.01	0.29	7.38E-02	4.00E-01	USP49	ubiquitin specific peptidase 49	chr6p21	242120_at	NM_018561
1.97	2.24	0.28	7.38E-02	4.00E-01	SMPDL3A	Sphingomyelin phosphodiesterase, acid-like 3A	chr6q22.31	1562512_at	NM_006714
2.14	2.41	0.27	7.38E-02	4.00E-01	---	---	---	244469_at	---
2.78	3.02	0.24	7.38E-02	4.00E-01	CARD14	caspase recruitment domain family, member 14	chr17q25	1555308_at	NM_024110 /// NM_052819
4.80	5.46	0.65	7.39E-02	4.00E-01	FASN	fatty acid synthase	chr17q25	212218_s_at	NM_004104
4.03	4.41	0.38	7.39E-02	4.00E-01	PIN1L	peptidylprolyl cis/trans isomerase, NIMA-interacting 1-like (pseudogene)	chr1p31	207582_at	NR_023916 /// XR_017802 /// XR_017814 /// XR_040597
3.84	4.31	0.47	7.39E-02	4.00E-01	LOC644192	hypothetical LOC644192	chr15q26.2	232878_at	XR_040009 /// XR_040010 /// XR_040011
2.96	3.20	0.24	7.40E-02	4.01E-01	LOC401320	Hypothetical LOC401320	chr7p15.1	1558458_at	XM_379482 /// XM_380098 /// XM_938539
4.26	4.90	0.64	7.40E-02	4.01E-01	---	---	---	1564733_at	---
2.95	3.28	0.34	7.40E-02	4.01E-01	LOC399900	Hypothetical gene supported by AK093779	chr11q12.3	237478_at	XR_040387
2.08	2.39	0.31	7.40E-02	4.01E-01	CLCA2	CLCA family member 2, chloride channel regulator	chr1p31-p22	206164_at	NM_006536
2.29	2.57	0.28	7.40E-02	4.01E-01	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	chr18q21.31	208064_s_at	NM_015879
4.44	4.84	0.40	7.40E-02	4.01E-01	KATNB1	katanin p80 (WD repeat containing) subunit B 1	chr16q13	203163_at	NM_005886
3.72	3.99	0.28	7.41E-02	4.01E-01	---	---	---	241514_at	---
2.36	2.57	0.21	7.41E-02	4.01E-01	---	---	---	237605_at	---
5.17	5.83	0.66	7.42E-02	4.01E-01	TRPS1	trichorhinophalangeal syndrome I	chr8q24.12	222651_s_at	NM_014112
8.61	9.00	0.39	7.42E-02	4.01E-01	LOC653566 /// SPCS2	signal peptidase complex subunit 2 homolog pseudogene /// signal peptidase complex subunit 2 homolog (S. cerevisiae)	chr11q13.4 /// chr1p35.3	201239_s_at	NM_014752
4.03	4.36	0.33	7.42E-02	4.01E-01	ZNF653	Zinc finger protein 653	chr19p13.2	244085_at	NM_138783
2.39	2.60	0.21	7.42E-02	4.01E-01	MORN1	MORN repeat containing 1	chr1p36.33-p36.32	222933_at	NM_024848
3.37	3.72	0.35	7.42E-02	4.01E-01	GRM8	glutamate receptor, metabotropic 8	chr7q31.3-q32.1	216256_at	NM_000845 /// NM_001127323 /// NM_001127326
4.81	5.04	0.23	7.42E-02	4.01E-01	ADAM33	ADAM metallopeptidase domain 33	chr20p13	233868_x_at	NM_025220 /// NM_153202
2.62	2.97	0.36	7.42E-02	4.01E-01	PDX1	pancreatic and duodenal homeobox 1	chr13q12.1	210938_at	NM_000209
3.98	4.30	0.33	7.42E-02	4.01E-01	---	---	---	228444_at	---
1.94	2.22	0.28	7.43E-02	4.01E-01	ALS2CR11	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	chr2q33.1	1558428_at	NM_152525
2.11	2.39	0.27	7.43E-02	4.01E-01	---	---	---	1554751_at	---
2.18	2.45	0.27	7.43E-02	4.01E-01	---	---	---	237857_at	---
2.14	2.39	0.25	7.43E-02	4.01E-01	---	---	---	235609_at	---
3.17	3.52	0.35	7.44E-02	4.01E-01	---	---	---	240684_at	---
2.59	2.94	0.35	7.44E-02	4.01E-01	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	chr9p24	206396_at	NM_004170
8.77	9.29	0.53	7.44E-02	4.01E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	200653_s_at	NM_001743 /// NM_005184 /// NM_006888
3.51	4.25	0.74	7.44E-02	4.01E-01	VPREB3	pre-B lymphocyte gene 3	chr22q11.23|22q11	220068_at	NM_013378
5.61	6.55	0.94	7.45E-02	4.02E-01	---	---	---	1562194_at	---
7.21	7.84	0.63	7.45E-02	4.02E-01	PLEKHB2	pleckstrin homology domain containing, family B (evectins) member 2	chr2q21.1	201411_s_at	NM_001100623 /// NM_017958
3.79	4.18	0.39	7.45E-02	4.02E-01	LOC440731	Similar to hCG1817424	chr1q42.2	1570243_at	XM_933693
2.70	3.07	0.37	7.45E-02	4.02E-01	FAM20A	family with sequence similarity 20, member A	chr17q24.2	242945_at	NM_017565
2.84	3.18	0.34	7.45E-02	4.02E-01	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	chr5q14.2	243477_at	NM_001131028 /// NM_031482
6.80	7.10	0.30	7.45E-02	4.02E-01	FAM62B	Family with sequence similarity 62 (C2 domain containing) member B	chr7q36.3	239334_at	NM_020728
2.07	2.30	0.23	7.45E-02	4.02E-01	PTEN	Phosphatase and tensin homolog	chr10q23.3	242622_x_at	NM_000314
1.79	2.02	0.23	7.45E-02	4.02E-01	KL	klotho	chr13q12	205978_at	NM_004795
2.19	3.08	0.90	7.45E-02	4.02E-01	AFF3	AF4/FMR2 family, member 3	chr2q11.2-q12	227198_at	NM_001025108 /// NM_002285
5.22	6.09	0.87	7.47E-02	4.02E-01	BPTF	bromodomain PHD finger transcription factor	chr17q24.3	207186_s_at	NM_004459 /// NM_182641
3.09	3.69	0.60	7.47E-02	4.02E-01	---	---	---	232916_at	---

4.99	5.59	0.60	7.46E-02	4.02E-01	STON1	stonin 1	chr2p16.3	213413_at	NM_006873
3.93	4.44	0.51	7.47E-02	4.02E-01	C10orf88	chromosome 10 open reading frame 88	chr10q26.13	222852_at	NM_024942
5.68	6.16	0.48	7.47E-02	4.02E-01	ARNT	aryl hydrocarbon receptor nuclear translocator	chr1q21	230619_at	NM_001668 /// NM_178426 /// NM_178427
2.30	2.69	0.38	7.47E-02	4.02E-01	FBXL14	F-box and leucine-rich repeat protein 14	chr12p13.33	1553683_s_at	NM_152441
3.76	4.13	0.38	7.46E-02	4.02E-01	LOC100128751	INM04	chr1q24.2	232623_at	XM_001719002 /// XM_001724165 /// XM_001726094
2.61	2.96	0.35	7.47E-02	4.02E-01	---	---	---	1556670_at	---
3.30	3.61	0.31	7.47E-02	4.02E-01	LOC100132618	hypothetical protein LOC100132618	chr1p31.1	231030_at	XM_001725824 /// XM_001726686 /// XM_001726739
4.46	4.67	0.21	7.47E-02	4.02E-01	NEURL	neuralized homolog (Drosophila)	chr10q25.1	204889_s_at	NM_004210
2.74	3.26	0.52	7.48E-02	4.02E-01	---	---	---	240214_at	---
4.19	4.45	0.26	7.48E-02	4.02E-01	---	---	---	1559806_at	---
4.96	5.31	0.36	7.48E-02	4.02E-01	TBXA2R	thromboxane A2 receptor	chr19p13.3	211590_x_at	NM_001060 /// NM_201636
3.74	4.18	0.45	7.48E-02	4.02E-01	C1orf69	chromosome 1 open reading frame 69	chr1q42.13	1558896_at	NM_001010867
4.53	4.89	0.36	7.48E-02	4.02E-01	HAB1	B1 for mucin	---	216878_x_at	---
6.67	7.03	0.36	7.48E-02	4.02E-01	AAK1	AP2 associated kinase 1	chr2p14	205434_s_at	NM_014911
2.48	2.81	0.34	7.48E-02	4.02E-01	---	---	---	1556401_a_at	---
6.20	6.92	0.72	7.49E-02	4.02E-01	IQWD1	IQ motif and WD repeats 1	chr1q24.2	232349_x_at	NM_001017977 /// NM_018442
2.45	2.67	0.22	7.49E-02	4.02E-01	CXCL14	chemokine (C-X-C motif) ligand 14	chr5q31	237038_at	NM_004887
3.67	3.93	0.27	7.49E-02	4.02E-01	---	---	---	239234_at	---
3.39	3.62	0.23	7.50E-02	4.02E-01	CLYBL	citrate lyase beta like	chr13q32	239683_at	NM_206808
6.30	6.89	0.59	7.50E-02	4.02E-01	GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide	chr9q21	224861_at	NM_002072
5.09	5.45	0.37	7.51E-02	4.02E-01	---	---	---	216736_at	---
2.63	2.99	0.36	7.51E-02	4.02E-01	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	chr2q33	208762_at	NM_001005781 /// NM_001005782 /// NM_003352
3.32	3.67	0.35	7.51E-02	4.02E-01	---	---	---	1569387_at	---
2.49	2.76	0.27	7.51E-02	4.02E-01	---	---	---	236009_at	---
2.55	2.78	0.23	7.51E-02	4.02E-01	MT1G	metallothionein 1G	chr16q13	210472_at	NM_005950
2.34	2.58	0.23	7.51E-02	4.02E-01	---	---	---	1563398_at	---
5.99	7.29	1.30	7.52E-02	4.02E-01	STAG2	stromal antigen 2	chrXq25	207983_s_at	NM_001042749 /// NM_001042750 /// NM_001042751 /// NM_006603
5.71	6.63	0.93	7.52E-02	4.02E-01	PECAM1	platelet/endothelial cell adhesion molecule	chr17q23	208981_at	NM_000442
6.64	7.04	0.40	7.51E-02	4.02E-01	ARF3	ADP-ribosylation factor 3	chr12q13	211622_s_at	NM_001659
3.30	3.62	0.32	7.52E-02	4.02E-01	KIAA0101	KIAA0101	chr15q22.31	211713_x_at	NM_001029989 /// NM_014736
2.19	2.43	0.25	7.52E-02	4.02E-01	PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	chr7p21.1	215486_at	NM_175886
4.92	5.47	0.55	7.52E-02	4.03E-01	CCPG1	cell cycle progression 1	chr15q21.1	214151_s_at	NM_004748 /// NM_020739
2.22	2.55	0.33	7.52E-02	4.03E-01	KLHL28	Kelch-like 28 (Drosophila)	chr14q21.3	243982_at	NM_017658
5.94	6.72	0.79	7.53E-02	4.03E-01	CPVL	carboxypeptidase, vitellogenic-like	chr7p15-p14	208146_s_at	NM_019029 /// NM_031311
3.29	3.57	0.28	7.53E-02	4.03E-01	---	---	---	1569776_at	---
4.23	4.47	0.24	7.53E-02	4.03E-01	---	---	---	231651_at	---
2.50	2.86	0.36	7.53E-02	4.03E-01	PCDHB7	protocadherin beta 7	chr5q31	231738_at	NM_018940
2.51	2.78	0.26	7.53E-02	4.03E-01	ADRA1D	adrenergic, alpha-1D-, receptor	chr20p13	210961_s_at	NM_000678
7.99	8.85	0.86	7.54E-02	4.03E-01	STEAP4	STEAP family member 4	chr7q21.12	225987_at	NM_024636
5.92	6.36	0.44	7.54E-02	4.03E-01	---	---	---	AFFX-BioB-3_at	---
5.83	6.17	0.34	7.54E-02	4.03E-01	TTLL3	tubulin tyrosine ligase-like family, member 3	chr3p25.3	203670_at	NM_001025930 /// NM_015644

2.13	2.43	0.30	7.54E-02	4.03E-01	LEPR	leptin receptor	chr1p31	207255_at	NM_001003679 /// NM_001003680 /// NM_002303																				
3.04	3.32	0.28	7.54E-02	4.03E-01	ONECUT2	one cut homeobox 2	chr18q21.1-q21.2	207676_at	NM_004852																				
2.00	2.23	0.23	7.54E-02	4.03E-01	---	---	---	1560797_s_at	---																				
3.76	4.45	0.69	7.55E-02	4.03E-01	---	---	---	230085_at	---																				
2.75	3.03	0.29	7.55E-02	4.03E-01	---	---	---	239424_at	---																				
2.13	2.40	0.27	7.55E-02	4.03E-01	---	---	---	238718_at	---																				
2.14	2.44	0.30	7.56E-02	4.04E-01	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	chr6q27	238871_at	NM_001040000 /// NM_001040001 /// NM_005936																				
5.00	5.57	0.57	7.56E-02	4.04E-01	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	chr4q21-q23	209614_at	NM_000668																				
3.33	3.66	0.32	7.56E-02	4.04E-01	ALPK1	alpha-kinase 1	chr4q25	243352_at	NM_001102406 /// NM_025144																				
2.37	2.64	0.28	7.56E-02	4.04E-01	---	---	---	241240_at	---																				
2.31	2.58	0.27	7.56E-02	4.04E-01	ZNF804A	zinc finger protein 804A	chr2q32.1	215767_at	NM_194250																				
7.22	7.74	0.51	7.57E-02	4.04E-01	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	chr5q31	200764_s_at	NM_001903																				
3.61	3.99	0.39	7.57E-02	4.04E-01	---	---	---	234891_at	---																				
2.36	2.69	0.33	7.57E-02	4.04E-01	FLJ20464	hypothetical protein FLJ20464	chr22q12.2	224073_at	XR_040036 /// XR_040037 /// XR_040038																				
1.93	2.21	0.28	7.57E-02	4.04E-01	ZNF391	zinc finger protein 391	chr6p22.1	1558658_at	NM_001076781																				
3.25	3.67	0.43	7.57E-02	4.04E-01	INTS3	integrator complex subunit 3	chr1q21.3	211132_at	NM_023015																				
3.44	3.76	0.32	7.57E-02	4.04E-01	KIAA0892	KIAA0892	chr19p13.11	216927_at	NM_015329																				
4.63	5.01	0.38	7.58E-02	4.04E-01	PDIA3	Protein disulfide isomerase family A, member 3	chr15q15	229453_at	NM_005313																				
3.84	4.26	0.42	7.58E-02	4.04E-01	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	chr3p14	240140_s_at	NM_015541																				
3.76	4.56	0.80	7.58E-02	4.04E-01	PIK3C2A	Phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	241905_at	NM_002645																				
7.79	8.56	0.77	7.59E-02	4.04E-01	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	chr2q24.2	212296_at	NM_005805																				
7.34	8.03	0.69	7.58E-02	4.04E-01	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	chr5q11.1	209303_at	NM_002495																				
3.62	4.19	0.56	7.58E-02	4.04E-01	CPD	carboxypeptidase D	chr17q11.2	201943_s_at	NM_001304																				
3.88	4.36	0.48	7.58E-02	4.04E-01	FGFR4	fibroblast growth factor receptor 4	chr5q35.1-qter	204579_at	NM_002011 /// NM_022963 /// NM_213647																				
2.24	2.56	0.32	7.58E-02	4.04E-01	---	---	---	1558803_at	---																				
7.81	8.12	0.30	7.59E-02	4.04E-01	COMMD1	copper metabolism (Murr1) domain containing 1	chr2p15	226024_at	NM_152516																				
3.19	3.47	0.28	7.59E-02	4.04E-01	---	---	---	243227_at	---																				
2.38	2.62	0.24	7.59E-02	4.04E-01	---	---	---	1564121_at	---																				
1.84	2.06	0.22	7.58E-02	4.04E-01	---	---	---	233392_at	---																				
6.27	6.65	0.38	7.60E-02	4.04E-01	---	---	---	AFFX-BioB-M_at	---																				
6.42	6.98	0.56	7.60E-02	4.04E-01	GCOM1 /// GRINL1A	GRINL1A complex locus /// glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	chr15q21.3 /// chr15q22.1	228568_at	NM_001018090 /// NM_001018091 /// NM_001018100 /// NM_001018102 /// NM_001018103 /// NM_015532 /// NM_152451																				
5.08	5.78	0.70	7.60E-02	4.05E-01	TRIM13	tripartite motif-containing 13	chr13q14	229943_at	NM_001007278 /// NM_005798 /// NM_052811 /// NM_213590																				
2.61	3.28	0.67	7.60E-02	4.05E-01	---	---	---	242126_at	---																				
5.71	6.24	0.52	7.60E-02	4.05E-01	---	---	---	213710_s_at	---																				
3.16	3.46	0.30	7.60E-02	4.05E-01	---	---	---	243914_at	---																				
2.56	2.85	0.29	7.60E-02	4.05E-01	---	---	---	242611_at	---																				
2.95	3.21	0.26	7.60E-02	4.05E-01	KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4	chr1p21	208251_at	NM_001039574 /// NM_004978 /// NM_153763																				

1.78	1.98	0.20	7.61E-02	4.05E-01	LOC100133319	PRO1804	chr17q24.3	224110_at	XM_001716232 /// XM_001725836 /// XM_001726474
5.83	6.56	0.73	7.61E-02	4.05E-01	POLR1D	polymerase (RNA) I polypeptide D, 16kDa	chr13q12.2	224874_at	NM_015972 /// NM_152705
2.07	2.36	0.29	7.61E-02	4.05E-01	LOC285194	hypothetical LOC285194	chr3q13.31	1558601_at	XR_040367 /// XR_040368 /// XR_040369
2.52	2.76	0.24	7.61E-02	4.05E-01	ZSCAN12	zinc finger and SCAN domain containing 12	chr6p22.2-p21.3	240181_at	XR_041200 /// XR_041201 /// XR_041202
2.19	2.50	0.31	7.61E-02	4.05E-01	PRKCE	Protein kinase C, epsilon	chr2p21	236459_at	NM_005400
8.12	8.68	0.55	7.62E-02	4.05E-01	LUM	lumican	chr12q21.3-q22	201744_s_at	NM_002345
3.18	3.47	0.28	7.62E-02	4.05E-01	---	---	---	241133_at	---
2.67	3.06	0.39	7.62E-02	4.05E-01	HOXD13	homeobox D13	chr2q31.1	207398_at	NM_000523
2.54	2.91	0.38	7.62E-02	4.05E-01	KLHL29	kelch-like 29 (Drosophila)	chr2p24.1	220348_at	XM_001717454 /// XM_001717533 /// XM_940375
3.44	3.76	0.32	7.63E-02	4.05E-01	SLC7A4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	chr22q11.21	214406_s_at	NM_004173
4.17	4.80	0.63	7.63E-02	4.05E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHG1 /// IGHG3 /// IGHM /// IGHV4-31 /// IGHV7-81 /// LOC100133739 /// LOC642131	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable 7-81 /// similar to hCG2038920 /// similar to hCG1812074	chr14q32.33 /// chr15q11.2	211635_x_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001718220
2.14	2.42	0.28	7.63E-02	4.05E-01	---	---	---	1561288_at	---
10.62	11.31	0.68	7.63E-02	4.05E-01	HSPA8	heat shock 70kDa protein 8	chr11q24.1	208687_x_at	NM_006597 /// NM_153201
2.66	3.00	0.34	7.63E-02	4.05E-01	---	---	---	238847_at	---
3.41	3.75	0.34	7.63E-02	4.05E-01	ZNF829	zinc finger protein 829	chr19q13.12	238952_x_at	NM_001037232
3.07	3.46	0.39	7.63E-02	4.05E-01	---	---	---	240315_at	---
3.30	3.86	0.56	7.64E-02	4.05E-01	CPEB1	cytoplasmic polyadenylation element binding protein 1	chr15q25.2	219578_s_at	NM_001079533 /// NM_001079534 /// NM_001079535 /// NM_030594
3.89	4.25	0.36	7.64E-02	4.05E-01	DDEF1	development and differentiation enhancing factor 1	chr8q24.1-q24.2	236533_at	NM_018482
8.93	9.46	0.53	7.64E-02	4.05E-01	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	chr5q31	210844_x_at	NM_001903
2.82	3.11	0.28	7.64E-02	4.05E-01	---	---	---	241400_at	---
2.23	2.46	0.23	7.64E-02	4.05E-01	---	---	---	1570264_at	---
5.29	6.74	1.45	7.64E-02	4.05E-01	JMJD1C	jumonji domain containing 1C	chr10q21.2-q21.3	224933_s_at	NM_004241 /// NM_032776
2.04	2.24	0.19	7.64E-02	4.05E-01	MYOT	myotilin	chr5q31	219728_at	NM_006790
2.07	2.28	0.22	7.65E-02	4.05E-01	IHPK3	inositol hexaphosphate kinase 3	chr6p21.31	231179_at	NM_054111
2.57	2.84	0.28	7.65E-02	4.06E-01	PSG1 /// PSG4	pregnancy specific beta-1-glycoprotein 1 /// pregnancy specific beta-1-glycoprotein 4	chr19q13.2	208191_x_at	NM_002780 /// NM_006905 /// NM_213633
3.05	3.39	0.34	7.66E-02	4.06E-01	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	chr1p31	227892_at	NM_006252
3.82	4.12	0.29	7.66E-02	4.06E-01	---	---	---	217390_x_at	---
5.02	5.31	0.29	7.66E-02	4.06E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	213688_at	NM_001743 /// NM_005184 /// NM_006888
2.34	2.77	0.44	7.66E-02	4.06E-01	---	---	---	240939_x_at	---
5.71	6.13	0.42	7.66E-02	4.06E-01	A4GALT	alpha 1,4-galactosyltransferase	chr22q11.2-q13.2	219488_at	NM_017436
5.64	6.25	0.61	7.67E-02	4.06E-01	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	chr11p15.1-p14	202451_at	NM_005316
2.28	2.68	0.41	7.68E-02	4.06E-01	---	---	---	1566959_at	---
2.04	2.29	0.25	7.67E-02	4.06E-01	LOC440981	similar to hCG1794790	chr3q24	241510_at	XM_001732842 /// XM_496663 /// XM_940896
2.81	3.05	0.24	7.67E-02	4.06E-01	---	---	---	230065_at	---
2.22	2.45	0.23	7.68E-02	4.06E-01	---	---	---	1563168_at	---

2.11	2.34	0.23	7.67E-02	4.06E-01	---	---	---	241011_at	---
2.70	3.09	0.39	7.68E-02	4.06E-01	---	---	---	229722_at	---
3.56	3.86	0.30	7.68E-02	4.06E-01	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	chr7q21-q22.1	243609_at	NM_000765
2.45	2.80	0.35	7.68E-02	4.06E-01	GHRHR	growth hormone releasing hormone receptor	chr7p14	211545_at	NM_000823 /// NM_001009824
4.14	4.70	0.55	7.69E-02	4.06E-01	PTPDC1	protein tyrosine phosphatase domain containing 1	chr9q22.32	238841_at	NM_152422 /// NM_177995
2.39	2.74	0.35	7.69E-02	4.06E-01	---	---	---	234172_at	---
2.33	2.60	0.27	7.69E-02	4.06E-01	C7orf53	chromosome 7 open reading frame 53	chr7q31.1	1569852_at	NM_001134468 /// NM_182597
2.05	2.36	0.31	7.69E-02	4.06E-01	ADRA1A	adrenergic, alpha-1A-, receptor	chr8p21-p11.2	211491_at	NM_000680 /// NM_033302 /// NM_033303 /// NM_033304
2.11	2.38	0.27	7.69E-02	4.06E-01	TP53INP1	Tumor protein p53 inducible nuclear protein 1	chr8q22	235602_at	NM_033285
7.18	7.56	0.38	7.70E-02	4.07E-01	CLPTM1	cleft lip and palate associated transmembrane protein 1	chr19q13.2-q13.3	201640_x_at	NM_001294
2.75	3.08	0.33	7.70E-02	4.07E-01	---	---	---	243745_at	---
3.18	3.47	0.29	7.70E-02	4.07E-01	LOC284373	Hypothetical protein LOC284373	chr19q13.41	236574_at	---
2.11	2.39	0.28	7.70E-02	4.07E-01	LOC652526 /// PDE4DIP	similar to phosphodiesterase 4D interacting protein isoform 2 /// phosphodiesterase 4D interacting protein	chr1q12	212392_s_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359 /// XM_942005
1.99	2.22	0.23	7.70E-02	4.07E-01	CR2	complement component (3d/Epstein Barr virus) receptor 2	chr1q32	244097_at	NM_001006658 /// NM_001877
8.86	9.41	0.55	7.71E-02	4.07E-01	RHBDD2	rhomboid domain containing 2	chr7q11.23	222995_s_at	NM_001040456 /// NM_001040457
4.47	4.99	0.53	7.71E-02	4.07E-01	ZNF148	zinc finger protein 148	chr3q21	239024_at	NM_021964
2.17	2.44	0.27	7.71E-02	4.07E-01	ZNF283	zinc finger protein 283	chr19q13.31	243188_at	NM_181845
2.54	3.05	0.51	7.71E-02	4.07E-01	SYT1	synaptotagmin I	chr12cen-q21	203999_at	NM_005639
2.73	3.16	0.43	7.71E-02	4.07E-01	DPF3	D4, zinc and double PHD fingers, family 3	chr14q24.3-q31.1	236442_at	NM_012074
2.33	2.62	0.29	7.71E-02	4.07E-01	DKFZp547J222	hypothetical LOC84237	chr4p15.33	234771_at	---
2.65	3.07	0.42	7.72E-02	4.07E-01	---	---	---	242421_at	---
1.99	2.24	0.25	7.72E-02	4.07E-01	---	---	---	237815_at	---
3.57	4.17	0.61	7.72E-02	4.07E-01	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	1563321_s_at	NM_001009569 /// NM_004641
3.30	3.61	0.31	7.72E-02	4.07E-01	C1orf183	chromosome 1 open reading frame 183	chr1p13.2	220476_s_at	NM_019099 /// NM_198926
4.63	5.12	0.49	7.72E-02	4.07E-01	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	chr12q24	242082_at	NM_052845
2.02	2.25	0.23	7.72E-02	4.07E-01	---	---	---	243850_at	---
6.94	7.43	0.49	7.73E-02	4.07E-01	APOO	apolipoprotein O	chrXp22.11	221620_s_at	NM_024122
2.00	2.25	0.25	7.73E-02	4.07E-01	PMCHL1	pro-melanin-concentrating hormone-like 1	chr5p14.3	224421_x_at	NR_003921
3.74	4.14	0.40	7.73E-02	4.07E-01	TMEM117	transmembrane protein 117	chr12q12	223594_at	NM_032256
2.31	2.59	0.28	7.73E-02	4.07E-01	hCG_1647286	hypothetical protein LOC728690	chr1p36.33	1563978_at	XM_001715625 /// XM_001718639 /// XM_001724958
3.05	3.33	0.28	7.73E-02	4.07E-01	LRRC23	leucine rich repeat containing 23	chr12p13	217609_at	NM_006992 /// NM_201650
5.42	5.74	0.31	7.73E-02	4.07E-01	ZNF793	zinc finger protein 793	chr19q13.12	244180_at	NM_001013659
5.05	6.59	1.54	7.74E-02	4.07E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	217148_x_at	---
1.97	2.28	0.31	7.74E-02	4.07E-01	LRRC34	leucine rich repeat containing 34	chr3q26.2	236918_s_at	NM_153353
3.27	3.54	0.26	7.74E-02	4.07E-01	LOC388419	galectin-3-binding protein-like	chr17q25.1	230445_at	NM_001080466
2.16	2.40	0.24	7.74E-02	4.07E-01	CCDC144C	coiled-coil domain containing 144C	chr17p11.2	1561271_at	NR_023380
4.78	5.00	0.22	7.74E-02	4.07E-01	---	---	---	241451_s_at	---
6.07	6.69	0.62	7.74E-02	4.07E-01	C14orf108	chromosome 14 open reading frame 108	chr14q23.1	218139_s_at	NM_018229

2.71	2.96	0.25	7.74E-02	4.07E-01	---	---	---	1557021_s_at	---
2.77	3.05	0.28	7.75E-02	4.07E-01	FBXO2	F-box protein 2	chr1p36.22	228036_s_at	NM_012168
3.91	4.92	1.01	7.75E-02	4.07E-01	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	chr5q33-q34	228602_at	NM_000337 /// NM_001128209 /// NM_172244
5.55	5.88	0.32	7.75E-02	4.07E-01	SIRT5	Sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	chr6p23	222080_s_at	NM_012241 /// NM_031244
3.04	3.45	0.42	7.76E-02	4.08E-01	---	---	---	238119_at	---
2.99	3.24	0.25	7.76E-02	4.08E-01	---	---	---	1562940_at	---
3.61	4.06	0.45	7.76E-02	4.08E-01	---	---	---	242080_at	---
2.60	2.88	0.28	7.76E-02	4.08E-01	CD48	CD48 molecule	chr1q21.3-q22	237759_at	NM_001778
3.03	3.32	0.29	7.76E-02	4.08E-01	GRAP2	GRB2-related adaptor protein 2	chr22q13.2	208406_s_at	NM_004810
6.02	6.38	0.36	7.77E-02	4.08E-01	MPRIP	myosin phosphatase Rho interacting protein	chr17p11.2	231255_at	NM_015134 /// NM_201274
2.88	3.19	0.31	7.77E-02	4.08E-01	C3orf32	chromosome 3 open reading frame 32	chr3p26.1	206741_at	NM_015931
2.65	2.96	0.31	7.77E-02	4.08E-01	LOC729285	hypothetical LOC729285	chr2p25.1	237880_at	XM_001129842 /// XM_001130009 /// XM_001716607
4.11	4.39	0.28	7.77E-02	4.08E-01	AK7	adenylate kinase 7	chr14q32.2	241326_at	NM_152327
4.35	4.62	0.27	7.77E-02	4.08E-01	PLXNB1	plexin B1	chr3p21.31	215668_s_at	NM_001130082 /// NM_002673
2.01	2.23	0.22	7.77E-02	4.08E-01	---	---	---	224050_s_at	---
3.71	4.14	0.43	7.78E-02	4.08E-01	---	---	---	232653_at	---
2.86	3.12	0.26	7.77E-02	4.08E-01	---	---	---	1569959_at	---
4.00	4.67	0.67	7.78E-02	4.08E-01	EXOC4	exocyst complex component 4	chr7q31	240528_s_at	NM_001037126 /// NM_021807
4.97	5.39	0.43	7.79E-02	4.08E-01	GPR153	G protein-coupled receptor 153	chr1p36.31	221902_at	NM_207370
4.36	4.75	0.39	7.79E-02	4.08E-01	---	---	---	1559667_at	---
2.89	3.28	0.39	7.78E-02	4.08E-01	---	---	---	240125_at	---
3.69	4.01	0.32	7.79E-02	4.08E-01	DHRS12	dehydrogenase/reductase (SDR family) member 12	chr13q14.3	204801_s_at	NM_001031719 /// NM_024705
3.24	3.54	0.30	7.78E-02	4.08E-01	CSF1	colony stimulating factor 1 (macrophage)	chr1p21-p13	211839_s_at	NM_000757 /// NM_172210 /// NM_172211 /// NM_172212
3.34	3.62	0.27	7.79E-02	4.08E-01	TRGV5	T cell receptor gamma variable 5	chr7p14	217381_s_at	---
1.90	2.14	0.24	7.78E-02	4.08E-01	---	---	---	217621_at	---
2.65	2.88	0.23	7.78E-02	4.08E-01	C9orf43	chromosome 9 open reading frame 43	chr9q32	1554280_a_at	NM_152786
1.99	2.21	0.22	7.79E-02	4.08E-01	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	chr7p12.1	244849_at	NM_006080
4.45	4.83	0.38	7.79E-02	4.08E-01	TMEM64	transmembrane protein 64	chr8q21.3	242338_at	NM_001008495
2.72	3.06	0.35	7.79E-02	4.08E-01	GALNT4 /// WDR51B	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) /// WD repeat domain 51B	chr12q21.3-q22 /// chr12q21.33	220442_at	NM_003774 /// NM_172240
2.29	2.64	0.34	7.79E-02	4.08E-01	WDR78	WD repeat domain 78	chr1p31.3	229816_at	NM_024763 /// NM_207014
4.03	4.30	0.28	7.79E-02	4.08E-01	---	---	---	241907_at	---
4.61	5.15	0.54	7.80E-02	4.08E-01	NCOA3	nuclear receptor coactivator 3	chr20q12	209060_x_at	NM_006534 /// NM_181659
5.15	5.53	0.37	7.80E-02	4.08E-01	KIAA0241	KIAA0241	chr7p14.3	212474_at	NM_015060
3.02	3.34	0.31	7.80E-02	4.08E-01	EML5	Echinoderm microtubule associated protein like 5	chr14q31.3	242443_at	NM_183387
2.71	2.97	0.26	7.80E-02	4.08E-01	ZNF787	zinc finger protein 787	chr19q13.42	1557888_at	NM_001002836
4.07	4.32	0.25	7.80E-02	4.08E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	208129_x_at	NM_001001890 /// NM_001122607 /// NM_001754
6.36	6.70	0.33	7.80E-02	4.08E-01	MUC3B	mucin 3B, cell surface associated	chr7q22	214898_x_at	XM_001125753 /// XM_001719326
5.62	6.21	0.60	7.81E-02	4.08E-01	TMEM140	transmembrane protein 140	chr7q33	218999_at	NM_018295
11.42	11.82	0.40	7.81E-02	4.08E-01	MGST1	microsomal glutathione S-transferase 1	chr12p12.3-p12.1	224918_x_at	NM_020300 /// NM_145764 /// NM_145791 /// NM_145792
6.38	6.76	0.38	7.81E-02	4.08E-01	TNRC6A	trinucleotide repeat containing 6A	chr16p11.2	243834_at	NM_014494
2.95	3.28	0.33	7.81E-02	4.08E-01	GPATCH4	G patch domain containing 4	chr1q22	221733_s_at	NM_015590 /// NM_182679

3.60	3.91	0.32	7.81E-02	4.08E-01	---	---	---	243202_at	---
4.63	4.89	0.27	7.81E-02	4.08E-01	RHPN1	rhophilin, Rho GTPase binding protein 1	chr8q24.3	235998_at	NM_052924
2.26	2.50	0.24	7.80E-02	4.08E-01	GRM7	glutamate receptor, metabotropic 7	chr3p26.1-p25.1	217008_s_at	NM_000844 /// NM_181874
1.82	2.03	0.21	7.81E-02	4.08E-01	---	---	---	240246_at	---
4.71	5.08	0.37	7.82E-02	4.08E-01	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	chr18q21	212448_at	NM_015277
3.56	3.93	0.36	7.82E-02	4.08E-01	DGCR9	DiGeorge syndrome critical region gene 9	chr22q11.21	215003_at	---
4.10	5.19	1.09	7.82E-02	4.08E-01	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	1553694_a_at	NM_002645
4.19	4.85	0.66	7.82E-02	4.08E-01	MYO10	myosin X	chr5p15.1-p14.3	201976_s_at	NM_012334
4.18	4.45	0.27	7.82E-02	4.08E-01	HRASLS2	HRAS-like suppressor 2	chr11q12.3	216759_at	NM_017878
3.57	4.02	0.45	7.83E-02	4.09E-01	---	---	---	232890_at	---
8.86	9.88	1.02	7.84E-02	4.09E-01	---	---	---	229606_at	---
7.53	8.50	0.96	7.83E-02	4.09E-01	RBPJ	recombination signal binding protein for immunoglobulin kappa J region	chr4p15.2	211974_x_at	NM_005349 /// NM_015874 /// NM_203283 /// NM_203284
2.89	3.27	0.39	7.84E-02	4.09E-01	DZIP3	DAZ interacting protein 3, zinc finger	chr3q13.13	207231_at	NM_014648
2.79	3.06	0.27	7.83E-02	4.09E-01	MUC4	mucin 4, cell surface associated	chr3q29	204895_x_at	NM_004532 /// NM_018406 /// NM_138297
3.97	4.24	0.26	7.83E-02	4.09E-01	---	---	---	1555374_at	---
2.96	3.18	0.22	7.83E-02	4.09E-01	LOC100129444	hypothetical protein LOC100129444	chr12q24.31	236272_at	XM_001716666 /// XM_001719053
4.03	4.80	0.77	7.84E-02	4.09E-01	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	chr1p13	201181_at	NM_006496
2.73	3.33	0.60	7.84E-02	4.09E-01	---	---	---	222313_at	---
2.00	2.25	0.26	7.85E-02	4.09E-01	LOC100129258	hypothetical protein LOC100129258	chr2q37.2	1557642_at	XM_001717571 /// XM_001721591 /// XM_001724116
2.85	3.19	0.34	7.86E-02	4.09E-01	FLJ16734	hypothetical LOC641928	chr7q36.2	243077_at	XR_040944 /// XR_040945 /// XR_040946
3.52	3.81	0.29	7.86E-02	4.09E-01	PLA2G12B	phospholipase A2, group XIIB	chr10q22.1	224411_at	NM_032562
2.22	2.96	0.74	7.86E-02	4.09E-01	NPAS3	neuronal PAS domain protein 3	chr14q12-q13	230412_at	NM_022123 /// NM_173159
2.34	2.62	0.28	7.86E-02	4.09E-01	FRY	furry homolog (Drosophila)	chr13q13.1	214318_s_at	NM_023037
2.01	2.21	0.21	7.86E-02	4.09E-01	---	---	---	1557439_at	---
3.89	4.21	0.32	7.87E-02	4.09E-01	ING3	inhibitor of growth family, member 3	chr7q31	242293_at	NM_019071 /// NM_198267
3.29	3.60	0.31	7.87E-02	4.09E-01	RAP2A	RAP2A, member of RAS oncogene family	chr13q34	214103_s_at	NM_021033
5.44	5.71	0.27	7.87E-02	4.09E-01	---	---	---	241467_at	---
4.26	4.59	0.33	7.88E-02	4.10E-01	---	---	---	239036_at	---
2.11	2.35	0.24	7.89E-02	4.10E-01	LOC283485	hypothetical protein LOC283485	chr13q34	1556476_at	---
4.23	4.54	0.31	7.89E-02	4.10E-01	GPRIN2	G protein regulated inducer of neurite outgrowth 2	chr10q11.22	206747_at	NM_014696
2.02	2.29	0.28	7.89E-02	4.10E-01	---	---	---	243865_x_at	---
4.55	5.16	0.61	7.90E-02	4.10E-01	ARID2	AT rich interactive domain 2 (ARID, RFX-like)	chr12q12	225490_at	NM_152641
3.05	3.53	0.49	7.90E-02	4.10E-01	---	---	---	1560171_at	---
6.64	7.01	0.37	7.89E-02	4.10E-01	DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22	chr12q13.12	244193_at	NM_024902
3.50	3.76	0.27	7.90E-02	4.10E-01	CHDH	choline dehydrogenase	chr3p21.1	231994_at	NM_018397
1.87	2.11	0.24	7.90E-02	4.10E-01	---	---	---	236198_at	---
2.80	3.15	0.35	7.91E-02	4.10E-01	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	chr17q23.3	221023_s_at	NM_030779 /// NM_173092
5.14	5.46	0.32	7.91E-02	4.10E-01	---	---	---	243374_x_at	---
2.25	2.54	0.29	7.91E-02	4.10E-01	KIAA0226	KIAA0226	chr3q29	1554612_at	NM_014687
1.83	2.10	0.27	7.91E-02	4.10E-01	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	chr16p13.2	242286_at	NM_000833 /// NM_001134407 /// NM_001134408
2.40	3.07	0.67	7.93E-02	4.10E-01	---	---	---	1563467_at	---
2.81	3.29	0.48	7.92E-02	4.10E-01	FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	chr1q22	217344_at	NM_002004
7.08	7.42	0.35	7.92E-02	4.10E-01	EPHB4	EPH receptor B4	chr7q22	216680_s_at	NM_004444
3.24	3.59	0.34	7.92E-02	4.10E-01	C20orf54	chromosome 20 open reading frame 54	chr20p13	228236_at	NM_033409
2.73	3.06	0.33	7.91E-02	4.10E-01	ITIH5	inter-alpha (globulin) inhibitor H5	chr10p14	219064_at	NM_001001851 /// NM_030569 /// NM_032817

3.93	4.24	0.31	7.92E-02	4.10E-01	SIGLEC8	sialic acid binding Ig-like lectin 8	chr19q13.33-q13.41	216327_s_at	NM_014442
2.61	2.88	0.27	7.92E-02	4.10E-01	---	---	---	236015_at	---
2.32	2.57	0.25	7.92E-02	4.10E-01	ITGB8	integrin, beta 8	chr7p15.3	242982_x_at	NM_002214
2.89	3.10	0.22	7.92E-02	4.10E-01	---	---	---	244772_at	---
2.33	2.55	0.21	7.91E-02	4.10E-01	---	---	---	244796_at	---
2.72	2.96	0.24	7.93E-02	4.11E-01	C5orf20 /// TIFAB	chromosome 5 open reading frame 20 /// TRAF-interacting protein with forkhead-associated domain, family member B	chr5q31.1	239529_at	NM_001099221 /// NM_130848
3.72	3.99	0.26	7.93E-02	4.11E-01	TMEM132A	transmembrane protein 132A	chr11q12.2	232419_at	NM_017870 /// NM_178031
2.06	2.39	0.32	7.93E-02	4.11E-01	---	---	---	230684_at	---
2.27	2.58	0.31	7.94E-02	4.11E-01	LRRC55	Leucine rich repeat containing 55	chr11q12.1	232856_at	NM_001005210
3.82	4.09	0.27	7.94E-02	4.11E-01	DIDO1	death inducer-obliterator 1	chr20q13.33	222595_s_at	NM_022105 /// NM_033081 /// NM_080796 /// NM_080797
3.05	3.57	0.52	7.94E-02	4.11E-01	---	---	---	233800_at	---
4.09	4.50	0.41	7.94E-02	4.11E-01	C4orf12	chromosome 4 open reading frame 12	chr4q21.3	1562953_s_at	NR_015359 /// XR_042111 /// XR_042112 /// XR_042113
4.00	4.44	0.44	7.95E-02	4.11E-01	CHST11	Carbohydrate (chondroitin 4) sulfotransferase 11	chr12q	226368_at	NM_018413
2.43	2.90	0.47	7.95E-02	4.11E-01	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	chr2p23.1	219271_at	NM_024572
3.63	3.91	0.29	7.95E-02	4.11E-01	KIAA1702	KIAA1702 protein	chr6p11	232029_at	XM_001722675 /// XM_001724453 /// XM_001726133
4.54	5.05	0.52	7.95E-02	4.11E-01	LARP4	La ribonucleoprotein domain family, member 4	chr12q13.13	238960_s_at	NM_052879 /// NM_199188 /// NM_199190
1.86	2.06	0.20	7.95E-02	4.11E-01	---	---	---	1559670_at	---
4.58	5.59	1.01	7.95E-02	4.11E-01	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	chr3p26-p25	211323_s_at	NM_001099952 /// NM_002222
5.90	6.44	0.53	7.95E-02	4.11E-01	ZBTB7A	zinc finger and BTB domain containing 7A	chr19p13.3	219186_at	NM_015898
6.25	6.87	0.63	7.95E-02	4.11E-01	PRKCI	protein kinase C, iota	chr3q26.3	209678_s_at	NM_002740
2.69	2.98	0.30	7.96E-02	4.11E-01	MAP3K2	mitogen-activated protein kinase kinase kinase 2	chr2q14.3	235011_at	NM_006609
3.23	3.50	0.27	7.96E-02	4.11E-01	AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	chr12p11.21 /// chr1p31.3	204347_at	NM_001002921 /// NM_001005353 /// NM_013410 /// NM_203464 /// XM_001132080 /// XM_001725174 /// XM_928632
4.07	4.34	0.27	7.96E-02	4.11E-01	---	---	---	211781_x_at	---
2.85	3.13	0.28	7.96E-02	4.11E-01	---	---	---	217239_x_at	---
3.37	3.69	0.32	7.97E-02	4.11E-01	STOX2	storkhead box 2	chr4q35.1	234317_s_at	NM_020225
2.18	2.50	0.31	7.97E-02	4.11E-01	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	chr17q22-q23	232020_at	NM_022739
2.86	3.15	0.29	7.97E-02	4.11E-01	LOC728012	hypothetical gene LOC728012	chr6q16.3	231129_at	XR_040015 /// XR_040016 /// XR_040017
2.18	2.41	0.24	7.97E-02	4.11E-01	C9orf102	chromosome 9 open reading frame 102	chr9q22.32	232801_at	NM_001010895 /// NM_001034155 /// NM_020207
4.43	4.75	0.32	7.97E-02	4.11E-01	---	---	---	244157_x_at	---
2.85	3.15	0.29	7.97E-02	4.11E-01	STXBP6	syntaxin binding protein 6 (amisyn)	chr14q12	226462_at	NM_014178
2.19	2.42	0.23	7.97E-02	4.11E-01	ZNF684	zinc finger protein 684	chr1p34.2	244398_x_at	NM_152373
2.09	2.28	0.20	7.97E-02	4.11E-01	C6orf54	chromosome 6 open reading frame 54	chr6q27	211351_at	NM_014354
7.96	9.23	1.27	7.99E-02	4.12E-01	COL3A1	collagen, type III, alpha 1	chr2q31	215076_s_at	NM_000090
2.59	2.93	0.34	7.98E-02	4.12E-01	LOC100132301	hypothetical protein LOC100132301	chr8p23.1	239642_at	XM_001720196 /// XM_001720295
3.56	3.89	0.33	7.99E-02	4.12E-01	DPF1	D4, zinc and double PHD fingers family 1	chr19q13.13-q13.2	206531_at	NM_004647

6.77	7.10	0.32	7.99E-02	4.12E-01	LOC100129701	Hypothetical protein LOC100129701	chr3q21.3	239662_x_at	XM_001723786 /// XM_001724509 /// XM_001725856																				
3.02	3.31	0.30	7.98E-02	4.12E-01	MEF2A	Myocyte enhancer factor 2A	chr15q26	242176_at	NM_001130926 /// NM_001130927 /// NM_001130928 /// NM_005587																				
6.32	6.59	0.27	7.98E-02	4.12E-01	SOCS1	suppressor of cytokine signaling 1	chr16p13.13	213337_s_at	NM_003745																				
5.77	6.02	0.25	7.99E-02	4.12E-01	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	chr11q13	206781_at	NM_005528																				
2.61	2.86	0.25	7.98E-02	4.12E-01	C1orf116	chromosome 1 open reading frame 116	chr1q32.1	228865_at	NM_001083924 /// NM_023938																				
2.05	2.28	0.22	7.99E-02	4.12E-01	---	---	---	240143_at	---																				
1.87	2.08	0.21	7.99E-02	4.12E-01	NLGN4Y	neuroligin 4, Y-linked	chrYq11.221	1554125_a_at	NM_014893																				
11.37	12.03	0.66	7.99E-02	4.12E-01	HSPD1	heat shock 60kDa protein 1 (chaperonin)	chr2q33.1	200807_s_at	NM_002156 /// NM_199440																				
2.40	2.74	0.34	7.99E-02	4.12E-01	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	chr5q21	230836_at	NM_005668 /// NM_175052																				
6.26	6.55	0.29	7.99E-02	4.12E-01	ATF5	activating transcription factor 5	chr19q13.3	217389_s_at	NM_012068																				
2.28	2.52	0.24	8.00E-02	4.12E-01	---	---	---	244143_at	---																				
4.00	4.58	0.58	8.01E-02	4.12E-01	DERL3	Der1-like domain family, member 3	chr22q11.23	229721_x_at	NM_001002862 /// NM_198440																				
3.99	4.42	0.43	8.01E-02	4.12E-01	MGC29506	hypothetical protein MGC29506	chr5q23-q31	221286_s_at	NM_016459																				
2.98	3.31	0.33	8.00E-02	4.12E-01	PPARGC1B	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	chr5q33.1	1555282_a_at	NM_133263																				
5.17	5.48	0.31	8.00E-02	4.12E-01	RBM47	RNA binding motif protein 47	chr4p13-p12	229439_s_at	NM_001098634 /// NM_019027																				
2.29	2.59	0.30	8.01E-02	4.12E-01	---	---	---	231639_at	---																				
2.02	2.29	0.28	8.00E-02	4.12E-01	IL4	interleukin 4	chr5q31.1	207539_s_at	NM_000589 /// NM_172348																				
3.52	3.77	0.25	8.01E-02	4.12E-01	---	---	---	236072_at	---																				
2.64	2.89	0.25	8.00E-02	4.12E-01	LPP	LIM domain containing preferred translocation partner in lipoma	chr3q28	230996_at	NM_005578																				
3.54	3.78	0.24	8.01E-02	4.12E-01	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	chr20q13.33	224171_at	NM_144703																				
2.06	2.30	0.23	8.00E-02	4.12E-01	---	---	---	1570196_at	---																				
2.18	2.38	0.20	8.01E-02	4.12E-01	---	---	---	243137_at	---																				
4.05	4.47	0.42	8.01E-02	4.12E-01	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	chr7q21.1	210998_s_at	NM_000601 /// NM_001010931 /// NM_001010932 /// NM_001010933 /// NM_001010934																				
4.91	5.23	0.33	8.01E-02	4.12E-01	MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	chr22q13.1	208058_s_at	NM_001098270 /// NM_002409																				
2.10	2.39	0.30	8.01E-02	4.12E-01	PDLIM4	PDZ and LIM domain 4	chr5q31.1	218691_s_at	NM_001131027 /// NM_003687																				
5.28	6.02	0.74	8.01E-02	4.12E-01	---	---	---	234998_at	---																				
4.14	5.00	0.87	8.02E-02	4.12E-01	UBXN7	UBX domain protein 7	chr3q29	217100_s_at	NM_015562																				
3.40	3.76	0.36	8.02E-02	4.12E-01	HOMER2	homer homolog 2 (Drosophila)	chr15q24.3	217080_s_at	NM_004839 /// NM_199330 /// NM_199331 /// NM_199332																				
3.39	3.64	0.25	8.03E-02	4.12E-01	---	---	---	242432_at	---																				
2.65	3.10	0.45	8.03E-02	4.12E-01	---	---	---	231109_at	---																				
2.23	2.44	0.20	8.03E-02	4.12E-01	---	---	---	216612_x_at	---																				
3.34	3.59	0.25	8.03E-02	4.12E-01	---	---	---	230798_at	---																				
3.08	3.35	0.26	8.04E-02	4.12E-01	ANKH	ankylosis, progressive homolog (mouse)	chr5p15.1	223093_at	NM_054027																				
2.40	2.76	0.36	8.04E-02	4.12E-01	---	---	---	232632_at	---																				
4.20	4.92	0.73	8.05E-02	4.12E-01	C2 /// CFB	complement component 2 /// complement factor B	chr6p21.3	202357_s_at	NM_000063 /// NM_001710																				
2.57	2.95	0.38	8.05E-02	4.12E-01	PITX1	paired-like homeodomain 1	chr5q31	208502_s_at	NM_002653																				
3.43	3.75	0.32	8.05E-02	4.12E-01	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	chr2q23.3	242569_at	NM_005843																				
1.99	2.29	0.30	8.05E-02	4.12E-01	---	---	---	241320_at	---																				

3.26	3.55	0.29	8.05E-02	4.12E-01	TADA2L	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	chr17q12-q21	210537_s_at	NM_001488 /// NM_133439
2.35	2.64	0.28	8.06E-02	4.12E-01	CEP152	centrosomal protein 152kDa	chr15q21.1	238535_at	NM_014985
2.05	2.33	0.28	8.05E-02	4.12E-01	ZNF780A /// ZNF780B	zinc finger protein 780A /// zinc finger protein 780B	chr19q13.2	215570_s_at	NM_001005851 /// NM_001010880
1.92	2.16	0.24	8.05E-02	4.12E-01	GALR1	galanin receptor 1	chr18q23	220821_at	NM_001480
2.00	2.24	0.24	8.05E-02	4.12E-01	---	---	---	230719_at	---
1.97	2.18	0.22	8.05E-02	4.12E-01	PRDM5	PR domain containing 5	chr4q25-q26	1569508_at	NM_018699
5.68	5.90	0.22	8.05E-02	4.12E-01	CHRNB2	cholinergic receptor, nicotinic, beta 2 (neuronal)	chr1q21.3	241389_at	NM_000748
3.55	3.96	0.41	8.06E-02	4.12E-01	IGHG1 /// LOC642131	Immunoglobulin heavy constant mu /// Similar to hCG1812074	chr14q32.33 /// chr15q11.2	217035_at	XM_001716198 /// XM_001716834 /// XM_001717736
6.00	6.76	0.77	8.08E-02	4.13E-01	MGC16169	hypothetical protein MGC16169	chr4q24	226126_at	NM_033115
3.81	4.49	0.68	8.07E-02	4.13E-01	ZFPM2	zinc finger protein, multitype 2	chr8q23	219778_at	NM_012082
4.56	5.20	0.64	8.06E-02	4.13E-01	ZNF451	zinc finger protein 451	chr6p12.1	215012_at	NM_001031623 /// NM_015555
3.39	3.78	0.39	8.07E-02	4.13E-01	NCOA2	nuclear receptor coactivator 2	chr8q13.3	205731_s_at	NM_006540
4.64	5.03	0.39	8.06E-02	4.13E-01	---	---	---	242657_at	---
2.76	3.09	0.33	8.07E-02	4.13E-01	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)	chr2p23	206938_at	NM_000348
3.41	3.73	0.32	8.07E-02	4.13E-01	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	chr19p13.11	211818_s_at	NM_000923 /// NM_001098818 /// NM_001098819
2.46	2.78	0.32	8.07E-02	4.13E-01	---	---	---	236678_at	---
4.11	4.41	0.30	8.06E-02	4.13E-01	---	---	---	233767_at	---
2.17	2.46	0.29	8.08E-02	4.13E-01	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	chr7p14.3	234233_s_at	NM_015483
2.75	3.03	0.29	8.07E-02	4.13E-01	---	---	---	238193_at	---
3.97	4.25	0.28	8.08E-02	4.13E-01	LOC100129105	Similar to hCG1821214	chr7q34	238016_s_at	XM_001714681 /// XM_001716713 /// XM_001717155
2.39	2.64	0.25	8.08E-02	4.13E-01	BCL2L14	BCL2-like 14 (apoptosis facilitator)	chr12p13-p12	221241_s_at	NM_030766 /// NM_138722 /// NM_138723 /// NM_138724
2.20	2.43	0.24	8.07E-02	4.13E-01	---	---	---	1562996_at	---
2.07	2.30	0.23	8.07E-02	4.13E-01	---	---	---	233869_x_at	---
2.06	2.28	0.23	8.07E-02	4.13E-01	---	---	---	241639_at	---
9.20	9.59	0.39	8.08E-02	4.13E-01	ECH1	enoyl Coenzyme A hydratase 1, peroxisomal	chr19q13.1	200789_at	NM_001398
5.46	5.89	0.44	8.08E-02	4.13E-01	GAL3ST4	galactose-3-O-sulfotransferase 4	chr7q22.1	219815_at	NM_024637
2.28	2.58	0.31	8.08E-02	4.13E-01	---	---	---	1570303_at	---
2.12	2.40	0.28	8.09E-02	4.13E-01	PLGLB1 /// PLGLB2	plasminogen-like B1 /// plasminogen-like B2	chr2p11-q11 /// chr2p11.2	214415_at	NM_001032392 /// NM_002665
2.94	3.20	0.27	8.08E-02	4.13E-01	IQCG	IQ motif containing G	chr3q29	1553757_at	NM_001134435 /// NM_032263
2.19	2.49	0.30	8.09E-02	4.13E-01	---	---	---	234625_at	---
4.68	5.02	0.34	8.09E-02	4.13E-01	---	---	---	231888_at	---
3.08	3.38	0.30	8.09E-02	4.13E-01	ATP2A3	ATPase, Ca++ transporting, ubiquitous	chr17p13.3	213042_s_at	NM_005173 /// NM_174953 /// NM_174954 /// NM_174955 /// NM_174956 /// NM_174957 /// NM_174958
6.35	6.63	0.27	8.09E-02	4.13E-01	SETD1A	SET domain containing 1A	chr16p11.2	213202_at	NM_014712
4.24	4.47	0.23	8.09E-02	4.13E-01	WDR31	WD repeat domain 31	chr9q32	241919_x_at	NM_001006615 /// NM_001012361 /// NM_145241
8.06	8.58	0.52	8.10E-02	4.13E-01	ARL8B	ADP-ribosylation factor-like 8B	chr3p26.2	217852_s_at	NM_018184
6.92	7.41	0.49	8.10E-02	4.13E-01	SNX9	sorting nexin 9	chr6q25.1-q26	223028_s_at	NM_016224
5.19	6.07	0.88	8.11E-02	4.13E-01	PAPD4	PAP associated domain containing 4	chr5q14.1	238706_at	NM_001114393 /// NM_001114394 /// NM_173797

4.39	5.13	0.74	8.10E-02	4.13E-01	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	chr1q25.2	227224_at	NM_018037 /// NM_152663
5.23	5.76	0.53	8.10E-02	4.13E-01	BAT2D1	BAT2 domain containing 1	chr1q23.3	211944_at	NM_015172
3.52	3.86	0.34	8.11E-02	4.13E-01	NSD1	nuclear receptor binding SET domain protein 1	chr5q35.2-q35.3	225654_at	NM_022455 /// NM_172349
2.80	3.14	0.34	8.10E-02	4.13E-01	NTF4	neurotrophin 4	chr19q13.3	231785_at	NM_006179
2.82	3.16	0.34	8.11E-02	4.13E-01	GNAT1	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1	chr3p21	207514_s_at	NM_000172 /// NM_144499
2.46	2.75	0.29	8.11E-02	4.13E-01	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	chr2p16	228421_s_at	NM_001039348 /// NM_001039349 /// NM_004105
2.11	2.39	0.28	8.10E-02	4.13E-01	---	---	---	217237_at	---
2.23	2.50	0.26	8.11E-02	4.13E-01	---	---	---	1569854_at	---
1.97	2.20	0.23	8.11E-02	4.13E-01	DUX1 /// DUX3 /// DUX5	double homeobox, 1 /// double homeobox, 3 /// double homeobox, 5	chr10q26.3	208582_s_at	NM_012146 /// NM_012148 /// NM_012149
1.96	2.18	0.23	8.10E-02	4.13E-01	---	---	---	244673_at	---
1.83	2.05	0.22	8.10E-02	4.13E-01	LOC728867	hypothetical LOC728867	chr17p13.1	243190_at	XM_001132876 /// XM_001133466 /// XM_001725020
6.21	6.59	0.38	8.11E-02	4.13E-01	GRASP	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	chr12q13.13	228263_at	NM_181711
2.57	3.00	0.43	8.11E-02	4.13E-01	---	---	---	1563468_at	---
2.87	3.25	0.38	8.12E-02	4.13E-01	---	---	---	235893_at	---
4.85	5.18	0.33	8.12E-02	4.13E-01	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	chr19p13.11	206791_s_at	NM_000923 /// NM_001098818 /// NM_001098819
4.43	4.73	0.30	8.12E-02	4.13E-01	---	---	---	216141_at	---
3.49	3.77	0.27	8.12E-02	4.13E-01	AHNAK	AHNAK nucleoprotein	chr11q12.2	238855_at	NM_001620 /// NM_024060
3.31	3.85	0.54	8.13E-02	4.13E-01	---	---	---	230254_at	---
6.93	7.25	0.32	8.13E-02	4.13E-01	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	chr15q22.3-q23	201051_at	NM_006305
3.37	3.66	0.29	8.13E-02	4.13E-01	KIRREL	kin of IRRE like (Drosophila)	chr1q21-q25	220825_s_at	NM_018240
4.73	5.14	0.41	8.14E-02	4.13E-01	PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	chr19q13.33	213368_x_at	NM_003660
2.06	2.29	0.24	8.15E-02	4.14E-01	BRUNOL4	bruno-like 4, RNA binding protein (Drosophila)	chr18q12	223654_s_at	NM_001025087 /// NM_001025088 /// NM_001025089 /// NM_020180
2.48	2.81	0.32	8.15E-02	4.14E-01	---	---	---	227929_at	---
5.63	6.53	0.91	8.15E-02	4.14E-01	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	chr12q12-q13.11	206989_s_at	NM_004719
4.24	4.90	0.66	8.16E-02	4.14E-01	DPEP1	dipeptidase 1 (renal)	chr16q24.3	205983_at	NM_001128141 /// NM_004413
5.62	6.11	0.49	8.15E-02	4.14E-01	VTA1	Vps20-associated 1 homolog (S. cerevisiae)	chr6q24.1	224437_s_at	NM_016485
2.38	2.72	0.33	8.16E-02	4.14E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHG1 /// IGHM /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	211636_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001724554 /// XM_941465
2.22	2.44	0.22	8.16E-02	4.14E-01	ALS2CR12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12	chr2q33.1	239458_at	NM_001127391 /// NM_139163
1.93	2.15	0.22	8.16E-02	4.14E-01	---	---	---	242406_at	---
2.83	3.10	0.26	8.16E-02	4.14E-01	RBM26	RNA binding motif protein 26	chr13q31.1	227355_at	NM_022118
2.06	2.31	0.25	8.16E-02	4.14E-01	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	chr1q32	244313_at	NM_000573 /// NM_000651
1.79	2.02	0.23	8.17E-02	4.14E-01	---	---	---	234827_at	---
3.35	3.89	0.54	8.17E-02	4.14E-01	---	---	---	244112_x_at	---
6.01	6.48	0.47	8.17E-02	4.14E-01	LOC645895	hypothetical LOC645895	chr8q13.1	231268_at	XM_928866 /// XM_938922
3.14	3.49	0.36	8.17E-02	4.14E-01	HAND2	heart and neural crest derivatives expressed 2	chr4q33	220480_at	NM_021973

2.22	2.56	0.34	8.17E-02	4.14E-01	SCN2B	sodium channel, voltage-gated, type II, beta	chr11q23	235225_at	NM_004588
2.98	3.22	0.24	8.17E-02	4.14E-01	TPSD1	tryptase delta 1	chr16p13.3	214568_at	NM_012217
4.79	6.14	1.35	8.18E-02	4.14E-01	OXR1	oxidation resistance 1	chr8q23	223879_s_at	NM_018002 /// NM_181354
3.02	3.68	0.66	8.18E-02	4.14E-01	---	---	---	236921_at	---
4.39	4.89	0.50	8.18E-02	4.14E-01	---	---	---	228172_at	---
5.05	5.48	0.44	8.18E-02	4.14E-01	SIGIRR	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	chr11p15.5	218921_at	NM_021805
3.67	4.07	0.40	8.18E-02	4.14E-01	LRFN1	leucine rich repeat and fibronectin type III domain containing 1	chr19q13.2	232486_at	NM_020862
5.65	5.99	0.34	8.18E-02	4.14E-01	MAN2C1	mannosidase, alpha, class 2C, member 1	chr15q11-q13	238230_x_at	NM_006715
4.02	4.36	0.34	8.18E-02	4.14E-01	SPTB	spectrin, beta, erythrocytic	chr14q23-q24.2	214145_s_at	NM_000347 /// NM_001024858
2.35	2.62	0.27	8.18E-02	4.14E-01	---	---	---	244851_at	---
2.27	2.49	0.22	8.18E-02	4.14E-01	LOC340581	hypothetical protein LOC340581	chrXq26.3	1563059_at	---
2.19	3.13	0.94	8.19E-02	4.14E-01	---	---	---	229118_at	---
4.27	4.77	0.50	8.19E-02	4.14E-01	C12orf4	chromosome 12 open reading frame 4	chr12p13.3	222613_at	NM_020374
2.36	2.67	0.32	8.19E-02	4.14E-01	LOC645355	hypothetical LOC645355	chr18p11.31	233610_at	XR_042014 /// XR_042015 /// XR_042016
1.82	2.03	0.21	8.19E-02	4.14E-01	---	---	---	1565875_at	---
2.08	2.27	0.19	8.19E-02	4.14E-01	SFRS3	Splicing factor, arginine/serine-rich 3	chr6p21	237485_at	NM_003017
4.85	5.15	0.30	8.19E-02	4.14E-01	HOXB3	homeobox B3	chr17q21.3	208414_s_at	NM_002146
5.76	6.39	0.63	8.20E-02	4.14E-01	CXXC5	CXXC finger 5	chr5q31.3	222996_s_at	NM_016463
3.90	4.26	0.37	8.20E-02	4.14E-01	SERPINA10	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	chr14q32.13	220626_at	NM_001100607 /// NM_016186
2.98	3.24	0.27	8.20E-02	4.14E-01	---	---	---	236986_at	---
2.55	2.88	0.33	8.20E-02	4.14E-01	ZNF717	zinc finger protein 717	chr3p12.3	240483_at	NM_001128223 /// XM_001714275 /// XM_001719548 /// XM_001719561
4.56	4.84	0.27	8.21E-02	4.14E-01	ARHGEF16	Rho guanine exchange factor (GEF) 16	chr1p36.3	208009_s_at	NM_014448
5.74	7.10	1.36	8.21E-02	4.15E-01	COL3A1	collagen, type III, alpha 1	chr2q31	211161_s_at	NM_000090
2.89	3.21	0.32	8.22E-02	4.15E-01	ASB10	ankyrin repeat and SOCS box-containing 10	chr7q36.1	1564537_a_at	NM_080871
3.44	3.75	0.31	8.22E-02	4.15E-01	---	---	---	233390_at	---
3.55	3.77	0.22	8.22E-02	4.15E-01	B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	chr11q13.4	1552834_at	NM_138706
2.23	2.44	0.20	8.22E-02	4.15E-01	C17orf39	Chromosome 17 open reading frame 39	chr17p11.2	241465_at	NM_024052
6.48	7.62	1.14	8.22E-02	4.15E-01	---	---	---	229823_at	---
2.40	2.74	0.34	8.22E-02	4.15E-01	---	---	---	236201_at	---
3.01	3.31	0.30	8.22E-02	4.15E-01	SYNPO2	synaptopodin 2	chr4q26	225894_at	NM_001128933 /// NM_001128934 /// NM_133477
2.05	2.27	0.22	8.22E-02	4.15E-01	ADCY2	adenylate cyclase 2 (brain)	chr5p15.3	213219_at	NM_020546
2.28	2.52	0.24	8.23E-02	4.15E-01	---	---	---	1569182_at	---
2.58	2.94	0.36	8.23E-02	4.15E-01	psiTPTE22	TPTE pseudogene	chr22q11.2	233469_at	NR_001591 /// XR_042159
6.58	6.95	0.36	8.23E-02	4.15E-01	SHARPIN	SHANK-associated RH domain interactor	chr8q24.3	220973_s_at	NM_030974
3.07	3.33	0.26	8.24E-02	4.15E-01	---	---	---	224287_at	---
4.37	5.58	1.21	8.24E-02	4.15E-01	WNK3	WNK lysine deficient protein kinase 3	chrXp11.23-p11.21	232282_at	NM_001002838 /// NM_020922
2.96	3.23	0.26	8.24E-02	4.15E-01	LOC728730	Hypothetical LOC728730	chr2p22.1	242835_s_at	XM_001132276 /// XM_001133148 /// XM_001718734
2.89	3.17	0.28	8.24E-02	4.15E-01	TM9SF3	Transmembrane 9 superfamily member 3	chr10q24.1	239626_x_at	NM_020123
4.48	5.32	0.84	8.25E-02	4.15E-01	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	chr5p13.1	230081_at	NM_001005473
5.29	5.84	0.55	8.25E-02	4.15E-01	EMILIN1	elastin microfibril interfacer 1	chr2p23.3-p23.2	204163_at	NM_007046
2.40	2.70	0.31	8.25E-02	4.15E-01	---	---	---	244238_at	---
2.46	2.73	0.27	8.25E-02	4.15E-01	LACE1	lactation elevated 1	chr6q22.1	1552490_at	NM_145315
2.30	2.55	0.25	8.25E-02	4.15E-01	WDR66	WD repeat domain 66	chr12q24.31	1555006_at	NM_144668
3.86	4.08	0.22	8.25E-02	4.15E-01	VIPR2	vasoactive intestinal peptide receptor 2	chr7q36.3	211598_x_at	NM_003382
2.32	2.52	0.20	8.25E-02	4.15E-01	---	---	---	1562817_at	---
4.24	4.82	0.58	8.26E-02	4.15E-01	DPT	dermatopontin	chr1q12-q23	213071_at	NM_001937

2.48	2.99	0.51	8.26E-02	4.15E-01	LIPA	lipase A, lysosomal acid, cholesterol esterase	chr10q23.2-q23.3	236156_at	NM_000235 /// NM_001127605
5.86	6.32	0.45	8.26E-02	4.15E-01	---	---	---	226756_at	---
6.57	6.94	0.37	8.26E-02	4.15E-01	CPEB3 /// LOC100130772	cytoplasmic polyadenylation element binding protein 3 /// hypothetical protein LOC100130772	chr10q23.32	243651_at	NM_014912 /// XM_001714491 /// XM_001717797 /// XM_001718020
3.39	3.66	0.27	8.26E-02	4.15E-01	GPR32	G protein-coupled receptor 32	chr19q13.3	221469_at	NM_001506
3.29	3.51	0.22	8.26E-02	4.15E-01	---	---	---	243123_at	---
3.37	4.11	0.74	8.27E-02	4.15E-01	---	---	---	228655_at	---
3.02	3.39	0.37	8.27E-02	4.15E-01	---	---	---	238072_at	---
3.76	4.06	0.31	8.27E-02	4.15E-01	tcag7.1228	hypothetical protein FLJ25778	chr7q34	238350_at	NM_173569
4.99	5.38	0.39	8.27E-02	4.16E-01	C3orf54	chromosome 3 open reading frame 54	chr3p21.31	229507_at	NM_203370
2.42	2.75	0.33	8.27E-02	4.16E-01	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	chr20q11.23	233813_at	NM_015568
2.57	2.89	0.32	8.27E-02	4.16E-01	ZFP64	Zinc finger protein 64 homolog (mouse)	chr20q13.2	229186_s_at	NM_018197 /// NM_022088 /// NM_199426 /// NM_199427
2.44	2.73	0.28	8.28E-02	4.16E-01	---	---	---	236299_at	---
2.05	2.32	0.27	8.28E-02	4.16E-01	CFHR3	complement factor H-related 3	chr1q32	1554459_s_at	NM_021023
2.34	2.60	0.26	8.28E-02	4.16E-01	MINA	MYC induced nuclear antigen	chr3q11.2	229675_at	NM_001042533 /// NM_032778 /// NM_153182
2.63	2.98	0.35	8.29E-02	4.16E-01	FLJ12825	hypothetical gene supported by AK022887; AK056417	chr12q13.13	233008_at	---
2.20	2.46	0.26	8.29E-02	4.16E-01	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	chr3p21.3	213597_s_at	NM_001008392 /// NM_005808
1.89	2.11	0.22	8.29E-02	4.16E-01	---	---	---	235506_at	---
4.50	5.95	1.46	8.29E-02	4.16E-01	MBNL1	muscleblind-like (Drosophila)	chr3q25	1558111_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297
2.99	3.32	0.33	8.30E-02	4.16E-01	---	---	---	233768_at	---
2.54	2.86	0.32	8.30E-02	4.16E-01	MGC40574	hypothetical protein MGC40574	chr2p21	1555124_at	XR_017938 /// XR_018006
2.46	2.77	0.31	8.30E-02	4.16E-01	UBASH3B	ubiquitin associated and SH3 domain containing, B	chr11q24.1	238587_at	NM_032873
4.04	4.91	0.87	8.31E-02	4.16E-01	---	---	---	1565598_at	---
6.50	7.30	0.80	8.31E-02	4.16E-01	RARS	arginyl-tRNA synthetase	chr5q35.1	201330_at	NM_002887
8.12	8.84	0.72	8.31E-02	4.16E-01	SEC31A	SEC31 homolog A (S. cerevisiae)	chr4q21.22	210616_s_at	NM_001077206 /// NM_001077207 /// NM_001077208 /// NM_014933 /// NM_016211
3.56	3.90	0.34	8.30E-02	4.16E-01	NLN	neurolysin (metallopeptidase M3 family)	chr5q12.3	225943_at	NM_020726
2.15	2.47	0.33	8.31E-02	4.16E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	1566269_at	NM_014990 /// NM_194301
5.38	5.69	0.31	8.30E-02	4.16E-01	GPR161	G protein-coupled receptor 161	chr1q24.2	232350_x_at	NM_007369 /// NM_153832
7.88	8.18	0.30	8.30E-02	4.16E-01	CPT1A	carnitine palmitoyltransferase 1A (liver)	chr11q13.1-q13.2	203633_at	NM_001031847 /// NM_001876
2.03	2.27	0.23	8.30E-02	4.16E-01	RBMY2FP	RNA binding motif protein, Y-linked, family 2, member F pseudogene	chrYq11.223	1552952_at	NR_002193
2.49	2.71	0.22	8.30E-02	4.16E-01	MUC17	mucin 17, cell surface associated	chr7q22.1	232321_at	NM_001040105 /// XM_001719956
6.68	7.30	0.61	8.31E-02	4.16E-01	IGF1R	insulin-like growth factor 1 receptor	chr15q26.3	203628_at	NM_000875
6.06	6.69	0.63	8.32E-02	4.16E-01	FBP1	fructose-1,6-bisphosphatase 1	chr9q22.3	209696_at	NM_000507 /// NM_001127628
7.78	8.22	0.43	8.32E-02	4.16E-01	GARS	glycyl-tRNA synthetase	chr7p15	208693_s_at	NM_002047
6.34	6.72	0.38	8.32E-02	4.16E-01	IGFALS	insulin-like growth factor binding protein, acid labile subunit	chr16p13.3	215712_s_at	NM_004970

2.56	2.90	0.34	8.32E-02	4.16E-01	PKNOX1	PBX/knotted 1 homeobox 1	chr21q22.3	204196_x_at	NM_004571
4.23	4.57	0.34	8.32E-02	4.16E-01	---	---	---	216789_at	---
3.75	4.85	1.10	8.32E-02	4.16E-01	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	chr21q22.3	211019_s_at	NM_001001438 /// NM_002340
5.57	6.05	0.47	8.33E-02	4.16E-01	ZFP91	zinc finger protein 91 homolog (mouse)	chr11q12	224631_at	NM_053023
2.10	2.37	0.27	8.33E-02	4.16E-01	---	---	---	216780_at	---
2.55	2.94	0.39	8.33E-02	4.17E-01	ZNF835	zinc finger protein 835	chr19q13.43	215826_x_at	NM_001005850
4.49	4.82	0.33	8.33E-02	4.17E-01	---	---	---	239112_at	---
2.38	2.63	0.25	8.33E-02	4.17E-01	---	---	---	1562137_at	---
4.59	5.39	0.80	8.33E-02	4.17E-01	C15orf27	chromosome 15 open reading frame 27	chr15q24.2	1552400_a_at	NM_152335
4.80	5.22	0.41	8.34E-02	4.17E-01	NKAIN1	Na+/K+ transporting ATPase interacting 1	chr1p35.2	219438_at	NM_024522
2.08	2.27	0.19	8.33E-02	4.17E-01	LOC100129266	Hypothetical protein LOC100129266	chr15q15.1	1557864_x_at	XM_001715005 /// XM_001717532 /// XM_001719008
2.22	2.40	0.18	8.34E-02	4.17E-01	---	---	---	235622_at	---
4.92	5.42	0.49	8.34E-02	4.17E-01	QSER1	glutamine and serine rich 1	chr11p13	229982_at	NM_001076786
3.72	4.00	0.28	8.34E-02	4.17E-01	FLT4	fms-related tyrosine kinase 4	chr5q35.3	234379_at	NM_002020 /// NM_182925
5.02	5.35	0.33	8.34E-02	4.17E-01	ZNF609	zinc finger protein 609	chr15q22.31	212620_at	NM_015042
2.39	2.67	0.28	8.34E-02	4.17E-01	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	chr21q22.13	211079_s_at	NM_001396 /// NM_101395 /// NM_130436 /// NM_130437 /// NM_130438
3.95	4.86	0.91	8.35E-02	4.17E-01	EBF1	early B-cell factor 1	chr5q34	232204_at	NM_024007
6.11	6.71	0.60	8.35E-02	4.17E-01	C14orf83	chromosome 14 open reading frame 83	chr14q24.1	227544_at	NM_182526
3.97	4.44	0.47	8.35E-02	4.17E-01	C1orf83	chromosome 1 open reading frame 83	chr1p32.3	238737_at	NM_153035
3.96	4.39	0.44	8.35E-02	4.17E-01	---	---	---	216707_at	---
4.07	4.46	0.39	8.35E-02	4.17E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	1553407_at	NM_012090 /// NM_033044
5.26	5.53	0.27	8.35E-02	4.17E-01	VCX2	variable charge, X-linked 2	chrXp22.32	207281_x_at	NM_016378
4.29	4.63	0.34	8.35E-02	4.17E-01	PCNX	pecanex homolog (Drosophila)	chr14q24.2	213173_at	NM_014982
2.04	2.30	0.27	8.36E-02	4.17E-01	CYBB	cytochrome b-245, beta polypeptide	chrXp21.1	217431_x_at	NM_000397
2.18	2.49	0.31	8.36E-02	4.17E-01	SNTG1	syntrophin, gamma 1	chr8q11-q12	234919_s_at	NM_018967
2.43	2.67	0.24	8.36E-02	4.17E-01	---	---	---	240410_at	---
3.47	4.37	0.90	8.36E-02	4.17E-01	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	chr8q21.13	225626_at	NM_018440
4.66	4.98	0.32	8.37E-02	4.17E-01	---	---	---	236784_s_at	---
2.03	2.34	0.32	8.36E-02	4.17E-01	ANKRD55	ankyrin repeat domain 55	chr5q11.2	220112_at	NM_001039935 /// NM_024669
6.48	7.50	1.02	8.37E-02	4.17E-01	OSBPL1A	oxysterol binding protein-like 1A	chr18q11.1	209485_s_at	NM_018030 /// NM_080597
5.92	6.59	0.67	8.37E-02	4.17E-01	---	---	---	223366_at	---
3.63	3.99	0.36	8.37E-02	4.17E-01	---	---	---	235823_at	---
2.88	3.40	0.53	8.38E-02	4.18E-01	---	---	---	234278_at	---
2.49	2.71	0.22	8.38E-02	4.18E-01	SERTAD4	SERTA domain containing 4	chr1q32.1-q41	233907_s_at	NM_019605
2.02	2.21	0.19	8.38E-02	4.18E-01	---	---	---	1567527_at	---
2.27	2.53	0.26	8.38E-02	4.18E-01	MLF1IP	MLF1 interacting protein	chr4q35.1	229305_at	NM_024629
4.33	5.09	0.76	8.39E-02	4.18E-01	ANKRD10	ankyrin repeat domain 10	chr13q34	226663_at	NM_017664
3.92	4.23	0.31	8.39E-02	4.18E-01	GSTTP1	glutathione S-transferase theta pseudogene 1	chr22q12	207215_at	NR_003081
5.27	5.53	0.26	8.39E-02	4.18E-01	NYX	nyctalopin	chrXp11.4	234496_x_at	NM_022567
2.62	2.87	0.24	8.40E-02	4.18E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	214360_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072
2.87	3.11	0.24	8.40E-02	4.18E-01	---	---	---	216112_at	---
2.94	3.41	0.47	8.40E-02	4.18E-01	ENPEP	glutamyl aminopeptidase (aminopeptidase A)	chr4q25	204844_at	NM_001977
3.73	4.28	0.55	8.41E-02	4.18E-01	CLIC2	chloride intracellular channel 2	chrXq28	213415_at	NM_001289
3.84	4.20	0.35	8.41E-02	4.18E-01	DZIP1L	DAZ interacting protein 1-like	chr3q22.3	239785_at	NM_173543
5.03	5.38	0.34	8.41E-02	4.18E-01	---	---	---	229948_at	---
4.04	4.31	0.27	8.41E-02	4.18E-01	---	---	---	233777_at	---

3.45	3.67	0.22	8.41E-02	4.18E-01	ZNF664	zinc finger protein 664	chr12q24.31	1558816_at	NM_152437
3.40	4.46	1.06	8.42E-02	4.19E-01	---	---	---	235693_at	---
2.12	2.38	0.26	8.42E-02	4.19E-01	LOC439949	hypothetical gene supported by AY007155	chr10p15.1	232001_at	XM_001128367 /// XM_001129241 /// XM_001723825
4.38	4.85	0.46	8.43E-02	4.19E-01	LOC100049716	hypothetical protein LOC100049716	chr12p13.33	228647_at	XR_041967 /// XR_041968 /// XR_041969
5.99	6.34	0.36	8.43E-02	4.19E-01	LOC284297	hypothetical LOC284297	chr19q13.42	230228_at	XM_001718392 /// XM_001718440 /// XM_001719242
2.74	3.09	0.35	8.42E-02	4.19E-01	ADAM33	ADAM metallopeptidase domain 33	chr20p13	232570_s_at	NM_025220 /// NM_153202
5.29	5.62	0.33	8.43E-02	4.19E-01	RCN3	reticulocalbin 3, EF-hand calcium binding domain	chr19q13.33	219102_at	NM_020650
4.86	5.14	0.28	8.42E-02	4.19E-01	LOC143188	hypothetical LOC143188	chr10q25.2	234054_at	XR_017700 /// XR_017867 /// XR_041028
3.07	3.39	0.32	8.43E-02	4.19E-01	TMC8	transmembrane channel-like 8	chr17q25.3	236554_x_at	NM_152468
5.22	6.25	1.04	8.43E-02	4.19E-01	CEP350	centrosomal protein 350kDa	chr1p36.13-q41	204373_s_at	NM_014810
2.35	2.77	0.42	8.43E-02	4.19E-01	RNF125	ring finger protein 125	chr18q12.1	235199_at	NM_017831
2.93	3.34	0.41	8.43E-02	4.19E-01	---	---	---	1558529_s_at	---
6.19	6.74	0.55	8.44E-02	4.19E-01	---	---	---	1556352_at	---
4.82	5.12	0.30	8.43E-02	4.19E-01	---	---	---	221715_at	---
3.44	3.77	0.33	8.44E-02	4.19E-01	MAPK8IP3	Mitogen-activated protein kinase 8 interacting protein 3	chr16p13.3	216137_s_at	NM_001040439 /// NM_015133
7.73	8.03	0.30	8.44E-02	4.19E-01	STX8	syntaxin 8	chr17p12	204690_at	NM_004853
2.46	2.72	0.25	8.44E-02	4.19E-01	ACOXL	acyl-Coenzyme A oxidase-like	chr2q13	240189_at	NM_001105516
2.54	2.83	0.29	8.44E-02	4.19E-01	CA6	carbonic anhydrase VI	chr1p36.2	206873_at	NM_001215
3.36	3.76	0.40	8.45E-02	4.19E-01	RAB17	RAB17, member RAS oncogene family	chr2q37.3	218931_at	NM_022449
3.69	4.27	0.58	8.45E-02	4.19E-01	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	chr6p21.1-p12.1	214153_at	NM_021814
2.53	2.85	0.32	8.45E-02	4.19E-01	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	chr12p12.1	204010_s_at	NM_004985 /// NM_033360
1.99	2.28	0.29	8.45E-02	4.19E-01	NCAM2	neural cell adhesion molecule 2	chr21q21.1	232390_at	NM_004540
9.31	9.63	0.31	8.45E-02	4.19E-01	EZR	ezrin	chr6q25.2-q26	208623_s_at	NM_001111077 /// NM_003379
2.73	3.25	0.51	8.45E-02	4.19E-01	WWP1	WW domain containing E3 ubiquitin protein ligase 1	chr8q21	212637_s_at	NM_007013
8.27	8.78	0.50	8.46E-02	4.19E-01	DEPDC6	DEP domain containing 6	chr8q24.12	218858_at	NM_022783
4.75	5.24	0.48	8.46E-02	4.19E-01	---	---	---	236571_at	---
4.66	5.50	0.84	8.47E-02	4.20E-01	---	---	---	232307_at	---
2.54	2.89	0.34	8.47E-02	4.20E-01	---	---	---	240256_at	---
2.95	3.33	0.38	8.47E-02	4.20E-01	KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	chr19q13.2	204401_at	NM_002250
6.71	7.07	0.36	8.48E-02	4.20E-01	CCM2	cerebral cavernous malformation 2	chr7p13	223164_at	NM_001029835 /// NM_031443
7.48	7.83	0.35	8.48E-02	4.20E-01	---	---	---	207730_x_at	---
4.25	4.60	0.35	8.48E-02	4.20E-01	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	chr22q12	213783_at	NM_002405
2.46	2.74	0.28	8.48E-02	4.20E-01	NEFM	neurofilament, medium polypeptide 150kDa	chr8p21	223902_at	NM_001105541 /// NM_005382
2.16	2.43	0.26	8.47E-02	4.20E-01	---	---	---	236740_at	---
1.85	2.11	0.26	8.48E-02	4.20E-01	---	---	---	232723_at	---
2.30	2.55	0.25	8.47E-02	4.20E-01	BRUNOL4	bruno-like 4, RNA binding protein (Drosophila)	chr18q12	231220_at	NM_001025087 /// NM_001025088 /// NM_001025089 /// NM_020180
2.36	2.60	0.24	8.48E-02	4.20E-01	HSH2D	hematopoietic SH2 domain containing	chr19p13.11	1552623_at	NM_032855
1.94	2.18	0.23	8.48E-02	4.20E-01	---	---	---	241420_at	---
1.90	2.14	0.23	8.48E-02	4.20E-01	LOC286434	hypothetical protein LOC286434	chrXp22.33	222196_at	XM_001717193
2.96	3.32	0.36	8.49E-02	4.20E-01	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	chr4p14-p13	216750_at	NM_173075
2.50	2.77	0.27	8.49E-02	4.20E-01	ZXDB	zinc finger, X-linked, duplicated B	chrXp11.21	216013_at	NM_007157
4.37	4.57	0.20	8.49E-02	4.20E-01	---	---	---	217162_at	---

3.39	3.80	0.41	8.49E-02	4.20E-01	CIB2	calcium and integrin binding family member 2	chr15q24	205007_s_at	NM_006383
2.76	3.11	0.35	8.49E-02	4.20E-01	FOXG1	forkhead box G1	chr14q13	207658_s_at	NM_005249
2.31	2.52	0.21	8.49E-02	4.20E-01	---	---	---	233081_at	---
4.85	5.35	0.49	8.50E-02	4.20E-01	CNOT6	CCR4-NOT transcription complex, subunit 6	chr5q35.3	222476_at	NM_015455
2.66	3.12	0.46	8.50E-02	4.20E-01	VDAC3	voltage-dependent anion channel 3	chr8p11.2	208844_at	NM_005662
3.41	3.83	0.42	8.51E-02	4.20E-01	RHOD	ras homolog gene family, member D	chr11q14.3	209885_at	NM_014578
3.43	3.82	0.39	8.50E-02	4.20E-01	LOC440731	Similar to hCG1817424	chr1q42.2	238973_s_at	XM_933693
6.50	6.87	0.37	8.52E-02	4.20E-01	SEC11C	SEC11 homolog C (S. cerevisiae)	chr18q21.32	223299_at	NM_033280
2.72	3.04	0.32	8.49E-02	4.20E-01	GRIA1	glutamate receptor, ionotropic, AMPA 1	chr5q33|5q31.1	209793_at	NM_000827 /// NM_001114183
2.41	2.72	0.31	8.51E-02	4.20E-01	---	---	---	1570230_at	---
2.85	3.14	0.30	8.51E-02	4.20E-01	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	chr2p23.3	233368_s_at	NM_016544
3.06	3.35	0.29	8.50E-02	4.20E-01	---	---	---	232324_x_at	---
3.37	3.65	0.28	8.50E-02	4.20E-01	PAX4	paired box 4	chr7q32	211176_s_at	NM_006193
2.74	3.02	0.28	8.51E-02	4.20E-01	---	---	---	217438_at	---
2.25	2.49	0.24	8.51E-02	4.20E-01	---	---	---	243244_at	---
2.19	2.43	0.24	8.52E-02	4.20E-01	---	---	---	241157_at	---
2.11	2.34	0.23	8.51E-02	4.20E-01	---	---	---	216761_at	---
4.76	4.98	0.22	8.51E-02	4.20E-01	TWF1	Twinfilin, actin-binding protein, homolog 1 (Drosophila)	chr12q12	244199_at	NM_002822
2.11	2.33	0.22	8.51E-02	4.20E-01	KIAA1622	KIAA1622	chr14q32.13	220672_at	NM_020958 /// NM_058237
2.31	2.53	0.21	8.50E-02	4.20E-01	PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	chr20q13.13	211907_s_at	NM_032521
2.19	2.45	0.26	8.53E-02	4.20E-01	---	---	---	243780_at	---
2.86	3.36	0.49	8.53E-02	4.20E-01	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	chr15q22.31	218349_s_at	NM_017975 /// NR_003105
2.75	3.03	0.28	8.53E-02	4.20E-01	NPPC	natriuretic peptide precursor C	chr2q24-qter	221348_at	NM_024409
2.32	2.66	0.34	8.53E-02	4.20E-01	PNOC	prepronociceptin	chr8p21	205901_at	NM_006228
2.69	2.91	0.22	8.53E-02	4.20E-01	ARHGEF4	Rho guanine nucleotide exchange factor (GEF) 4	chr2q22	216912_at	NM_015320 /// NM_032995
7.90	8.73	0.83	8.54E-02	4.20E-01	EIF5	eukaryotic translation initiation factor 5	chr14q32.32	208705_s_at	NM_001969 /// NM_183004
3.27	3.86	0.59	8.54E-02	4.20E-01	ACVR2A	activin A receptor, type IIA	chr2q22.3	228416_at	NM_001616
4.68	5.04	0.36	8.54E-02	4.20E-01	HFE	hemochromatosis	chr6p21.3	211863_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
2.36	2.69	0.33	8.54E-02	4.20E-01	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	chr9q31-q32	223859_at	NM_018424 /// NM_019114
2.57	2.88	0.31	8.54E-02	4.20E-01	---	---	---	243620_at	---
4.39	4.65	0.26	8.54E-02	4.20E-01	PRKCE	protein kinase C, epsilon	chr2p21	226101_at	NM_005400
2.78	2.99	0.21	8.55E-02	4.20E-01	NXF5	nuclear RNA export factor 5	chrXq22	234648_s_at	NM_032946
3.94	4.66	0.71	8.55E-02	4.20E-01	CPD	carboxypeptidase D	chr17q11.2	201940_at	NM_001304
4.64	5.92	1.28	8.55E-02	4.20E-01	---	---	---	228582_x_at	---
1.99	2.28	0.29	8.56E-02	4.20E-01	---	---	---	1567663_at	---
2.03	2.27	0.24	8.56E-02	4.21E-01	---	---	---	244604_at	---
5.41	5.95	0.54	8.57E-02	4.21E-01	---	---	---	229319_at	---
3.65	4.14	0.49	8.57E-02	4.21E-01	EIF5B	eukaryotic translation initiation factor 5B	chr2q11.2	201025_at	NM_015904
2.87	3.26	0.39	8.57E-02	4.21E-01	PNMA2	paraneoplastic antigen MA2	chr8p21.2	209598_at	NM_007257
3.74	4.10	0.36	8.57E-02	4.21E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	214634_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054

3.32	3.64	0.32	8.56E-02	4.21E-01	VWA3A	von Willebrand factor A domain containing 3A	chr16p12.1	238864_at	NM_173615
2.45	2.70	0.25	8.56E-02	4.21E-01	---	---	---	1569237_at	---
2.59	2.82	0.23	8.57E-02	4.21E-01	GPHB5	glycoprotein hormone beta 5	chr14q23.2	1553945_at	NM_145171
4.30	4.70	0.40	8.57E-02	4.21E-01	DMPK	Dystrophia myotonica-protein kinase	chr19q13.3	217062_at	NM_001081560 /// NM_001081562 /// NM_001081563 /// NM_004409
4.18	5.27	1.09	8.57E-02	4.21E-01	MAK10	MAK10 homolog, amino-acid N-acetyltransferase subunit (S. cerevisiae)	chr9q21.33	220925_at	NM_024635
2.85	3.26	0.41	8.58E-02	4.21E-01	RBM25	RNA binding motif protein 25	chr14q24.3	1557081_at	NM_021239
2.59	3.00	0.40	8.59E-02	4.21E-01	STOX1	storkhead box 1	chr10q21.3	1553202_at	NM_001130159 /// NM_001130160 /// NM_001130161 /// NM_001130162 /// NM_152709
2.21	2.46	0.25	8.59E-02	4.21E-01	SLC22A17	solute carrier family 22, member 17	chr14q11.2	221106_at	NM_016609 /// NM_020372
4.32	4.86	0.55	8.59E-02	4.21E-01	LMLN	leishmanolysin-like (metallopeptidase M8 family)	chr3q29	244881_at	NM_033029
5.84	6.20	0.36	8.59E-02	4.21E-01	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	chr17q21-q23	202630_at	NM_006380
2.08	2.29	0.21	8.60E-02	4.21E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	208026_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054
4.26	4.72	0.46	8.60E-02	4.22E-01	WDR35	WD repeat domain 35	chr2p24.1	226889_at	NM_001006657 /// NM_020779
2.02	2.30	0.28	8.63E-02	4.23E-01	CNPY1	canopy 1 homolog (zebrafish)	chr7q36.3	1559283_a_at	NM_001103176
2.34	2.55	0.21	8.64E-02	4.23E-01	TTLL5	tubulin tyrosine ligase-like family, member 5	chr14q24.3	215898_at	NM_015072
2.06	2.28	0.22	8.64E-02	4.23E-01	TMEM144	transmembrane protein 144	chr4q32.1	1558452_at	NM_018342
2.91	3.19	0.28	8.64E-02	4.23E-01	C17orf80	chromosome 17 open reading frame 80	chr17q25.1	221048_x_at	NM_001100621 /// NM_001100622 /// NM_017941
2.24	2.52	0.28	8.64E-02	4.23E-01	---	---	---	1562928_at	---
6.34	7.01	0.67	8.64E-02	4.23E-01	EIF5B	eukaryotic translation initiation factor 5B	chr2q11.2	201027_s_at	NM_015904
2.03	2.27	0.24	8.65E-02	4.23E-01	C18orf2	chromosome 18 open reading frame 2	---	223977_s_at	NM_031416 /// NR_023925 /// NR_023926 /// NR_023927 /// NR_023928
2.21	2.48	0.27	8.65E-02	4.23E-01	LOC283904	hypothetical protein LOC283904	chr16q24.1	243059_at	XM_001713951 /// XM_001718298 /// XM_001719681
2.93	3.25	0.32	8.65E-02	4.23E-01	KLF8	Kruppel-like factor 8	chrXp11.21	230986_at	NM_007250
2.95	3.29	0.34	8.66E-02	4.24E-01	C4orf32	chromosome 4 open reading frame 32	chr4q25	240465_at	NM_152400
2.05	2.32	0.27	8.66E-02	4.24E-01	---	---	---	217533_x_at	---
4.50	5.04	0.54	8.66E-02	4.24E-01	MCAM	melanoma cell adhesion molecule	chr11q23.3	209086_x_at	NM_006500
3.51	3.83	0.32	8.66E-02	4.24E-01	---	---	---	237264_at	---

3.13	3.46	0.34	8.66E-02	4.24E-01	---	---	---	234555_at	---
4.49	4.88	0.39	8.66E-02	4.24E-01	ANKRD35	ankyrin repeat domain 35	chr1q21.1	231118_at	NM_144698
3.63	3.90	0.26	8.66E-02	4.24E-01	PHOX2A	paired-like homeobox 2a	chr11q13.2	214609_at	NM_005169
6.64	7.50	0.86	8.67E-02	4.24E-01	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	chr5q31.3	201865_x_at	NM_000176 /// NM_001018074 /// NM_001018075 /// NM_001018076 /// NM_001018077 /// NM_001020825 /// NM_001024094
4.08	4.57	0.49	8.67E-02	4.24E-01	CNFN	cornifelin	chr19q13.2	224329_s_at	NM_032488
2.56	2.84	0.28	8.67E-02	4.24E-01	---	---	---	1564789_at	---
1.97	2.25	0.28	8.67E-02	4.24E-01	---	---	---	1570593_at	---
2.64	2.85	0.21	8.68E-02	4.24E-01	LOC126536	hypothetical protein LOC126536	chr19p13.12	1555988_a_at	XR_041168 /// XR_041169 /// XR_041170
5.89	6.22	0.32	8.68E-02	4.24E-01	ITFG3	integrin alpha FG-GAP repeat containing 3	chr16p13.3	224749_at	NM_032039
2.43	2.68	0.25	8.69E-02	4.24E-01	IGF1R	insulin-like growth factor 1 receptor	chr15q26.3	208441_at	NM_000875
4.56	4.83	0.27	8.69E-02	4.24E-01	NES	nestin	chr1q23.1	229346_at	NM_006617
3.50	3.90	0.39	8.69E-02	4.24E-01	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16	chr1p36.1	217358_at	NM_015291
4.04	4.71	0.67	8.70E-02	4.25E-01	ZNF43	zinc finger protein 43	chr19p13.1-p12	206695_x_at	NM_003423
3.55	3.84	0.30	8.70E-02	4.25E-01	---	---	---	244728_at	---
2.60	3.01	0.41	8.70E-02	4.25E-01	COL14A1	collagen, type XIV, alpha 1	chr8q23	212865_s_at	NM_021110
3.23	3.58	0.35	8.70E-02	4.25E-01	USP53	ubiquitin specific peptidase 53	chr4q26	237465_at	NM_019050
2.25	2.47	0.23	8.70E-02	4.25E-01	IMPG2	interphotoreceptor matrix proteoglycan 2	chr3q12.2-q12.3	220830_at	NM_016247
3.72	3.96	0.23	8.71E-02	4.25E-01	C21orf96	chromosome 21 open reading frame 96	chr21q22.12	220918_at	XR_039434 /// XR_040895 /// XR_040896
3.63	3.93	0.30	8.71E-02	4.25E-01	LHX1	LIM homeobox 1	chr17q12	206230_at	NM_005568
2.04	2.30	0.26	8.71E-02	4.25E-01	---	---	---	1560962_at	---
4.77	5.43	0.66	8.71E-02	4.25E-01	TMEM64	transmembrane protein 64	chr8q21.3	225972_at	NM_001008495
6.63	6.95	0.32	8.71E-02	4.25E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	228823_at	NR_003655 /// XR_042143 /// XR_042182
6.22	6.51	0.29	8.71E-02	4.25E-01	RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	chr2q37.3	218301_at	NM_018226
3.21	3.71	0.50	8.72E-02	4.25E-01	---	---	---	230180_at	---
3.28	3.68	0.40	8.72E-02	4.25E-01	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	chr16p12	219697_at	NM_006043
4.60	5.47	0.87	8.72E-02	4.25E-01	NARG1	NMDA receptor regulated 1	chr4q31.1	219158_s_at	NM_057175
2.11	2.44	0.32	8.73E-02	4.25E-01	MAN1A2	mannosidase, alpha, class 1A, member 2	chr1p13	217282_at	NM_006699
2.30	2.59	0.28	8.73E-02	4.25E-01	CDH11	Cadherin 11, type 2, OB-cadherin (osteoblast)	chr16q22.1	239769_at	NM_001797
5.15	5.40	0.25	8.73E-02	4.25E-01	C16orf88	chromosome 16 open reading frame 88	chr16p12.3	213235_at	NM_001012991
2.40	2.59	0.19	8.73E-02	4.25E-01	PLAC4	placenta-specific 4	chr21q22.3	227519_at	NM_182832
2.27	2.51	0.24	8.74E-02	4.26E-01	SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	chr3p25-p24	205152_at	NM_003042
2.59	2.90	0.31	8.74E-02	4.26E-01	---	---	---	234177_at	---
2.18	2.52	0.34	8.74E-02	4.26E-01	---	---	---	240899_at	---
6.46	7.52	1.06	8.76E-02	4.26E-01	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta	chr2p22.2	203341_at	NM_005760
7.46	8.41	0.95	8.76E-02	4.26E-01	DLD	dihydrolipoamide dehydrogenase	chr7q31-q32	209095_at	NM_000108
6.08	6.70	0.62	8.76E-02	4.26E-01	EPB41L1	erythrocyte membrane protein band 4.1-like 1	chr20q11.2-q12	212336_at	NM_012156 /// NM_177996
3.33	3.86	0.53	8.76E-02	4.26E-01	---	---	---	1560926_at	---
5.51	5.94	0.43	8.75E-02	4.26E-01	---	---	---	227031_at	---
4.78	5.20	0.43	8.76E-02	4.26E-01	PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	chr19q13.33	215280_s_at	NM_003660
3.98	4.35	0.37	8.75E-02	4.26E-01	ENAH	enabled homolog (Drosophila)	chr1q42.12	228310_at	NM_001008493 /// NM_018212
1.94	2.29	0.35	8.76E-02	4.26E-01	DNAJC24	DnaJ (Hsp40) homolog, subfamily C, member 24	chr11p13	242562_at	NM_181706
3.09	3.40	0.32	8.76E-02	4.26E-01	LOC644714	hypothetical protein LOC644714	chr3p21.31	233541_at	XM_001724774 /// XM_934514 /// XM_945782
3.99	4.28	0.29	8.76E-02	4.26E-01	WDR68	WD repeat domain 68	chr17q23.3	236134_at	NM_005828
2.94	3.20	0.26	8.75E-02	4.26E-01	STAG3L4	Stromal antigen 3-like 4	chr7p11.2-q11.2	231521_at	NM_022906
2.13	2.34	0.21	8.75E-02	4.26E-01	---	---	---	234636_at	---
2.80	3.19	0.39	8.76E-02	4.26E-01	---	---	---	243050_at	---
3.94	4.22	0.28	8.77E-02	4.26E-01	---	---	---	231079_at	---
7.14	7.50	0.37	8.77E-02	4.26E-01	ZBTB7B	zinc finger and BTB domain containing 7B	chr1q21.3	235145_at	NM_015872

3.23	3.81	0.58	8.78E-02	4.26E-01	SUSD4	sushi domain containing 4	chr1q41	219389_at	NM_001037175 /// NM_017982
4.11	4.37	0.27	8.78E-02	4.26E-01	FNDC5	Fibronectin type III domain containing 5	chr1p35.1	230646_at	NM_153756
2.63	2.90	0.27	8.78E-02	4.26E-01	---	---	---	233107_at	---
3.69	4.02	0.33	8.78E-02	4.26E-01	DACT3	Dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	chr19q13.32	229745_x_at	NM_145056
5.30	5.97	0.67	8.78E-02	4.26E-01	DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14	chr4q23	219237_s_at	NM_001031723 /// NM_024920
3.50	3.88	0.38	8.79E-02	4.26E-01	CDH6	Hypothetical protein LOC100128783	chr5p15.1-p14	232631_at	NM_004932
1.82	2.09	0.27	8.79E-02	4.26E-01	---	---	---	1558449_at	---
2.21	2.47	0.26	8.79E-02	4.27E-01	---	---	---	237628_at	---
3.28	3.56	0.28	8.80E-02	4.27E-01	STRC	stereocilin	chr15q15.3	240048_at	NM_153700 /// XM_001715128 /// XM_001718339
5.39	6.56	1.17	8.80E-02	4.27E-01	---	---	---	225856_at	---
2.19	2.53	0.34	8.80E-02	4.27E-01	---	---	---	244869_at	---
2.03	2.26	0.23	8.80E-02	4.27E-01	ZNF702P	zinc finger protein 702 pseudogene	chr19q13.41	206557_at	NR_003578
5.35	5.83	0.48	8.81E-02	4.27E-01	RAB3A	RAB3A, member RAS oncogene family	chr19p13.2	204974_at	NM_002866
3.31	3.62	0.31	8.81E-02	4.27E-01	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	chr10q25.3	222072_at	NM_020383
2.10	2.34	0.24	8.81E-02	4.27E-01	---	---	---	231160_at	---
2.06	2.28	0.23	8.81E-02	4.27E-01	LECT2	leukocyte cell-derived chemotaxin 2	chr5q31.1-q32	207409_at	NM_002302
2.41	2.62	0.20	8.81E-02	4.27E-01	---	---	---	1561311_at	---
6.35	6.71	0.36	8.81E-02	4.27E-01	LDB1	LIM domain binding 1	chr10q24-q25	203451_at	NM_001113407 /// NM_003893
2.50	2.73	0.24	8.82E-02	4.27E-01	IRG1	immunoresponsive 1 homolog (mouse)	chr13q22.3	240287_at	XM_001127275 /// XM_001133269 /// XM_001722295
4.55	4.90	0.35	8.83E-02	4.27E-01	APLN	apelin	chrXq25-q26.3	222856_at	NM_017413
1.95	2.25	0.31	8.83E-02	4.27E-01	CADPS	Ca++-dependent secretion activator	chr3p14.2	204814_at	NM_003716 /// NM_183393 /// NM_183394
3.08	3.44	0.36	8.83E-02	4.27E-01	PUM2	Pumilio homolog 2 (Drosophila)	chr2p22-p21	235995_at	NM_015317
2.98	3.33	0.35	8.84E-02	4.27E-01	---	---	---	234267_at	---
2.43	2.72	0.29	8.84E-02	4.27E-01	DKFZP434C153	DKFZP434C153 protein	chr1q42.13	216085_at	---
2.63	2.89	0.26	8.84E-02	4.27E-01	hCG_1776018	phosphoinositide-interacting regulator of transient receptor potential channels	chr17p13.1	232887_at	NM_001101387
4.02	4.26	0.24	8.84E-02	4.27E-01	ADAM28	ADAM metallopeptidase domain 28	chr8p21.2	208269_s_at	NM_014265 /// NM_021777
1.90	2.10	0.20	8.84E-02	4.27E-01	NPY2R	neuropeptide Y receptor Y2	chr4q31	210729_at	NM_000910
2.21	2.40	0.19	8.83E-02	4.27E-01	---	---	---	1566485_at	---
2.38	2.62	0.24	8.84E-02	4.27E-01	OR10D1P	olfactory receptor, family 10, subfamily D, member 1 pseudogene	chr11q24.2	1567254_at	---
4.25	4.47	0.22	8.84E-02	4.27E-01	---	---	---	233313_at	---
4.64	4.93	0.29	8.84E-02	4.27E-01	---	---	---	237533_at	---
2.09	2.27	0.18	8.84E-02	4.27E-01	---	---	---	1568795_at	---
4.39	4.75	0.36	8.84E-02	4.27E-01	DKFZP434A062	DKFZP434A062 protein	chr9q34.3	216608_at	XM_001719952 /// XM_001722610 /// XM_001723271
1.90	2.10	0.20	8.84E-02	4.27E-01	DIRAS2	DIRAS family, GTP-binding RAS-like 2	chr9q22.2	219619_at	NM_017594
4.38	4.70	0.33	8.85E-02	4.28E-01	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	chr19q13.2	208052_x_at	NM_001815
3.45	3.89	0.43	8.85E-02	4.28E-01	KLF14	Kruppel-like factor 14	chr7q32.2	1552813_at	NM_138693
3.16	3.48	0.32	8.85E-02	4.28E-01	GPR182	G protein-coupled receptor 182	chr12q13.3	214506_at	NM_007264
2.71	2.95	0.24	8.86E-02	4.28E-01	OTOF	otoferlin	chr2p23.1	220492_s_at	NM_004802 /// NM_194248 /// NM_194322 /// NM_194323
3.96	4.18	0.22	8.86E-02	4.28E-01	PHLDA2	pleckstrin homology-like domain, family A, member 2	chr11p15.5	209802_at	NM_003311
6.53	7.01	0.47	8.86E-02	4.28E-01	ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	chr1p21.3	1553954_at	NM_144988
2.52	2.74	0.23	8.86E-02	4.28E-01	ZP2	zona pellucida glycoprotein 2 (sperm receptor)	chr16p12	207933_at	NM_003460
3.10	3.36	0.27	8.86E-02	4.28E-01	TBC1D2B	TBC1 domain family, member 2B	chr15q24.3-q25.1	215951_at	NM_015079 /// NM_144572
2.77	3.08	0.30	8.87E-02	4.28E-01	BSPRY	B-box and SPRY domain containing	chr9q32	222746_s_at	NM_017688
5.10	6.11	1.01	8.87E-02	4.28E-01	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	chr12p11	202662_s_at	NM_002223
7.21	7.58	0.37	8.87E-02	4.28E-01	---	---	---	AFFX-BioC-3_at	---
2.52	2.85	0.33	8.87E-02	4.28E-01	CD72	CD72 molecule	chr9p13.3	215925_s_at	NM_001782
2.45	2.81	0.36	8.87E-02	4.28E-01	FAM82A1	family with sequence similarity 82, member A1	chr2p22.2	1560042_at	NM_144713
2.92	3.20	0.28	8.87E-02	4.28E-01	C7orf41	chromosome 7 open reading frame 41	chr7p15.1	227000_at	NM_152793

4.18	4.51	0.32	8.88E-02	4.28E-01	C18orf49	chromosome 18 open reading frame 49	chr18q21.33	232222_at	---
4.34	4.69	0.35	8.88E-02	4.28E-01	LOC90379	Hypothetical protein BC002926	chr19p13.12	222012_at	NM_138353
1.94	2.13	0.19	8.88E-02	4.28E-01	GLS	glutaminase	chr2q32-q34	241034_at	NM_014905
3.27	3.94	0.66	8.89E-02	4.29E-01	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	chr5q33-q34	230730_at	NM_000337 /// NM_001128209 /// NM_172244
4.77	5.14	0.36	8.89E-02	4.29E-01	SOX10	SRY (sex determining region Y)-box 10	chr22q13.1	209843_s_at	NM_006941
3.06	3.35	0.29	8.89E-02	4.29E-01	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	chr19q13.2	211657_at	NM_002483
4.01	4.32	0.31	8.89E-02	4.29E-01	---	---	---	232835_at	---
6.00	6.56	0.55	8.89E-02	4.29E-01	---	---	---	235804_at	---
2.41	2.66	0.25	8.90E-02	4.29E-01	C20orf117	chromosome 20 open reading frame 117	chr20q11.23	241362_at	NM_199181
2.26	2.49	0.23	8.90E-02	4.29E-01	ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	chr19p13.2-cen	207194_s_at	NM_001039132 /// NM_001544 /// NM_022377
5.79	6.52	0.73	8.90E-02	4.29E-01	---	---	---	212605_s_at	---
6.05	6.87	0.82	8.90E-02	4.29E-01	THY1	Thy-1 cell surface antigen	chr11q22.3-q23	208851_s_at	NM_006288
3.05	4.60	1.55	8.90E-02	4.29E-01	---	---	---	243543_at	---
3.09	3.79	0.70	8.90E-02	4.29E-01	---	---	---	236778_at	---
2.43	2.65	0.22	8.90E-02	4.29E-01	---	---	---	1560156_at	---
3.45	3.87	0.42	8.91E-02	4.29E-01	---	---	---	241924_at	---
2.73	3.07	0.34	8.91E-02	4.29E-01	---	---	---	233117_at	---
3.49	3.74	0.25	8.91E-02	4.29E-01	---	---	---	238739_at	---
5.21	5.44	0.23	8.91E-02	4.29E-01	---	---	---	244222_at	---
2.10	2.31	0.21	8.91E-02	4.29E-01	---	---	---	1562907_at	---
2.61	2.92	0.31	8.92E-02	4.29E-01	ZNF556	zinc finger protein 556	chr19p13.3	220709_at	NM_024967
2.88	3.25	0.37	8.93E-02	4.29E-01	XKR6	XK, Kell blood group complex subunit-related family, member 6	chr8p23.1	1553640_at	NM_173683
9.40	10.12	0.71	8.93E-02	4.30E-01	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	226880_at	NM_022731
4.41	4.79	0.38	8.93E-02	4.30E-01	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	chr10q24	209636_at	NM_001077493 /// NM_001077494 /// NM_002502
2.95	3.22	0.27	8.93E-02	4.30E-01	AFAP1L1	actin filament associated protein 1-like 1	chr5q33.1	1555542_at	NM_152406
3.36	3.64	0.27	8.93E-02	4.30E-01	TMED5	transmembrane emp24 protein transport domain containing 5	chr1pter-q31.3	1558814_s_at	NM_016040
3.44	3.98	0.54	8.94E-02	4.30E-01	KLRK1	killer cell lectin-like receptor subfamily K, member 1	chr12p13.2-p12.3	205821_at	NM_007360
4.74	5.24	0.50	8.94E-02	4.30E-01	FRG1B	Hypothetical protein LOC283788	chr20q11.1	228247_at	NR_003579
3.74	4.16	0.42	8.94E-02	4.30E-01	FLJ39632 /// LOC100131139	hypothetical LOC642477 /// similar to double homeobox A	chr14q11.1	231882_at	XR_015133 /// XR_037336 /// XR_037869 /// XR_041395
4.16	4.50	0.35	8.94E-02	4.30E-01	tcag7.1196	Similar to GLI-Kruppel family member HKR1	chr7q36.1	235499_at	XR_041712 /// XR_041713 /// XR_041714
2.22	2.54	0.31	8.94E-02	4.30E-01	---	---	---	220568_at	---
2.15	2.43	0.27	8.94E-02	4.30E-01	---	---	---	213790_at	---
5.07	5.41	0.33	8.95E-02	4.30E-01	RAB7L1	RAB7, member RAS oncogene family-like 1	chr1q32	218700_s_at	NM_003929
5.74	5.99	0.24	8.95E-02	4.30E-01	SRL	sarcalumenin	chr16p13.3	235718_at	NM_001098814
9.59	10.03	0.44	8.95E-02	4.30E-01	YBX1	Y box binding protein 1	chr1p34	208627_s_at	NM_004559
7.98	8.56	0.58	8.96E-02	4.30E-01	USP9X	ubiquitin specific peptidase 9, X-linked	chrXp11.4	201100_s_at	NM_001039590 /// NM_001039591
3.29	3.67	0.38	8.96E-02	4.30E-01	F5	coagulation factor V (proaccelerin, labile factor)	chr1q23	204713_s_at	NM_000130
7.40	7.72	0.32	8.96E-02	4.30E-01	TIGD5	tigger transposable element derived 5	chr8q24.3	229758_at	NM_032862
2.71	2.98	0.27	8.96E-02	4.30E-01	---	---	---	239544_at	---
2.34	2.60	0.26	8.96E-02	4.30E-01	hCG_17324	primary ciliary dyskinesia protein 1	chr2q14.2	237152_at	NM_001029996
2.59	2.83	0.24	8.96E-02	4.30E-01	MDFIC	MyoD family inhibitor domain containing	chr7q31.1-q31.2	217599_s_at	NM_199072
3.39	3.63	0.24	8.96E-02	4.30E-01	---	---	---	217224_at	---
2.43	2.66	0.23	8.96E-02	4.30E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	222023_at	NM_006738 /// NM_007200 /// NM_144767
2.23	2.43	0.20	8.96E-02	4.30E-01	LOC344887	similar to hCG2041270	chr3q27.2	241418_at	XR_017497 /// XR_019323 /// XR_038616

1.98	2.38	0.39	8.96E-02	4.30E-01	FSTL5	follistatin-like 5	chr4q32.3	232010_at	NM_001128427 /// NM_001128428 /// NM_020116																				
2.33	2.54	0.21	8.97E-02	4.30E-01	---	---	---	1569114_at	---																				
6.50	7.67	1.17	8.97E-02	4.30E-01	INSIG1	insulin induced gene 1	chr7q36	201626_at	NM_005542 /// NM_198336 /// NM_198337																				
3.35	3.82	0.47	8.97E-02	4.30E-01	MED1	mediator complex subunit 1	chr17q12-q21.1	203496_s_at	NM_004774																				
2.53	2.72	0.20	8.97E-02	4.30E-01	---	---	---	244449_at	---																				
6.57	7.23	0.67	8.97E-02	4.30E-01	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	chr5q13.3	226277_at	NM_001130105 /// NM_005713 /// NM_031361																				
3.64	4.29	0.66	8.97E-02	4.30E-01	---	---	---	244464_at	---																				
4.79	5.12	0.33	8.97E-02	4.30E-01	NUMBL	numb homolog (Drosophila)-like	chr19q13.13-q13.2	224059_s_at	NM_004756																				
5.25	6.18	0.93	8.98E-02	4.30E-01	NPTX1	neuronal pentraxin I	chr17q25.1-q25.2	204684_at	NM_002522																				
3.33	3.74	0.41	8.98E-02	4.30E-01	---	---	---	237452_at	---																				
5.69	6.04	0.35	8.98E-02	4.30E-01	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	chr19q13.3	208916_at	NM_005628																				
5.34	5.79	0.46	8.98E-02	4.30E-01	---	---	---	232808_at	---																				
3.52	3.84	0.31	8.98E-02	4.30E-01	---	---	---	239779_at	---																				
3.16	3.46	0.30	8.98E-02	4.30E-01	C2orf54	chromosome 2 open reading frame 54	chr2q37.3	220149_at	NM_001085437 /// NM_024861																				
2.37	2.67	0.30	8.98E-02	4.30E-01	---	---	---	243490_at	---																				
2.90	3.85	0.95	8.99E-02	4.30E-01	KIAA0746 /// SERINC2	KIAA0746 protein /// serine incorporator 2	chr1p35.1 /// chr4p15.2	212311_at	NM_015187 /// NM_178865																				
4.05	4.74	0.69	8.99E-02	4.30E-01	C3orf23	chromosome 3 open reading frame 23	chr3p21.33-p21.32	226688_at	NM_001029839 /// NM_001029840 /// NM_173826																				
3.66	4.11	0.45	8.99E-02	4.30E-01	ALPK3	alpha-kinase 3	chr15q25.2	214846_s_at	NM_020778																				
4.19	4.56	0.37	8.99E-02	4.30E-01	LOC401463	hypothetical gene supported by BC022555; BC050012	chr8q12.3	243820_at	NR_015374																				
4.48	4.80	0.32	8.99E-02	4.30E-01	RAB6A	RAB6A, member RAS oncogene family	chr11q13.3	201045_s_at	NM_002869 /// NM_198896																				
2.93	3.21	0.28	8.99E-02	4.30E-01	NLN	neurolysin (metallopeptidase M3 family)	chr5q12.3	225944_at	NM_020726																				
1.95	2.15	0.20	8.99E-02	4.30E-01	GFM1	G elongation factor, mitochondrial 1	chr3q25.1-q26.2	232295_at	NM_024996																				
3.72	4.07	0.35	9.00E-02	4.31E-01	KCNC2	Potassium voltage-gated channel, Shaw-related subfamily, member 2	chr12q14.1	222289_at	NM_139136 /// NM_139137 /// NM_153748																				
3.27	3.53	0.27	9.00E-02	4.31E-01	C7orf50	chromosome 7 open reading frame 50	chr7p22.3	240900_at	NM_001134395 /// NM_001134396 /// NM_032350																				
4.57	4.90	0.33	9.00E-02	4.31E-01	BCAS1	breast carcinoma amplified sequence 1	chr20q13.2	204378_at	NM_003657																				
3.16	3.42	0.26	9.00E-02	4.31E-01	---	---	---	1562208_a_at	---																				
5.38	6.26	0.89	9.01E-02	4.31E-01	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	chr7q21.3-q22.1	1557953_at	NM_003439																				
7.93	8.41	0.48	9.01E-02	4.31E-01	RHBDD2	rhomboid domain containing 2	chr7q11.23	232053_x_at	NM_001040456 /// NM_001040457																				
5.00	5.47	0.47	9.01E-02	4.31E-01	FGF18	fibroblast growth factor 18	chr5q34	206986_at	NM_003862																				
3.83	4.16	0.33	9.01E-02	4.31E-01	TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	chr17p11.2	207641_at	NM_012452																				
2.19	2.47	0.28	9.01E-02	4.31E-01	SCRN3	secernin 3	chr2q31.1	1555595_at	NM_024583																				
4.86	5.49	0.64	9.02E-02	4.31E-01	GDAP2	ganglioside induced differentiation associated protein 2	chr1p12	1554154_at	NM_017686																				
3.37	3.67	0.29	9.02E-02	4.31E-01	RLTPR	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing	chr16q22.1	227216_at	NM_001013838																				
7.16	7.64	0.48	9.02E-02	4.31E-01	EPB41L1	erythrocyte membrane protein band 4.1-like 1	chr20q11.2-q12	212339_at	NM_012156 /// NM_177996																				
2.70	2.91	0.21	9.02E-02	4.31E-01	C20orf94	chromosome 20 open reading frame 94	chr20p12.2	236390_at	NM_001009608																				

2.70	3.27	0.57	9.03E-02	4.31E-01	SYTL2	synaptotagmin-like 2	chr11q14	220613_s_at	NM_032379 /// NM_032943 /// NM_206927 /// NM_206928 /// NM_206929 /// NM_206930
3.32	3.62	0.29	9.03E-02	4.31E-01	CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S subunit	chr1q32	217515_s_at	NM_000069
3.90	4.24	0.35	9.03E-02	4.31E-01	ZNF93	zinc finger protein 93	chr19p12	208119_s_at	NM_031218
3.81	4.14	0.33	9.03E-02	4.31E-01	TJP3	tight junction protein 3 (zona occludens 3)	chr19p13.3	213412_at	NM_014428
2.74	3.03	0.29	9.03E-02	4.31E-01	NBPF4	neuroblastoma breakpoint family, member 4	chr1p13.3	1553910_at	XR_040171
3.01	3.23	0.22	9.03E-02	4.31E-01	---	---	---	239737_at	---
2.48	2.80	0.32	9.04E-02	4.31E-01	---	---	---	1555194_at	---
6.19	6.77	0.58	9.04E-02	4.32E-01	THEM2	thioesterase superfamily member 2	chr6p22.2	204565_at	NM_018473
2.11	2.33	0.23	9.05E-02	4.32E-01	---	---	---	1566115_at	---
6.48	7.32	0.84	9.05E-02	4.32E-01	C5orf41	chromosome 5 open reading frame 41	chr5q35.2	225957_at	NM_153607
2.58	2.88	0.29	9.06E-02	4.32E-01	FEV	FEV (ETS oncogene family)	chr2q36	207260_at	NM_017521
2.48	2.73	0.25	9.05E-02	4.32E-01	AMOTL1	angiomotin like 1	chr11q14.3	235277_at	NM_130847
2.09	2.38	0.28	9.06E-02	4.32E-01	---	---	---	1568851_at	---
6.35	6.80	0.44	9.06E-02	4.32E-01	CSF1	colony stimulating factor 1 (macrophage)	chr1p21-p13	209716_at	NM_000757 /// NM_172210 /// NM_172211 /// NM_172212
3.32	3.75	0.43	9.06E-02	4.32E-01	---	---	---	234245_at	---
2.70	2.93	0.23	9.06E-02	4.32E-01	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	220546_at	NM_005933
1.93	2.16	0.23	9.07E-02	4.32E-01	---	---	---	244045_at	---
5.09	5.87	0.78	9.07E-02	4.32E-01	HIST1H2AC	histone cluster 1, H2ac	chr6p21.3	215071_s_at	NM_003512
4.90	5.43	0.53	9.07E-02	4.32E-01	---	---	---	215279_at	---
1.86	2.14	0.27	9.07E-02	4.32E-01	ZC3H15	Zinc finger CCCH-type containing 15	chr2q32.1	210709_at	NM_018471
4.16	4.40	0.24	9.07E-02	4.32E-01	ADRBK2	adrenergic, beta, receptor kinase 2	chr22q11|22q12.1	204183_s_at	NM_005160
3.92	4.56	0.64	9.08E-02	4.32E-01	TRIP11	thyroid hormone receptor interactor 11	chr14q31-q32	236160_at	NM_004239
3.19	3.66	0.47	9.08E-02	4.32E-01	RB1	retinoblastoma 1	chr13q14.2	211540_s_at	NM_000321
7.12	7.71	0.59	9.09E-02	4.32E-01	MAP1B	microtubule-associated protein 1B	chr5q13	226084_at	NM_005909
4.38	4.86	0.48	9.09E-02	4.32E-01	TBC1D16	TBC1 domain family, member 16	chr17q25.3	228488_at	NM_019020
4.20	4.65	0.46	9.09E-02	4.32E-01	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	chr22q13.1	207265_s_at	NM_006855 /// NM_016657
5.21	5.62	0.42	9.08E-02	4.32E-01	B3GNT8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	chr19q13.2	237338_at	NM_198540
2.30	2.62	0.31	9.08E-02	4.32E-01	VNN1	vanin 1	chr6q23-q24	205844_at	NM_004666
3.88	4.18	0.30	9.08E-02	4.32E-01	---	---	---	244872_at	---
2.29	2.58	0.29	9.09E-02	4.32E-01	LOC100131056	similar to hCG2041870	chr1p34.2	231105_at	XM_001718780 /// XM_001718793
3.97	4.22	0.25	9.09E-02	4.32E-01	---	---	---	216811_at	---
2.06	2.26	0.20	9.09E-02	4.32E-01	---	---	---	237898_at	---
6.10	6.64	0.55	9.09E-02	4.32E-01	MGLL	monoglyceride lipase	chr3q21.3	225102_at	NM_001003794 /// NM_007283
4.53	4.86	0.32	9.09E-02	4.32E-01	---	---	---	238202_at	---
3.99	4.61	0.62	9.09E-02	4.32E-01	PHCA	phytoceramidase, alkaline	chr11q13.5	222688_at	NM_018367
2.40	2.66	0.26	9.10E-02	4.32E-01	CNTN2	contactin 2 (axonal)	chr1q32.1	230045_at	NM_005076
1.93	2.19	0.26	9.10E-02	4.32E-01	---	---	---	215924_at	---
2.32	2.53	0.21	9.10E-02	4.32E-01	---	---	---	241288_at	---
3.08	3.38	0.30	9.10E-02	4.32E-01	DAZAP2	DAZ associated protein 2	chr12q12	238300_s_at	NM_014764
3.47	3.84	0.38	9.10E-02	4.32E-01	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	chr3q22.1	209632_at	NM_002718 /// NM_181897
3.50	3.79	0.30	9.10E-02	4.32E-01	LOC284014	hypothetical protein LOC284014	chr17p13.3	1558723_at	---
2.37	2.64	0.27	9.10E-02	4.32E-01	NPAL3	NIPA-like domain containing 3	chr1p36.12-p35.1	210267_at	NM_020448
3.88	4.29	0.40	9.11E-02	4.32E-01	---	---	---	242058_at	---
3.57	3.89	0.32	9.11E-02	4.33E-01	GATM	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	chr15q21.1	235426_at	NM_001482
3.30	3.65	0.35	9.12E-02	4.33E-01	JPH3	junctophilin 3	chr16q24.3	243679_at	NM_020655
2.27	2.51	0.24	9.12E-02	4.33E-01	---	---	---	1560298_at	---
2.38	2.58	0.20	9.12E-02	4.33E-01	---	---	---	1556847_s_at	---
3.45	3.99	0.54	9.12E-02	4.33E-01	PDZK1IP1	PDZK1 interacting protein 1	chr1p33	219630_at	NM_005764
2.02	2.19	0.18	9.12E-02	4.33E-01	---	---	---	1556393_at	---
4.85	5.81	0.96	9.13E-02	4.33E-01	CXADR	coxsackie virus and adenovirus receptor	chr21q21.1	203917_at	NM_001338
2.41	2.72	0.30	9.13E-02	4.33E-01	GPR61	G protein-coupled receptor 61	chr1p13.3	224531_at	NM_031936

4.14	4.44	0.30	9.13E-02	4.33E-01	LOC100130339	hypothetical protein LOC100130339	chr22q13.1	244104_at	XM_001723579 /// XM_001725317 /// XM_001726760																				
3.41	3.70	0.29	9.13E-02	4.33E-01	ANO9	anoctamin 9	chr11p15.5	227393_at	NM_001012302																				
1.80	2.00	0.20	9.13E-02	4.33E-01	---	---	---	237667_at	---																				
2.80	3.02	0.22	9.13E-02	4.33E-01	NUP188	nucleoporin 188kDa	chr9q34.11	214675_at	NM_015354																				
2.80	3.59	0.78	9.13E-02	4.33E-01	NPY	neuropeptide Y	chr7p15.1	206001_at	NM_000905																				
2.13	2.45	0.32	9.14E-02	4.33E-01	LOC283486	hypothetical protein LOC283486	chr13q34	1559079_at	---																				
1.93	2.15	0.22	9.13E-02	4.33E-01	---	---	---	238390_at	---																				
2.07	2.27	0.20	9.14E-02	4.33E-01	TAS2R16	taste receptor, type 2, member 16	chr7q31.1-q31.3|7q31	221444_at	NM_016945																				
2.20	2.38	0.18	9.13E-02	4.33E-01	---	---	---	238354_x_at	---																				
4.62	5.52	0.90	9.14E-02	4.33E-01	DLG2	discs, large homolog 2, chapsyn-110 (Drosophila)	chr11q14.1	228973_at	NM_001364																				
4.34	4.67	0.33	9.15E-02	4.33E-01	EPO	erythropoietin	chr7q22	217254_s_at	NM_000799																				
2.90	3.10	0.20	9.15E-02	4.33E-01	PSG11	pregnancy specific beta-1-glycoprotein 11	chr19q13.2	206570_s_at	NM_001113410 /// NM_002785 /// NM_203287																				
2.65	2.93	0.28	9.15E-02	4.33E-01	C11orf64	chromosome 11 open reading frame 64	chr11q12.2	1554765_a_at	XR_039987 /// XR_039988 /// XR_039989																				
5.44	6.57	1.12	9.16E-02	4.33E-01	KPNA3	karyopherin alpha 3 (importin alpha 4)	chr13q14.3	221503_s_at	NM_002267																				
4.11	4.56	0.46	9.16E-02	4.33E-01	LOC100131419 /// SLC38A10	hypothetical protein LOC100131419 /// solute carrier family 38, member 10	chr17q25.3	242942_at	NM_001037984 /// NM_138570 /// XM_001717284 /// XM_001721800 /// XM_001726788																				
3.57	3.93	0.36	9.16E-02	4.33E-01	POLDIP3	polymerase (DNA-directed), delta interacting protein 3	chr22q13.2	210583_at	NM_032311 /// NM_178136																				
5.96	6.32	0.36	9.16E-02	4.33E-01	FBRS	fibrosin	chr16p11.2	218255_s_at	NM_001105079																				
9.02	9.35	0.33	9.16E-02	4.33E-01	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	chr12q24.2	201425_at	NM_000690																				
3.29	3.55	0.26	9.16E-02	4.33E-01	CXorf62	chromosome X open reading frame 62	chrXq13.1	1553457_at	---																				
2.02	2.23	0.21	9.16E-02	4.33E-01	LAMA3	laminin, alpha 3	chr18q11.2	234608_at	NM_000227 /// NM_001127717 /// NM_001127718 /// NM_198129																				
2.49	2.79	0.30	9.16E-02	4.33E-01	---	---	---	242174_at	---																				
2.69	2.91	0.22	9.17E-02	4.33E-01	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	chr6p22.3-p22.2	206266_at	NM_001503 /// NM_177483																				
2.33	2.65	0.32	9.17E-02	4.33E-01	PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1	chr11q13.5-q14.1	209504_s_at	NM_001130033 /// NM_001130034 /// NM_001130035 /// NM_001130036 /// NM_021200																				
1.98	2.32	0.34	9.17E-02	4.34E-01	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	chr12q21.3	240419_at	NM_018057 /// NM_182767																				
1.86	2.09	0.23	9.17E-02	4.34E-01	COL8A1	collagen, type VIII, alpha 1	chr3q12.3	221152_at	NM_001850 /// NM_020351																				
2.50	2.80	0.30	9.18E-02	4.34E-01	ZNF555	zinc finger protein 555	chr19p13.3	239839_at	NM_152791																				
2.69	2.92	0.23	9.18E-02	4.34E-01	---	---	---	236935_at	---																				
2.11	2.33	0.22	9.18E-02	4.34E-01	---	---	---	235960_at	---																				
4.04	4.61	0.57	9.19E-02	4.34E-01	---	---	---	222306_at	---																				
4.75	5.15	0.39	9.19E-02	4.34E-01	LOC100132540 /// LOC100132620 /// LOC339047 /// NPIP	similar to LOC339047 protein /// similar to LOC339047 protein /// hypothetical protein LOC339047 /// nuclear pore complex interacting protein	chr16p12.3 /// chr16p13-p11 /// chr16p13.11	240376_s_at	NM_006985 /// NM_178541 /// XM_001134445 /// XM_001723375 /// XM_001724221																				
2.27	2.54	0.27	9.19E-02	4.34E-01	---	---	---	241121_at	---																				
5.98	6.30	0.32	9.19E-02	4.34E-01	---	---	---	244842_x_at	---																				

2.28	2.57	0.29	9.19E-02	4.34E-01	---	---	---	233280_at	---
7.56	8.39	0.83	9.20E-02	4.34E-01	PURA	purine-rich element binding protein A	chr5q31	204020_at	NM_005859
4.75	5.07	0.31	9.20E-02	4.34E-01	APOL6	apolipoprotein L, 6	chr22q12.3	1557116_at	NM_030641
2.12	2.42	0.30	9.20E-02	4.34E-01	---	---	---	1561400_at	---
2.88	3.17	0.29	9.19E-02	4.34E-01	---	---	---	217396_at	---
8.93	9.49	0.56	9.20E-02	4.34E-01	MORF4L1	mortality factor 4 like 1	chr15q24	224561_s_at	NM_006791 /// NM_206839
3.54	4.12	0.58	9.20E-02	4.34E-01	PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	chrXp11.23	218952_at	NM_013271
3.63	3.88	0.26	9.21E-02	4.34E-01	PCBP3	poly(rC) binding protein 3	chr21q22.3	205663_at	NM_001130141 /// NM_020528
5.07	5.68	0.61	9.21E-02	4.34E-01	RAB6B	RAB6B, member RAS oncogene family	chr3q22.1	221792_at	NM_016577
3.19	3.77	0.58	9.22E-02	4.34E-01	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	chr3p26-p25	240052_at	NM_001099952 /// NM_002222
3.91	4.41	0.50	9.22E-02	4.34E-01	CARTPT	CART prepropeptide	chr5q13.2	206339_at	NM_004291
2.57	3.04	0.47	9.22E-02	4.34E-01	---	---	---	239673_at	---
4.43	4.85	0.41	9.22E-02	4.34E-01	BBS4	Bardet-Biedl syndrome 4	chr15q22.3-q23	212744_at	NM_033028
4.00	4.31	0.32	9.22E-02	4.34E-01	TBCE	tubulin folding cofactor E	chr1q42.3	203715_at	NM_001079515 /// NM_003193
3.68	3.96	0.28	9.22E-02	4.34E-01	---	---	---	242357_x_at	---
2.31	2.58	0.27	9.22E-02	4.35E-01	---	---	---	1563601_at	---
3.96	4.17	0.21	9.23E-02	4.35E-01	KRBA2	KRAB-A domain containing 2	chr17p13.1	1558533_at	NM_213597
2.76	3.08	0.32	9.23E-02	4.35E-01	---	---	---	1570180_at	---
2.06	2.32	0.26	9.23E-02	4.35E-01	VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	chr13q14.3	240086_at	NM_016075
1.89	2.10	0.21	9.23E-02	4.35E-01	---	---	---	242952_at	---
2.28	2.53	0.25	9.23E-02	4.35E-01	LOC647121	embigin homolog (mouse) pseudogene	chr1p11.2	239072_at	NR_003955
2.33	2.55	0.22	9.23E-02	4.35E-01	---	---	---	1563143_at	---
2.95	3.17	0.22	9.24E-02	4.35E-01	PCDH10	protocadherin 10	chr4q28.3	1552925_at	NM_020815 /// NM_032961
2.27	2.48	0.22	9.24E-02	4.35E-01	FAM44A	family with sequence similarity 44, member A	chr4p16.1	235009_at	NM_148894
2.00	2.19	0.19	9.24E-02	4.35E-01	---	---	---	233095_at	---
5.07	5.85	0.78	9.25E-02	4.35E-01	GALK2	galactokinase 2	chr15q21.1	205219_s_at	NM_001001556 /// NM_002044
4.64	4.87	0.24	9.25E-02	4.35E-01	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	chr17q21.32	243899_at	NM_001113738 /// NM_016632
5.30	5.58	0.28	9.25E-02	4.35E-01	TRAPPC9	trafficking protein particle complex 9	chr8q24.3	221836_s_at	NM_031466
4.44	5.19	0.75	9.26E-02	4.35E-01	IMPACT	Impact homolog (mouse)	chr18q11.2-q12.1	222698_s_at	NM_018439
5.51	5.81	0.31	9.26E-02	4.35E-01	TMUB1	transmembrane and ubiquitin-like domain containing 1	chr7q36.1	223153_x_at	NM_031434
3.63	3.92	0.29	9.26E-02	4.35E-01	KREMEN2	kringle containing transmembrane protein 2	chr16p13.3	219692_at	NM_024507 /// NM_172229
6.67	6.95	0.28	9.26E-02	4.35E-01	TMEM184A	transmembrane protein 184A	chr7p22.3	235817_at	NM_001097620
1.92	2.20	0.28	9.26E-02	4.35E-01	---	---	---	241507_x_at	---
3.61	3.88	0.27	9.26E-02	4.35E-01	---	---	---	233519_at	---
2.52	2.78	0.26	9.26E-02	4.35E-01	---	---	---	235560_at	---
1.88	2.11	0.24	9.26E-02	4.35E-01	BEST3	bestrophin 3	chr12q14.2-q15	224520_s_at	NM_032735 /// NM_152439
2.06	2.29	0.23	9.26E-02	4.35E-01	MIA2	melanoma inhibitory activity 2	chr14q13.2	1553944_at	NM_054024
1.98	2.17	0.19	9.26E-02	4.35E-01	---	---	---	244148_at	---
2.75	2.98	0.24	9.27E-02	4.35E-01	---	---	---	241153_at	---
2.14	2.35	0.21	9.27E-02	4.35E-01	---	---	---	1566176_at	---
2.36	2.67	0.31	9.27E-02	4.35E-01	---	---	---	232783_at	---
2.57	2.94	0.37	9.27E-02	4.35E-01	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	chr9q22.33	234605_at	NM_001077181 /// NM_003671 /// NM_033331
3.95	4.16	0.22	9.28E-02	4.35E-01	COL6A1	collagen, type VI, alpha 1	chr21q22.3	212938_at	NM_001848
2.35	2.59	0.24	9.28E-02	4.35E-01	---	---	---	242257_at	---
8.38	8.93	0.54	9.29E-02	4.36E-01	TCP1	t-complex 1	chr6q25.3-q26	208778_s_at	NM_001008897 /// NM_030752
3.86	4.27	0.41	9.29E-02	4.36E-01	API5	apoptosis inhibitor 5	chr11p11.2	214960_at	NM_006595
2.23	2.52	0.29	9.29E-02	4.36E-01	---	---	---	242655_at	---
2.31	2.59	0.28	9.29E-02	4.36E-01	---	---	---	1561555_at	---
3.13	3.40	0.27	9.29E-02	4.36E-01	FAM55C	family with sequence similarity 55, member C	chr3q12.3	243011_at	NM_001134456 /// NM_145037
2.42	2.68	0.26	9.29E-02	4.36E-01	---	---	---	240540_at	---
2.41	2.65	0.24	9.30E-02	4.36E-01	---	---	---	231465_at	---
2.22	2.41	0.20	9.30E-02	4.36E-01	ARHGAP29	Rho GTPase activating protein 29	chr1p22.1	1558280_s_at	NM_004815
3.61	4.43	0.82	9.30E-02	4.36E-01	ZNF195	zinc finger protein 195	chr11p15.5	204234_s_at	NM_001130519 /// NM_001130520 /// NM_007152

6.36	6.94	0.58	9.30E-02	4.36E-01	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	chr18p11.32	226567_at	NM_001037334 /// NM_005151
2.44	2.72	0.28	9.30E-02	4.36E-01	---	---	---	241189_at	---
2.02	2.28	0.25	9.30E-02	4.36E-01	ZSCAN23	zinc finger and SCAN domain containing 23	chr6p22.1	1563670_at	NM_001012455 /// XM_001715453 /// XM_001715639 /// XM_001717784
1.83	2.03	0.20	9.30E-02	4.36E-01	---	---	---	238362_at	---
6.91	7.26	0.35	9.31E-02	4.36E-01	NAG	neuroblastoma-amplified protein	chr2p24	202926_at	NM_015909
3.21	3.50	0.30	9.31E-02	4.36E-01	FLJ14100	hypothetical protein FLJ14100	chr1p36.33	220579_at	XR_041871 /// XR_041872 /// XR_041873
2.00	2.29	0.28	9.31E-02	4.36E-01	---	---	---	1565596_at	---
2.61	2.87	0.26	9.31E-02	4.36E-01	---	---	---	1562432_at	---
2.47	2.70	0.22	9.31E-02	4.36E-01	---	---	---	242044_at	---
2.82	3.71	0.89	9.32E-02	4.36E-01	---	---	---	1570482_at	---
3.72	4.32	0.60	9.32E-02	4.36E-01	NT5E	5'-nucleotidase, ecto (CD73)	chr6q14-q21	203939_at	NM_002526
5.03	5.25	0.22	9.32E-02	4.36E-01	---	---	---	227097_at	---
2.47	2.71	0.23	9.32E-02	4.36E-01	---	---	---	233796_at	---
2.51	2.80	0.29	9.32E-02	4.36E-01	---	---	---	244068_at	---
5.70	5.95	0.26	9.33E-02	4.36E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	211693_at	---
2.09	2.36	0.27	9.33E-02	4.36E-01	---	---	---	234852_at	---
4.26	4.85	0.59	9.33E-02	4.36E-01	APC	adenomatous polyposis coli	chr5q21-q22	203525_s_at	NM_000038 /// NM_001127510 /// NM_001127511
9.44	9.92	0.48	9.33E-02	4.36E-01	PEG3	paternally expressed 3	chr19q13.4	209242_at	NM_006210
3.22	3.54	0.32	9.33E-02	4.36E-01	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	chr1p36.22	220221_at	NM_015378 /// NM_018156
4.84	5.49	0.65	9.34E-02	4.36E-01	---	---	---	243003_at	---
4.86	5.49	0.62	9.34E-02	4.36E-01	ZNF22	zinc finger protein 22 (KOX 15)	chr10q11	218005_at	NM_006963
3.33	3.86	0.54	9.34E-02	4.36E-01	PCDHA1 /// PCDHA10 /// PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2	protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	chr5q31	223435_s_at	NM_014005 /// NM_018898 /// NM_018899 /// NM_018900 /// NM_018901 /// NM_018902 /// NM_018903 /// NM_018904 /// NM_018905 /// NM_018906 /// NM_018907 /// NM_018908 /// NM_018909 /// NM_018910 /// NM_018911 /// NM_031410 /// NM_031411 /// NM_031495 /// NM_031496 /// NM_031497 /// NM_031500 /// NM_031501 /// NM_031848 /// NM_031849 /// NM_031852 /// NM_031856 /// NM_031857 /// NM_031859 /// NM_031860 /// NM_031861 /// NM_031864 /// NM_031865 /// NM_031882 /// NM_031883
3.42	3.77	0.36	9.34E-02	4.36E-01	TFCP2L1	Transcription factor CP2-like 1	chr2q14	229341_at	NM_014553
2.91	3.26	0.35	9.34E-02	4.36E-01	JARID1A	jumonji, AT rich interactive domain 1A	chr12p11	226367_at	NM_001042603 /// NM_005056
2.99	3.27	0.28	9.34E-02	4.36E-01	TIGD3	tigger transposable element derived 3	chr11q13.1	229789_at	NM_145719
2.07	2.33	0.25	9.34E-02	4.36E-01	CEP55	centrosomal protein 55kDa	chr10q23.33	218542_at	NM_001127182 /// NM_018131

2.12	2.37	0.24	9.34E-02	4.36E-01	KIAA0174	KIAA0174	chr16q22.3	215585_at	NM_014761
2.94	3.13	0.19	9.34E-02	4.36E-01	LOC387647	patched domain containing 3 pseudogene	chr10p11.23	230736_at	NR_003930
2.20	2.37	0.17	9.34E-02	4.36E-01	CLDN23	Claudin 23	chr8p23.1	228704_s_at	NM_194284
2.37	3.03	0.66	9.35E-02	4.36E-01	FAP	fibroblast activation protein, alpha	chr2q23	209955_s_at	NM_004460
3.83	4.29	0.46	9.35E-02	4.36E-01	FBLIM1	filamin binding LIM protein 1	chr1p36.21	1555483_x_at	NM_001024215 /// NM_001024216 /// NM_017556
3.24	3.92	0.68	9.35E-02	4.37E-01	MYH11	myosin, heavy chain 11, smooth muscle	chr16p13.11	201496_x_at	NM_001040113 /// NM_001040114 /// NM_002474 /// NM_022844
7.32	7.85	0.53	9.35E-02	4.37E-01	ZCRB1	zinc finger CCHC-type and RNA binding motif 1	chr12q12	227416_s_at	NM_033114
3.40	3.62	0.22	9.35E-02	4.37E-01	---	---	---	243044_at	---
4.16	4.52	0.35	9.36E-02	4.37E-01	---	---	---	1563030_at	---
3.28	3.59	0.30	9.36E-02	4.37E-01	---	---	---	222069_s_at	---
2.96	3.23	0.27	9.36E-02	4.37E-01	ARID5B	AT rich interactive domain 5B (MRF1-like)	chr10q21.2	235404_at	NM_032199
3.33	3.59	0.26	9.36E-02	4.37E-01	---	---	---	1563109_at	---
3.26	3.52	0.26	9.36E-02	4.37E-01	KIAA1654	KIAA1654 protein	---	215681_at	---
4.55	4.81	0.25	9.36E-02	4.37E-01	SLAIN2	SLAIN motif family, member 2	chr4p12	224854_s_at	NM_020846
2.83	3.08	0.25	9.36E-02	4.37E-01	PTPRB	protein tyrosine phosphatase, receptor type, B	chr12q15-q21	217177_s_at	NM_001109754 /// NM_002837
3.10	3.34	0.23	9.35E-02	4.37E-01	IGSF9	immunoglobulin superfamily, member 9	chr1q22-q23	229276_at	NM_020789
5.33	6.51	1.18	9.37E-02	4.37E-01	USO1	USO1 homolog, vesicle docking protein (yeast)	chr4q21.1	201831_s_at	NM_003715
3.22	3.51	0.29	9.37E-02	4.37E-01	APOL4	apolipoprotein L, 4	chr22q11.2-q13.2	223801_s_at	NM_030643 /// NM_145660
9.35	10.03	0.68	9.38E-02	4.37E-01	METTL9	methyltransferase like 9	chr16p13-p12	217868_s_at	NM_001077180 /// NM_016025
9.97	10.34	0.37	9.39E-02	4.37E-01	---	---	---	AFFX-r2-Ec-bioD-5_at	---
3.02	3.35	0.33	9.39E-02	4.37E-01	PCDHGA1	protocadherin gamma subfamily A, 1	chr5q31	211880_x_at	NM_018912 /// NM_031993
3.34	3.67	0.33	9.38E-02	4.37E-01	C20orf71	chromosome 20 open reading frame 71	chr20q11.21	240359_at	NM_001042439 /// NM_178466
6.03	6.34	0.31	9.38E-02	4.37E-01	GNAS	GNAS complex locus	chr20q13.3	217058_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259
3.03	3.33	0.31	9.38E-02	4.37E-01	ATXN1	ataxin 1	chr6p23	1559249_at	NM_000332 /// NM_001128164
2.80	3.07	0.27	9.38E-02	4.37E-01	CYP2E1	Cytochrome P450, family 2, subfamily E, polypeptide 1	chr10q24.3-qter	222100_at	NM_000773
6.24	6.51	0.27	9.39E-02	4.37E-01	COL1A1	collagen, type I, alpha 1	chr17q21.33	202312_s_at	NM_000088
2.51	2.77	0.26	9.39E-02	4.37E-01	---	---	---	243160_at	---
2.29	2.52	0.23	9.38E-02	4.37E-01	---	---	---	236215_at	---
1.97	2.17	0.20	9.38E-02	4.37E-01	---	---	---	1558373_s_at	---
8.53	9.33	0.79	9.39E-02	4.37E-01	IQGAP1	IQ motif containing GTPase activating protein 1	chr15q26.1	200791_s_at	NM_003870
2.47	2.72	0.25	9.39E-02	4.37E-01	---	---	---	238134_at	---
2.30	2.54	0.23	9.39E-02	4.37E-01	---	---	---	235100_at	---
5.16	5.38	0.22	9.40E-02	4.37E-01	KRT81	keratin 81	chr12q13	213711_at	NM_002281
6.21	7.17	0.95	9.41E-02	4.37E-01	CLEC2B	C-type lectin domain family 2, member B	chr12p13-p12	209732_at	NM_005127
6.40	7.16	0.77	9.40E-02	4.37E-01	PRKCA	protein kinase C, alpha	chr17q22-q23.2	213093_at	NM_002737
2.88	3.24	0.37	9.41E-02	4.37E-01	RDX	radixin	chr11q23	244739_at	NM_002906
2.75	3.05	0.30	9.41E-02	4.37E-01	MEF2A	myocyte enhancer factor 2A	chr15q26	208328_s_at	NM_001130926 /// NM_001130927 /// NM_001130928 /// NM_005587
2.91	3.16	0.25	9.41E-02	4.37E-01	---	---	---	231049_at	---

2.02	2.26	0.24	9.40E-02	4.37E-01	CLEC4C	C-type lectin domain family 4, member C	chr12p13.2-p12.3	1552552_s_at	NM_130441 /// NM_203503
4.67	5.03	0.35	9.41E-02	4.38E-01	GPR68	G protein-coupled receptor 68	chr14q31	229055_at	NM_003485
10.19	10.86	0.67	9.42E-02	4.38E-01	CLTC	clathrin, heavy chain (Hc)	chr17q11-qter	200614_at	NM_004859
4.10	4.35	0.25	9.42E-02	4.38E-01	CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B subunit	chr9q34	207162_s_at	NM_000718
3.57	3.86	0.29	9.42E-02	4.38E-01	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	chr12q23.2	240106_at	NM_024312
2.56	2.81	0.25	9.43E-02	4.38E-01	C6orf54	chromosome 6 open reading frame 54	chr6q27	207963_at	NM_014354
2.31	2.60	0.30	9.43E-02	4.38E-01	---	---	---	241831_at	---
2.82	3.11	0.29	9.43E-02	4.38E-01	FOXL1	forkhead box L1	chr16q24	216572_at	NM_005250
2.82	3.09	0.27	9.43E-02	4.38E-01	UNKL	unkempt homolog (Drosophila)-like	chr16p13.3	235087_at	NM_001037125 /// NM_023076
2.18	2.38	0.20	9.43E-02	4.38E-01	LOC283033	Hypothetical protein LOC283033	chr10q11.21	244465_at	---
3.78	3.98	0.20	9.43E-02	4.38E-01	---	---	---	231272_at	---
4.72	5.03	0.31	9.44E-02	4.38E-01	LOC646014	hypothetical protein LOC646014	chr17q24.1	238715_at	XM_001724434 /// XM_001726150 /// XM_928978
2.30	2.74	0.44	9.44E-02	4.38E-01	TCEAL7	transcription elongation factor A (SII)-like 7	chrXq22.1	227705_at	NM_152278
2.54	2.79	0.25	9.44E-02	4.38E-01	UGT8	UDP glycosyltransferase 8	chr4q26	208358_s_at	NM_001128174 /// NM_003360
2.48	3.09	0.61	9.44E-02	4.38E-01	ZNF294	zinc finger protein 294	chr21q22.11	233819_s_at	NM_015565
4.53	4.87	0.34	9.44E-02	4.38E-01	LOC440792	proline dehydrogenase (oxidase) 1 pseudogene	chr22q11.21	215682_at	---
3.87	4.23	0.36	9.45E-02	4.39E-01	CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	chr22q13.1	207498_s_at	NM_000106 /// NM_001025161
2.32	2.55	0.23	9.45E-02	4.39E-01	TBX5	T-box 5	chr12q24.1	207155_at	NM_000192 /// NM_080717 /// NM_080718 /// NM_181486
4.89	5.57	0.68	9.45E-02	4.39E-01	---	---	---	243933_at	---
3.46	3.82	0.36	9.45E-02	4.39E-01	---	---	---	243212_at	---
4.38	4.65	0.27	9.45E-02	4.39E-01	PTK2B	PTK2B protein tyrosine kinase 2 beta	chr8p21.1	203111_s_at	NM_004103 /// NM_173174 /// NM_173175 /// NM_173176
1.95	2.20	0.25	9.45E-02	4.39E-01	AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	chr10p15-p14	210558_at	NM_001818
2.18	2.38	0.20	9.45E-02	4.39E-01	PTCH1	patched homolog 1 (Drosophila)	chr9q22.3	209816_at	NM_000264 /// NM_001083602 /// NM_001083603 /// NM_001083604 /// NM_001083605 /// NM_001083606 /// NM_001083607
2.71	3.48	0.78	9.47E-02	4.39E-01	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	chr1q32.1	209395_at	NM_001276
4.16	4.91	0.76	9.46E-02	4.39E-01	NCBP1	nuclear cap binding protein subunit 1, 80kDa	chr9q34.1	209520_s_at	NM_002486
7.06	7.62	0.56	9.47E-02	4.39E-01	KTN1	kinectin 1 (kinesin receptor)	chr14q22.1	214709_s_at	NM_001079521 /// NM_001079522 /// NM_004986 /// NM_182926
3.64	4.08	0.44	9.46E-02	4.39E-01	SCAPER	S phase cyclin A-associated protein in the ER	chr15q24	216399_s_at	NM_020843
4.05	4.42	0.37	9.46E-02	4.39E-01	RASL10B	RAS-like, family 10, member B	chr17q12	235488_at	NM_033315
6.52	6.86	0.34	9.46E-02	4.39E-01	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	chr7q11.23	213336_at	NM_032408
2.42	2.72	0.30	9.47E-02	4.39E-01	POU2F2	POU class 2 homeobox 2	chr19q13.2	228343_at	NM_002698
2.12	2.40	0.28	9.47E-02	4.39E-01	---	---	---	235860_at	---
2.05	2.30	0.25	9.46E-02	4.39E-01	LCA5	Leber congenital amaurosis 5	chr6q14.1	242006_at	NM_001122769 /// NM_181714
1.95	2.17	0.22	9.46E-02	4.39E-01	NEBL	Nebulette	chr10p12	241782_at	NM_006393 /// NM_213569
2.93	3.13	0.20	9.47E-02	4.39E-01	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	chr2q37.3	214260_at	NM_006710 /// NM_198189
2.30	2.58	0.28	9.48E-02	4.39E-01	---	---	---	240847_at	---

3.43	3.73	0.30	9.48E-02	4.39E-01	OSBPL10	oxysterol binding protein-like 10	chr3p22.3	216755_at	NM_017784
3.15	3.61	0.46	9.48E-02	4.39E-01	---	---	---	1553439_at	---
3.08	3.39	0.31	9.49E-02	4.39E-01	ZNF7	Zinc finger protein 7	chr8q24	234914_at	NM_003416
4.54	4.83	0.30	9.49E-02	4.39E-01	GATA2	GATA binding protein 2	chr3q21.3	210358_x_at	NM_032638
2.65	2.95	0.29	9.48E-02	4.39E-01	---	---	---	217435_x_at	---
2.12	2.35	0.23	9.48E-02	4.39E-01	PXMP3	Peroxisomal membrane protein 3, 35kDa	chr8q21.1	1561238_at	NM_000318 /// NM_001079867
2.48	2.71	0.22	9.48E-02	4.39E-01	---	---	---	233831_at	---
5.21	5.48	0.27	9.49E-02	4.39E-01	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	chr15q24.2	220705_s_at	NM_014272
3.69	3.95	0.26	9.49E-02	4.39E-01	TRPM5	transient receptor potential cation channel, subfamily M, member 5	chr11p15.5	223935_at	NM_014555
5.59	6.42	0.83	9.49E-02	4.39E-01	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	215338_s_at	NM_005385
2.65	2.96	0.30	9.49E-02	4.39E-01	SOX1	SRY (sex determining region Y)-box 1	chr13q34	208533_at	NM_005986
2.98	4.09	1.12	9.50E-02	4.39E-01	IGL@ /// IGLV1-36 /// IGLV1-44	immunoglobulin lambda locus /// immunoglobulin lambda variable 1-36 /// immunoglobulin lambda variable 1-44	chr22q11.1-q11.2 /// chr22q11.2	234764_x_at	---
2.26	2.69	0.43	9.50E-02	4.39E-01	C14orf145	chromosome 14 open reading frame 145	chr14q31.1	244033_at	NM_152446
1.86	2.06	0.20	9.50E-02	4.39E-01	C15orf21	chromosome 15 open reading frame 21	chr15q21.1	242649_x_at	NM_001005266 /// NM_001005267 /// NM_001005268 /// NM_001005269 /// NM_173609 /// NR_022014
4.63	4.90	0.27	9.50E-02	4.39E-01	HLCS	holocarboxylase synthetase (biotin-(proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)) ligase)	chr21q22.1|21q22.13	209399_at	NM_000411
4.22	4.83	0.60	9.50E-02	4.39E-01	---	---	---	241302_at	---
3.39	3.74	0.35	9.51E-02	4.39E-01	FOLR3	folate receptor 3 (gamma)	chr11q13	206371_at	NM_000804
4.99	5.33	0.34	9.52E-02	4.40E-01	C16orf13	Chromosome 16 open reading frame 13	chr16p13.3	227380_x_at	NM_001040160 /// NM_001040161 /// NM_001040162 /// NM_001040165 /// NM_032366
6.29	6.99	0.70	9.52E-02	4.40E-01	OXR1	oxidation resistance 1	chr8q23	222553_x_at	NM_018002 /// NM_181354
3.09	3.55	0.46	9.52E-02	4.40E-01	---	---	---	233820_at	---
5.25	5.63	0.38	9.52E-02	4.40E-01	---	---	---	228389_at	---
4.37	4.72	0.34	9.52E-02	4.40E-01	NENF	Neuron derived neurotrophic factor	chr1q32.3	214125_s_at	NM_013349
3.21	3.40	0.19	9.52E-02	4.40E-01	---	---	---	240080_at	---
4.59	4.97	0.37	9.53E-02	4.40E-01	---	---	---	232716_at	---
6.01	6.35	0.34	9.53E-02	4.40E-01	---	---	---	229355_at	---
4.50	5.40	0.90	9.53E-02	4.40E-01	CAV2	caveolin 2	chr7q31.1	203323_at	NM_001233 /// NM_198212
4.40	4.74	0.33	9.54E-02	4.40E-01	---	---	---	215607_x_at	---
2.71	3.03	0.32	9.53E-02	4.40E-01	RP4-692D3.1	hypothetical protein LOC728621	chr1p34.2	221171_at	NM_001080850
2.11	2.34	0.22	9.54E-02	4.40E-01	PDZRN4	PDZ domain containing ring finger 4	chr12q12	220595_at	NM_013377
2.39	2.68	0.29	9.55E-02	4.40E-01	---	---	---	244588_at	---
2.14	2.40	0.25	9.55E-02	4.40E-01	LIX1	Lix1 homolog (chicken)	chr5q15	236163_at	NM_153234
5.18	5.65	0.47	9.55E-02	4.40E-01	---	---	---	228156_at	---
7.05	7.47	0.42	9.55E-02	4.40E-01	CALD1	caldesmon 1	chr7q33	214880_x_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
2.63	2.88	0.25	9.55E-02	4.40E-01	---	---	---	244595_at	---
3.54	4.04	0.50	9.55E-02	4.40E-01	ZNF420	zinc finger protein 420	chr19q13.12	238937_at	NM_144689
2.74	3.49	0.75	9.56E-02	4.40E-01	---	---	---	235805_at	---
6.15	6.58	0.44	9.56E-02	4.40E-01	OPTN	optineurin	chr10p13	202073_at	NM_001008211 /// NM_001008212 /// NM_001008213 /// NM_021980
2.33	2.56	0.23	9.56E-02	4.40E-01	ERVWE1	endogenous retroviral family W, env(C7), member 1	chr7q21-q22	1555299_s_at	NM_001130925 /// NM_014590
7.19	7.71	0.52	9.56E-02	4.40E-01	---	---	---	213574_s_at	---

4.20	4.58	0.37	9.57E-02	4.41E-01	OGFR	opioid growth factor receptor	chr20q13.3	211513_s_at	NM_007346
2.35	2.60	0.25	9.57E-02	4.41E-01	ACSL6	acyl-CoA synthetase long-chain family member 6	chr5q31	213683_at	NM_001009185 /// NM_015256
5.77	6.33	0.56	9.58E-02	4.41E-01	S100A9	S100 calcium binding protein A9	chr1q21	203535_at	NM_002965
4.74	5.19	0.45	9.58E-02	4.41E-01	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	chr20q13.33	232518_at	NM_001037335 /// NM_033405
4.82	5.15	0.32	9.58E-02	4.41E-01	EXTL1	exostoses (multiple)-like 1	chr1p36.1	206329_at	NM_004455
2.02	2.31	0.29	9.58E-02	4.41E-01	SV2C	synaptic vesicle glycoprotein 2C	chr5q13.3	216086_at	NM_014979
5.51	5.74	0.23	9.58E-02	4.41E-01	---	---	---	221155_x_at	---
2.66	3.00	0.33	9.58E-02	4.41E-01	---	---	---	1561611_at	---
5.25	6.15	0.89	9.59E-02	4.41E-01	PC	pyruvate carboxylase	chr11q13.4-q13.5	204476_s_at	NM_000920 /// NM_001040716 /// NM_022172
4.34	4.88	0.53	9.60E-02	4.41E-01	PSME4	Proteasome (prosome, macropain) activator subunit 4	chr2p16.2	237180_at	NM_014614
3.19	3.61	0.42	9.59E-02	4.41E-01	NHEDC2	Na+/H+ exchanger domain containing 2	chr4q24	229491_at	NM_178833
3.61	4.01	0.40	9.60E-02	4.41E-01	---	---	---	242614_at	---
6.23	6.60	0.37	9.60E-02	4.41E-01	PWWP2B	PWWP domain containing 2B	chr10q26.3	238046_x_at	NM_001098637 /// NM_138499
2.91	3.27	0.35	9.59E-02	4.41E-01	---	---	---	1564369_at	---
3.06	3.33	0.27	9.60E-02	4.41E-01	---	---	---	1559641_at	---
2.71	2.95	0.24	9.60E-02	4.41E-01	CCDC88A	coiled-coil domain containing 88A	chr2p16.1	238759_at	NM_018084
2.00	2.23	0.24	9.60E-02	4.41E-01	ANKRD40	Ankyrin repeat domain 40	chr17q21.33	241032_at	NM_052855
2.58	2.81	0.23	9.60E-02	4.41E-01	EBF2	early B-cell factor 2	chr8p21.2	220392_at	NM_022659
4.55	4.78	0.23	9.59E-02	4.41E-01	DPF1	D4, zinc and double PHD fingers family 1	chr19q13.13-q13.2	231599_x_at	NM_004647
2.34	2.54	0.20	9.60E-02	4.41E-01	PATL1	protein associated with topoisomerase II homolog 1 (yeast)	chr11q12.1	244342_at	NM_152716
1.89	2.08	0.19	9.60E-02	4.41E-01	COPA	coatomer protein complex, subunit alpha	chr1q23-q25	1559862_at	NM_001098398 /// NM_004371
2.23	2.41	0.18	9.60E-02	4.41E-01	CD8B	CD8b molecule	chr2p12	215332_s_at	NM_004931 /// NM_172099 /// NM_172101 /// NM_172102 /// NM_172213
2.98	3.30	0.32	9.61E-02	4.41E-01	---	---	---	239515_at	---
1.92	2.19	0.27	9.61E-02	4.41E-01	---	---	---	1562431_x_at	---
2.15	2.38	0.24	9.61E-02	4.41E-01	KRT84	keratin 84	chr12q13	217031_at	NM_033045
2.04	2.23	0.19	9.61E-02	4.41E-01	---	---	---	206532_at	---
4.83	5.61	0.78	9.62E-02	4.41E-01	CDC27	cell division cycle 27 homolog (S. cerevisiae)	chr17q12-q23.2	217881_s_at	NM_001114091 /// NM_001256
3.19	3.56	0.37	9.62E-02	4.41E-01	---	---	---	233717_x_at	---
3.32	3.63	0.31	9.61E-02	4.41E-01	---	---	---	243513_at	---
3.76	4.02	0.26	9.62E-02	4.41E-01	RBP3	retinol binding protein 3, interstitial	chr10q11.2	210318_at	NM_002900
2.47	2.70	0.23	9.61E-02	4.41E-01	LOC100132116	hypothetical LOC100132116	chr10q23.31	1564257_at	XM_001720537 /// XM_001723915 /// XM_001724437
2.54	2.72	0.18	9.61E-02	4.41E-01	---	---	---	236628_at	---
7.21	7.53	0.32	9.63E-02	4.41E-01	TRABD	TraB domain containing	chr22q13.33	232706_s_at	NM_025204
3.72	4.01	0.29	9.63E-02	4.41E-01	MOCS2	molybdenum cofactor synthesis 2	chr5q11	236208_at	NM_004531 /// NM_176806
2.00	2.29	0.29	9.63E-02	4.41E-01	---	---	---	241220_at	---
2.53	2.76	0.23	9.64E-02	4.41E-01	---	---	---	213658_at	---
2.63	2.84	0.21	9.63E-02	4.41E-01	NCOA1	Nuclear receptor coactivator 1	chr2p23	231289_at	NM_003743 /// NM_147223 /// NM_147233
2.95	3.13	0.18	9.64E-02	4.41E-01	KCNB1	potassium voltage-gated channel, Shab-related subfamily, member 1	chr20q13.2	211006_s_at	NM_004975
3.86	4.51	0.65	9.64E-02	4.41E-01	OSBPL11	oxysterol binding protein-like 11	chr3q21	222586_s_at	NM_022776
4.78	5.12	0.34	9.64E-02	4.41E-01	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	chr9p13	201882_x_at	NM_001497
2.19	2.44	0.26	9.64E-02	4.41E-01	HRH3	histamine receptor H3	chr20q13.33	220447_at	NM_007232
2.12	2.32	0.20	9.64E-02	4.41E-01	SMAD2	SMAD family member 2	chr18q21.1	239271_at	NM_001003652 /// NM_005901
3.82	4.50	0.68	9.64E-02	4.42E-01	PTPRF	protein tyrosine phosphatase, receptor type, F	chr1p34	200637_s_at	NM_002840 /// NM_130440
2.17	2.82	0.65	9.65E-02	4.42E-01	CDH19	cadherin 19, type 2	chr18q22-q23	206898_at	NM_021153

3.27	3.60	0.33	9.65E-02	4.42E-01	MUPCDH	mucin-like protocadherin	chr11p15.5	220074_at	NM_021924 /// NM_031264
2.52	2.83	0.31	9.65E-02	4.42E-01	TMEM20	transmembrane protein 20	chr10q23.33	239265_at	NM_001134658 /// NM_153226
7.72	8.26	0.54	9.65E-02	4.42E-01	SRPRB	signal recognition particle receptor, B subunit	chr3q22.1	218140_x_at	NM_021203
3.44	3.95	0.51	9.65E-02	4.42E-01	ZNF573	zinc finger protein 573	chr19q13.12	217627_at	NM_152360
8.19	8.53	0.33	9.65E-02	4.42E-01	HAB1	B1 for mucin	---	215778_x_at	---
2.17	2.46	0.30	9.65E-02	4.42E-01	---	---	---	242249_at	---
3.02	3.39	0.37	9.66E-02	4.42E-01	FABP2	fatty acid binding protein 2, intestinal	chr4q28-q31	207475_at	NM_000134
5.63	5.96	0.34	9.67E-02	4.42E-01	REM1	RAS (RAD and GEM)-like GTP-binding 1	chr20q11.21	210300_at	NM_014012
2.09	2.32	0.23	9.66E-02	4.42E-01	---	---	---	244162_at	---
2.36	2.53	0.17	9.67E-02	4.42E-01	EDA	ectodysplasin A	chrXq12-q13.1|Xq12	211127_x_at	NM_001005609 /// NM_001005610 /// NM_001005611 /// NM_001005612 /// NM_001005615 /// NM_001399
6.73	7.09	0.36	9.67E-02	4.42E-01	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	chr9q34.3	32837_at	NM_001012727 /// NM_006412
2.85	3.18	0.32	9.67E-02	4.42E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	214886_s_at	NM_001079691 /// NM_052818
2.14	2.35	0.21	9.67E-02	4.42E-01	---	---	---	1570653_at	---
4.12	4.49	0.38	9.67E-02	4.42E-01	FLJ46026	FLJ46026 protein	chr17q25.3	1565905_at	XR_041189 /// XR_041190
2.18	2.43	0.25	9.68E-02	4.42E-01	---	---	---	240986_at	---
3.44	3.71	0.26	9.68E-02	4.42E-01	TSPAN32	tetraspanin 32	chr11p15.5	233467_s_at	NM_005705 /// NM_139022
4.55	4.79	0.24	9.68E-02	4.42E-01	LGI3	leucine-rich repeat LGI family, member 3	chr8p21.3	238061_at	NM_139278
2.53	2.87	0.34	9.68E-02	4.42E-01	---	---	---	236579_at	---
5.88	6.38	0.50	9.69E-02	4.42E-01	ITM2C	integral membrane protein 2C	chr2q37	221004_s_at	NM_001012514 /// NM_001012516 /// NM_030926
3.01	3.40	0.38	9.69E-02	4.42E-01	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	chr22q11.21	211147_s_at	NM_005446
5.30	5.57	0.27	9.69E-02	4.42E-01	APOA5	apolipoprotein A-V	chr11q23	224243_at	NM_052968
2.25	2.56	0.31	9.69E-02	4.42E-01	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	chr9q32	219552_at	NM_153366
2.99	3.20	0.21	9.69E-02	4.42E-01	---	---	---	242848_x_at	---
2.69	3.01	0.32	9.70E-02	4.43E-01	RPS27A	ribosomal protein S27a	chr2p16	244624_at	NM_002954
4.01	4.74	0.73	9.70E-02	4.43E-01	IGKV4-1	immunoglobulin kappa variable 4-1	chr2p12	214777_at	---
2.16	2.47	0.31	9.70E-02	4.43E-01	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	chr9q32	1566722_a_at	NM_153366
3.72	4.22	0.50	9.71E-02	4.43E-01	tcag7.903	hypothetical protein LOC729852	chr7p21.3	226596_x_at	XR_040869 /// XR_040870
3.05	3.50	0.45	9.71E-02	4.43E-01	---	---	---	235111_at	---
2.91	3.19	0.27	9.71E-02	4.43E-01	FXYD2	FXYD domain containing ion transport regulator 2	chr11q23	207434_s_at	NM_001127489 /// NM_001680 /// NM_021603
1.81	2.03	0.22	9.71E-02	4.43E-01	---	---	---	1555718_x_at	---
8.62	9.02	0.40	9.72E-02	4.43E-01	C20orf199	chromosome 20 open reading frame 199	chr20q13.13	226227_x_at	NR_003604 /// NR_003605 /// NR_003606
3.34	3.59	0.26	9.72E-02	4.43E-01	---	---	---	236455_at	---
2.20	2.45	0.25	9.73E-02	4.43E-01	---	---	---	241205_at	---
2.11	2.31	0.20	9.73E-02	4.43E-01	---	---	---	1564676_a_at	---
3.10	3.40	0.30	9.73E-02	4.43E-01	RNF213	ring finger protein 213	chr17q25.3	241480_at	NM_020914
2.07	2.30	0.23	9.74E-02	4.43E-01	FLJ40434	hypothetical FLJ40434	chr1p32.3	1560944_at	NR_002314
10.30	10.69	0.40	9.74E-02	4.44E-01	---	---	---	AFFX-r2-Ec-bioD-3_at	---
2.45	2.77	0.32	9.74E-02	4.44E-01	---	---	---	242926_at	---
4.38	4.67	0.29	9.74E-02	4.44E-01	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	chr19q13.42	214380_at	NM_015629
2.42	2.70	0.28	9.74E-02	4.44E-01	41528	septin 11	chr4q21.1	201308_s_at	NM_018243
2.00	2.22	0.22	9.74E-02	4.44E-01	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	chr3p21.3	1555118_at	NM_001248
2.93	3.22	0.29	9.75E-02	4.44E-01	LOC400084	hypothetical gene supported by AK057632; AL137270; BC057846	chr12q24.31	216209_at	---
1.82	2.03	0.21	9.75E-02	4.44E-01	TRDN	triadin	chr6q22-q23	222287_at	NM_006073

4.18	4.56	0.38	9.75E-02	4.44E-01	SPAG9	sperm associated antigen 9	chr17q21.33	212468_at	NM_001130528 /// NM_003971																				
2.08	2.34	0.26	9.75E-02	4.44E-01	---	---	---	241128_at	---																				
7.36	8.35	0.99	9.77E-02	4.44E-01	RAB18	RAB18, member RAS oncogene family	chr10p12.1	224787_s_at	NM_021252																				
7.81	8.74	0.93	9.77E-02	4.44E-01	SERINC1	serine incorporator 1	chr6q22.31	208671_at	NM_020755																				
2.86	3.60	0.75	9.77E-02	4.44E-01	KRT222P	keratin 222 pseudogene	chr17q21.2	244111_at	NM_152349																				
3.91	4.37	0.46	9.77E-02	4.44E-01	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	chr9q34.3	205914_s_at	NM_000832 /// NM_007327 /// NM_021569																				
3.29	3.63	0.34	9.76E-02	4.44E-01	ZNF532	zinc finger protein 532	chr18q21.32	225021_at	NM_018181																				
2.61	2.92	0.31	9.77E-02	4.44E-01	NPHS2	nephrosis 2, idiopathic, steroid-resistant (podocin)	chr1q25.2	220424_at	NM_014625																				
3.11	3.39	0.28	9.76E-02	4.44E-01	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	chr12q13.3	1555385_at	NM_001478																				
2.21	2.48	0.27	9.76E-02	4.44E-01	LOC100130288	Hypothetical protein LOC100130288	chr3p24.3	1557840_at	XM_001716704 /// XM_001717724 /// XM_001718096																				
5.80	6.15	0.35	9.77E-02	4.44E-01	---	---	---	243567_at	---																				
4.10	4.40	0.30	9.77E-02	4.44E-01	LOC100134128	similar to hCG15011	---	213747_at	XM_001717560																				
6.42	6.70	0.28	9.77E-02	4.44E-01	CD6	CD6 molecule	chr11q13	213958_at	NM_006725																				
3.41	3.67	0.25	9.77E-02	4.44E-01	---	---	---	236457_at	---																				
3.57	3.84	0.27	9.78E-02	4.44E-01	---	---	---	237541_at	---																				
7.67	8.13	0.46	9.78E-02	4.44E-01	CTSH	cathepsin H	chr15q24-q25	202295_s_at	NM_004390 /// NM_148979																				
2.85	3.10	0.25	9.78E-02	4.44E-01	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	chr19p13.3	214088_s_at	NM_000149 /// NM_001097639 /// NM_001097640 /// NM_001097641																				
6.01	6.74	0.73	9.79E-02	4.44E-01	NFIA	nuclear factor I/A	chr1p31.3-p31.2	224976_at	NM_001134673 /// NM_005595																				
3.09	3.38	0.29	9.79E-02	4.44E-01	PCGF2	Polycomb group ring finger 2	chr17q12	240752_at	NM_007144																				
4.50	5.23	0.74	9.79E-02	4.45E-01	EBF1	early B-cell factor 1	chr5q34	227646_at	NM_024007																				
2.12	2.37	0.25	9.80E-02	4.45E-01	KRTAP4-8	keratin associated protein 4-8	chr17q12-q21	234631_at	XM_001130332 /// XM_001130340 /// XM_001721146 /// XM_001721148 /// XM_001722576 /// XM_927495																				
2.80	3.21	0.42	9.80E-02	4.45E-01	OR7C1	olfactory receptor, family 7, subfamily C, member 1	chr19p13.1	216690_at	NM_198944																				
3.51	3.89	0.38	9.81E-02	4.45E-01	LOC100129845	hypothetical LOC100129845	chr7q22.1	1560939_at	XM_001714950 /// XM_001724851 /// XM_001724864 /// XM_001725295																				
2.92	3.23	0.31	9.81E-02	4.45E-01	IGH@ /// IGHA1 /// IGHD /// IGHG1 /// IGHG3 /// IGHM /// IGHV@ /// LOC100133739	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable group /// similar to hCG2038920	chr14q32.33	234419_x_at	XM_001718220																				
5.22	5.64	0.42	9.81E-02	4.45E-01	AQP7	aquaporin 7	chr9p13	206955_at	NM_001170																				
2.29	2.51	0.22	9.81E-02	4.45E-01	---	---	---	1561686_at	---																				
6.05	6.61	0.56	9.82E-02	4.45E-01	FRYL	FRY-like	chr4p12	212548_s_at	NM_015030																				
7.36	7.96	0.60	9.82E-02	4.45E-01	ALG5	asparagine-linked glycosylation 5 homolog (S. cerevisiae, dolichyl-phosphate beta-glucosyltransferase)	chr13q13.3	218203_at	NM_013338																				
6.61	6.93	0.32	9.82E-02	4.45E-01	FAM115A	family with sequence similarity 115, member A	chr7q35	204403_x_at	NM_014719																				
5.75	6.72	0.97	9.82E-02	4.45E-01	TBC1D15	TBC1 domain family, member 15	chr12q21.1	218268_at	NM_022771																				

3.36	3.59	0.22	9.82E-02	4.45E-01	ALAS2	aminolevulinate, delta-, synthase 2	chrXp11.21	211560_s_at	NM_000032 /// NM_001037967 /// NM_001037968 /// NM_001037969
3.93	5.05	1.12	9.83E-02	4.46E-01	CLIC4	chloride intracellular channel 4	chr1p36.11	201559_s_at	NM_013943
4.15	4.51	0.36	9.83E-02	4.46E-01	---	---	---	238728_at	---
2.61	2.90	0.28	9.83E-02	4.46E-01	---	---	---	217587_at	---
4.83	5.16	0.33	9.83E-02	4.46E-01	SLC39A3	solute carrier family 39 (zinc transporter), member 3	chr19p13.3	229677_at	NM_144564 /// NM_213568
2.58	2.95	0.37	9.84E-02	4.46E-01	---	---	---	234105_at	---
2.65	2.96	0.31	9.84E-02	4.46E-01	---	---	---	235962_at	---
2.07	2.33	0.26	9.84E-02	4.46E-01	TMPRSS3	transmembrane protease, serine 3	chr21q22.3	220177_s_at	NM_024022 /// NM_032401 /// NM_032404 /// NM_032405
2.24	2.47	0.23	9.84E-02	4.46E-01	---	---	---	230908_at	---
2.03	2.22	0.19	9.84E-02	4.46E-01	TRPM1	transient receptor potential cation channel, subfamily M, member 1	chr15q13-q14	206479_at	NM_002420
5.91	6.70	0.79	9.85E-02	4.46E-01	NR1D2	nuclear receptor subfamily 1, group D, member 2	chr3p24.2	209750_at	NM_005126
8.86	9.50	0.65	9.85E-02	4.46E-01	CD59	CD59 molecule, complement regulatory protein	chr11p13	200985_s_at	NM_000611 /// NM_001127223 /// NM_001127225 /// NM_001127226 /// NM_001127227 /// NM_203329 /// NM_203330 /// NM_203331
3.43	3.71	0.27	9.85E-02	4.46E-01	---	---	---	233114_at	---
2.24	2.48	0.23	9.85E-02	4.46E-01	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	chr3q13.31	1560696_x_at	NM_024638
2.30	2.53	0.22	9.85E-02	4.46E-01	SEMA3D	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	chr7q21.11	215324_at	NM_152754
2.52	2.74	0.22	9.85E-02	4.46E-01	---	---	---	237637_at	---
4.53	4.97	0.44	9.85E-02	4.46E-01	ZNF414	Zinc finger protein 414	chr19p13.2	239145_at	NM_032370
5.84	6.12	0.28	9.85E-02	4.46E-01	---	---	---	215372_x_at	---
3.97	4.22	0.25	9.86E-02	4.46E-01	C17orf70	Chromosome 17 open reading frame 70	chr17q25.3	228136_s_at	NM_001109760 /// NM_025161
4.88	5.79	0.91	9.86E-02	4.46E-01	TMEM97	transmembrane protein 97	chr17q11.2	214283_at	NM_014573
8.13	8.75	0.62	9.86E-02	4.46E-01	IARS	isoleucyl-tRNA synthetase	chr9q21	204744_s_at	NM_002161 /// NM_013417
3.46	3.87	0.41	9.86E-02	4.46E-01	PDK3	pyruvate dehydrogenase kinase, isozyme 3	chrXp22.11	221957_at	NM_005391
5.06	5.43	0.37	9.87E-02	4.46E-01	KLK1	kallikrein 1	chr19q13.3	216699_s_at	NM_002257
4.06	4.40	0.34	9.87E-02	4.46E-01	ZNF33B	zinc finger protein 33B	chr10q11.2	215022_x_at	NM_006955
2.90	3.24	0.33	9.86E-02	4.46E-01	SERTAD4	SERTA domain containing 4	chr1q32.1-q41	229674_at	NM_019605
2.59	2.87	0.28	9.86E-02	4.46E-01	TPM3	tropomyosin 3	chr1q21.2	238065_at	NM_001043351 /// NM_001043352 /// NM_001043353 /// NM_152263 /// NM_153649
3.65	3.91	0.26	9.87E-02	4.46E-01	GPR21	G protein-coupled receptor 21	chr9q33	221294_at	NM_005294
6.32	6.55	0.23	9.86E-02	4.46E-01	ISY1	ISY1 splicing factor homolog (S. cerevisiae)	chr3q21.3	223428_s_at	NM_020701
3.35	3.57	0.22	9.86E-02	4.46E-01	RAD18	RAD18 homolog (S. cerevisiae)	chr3p25-p24	223417_at	NM_020165
1.94	2.15	0.21	9.87E-02	4.46E-01	---	---	---	1555623_at	---

7.66	8.15	0.50	9.88E-02	4.46E-01	TPM1	tropomyosin 1 (alpha)	chr15q22.1	210986_s_at	NM_000366 /// NM_001018004 /// NM_001018005 /// NM_001018006 /// NM_001018007 /// NM_001018008 /// NM_001018020
3.05	3.52	0.47	9.87E-02	4.46E-01	---	---	---	236327_at	---
6.11	6.51	0.39	9.87E-02	4.46E-01	RCE1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	chr11q13	205333_s_at	NM_001032279 /// NM_005133
4.77	5.10	0.33	9.88E-02	4.46E-01	REEP2	receptor accessory protein 2	chr5q31	205331_s_at	NM_016606
2.46	2.74	0.28	9.87E-02	4.46E-01	---	---	---	242799_at	---
2.33	2.59	0.26	9.88E-02	4.46E-01	---	---	---	237763_at	---
2.02	2.24	0.23	9.87E-02	4.46E-01	---	---	---	1560717_at	---
2.10	2.32	0.22	9.88E-02	4.46E-01	---	---	---	1564836_at	---
2.06	2.28	0.22	9.87E-02	4.46E-01	---	---	---	241179_at	---
2.57	2.86	0.29	9.88E-02	4.46E-01	GRHL1	grainyhead-like 1 (Drosophila)	chr2p25.1	1552685_a_at	NM_014552 /// NM_198182
3.45	3.82	0.36	9.89E-02	4.46E-01	DGAT2	diacylglycerol O-acyltransferase homolog 2 (mouse)	chr11q13.5	226064_s_at	NM_032564
3.30	3.65	0.35	9.89E-02	4.46E-01	---	---	---	237926_s_at	---
2.42	2.64	0.22	9.89E-02	4.46E-01	SNX32	sorting nexin 32	chr11q13.1	1554181_at	NM_152760
3.58	3.92	0.34	9.89E-02	4.46E-01	WDR27	WD repeat domain 27	chr6q27	238074_at	NM_182552
3.55	3.87	0.32	9.89E-02	4.46E-01	CIITA	class II, major histocompatibility complex, transactivator	chr16p13	211884_s_at	NM_000246
1.98	2.22	0.24	9.89E-02	4.46E-01	---	---	---	240141_at	---
2.64	2.86	0.22	9.89E-02	4.46E-01	CCDC129	coiled-coil domain containing 129	chr7p15.1	234027_at	NM_194300
8.45	8.83	0.38	9.90E-02	4.46E-01	SUCLG1	succinate-CoA ligase, alpha subunit	chr2p11.2	217874_at	NM_003849
2.63	2.83	0.20	9.90E-02	4.46E-01	---	---	---	239495_at	---
3.57	3.89	0.32	9.90E-02	4.46E-01	---	---	---	240727_s_at	---
5.16	5.51	0.36	9.90E-02	4.47E-01	DKFZp564N2472	hypothetical protein DKFZp564N2472	chr7p12.1	1556291_at	NM_182595
2.22	2.47	0.25	9.91E-02	4.47E-01	hCG_2036596	HCG2036596	chr1p36.32	1566735_at	XM_001132281 /// XM_001134291 /// XM_001134292 /// XM_001724323
2.41	2.63	0.21	9.90E-02	4.47E-01	PLA2R1	phospholipase A2 receptor 1, 180kDa	chr2q23-q24	235746_s_at	NM_001007267 /// NM_007366
2.17	2.41	0.24	9.91E-02	4.47E-01	---	---	---	1568755_a_at	---
6.57	7.12	0.55	9.91E-02	4.47E-01	MDFIC	MyoD family inhibitor domain containing	chr7q31.1-q31.2	211675_s_at	NM_199072
8.06	8.50	0.44	9.91E-02	4.47E-01	CTSD	cathepsin D	chr11p15.5	200766_at	NM_001909
2.26	2.55	0.29	9.92E-02	4.47E-01	P11	26 serine protease	chr12q13.1	206605_at	NM_006025
5.01	5.50	0.49	9.92E-02	4.47E-01	---	---	---	238108_at	---
2.62	2.90	0.28	9.92E-02	4.47E-01	HIST1H1B	histone cluster 1, H1b	chr6p22-p21.3	214534_at	NM_005322
2.43	2.65	0.21	9.92E-02	4.47E-01	EIF5A2	eukaryotic translation initiation factor 5A2	chr3q26.2	235296_at	NM_020390
6.42	7.19	0.77	9.93E-02	4.47E-01	ERMP1	endoplasmic reticulum metallopeptidase 1	chr9p24	218342_s_at	NM_024896
2.23	2.45	0.22	9.93E-02	4.47E-01	CLDN10	claudin 10	chr13q31-q34	1556687_a_at	NM_006984 /// NM_182848
2.86	3.11	0.25	9.93E-02	4.47E-01	ZNF416	zinc finger protein 416	chr19q13.4	234902_s_at	NM_017879
2.51	3.03	0.51	9.94E-02	4.47E-01	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	chr6p21.1-p12.2	214581_x_at	NM_014452
2.32	2.65	0.33	9.94E-02	4.47E-01	---	---	---	1559911_at	---
3.07	3.36	0.29	9.94E-02	4.47E-01	---	---	---	1556835_s_at	---
7.65	8.28	0.62	9.94E-02	4.47E-01	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	chr1q32.1	212135_s_at	NM_001001396 /// NM_001684

2.40	2.69	0.29	9.95E-02	4.47E-01	FLJ43663	hypothetical LOC378805	chr7q32.3	238986_at	XM_380146 /// XM_930545 /// XM_935361 /// XM_935362 /// XM_935363 /// XM_935364 /// XM_935365 /// XM_935366 /// XM_935367 /// XM_935688 /// XM_935957 /// XM_935958 /// XM_935959 /// XM_935960 /// XM_935961 /// XM_935962 /// XM_935963 /// XM_935964 /// XM_940526 /// XM_944629 /// XM_944633 /// XM_944638 /// XM_944640 /// XM_944641 /// XM_944643 /// XM_944645 /// XM_944647																					
2.67	2.95	0.28	9.95E-02	4.47E-01	GFAP	glial fibrillary acidic protein	chr17q21	203540_at	NM_001131019 /// NM_002055																				
5.96	6.24	0.28	9.95E-02	4.47E-01	HEATR6	HEAT repeat containing 6	chr17q23.1	218991_at	NM_022070																				
2.62	2.86	0.24	9.94E-02	4.47E-01	---	---	---	244027_at	---																				
1.90	2.14	0.23	9.94E-02	4.47E-01	F13B	coagulation factor XIII, B polypeptide	chr1q31-q32.1	207810_at	NM_001994																				
1.87	2.06	0.19	9.95E-02	4.47E-01	TAF13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	chr1p13.3	205966_at	NM_005645																				
4.29	4.61	0.32	9.95E-02	4.47E-01	TRIM17	tripartite motif-containing 17	chr1q42	220279_at	NM_001024940 /// NM_001024941 /// NM_016102																				
2.65	2.95	0.29	9.95E-02	4.47E-01	FLJ30428	similar to hypothetical protein A230046P18; cDNA sequence BC055759	chr2q21.1	226809_at	XM_001718192 /// XM_001723916 /// XM_496597																				
2.13	2.37	0.24	9.95E-02	4.47E-01	---	---	---	217674_at	---																				
4.42	5.12	0.70	9.96E-02	4.47E-01	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	chr6q14-q15	1555427_s_at	NM_006372																				
2.59	2.80	0.21	9.96E-02	4.47E-01	RERE	arginine-glutamic acid dipeptide (RE) repeats	chr1p36.2-p36.1	200939_s_at	NM_001042681 /// NM_001042682 /// NM_012102																				
4.37	5.03	0.66	9.96E-02	4.47E-01	DTWD1	DTW domain containing 1	chr15q21.2	236649_at	NM_020234																				
4.40	4.76	0.35	9.97E-02	4.47E-01	DERL3	Der1-like domain family, member 3	chr22q11.23	228897_at	NM_001002862 /// NM_198440																				
3.93	4.24	0.30	9.97E-02	4.48E-01	---	---	---	233258_at	---																				

2.75	4.02	1.27	9.97E-02	4.48E-01	PRAME	preferentially expressed antigen in melanoma	chr22q11.22	204086_at	NM_006115 /// NM_206953 /// NM_206954 /// NM_206955 /// NM_206956																				
2.69	2.95	0.25	9.98E-02	4.48E-01	---	---	---	1561459_at	---																				
3.29	3.58	0.29	9.99E-02	4.48E-01	ELFN1	extracellular leucine-rich repeat and fibronectin type III domain containing 1	chr7p22.3	229581_at	NM_001128636 /// XM_001132524 /// XM_001717054 /// XM_001732882 /// XM_374386																				
5.16	5.85	0.70	1.00E-01	4.48E-01	RNPC3	RNA-binding region (RNP1, RRM) containing 3	chr1p21	226975_at	NM_017619																				
6.23	7.29	1.06	1.00E-01	4.49E-01	MYCBP2	MYC binding protein 2	chr13q22	201959_s_at	NM_015057																				
3.81	4.66	0.85	1.00E-01	4.49E-01	PAX6	paired box 6	chr11p13	205646_s_at	NM_000280 /// NM_001127612 /// NM_001604																				
3.58	4.23	0.65	1.00E-01	4.49E-01	---	---	---	215164_at	---																				
3.54	3.78	0.24	1.00E-01	4.49E-01	TAT	tyrosine aminotransferase	chr16q22.1	206916_x_at	NM_000353																				
1.93	2.13	0.20	1.00E-01	4.49E-01	SPDYA	speedy homolog A (Drosophila)	chr2p23.2	238262_at	NM_001008779 /// NM_182756																				
5.22	6.46	1.24	1.00E-01	4.49E-01	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	chr3q13.2-q13.31	201971_s_at	NM_001690																				
1.94	2.22	0.28	1.00E-01	4.49E-01	---	---	---	239984_at	---																				
2.06	2.33	0.27	1.00E-01	4.49E-01	---	---	---	243122_at	---																				
2.26	2.52	0.26	1.00E-01	4.49E-01	MUPCDH	mucin-like protocadherin	chr11p15.5	220075_s_at	NM_021924 /// NM_031264																				
2.28	2.56	0.28	1.00E-01	4.49E-01	ZNF396	zinc finger protein 396	chr18q12	1554985_at	NM_145756																				
2.03	2.27	0.24	1.00E-01	4.49E-01	---	---	---	1566540_at	---																				
2.60	2.90	0.30	1.00E-01	4.49E-01	CASR	calcium-sensing receptor	chr3q13	242745_at	NM_000388																				
4.96	5.42	0.46	1.00E-01	4.49E-01	C17orf55	chromosome 17 open reading frame 55	chr17q25.3	243263_at	NM_178519																				
6.40	6.86	0.46	1.00E-01	4.49E-01	PTAFR	platelet-activating factor receptor	chr1p35-p34.3	206278_at	NM_000952																				
2.30	2.52	0.22	1.00E-01	4.49E-01	---	---	---	1560547_at	---																				
2.95	3.42	0.47	1.00E-01	4.49E-01	PLAA	phospholipase A2-activating protein	chr9p21	209532_at	NM_001031689 /// NM_004253																				
3.82	4.19	0.37	1.00E-01	4.49E-01	ZNF286A	zinc finger protein 286A	chr17p11.2	1557684_at	NM_001130842 /// NM_020652																				
4.23	4.57	0.34	1.00E-01	4.49E-01	ZFP64	zinc finger protein 64 homolog (mouse)	chr20q13.2	219536_s_at	NM_018197 /// NM_022088 /// NM_199426 /// NM_199427																				
2.64	2.82	0.18	1.00E-01	4.49E-01	SLC25A30	solute carrier family 25, member 30	chr13q14.12	238171_at	NM_001010875																				
5.93	6.28	0.35	1.00E-01	4.49E-01	SHROOM1	shroom family member 1	chr5q31.1	241935_at	NM_133456																				
6.86	7.44	0.58	1.00E-01	4.49E-01	PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	chr2p23	201409_s_at	NM_002709 /// NM_206876																				
2.35	2.65	0.31	1.00E-01	4.49E-01	---	---	---	220873_at	---																				
4.13	4.43	0.30	1.00E-01	4.49E-01	MATK	megakaryocyte-associated tyrosine kinase	chr19p13.3	206267_s_at	NM_002378 /// NM_139354 /// NM_139355																				
6.46	6.99	0.53	1.00E-01	4.49E-01	FOXO3	forkhead box O3	chr6q21	224889_at	NM_001455 /// NM_201559																				
5.00	5.88	0.88	1.01E-01	4.49E-01	PHIP	pleckstrin homology domain interacting protein	chr6q14	212542_s_at	NM_017934																				
3.21	3.60	0.38	1.01E-01	4.49E-01	---	---	---	228742_at	---																				
2.86	3.20	0.34	1.01E-01	4.49E-01	AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	chr12p11.21 /// chr1p31.3	225342_at	NM_001002921 /// NM_001005353 /// NM_013410 /// NM_203464 /// XM_001132080 /// XM_001725174 /// XM_928632																				
4.32	4.65	0.33	1.01E-01	4.49E-01	---	---	---	238842_at	---																				
2.36	2.62	0.27	1.01E-01	4.49E-01	SCML4	sex comb on midleg-like 4 (Drosophila)	chr6q21	1569225_a_at	NM_198081																				

2.16	2.40	0.24	1.01E-01	4.49E-01	LOC202451	hypothetical protein LOC202451	chr6q23.3	228051_at	XM_928403 /// XM_941101
2.81	3.02	0.21	1.01E-01	4.49E-01	---	---	---	1569758_at	---
2.81	3.09	0.28	1.01E-01	4.50E-01	CXCR5	chemokine (C-X-C motif) receptor 5	chr11q23.3	206126_at	NM_001716 /// NM_032966
2.51	2.85	0.34	1.01E-01	4.50E-01	ATP8A2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	chr13q12	219660_s_at	NM_016529
6.68	6.99	0.31	1.01E-01	4.50E-01	PTCRA	pre T-cell antigen receptor alpha	chr6p21.3	211252_x_at	NM_138296
2.08	2.31	0.24	1.01E-01	4.50E-01	POLK	polymerase (DNA directed) kappa	chr5q13	1555317_at	NM_016218
2.68	3.06	0.39	1.01E-01	4.50E-01	DMRTA2	DMRT-like family A2	chr1p33	1558856_at	NM_032110
4.86	5.19	0.33	1.01E-01	4.50E-01	---	---	---	226362_at	---
5.47	6.15	0.68	1.01E-01	4.50E-01	TPM4	tropomyosin 4	chr19p13.1	209344_at	NM_003290
2.59	2.83	0.24	1.01E-01	4.50E-01	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	chr11q24.2	205973_at	NM_005103 /// NM_022549
5.86	6.07	0.21	1.01E-01	4.50E-01	---	---	---	242589_x_at	---
3.95	4.34	0.40	1.01E-01	4.50E-01	RNGTT	RNA guanylyltransferase and 5'-phosphatase	chr6q16	211387_x_at	NM_003800
2.34	2.63	0.30	1.01E-01	4.50E-01	LOC641518	hypothetical protein LOC641518	chr4q23-q25	243362_s_at	XR_017788 /// XR_017912 /// XR_040484
2.37	2.59	0.22	1.01E-01	4.50E-01	OR2L1P	olfactory receptor, family 2, subfamily L, member 1 pseudogene	chr1q44	1567242_at	NR_002145
2.81	3.53	0.72	1.01E-01	4.50E-01	---	---	---	229692_at	---
2.70	2.96	0.25	1.01E-01	4.50E-01	SYTL5	synaptotagmin-like 5	chrXp21.1	1553033_at	NM_138780
3.40	3.96	0.56	1.01E-01	4.50E-01	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	---	1552625_a_at	NM_182916
4.23	4.47	0.24	1.01E-01	4.51E-01	LOC283904	hypothetical protein LOC283904	chr16q24.1	242332_at	XM_001713951 /// XM_001718298 /// XM_001719681
3.55	3.87	0.32	1.01E-01	4.51E-01	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	chrXp11.4-p11.21	205400_at	NM_000377
2.12	2.34	0.22	1.01E-01	4.51E-01	---	---	---	1559895_x_at	---
2.18	2.42	0.24	1.01E-01	4.51E-01	---	---	---	234817_at	---
2.07	2.29	0.22	1.01E-01	4.51E-01	FPR2	formyl peptide receptor 2	chr19q13.3-q13.4	210772_at	NM_001005738 /// NM_001462
2.82	3.15	0.33	1.01E-01	4.51E-01	KCNA10	potassium voltage-gated channel, shaker-related subfamily, member 10	chr1p13.1	208560_at	NM_005549
2.27	2.53	0.26	1.01E-01	4.51E-01	IL13RA2	interleukin 13 receptor, alpha 2	chrXq13.1-q28	206172_at	NM_000640
5.39	5.89	0.51	1.01E-01	4.51E-01	DENND2D	DENN/MADD domain containing 2D	chr1p13.3	221081_s_at	NM_024901
3.43	3.86	0.43	1.01E-01	4.51E-01	---	---	---	239790_s_at	---
3.52	3.84	0.32	1.01E-01	4.51E-01	---	---	---	237386_at	---
2.43	2.72	0.30	1.01E-01	4.51E-01	ERC1	ELKS/RAB6-interacting/CAST family member 1	chr12p13.3	1563947_a_at	NM_015064 /// NM_178037 /// NM_178038 /// NM_178039 /// NM_178040
1.99	2.26	0.27	1.01E-01	4.51E-01	---	---	---	236161_at	---
2.81	3.11	0.30	1.01E-01	4.51E-01	C8orf16	chromosome 8 open reading frame 16	chr8p23.1	230702_at	NM_001014439
5.16	6.51	1.35	1.01E-01	4.51E-01	LOC653071	similar to CG32820-PA, isoform A	---	226558_at	XM_001720564 /// XM_001726969
4.27	4.72	0.45	1.01E-01	4.51E-01	METT5D1	methyltransferase 5 domain containing 1	chr11p14.1	238773_at	NM_001113528 /// NM_152636
2.13	2.44	0.30	1.01E-01	4.51E-01	DTNA	dystrobrevin, alpha	chr18q12	210091_s_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981
5.19	6.07	0.88	1.01E-01	4.51E-01	MYCBP2	MYC binding protein 2	chr13q22	1557370_s_at	NM_015057
8.40	9.03	0.63	1.01E-01	4.51E-01	AIDA	axin interactor, dorsalization associated	chr1q41	226801_s_at	NM_022831
1.98	2.17	0.18	1.01E-01	4.51E-01	---	---	---	AFFX-PheX-M_at	---
2.86	3.14	0.28	1.01E-01	4.51E-01	---	---	---	235782_at	---
5.96	6.89	0.93	1.01E-01	4.51E-01	TMEM87A	transmembrane protein 87A	chr15q15.1	212202_s_at	NM_001110503 /// NM_015497

6.32	6.86	0.54	1.01E-01	4.51E-01	FXR1	fragile X mental retardation, autosomal homolog 1	chr3q28	201636_at	NM_001013438 /// NM_001013439 /// NM_005087																				
3.21	3.47	0.27	1.01E-01	4.51E-01	OTX1	orthodenticle homeobox 1	chr2p13	238839_at	NM_014562																				
1.67	1.89	0.22	1.01E-01	4.51E-01	---	---	---	1570244_at	---																				
2.13	2.31	0.19	1.01E-01	4.51E-01	---	---	---	1569568_at	---																				
2.19	2.43	0.25	1.01E-01	4.51E-01	DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	chr11q24	219945_at	NM_013264																				
1.86	2.07	0.21	1.01E-01	4.51E-01	SYT14	synaptotagmin XIV	chr1q32.2	1553654_at	NM_153262																				
4.64	5.00	0.37	1.02E-01	4.51E-01	SYNJ2	synaptojanin 2	chr6q25.3	216180_s_at	NM_003898																				
2.21	2.52	0.31	1.02E-01	4.51E-01	ADAM28	ADAM metallopeptidase domain 28	chr8p21.2	208268_at	NM_014265 /// NM_021777																				
2.58	2.88	0.30	1.01E-01	4.51E-01	C1orf112	chromosome 1 open reading frame 112	chr1q24.2	220840_s_at	NM_018186																				
2.46	2.74	0.27	1.01E-01	4.51E-01	FER1L4	fer-1-like 4 (C. elegans)	chr20q11.22	220388_at	XM_001732892 /// XM_001732893 /// XM_001732894																				
3.48	3.72	0.24	1.02E-01	4.51E-01	NR6A1	nuclear receptor subfamily 6, group A, member 1	chr9q33-q34.1	207742_s_at	NM_001489 /// NM_033334																				
1.99	2.22	0.24	1.02E-01	4.51E-01	---	---	---	1562473_at	---																				
3.43	3.65	0.22	1.02E-01	4.51E-01	GPR31	G protein-coupled receptor 31	chr6q27	208556_at	NM_005299																				
2.07	2.26	0.20	1.02E-01	4.51E-01	---	---	---	232261_at	---																				
1.90	2.08	0.18	1.02E-01	4.51E-01	---	---	---	1562079_at	---																				
3.00	3.29	0.30	1.02E-01	4.51E-01	ADARB1	Adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	chr21q22.3	234539_at	NM_001033049 /// NM_001112 /// NM_015833 /// NM_015834																				
6.26	7.22	0.96	1.02E-01	4.52E-01	PHKB	phosphorylase kinase, beta	chr16q12-q13	202738_s_at	NM_000293 /// NM_001031835																				
5.55	6.42	0.87	1.02E-01	4.52E-01	PHF14	PHD finger protein 14	chr7p21.3	228095_at	NM_001007157 /// NM_014660																				
2.07	2.75	0.67	1.02E-01	4.52E-01	FAM40B	family with sequence similarity 40, member B	chr7q32.1	231880_at	NM_001134336 /// NM_020704																				
3.99	4.61	0.62	1.02E-01	4.52E-01	FBLIM1	filamin binding LIM protein 1	chr1p36.21	1555480_a_at	NM_001024215 /// NM_001024216 /// NM_017556																				
4.22	4.63	0.41	1.02E-01	4.52E-01	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	chr10p14-p13	219654_at	NM_014241																				
3.92	4.25	0.33	1.02E-01	4.52E-01	---	---	---	227714_s_at	---																				
3.18	3.50	0.33	1.02E-01	4.52E-01	C21orf34	chromosome 21 open reading frame 34	chr21q21.1	1559901_s_at	NM_001005732 /// NM_001005733 /// NM_001005734																				
2.99	3.32	0.32	1.02E-01	4.52E-01	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	chr4q12	205121_at	NM_000232																				
2.44	2.70	0.26	1.02E-01	4.52E-01	---	---	---	236301_at	---																				
2.40	2.64	0.23	1.02E-01	4.52E-01	NKX2-1	NK2 homeobox 1	chr14q13	211024_s_at	NM_001079668 /// NM_003317																				
2.34	2.56	0.23	1.02E-01	4.52E-01	LOC100130219	Similar to hCG2041987	chr12p13.33	235820_at	XM_001714414 /// XM_001716247																				
2.40	2.60	0.20	1.02E-01	4.52E-01	NUDC	nuclear distribution gene C homolog (A. nidulans)	chr1p35-p34	210575_at	NM_006600																				
6.89	7.44	0.55	1.02E-01	4.52E-01	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	chrXp11.4	211208_s_at	NM_001126054 /// NM_001126055 /// NM_003688																				
2.29	2.64	0.35	1.02E-01	4.52E-01	---	---	---	1563480_at	---																				
2.31	2.55	0.24	1.02E-01	4.52E-01	---	---	---	1561777_at	---																				
6.36	7.16	0.80	1.02E-01	4.52E-01	TCF4	transcription factor 4	chr18q21.1	212382_at	NM_001083962 /// NM_003199																				
6.20	6.51	0.31	1.02E-01	4.52E-01	FMN2	Formin 2	chr1q43	230946_at	NM_020066																				
2.76	2.98	0.22	1.02E-01	4.52E-01	---	---	---	1563482_at	---																				

3.76	4.46	0.70	1.02E-01	4.52E-01	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	chr10q24	209474_s_at	NM_001098175 /// NM_001776
3.08	3.67	0.59	1.02E-01	4.52E-01	ULK4	unc-51-like kinase 4 (C. elegans)	chr3p22.1	232206_at	NM_017886
3.66	3.94	0.28	1.02E-01	4.52E-01	LOC100132540 /// LOC100132620 /// LOC339047 /// NPIP	similar to LOC339047 protein /// similar to LOC339047 protein /// hypothetical protein LOC339047 /// nuclear pore complex interacting protein	chr16p12.3 /// chr16p13-p11 /// chr16p13.11	240377_at	NM_006985 /// NM_178541 /// XM_001134445 /// XM_001723375 /// XM_001724221
4.46	4.67	0.21	1.02E-01	4.52E-01	WWOX	WW domain containing oxidoreductase	chr16q23.3-q24.1	223747_x_at	NM_016373 /// NM_130791 /// NM_130844
2.31	2.48	0.17	1.02E-01	4.52E-01	MFSD9	major facilitator superfamily domain containing 9	chr2q12.1	224483_s_at	NM_032718
2.37	2.58	0.21	1.02E-01	4.52E-01	METTL7A	methyltransferase like 7A	chr12q13.13	211424_x_at	NM_014033
2.63	2.88	0.24	1.02E-01	4.52E-01	---	---	---	232871_at	---
2.27	2.46	0.19	1.02E-01	4.52E-01	PIWIL1	piwi-like 1 (Drosophila)	chr12q24.33	214868_at	NM_004764
3.60	3.95	0.35	1.02E-01	4.52E-01	RHOF	ras homolog gene family, member F (in filopodia)	chr12q24.31	1554538_at	NM_019034
4.46	5.30	0.84	1.02E-01	4.52E-01	IGLJ3	immunoglobulin lambda joining 3	chr22q11.1-q11.2	211798_x_at	---
2.71	3.04	0.33	1.02E-01	4.52E-01	---	---	---	216766_at	---
2.00	2.23	0.23	1.02E-01	4.52E-01	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	chr6p12	215686_x_at	NM_003221
2.31	2.59	0.27	1.02E-01	4.52E-01	---	---	---	234826_at	---
2.32	2.55	0.23	1.02E-01	4.52E-01	GTPBP10	GTP-binding protein 10 (putative)	chr7q21.13	239773_at	NM_001042717 /// NM_033107
4.68	5.36	0.68	1.02E-01	4.52E-01	NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	chr12q13.3	218484_at	NM_020142
4.76	5.20	0.43	1.02E-01	4.52E-01	SERGEF	secretion regulating guanine nucleotide exchange factor	chr11p14.3	220482_s_at	NM_012139
7.62	8.02	0.40	1.02E-01	4.52E-01	MRPS22	mitochondrial ribosomal protein S22	chr3q23	223448_x_at	NM_020191
7.13	8.50	1.37	1.02E-01	4.52E-01	GSTM1	glutathione S-transferase M1	chr1p13.3	204550_x_at	NM_000561 /// NM_146421
3.16	4.20	1.04	1.02E-01	4.52E-01	CST5	cystatin D	chr20p11.21	207925_at	NM_001900
4.07	4.91	0.84	1.02E-01	4.52E-01	PCDH18	protocadherin 18	chr4q31	225975_at	NM_019035
5.90	6.43	0.53	1.02E-01	4.52E-01	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	chr8q13	203448_s_at	NM_003218 /// NM_017489
3.16	3.59	0.43	1.02E-01	4.52E-01	---	---	---	240758_at	---
5.53	5.93	0.40	1.02E-01	4.52E-01	BLOC1S3	Biogenesis of lysosomal organelles complex-1, subunit 3	chr19q13.32	230576_at	NM_212550
5.11	5.49	0.39	1.02E-01	4.52E-01	---	---	---	236447_at	---
2.60	2.98	0.38	1.02E-01	4.52E-01	LDLR	low density lipoprotein receptor	chr19p13.3	217103_at	NM_000527
2.62	2.98	0.36	1.02E-01	4.52E-01	GK	glycerol kinase	chrXp21.3	215975_x_at	NM_000167 /// NM_001128127 /// NM_203391
3.60	3.95	0.36	1.02E-01	4.52E-01	SPINK5L3	serine PI Kazal type 5-like 3	chr5q33.1	233340_at	NM_001040129
2.53	2.88	0.35	1.02E-01	4.52E-01	BMP2K	BMP2 inducible kinase	chr4q21.21	232688_at	NM_017593 /// NM_198892
3.03	3.37	0.34	1.02E-01	4.52E-01	LOC100128918	hypothetical protein LOC100128918	chr6p21.1	238028_at	XM_001716725 /// XM_001717510 /// XM_001718466
3.43	3.77	0.34	1.02E-01	4.52E-01	hCG_1993592	hypothetical LOC644903	chr2q12.3	224141_at	XR_040182 /// XR_040183 /// XR_040184
4.46	4.80	0.34	1.02E-01	4.52E-01	AURKAIP1	aurora kinase A interacting protein 1	chr1p36.33	228800_x_at	NM_001127229 /// NM_001127230 /// NM_017900
3.57	3.90	0.33	1.02E-01	4.52E-01	NCLN	nicalin homolog (zebrafish)	chr19p13.3	215857_at	NM_020170
4.36	4.66	0.30	1.02E-01	4.52E-01	TSPAN9	tetraspanin 9	chr12p13.33-p13.32	205665_at	NM_006675
2.54	2.82	0.28	1.02E-01	4.52E-01	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	chr15q24	210550_s_at	NM_002891 /// NM_153815
2.28	2.55	0.27	1.02E-01	4.52E-01	FAM111A	family with sequence similarity 111, member A	chr11q12.1	229196_at	NM_022074 /// NM_198847
2.35	2.60	0.24	1.02E-01	4.52E-01	---	---	---	1561984_at	---
1.93	2.16	0.23	1.02E-01	4.52E-01	HFM1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)	chr1p22.2	241469_at	NM_001017975
6.46	7.26	0.80	1.02E-01	4.52E-01	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	chr1q41	202373_s_at	NM_012414
5.96	7.21	1.25	1.03E-01	4.52E-01	LPHN3	latrophilin 3	chr4q13.1	209866_s_at	NM_015236
4.86	6.07	1.20	1.03E-01	4.52E-01	THY1	Thy-1 cell surface antigen	chr11q22.3-q23	208850_s_at	NM_006288

5.78	6.69	0.91	1.03E-01	4.52E-01	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	chr5q31.3	211671_s_at	NM_000176 /// NM_001018074 /// NM_001018075 /// NM_001018076 /// NM_001018077 /// NM_001020825 /// NM_001024094
4.09	4.85	0.77	1.03E-01	4.52E-01	PHF17	PHD finger protein 17	chr4q26-q27	225820_at	NM_024900 /// NM_199320
4.12	4.77	0.65	1.02E-01	4.52E-01	JAK1	Janus kinase 1 (a protein tyrosine kinase)	chr1p32.3-p31.3	1552611_a_at	NM_002227
4.70	5.33	0.63	1.03E-01	4.52E-01	CREB1	cAMP responsive element binding protein 1	chr2q34	214513_s_at	NM_004379 /// NM_134442
8.46	9.07	0.61	1.02E-01	4.52E-01	NFIA	nuclear factor I/A	chr1p31.3-p31.2	224970_at	NM_001134673 /// NM_005595
2.45	3.04	0.59	1.02E-01	4.52E-01	FGG	fibrinogen gamma chain	chr4q28	219612_s_at	NM_000509 /// NM_021870
2.44	2.96	0.52	1.03E-01	4.52E-01	---	---	---	234036_x_at	---
3.44	3.78	0.34	1.03E-01	4.52E-01	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	chr18q23	209664_x_at	NM_006162 /// NM_172387 /// NM_172388 /// NM_172389 /// NM_172390
2.25	2.57	0.33	1.03E-01	4.52E-01	MUSK	muscle, skeletal, receptor tyrosine kinase	chr9q31.3-q32	241122_s_at	NM_005592
4.11	4.40	0.29	1.03E-01	4.52E-01	C7orf54	chromosome 7 open reading frame 54	chr7q31	210109_at	NM_014411
3.81	4.10	0.29	1.02E-01	4.52E-01	FFAR3 /// GPR42P	free fatty acid receptor 3 /// G protein-coupled receptor 42 pseudogene	chr19q13.1	221385_s_at	NM_005304 /// NM_005305
2.40	2.67	0.27	1.03E-01	4.52E-01	AKR1C2	Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	chr10p15-p14	244266_at	NM_001354 /// NM_205845
3.30	3.57	0.27	1.03E-01	4.52E-01	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	chr1p34	206051_at	NM_021952
3.28	3.47	0.19	1.03E-01	4.52E-01	MRPS5	Mitochondrial ribosomal protein S5	chr2p11.2-q11.2	237560_at	NM_031902
1.96	2.23	0.27	1.03E-01	4.53E-01	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	chr11q13	207496_at	NM_000139
2.38	2.63	0.24	1.03E-01	4.53E-01	VWA5B1	von Willebrand factor A domain containing 5B1	chr1p36.12	1552853_at	XM_001720309 /// XM_001722222 /// XM_001722706
2.61	2.83	0.22	1.03E-01	4.53E-01	C20orf132	chromosome 20 open reading frame 132	chr20q11.22	236618_at	NM_152503 /// NM_213631 /// NM_213632
5.09	5.53	0.44	1.03E-01	4.53E-01	TBC1D22A	TBC1 domain family, member 22A	chr22q13.3	210144_at	NM_014346
4.63	4.94	0.32	1.03E-01	4.53E-01	WDTC1	WD and tetratricopeptide repeats 1	chr1p36.11	216036_x_at	NM_015023
5.85	6.11	0.25	1.03E-01	4.53E-01	EML2	Echinoderm microtubule associated protein like 2	chr19q13.32	234026_at	NM_012155
5.18	5.68	0.50	1.03E-01	4.53E-01	---	---	---	235556_at	---
4.38	4.68	0.30	1.03E-01	4.53E-01	FOXN4	forkhead box N4	chr12q24.11	1564713_a_at	NM_213596
7.08	7.61	0.54	1.03E-01	4.53E-01	UBQLN1	ubiquilin 1	chr9q22|9q21.2-q21.3	222990_at	NM_013438 /// NM_053067
4.24	5.23	0.98	1.03E-01	4.53E-01	---	---	---	228694_at	---
6.32	6.52	0.20	1.03E-01	4.53E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	232168_x_at	NM_012090 /// NM_033044
7.56	8.26	0.70	1.03E-01	4.53E-01	TCF4	transcription factor 4	chr18q21.1	212387_at	NM_001083962 /// NM_003199
2.19	2.42	0.23	1.03E-01	4.53E-01	---	---	---	1562718_at	---
2.51	2.84	0.33	1.03E-01	4.53E-01	SCNN1G	sodium channel, nonvoltage-gated 1, gamma	chr16p12	207295_at	NM_001039
2.15	2.36	0.21	1.03E-01	4.53E-01	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	chr12q24.2|12q24.2	234876_at	NM_004373
3.00	4.01	1.01	1.03E-01	4.53E-01	TPSAB1 /// TPSB2	tryptase alpha/beta 1 /// tryptase beta 2	chr16p13.3	205683_x_at	NM_003294 /// NM_024164 /// XM_001720738 /// XM_001720740

2.16	2.41	0.25	1.03E-01	4.53E-01	LOC645249	hypothetical protein LOC645249	chr7q36.3	236967_at	XM_001715163 /// XM_928291 /// XM_935704 /// XM_938677
2.76	2.99	0.23	1.03E-01	4.53E-01	CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9q34.3	228995_at	NM_015447
4.77	5.27	0.51	1.03E-01	4.53E-01	MID1	midline 1 (Opitz/BBB syndrome)	chrXp22	203636_at	NM_000381 /// NM_001098624 /// NM_033290
2.98	3.35	0.37	1.03E-01	4.53E-01	---	---	---	214781_at	---
7.20	7.53	0.33	1.03E-01	4.53E-01	---	---	---	AFFX-BioC-5_at	---
2.09	2.39	0.30	1.03E-01	4.53E-01	EVI1	ecotropic viral integration site 1	chr3q24-q28	226420_at	NM_001105077 /// NM_001105078 /// NM_005241
2.77	3.01	0.24	1.03E-01	4.53E-01	HSPB8	heat shock 22kDa protein 8	chr12q24.23	233057_at	NM_014365 /// XR_017379 /// XR_019602 /// XR_038402
2.51	2.76	0.25	1.03E-01	4.53E-01	CASC4	cancer susceptibility candidate 4	chr15q15.3	1559635_at	NM_138423 /// NM_177974
7.01	7.60	0.59	1.03E-01	4.53E-01	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	chr17q11.2	224939_at	NM_020772
2.53	2.88	0.35	1.03E-01	4.54E-01	CNOT4	CCR4-NOT transcription complex, subunit 4	chr7q22-qter	210867_at	NM_001008225 /// NM_013316
2.81	3.01	0.20	1.03E-01	4.54E-01	FMNL1	formin-like 1	chr17q21	1569257_at	NM_005892
2.30	2.72	0.42	1.03E-01	4.54E-01	MPPE1	Metallophosphoesterase 1	chr18p11.21	214071_at	NM_023075
5.89	6.31	0.42	1.03E-01	4.54E-01	ITFG2	integrin alpha FG-GAP repeat containing 2	chr12p13.33	226295_at	NM_018463
3.30	3.58	0.28	1.03E-01	4.54E-01	RLBP1	retinaldehyde binding protein 1	chr15q26	206154_at	NM_000326
6.31	7.36	1.05	1.03E-01	4.54E-01	UBXN4	UBX domain protein 4	chr2q21.3	212007_at	NM_014607
4.87	5.34	0.48	1.03E-01	4.54E-01	ZBTB43	zinc finger and BTB domain containing 43	chr9q33-q34	204180_s_at	NM_014007
3.86	4.69	0.83	1.03E-01	4.54E-01	COL5A2	collagen, type V, alpha 2	chr2q14-q32	221729_at	NM_000393
1.99	2.18	0.18	1.03E-01	4.54E-01	CCDC4	coiled-coil domain containing 4	chr4p13	230896_at	NM_207406
2.26	2.59	0.33	1.04E-01	4.54E-01	---	---	---	242629_at	---
2.03	2.25	0.23	1.04E-01	4.54E-01	---	---	---	224236_s_at	---
3.88	4.10	0.22	1.04E-01	4.54E-01	---	---	---	241787_at	---
2.43	2.63	0.20	1.04E-01	4.54E-01	---	---	---	1556618_at	---
2.37	2.62	0.25	1.04E-01	4.54E-01	PDCL3	phosducin-like 3	chr2q11.2	243049_at	NM_024065
2.34	2.56	0.23	1.04E-01	4.54E-01	SRD5A2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)	chr2p23	235945_at	NM_000348
5.06	5.82	0.76	1.04E-01	4.54E-01	C1orf27	chromosome 1 open reading frame 27	chr1q25	218721_s_at	NM_017847
4.33	4.63	0.30	1.04E-01	4.54E-01	SIGLEC7	sialic acid binding Ig-like lectin 7	chr19q13.3	217159_x_at	NM_014385 /// NM_016543
2.53	2.81	0.28	1.04E-01	4.54E-01	FYN	FYN oncogene related to SRC, FGR, YES	chr6q21	212486_s_at	NM_002037 /// NM_153047 /// NM_153048
3.14	3.39	0.25	1.04E-01	4.54E-01	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	chr1p32	214185_at	NM_006559
2.73	2.95	0.22	1.04E-01	4.54E-01	CD300C	CD300c molecule	chr17q25.1	207270_x_at	NM_006678
4.26	5.04	0.78	1.04E-01	4.55E-01	USP38	ubiquitin specific peptidase 38	---	223289_s_at	NM_032557
3.76	4.32	0.56	1.04E-01	4.55E-01	ATF6	Activating transcription factor 6	chr1q22-q23	231927_at	NM_007348
3.65	4.11	0.46	1.04E-01	4.55E-01	MBP	myelin basic protein	chr18q23	1554544_a_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385
3.36	3.68	0.32	1.04E-01	4.55E-01	TSC22D1	TSC22 domain family, member 1	chr13q14	243133_at	NM_006022 /// NM_183422
4.59	4.85	0.26	1.04E-01	4.55E-01	MINK1	misshapen-like kinase 1 (zebrafish)	chr17p13.2	214625_s_at	NM_001024937 /// NM_015716 /// NM_153827 /// NM_170663
2.58	2.80	0.22	1.04E-01	4.55E-01	---	---	---	1558831_x_at	---
6.52	6.93	0.41	1.04E-01	4.55E-01	DHRS7B	dehydrogenase/reductase (SDR family) member 7B	chr17p12	220690_s_at	NM_015510
2.95	3.30	0.36	1.04E-01	4.55E-01	MGC42105	hypothetical protein MGC42105	chr5p12	230864_at	NM_153361
3.64	4.00	0.35	1.04E-01	4.55E-01	UHMK1	U2AF homology motif (UHM) kinase 1	chr1q23.3	1552656_s_at	NM_175866
3.89	4.25	0.35	1.04E-01	4.55E-01	---	---	---	217469_at	---

2.52	2.85	0.32	1.04E-01	4.55E-01	SCAND2	SCAN domain containing 2 pseudogene	chr15q25-q26	206021_at	NM_022050 /// NM_033633 /// NM_033634 /// NM_033635 /// NM_033636 /// NM_033640 /// NR_003654 /// NR_004859
6.16	6.47	0.31	1.04E-01	4.55E-01	LOC126075	hypothetical protein LOC126075	chr19p13.2	227043_at	NM_001080503
2.11	2.41	0.31	1.04E-01	4.55E-01	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	chr1p22.2	231578_at	NM_002053
2.53	2.82	0.29	1.04E-01	4.55E-01	KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2	chr12q14.1	240614_at	NM_139136 /// NM_139137 /// NM_153748
2.74	3.00	0.25	1.04E-01	4.55E-01	HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	chr1p34	235122_at	NM_001127714 /// NM_024503
2.56	2.88	0.32	1.04E-01	4.55E-01	KLHL34	Kelch-like 34 (Drosophila)	chrXp22.12	238832_at	NM_153270
4.58	5.15	0.57	1.04E-01	4.55E-01	NFIB	nuclear factor I/B	chr9p24.1	211467_s_at	NM_005596
2.45	2.69	0.24	1.04E-01	4.55E-01	---	---	---	237235_at	---
3.05	3.40	0.35	1.04E-01	4.55E-01	MYO5A	myosin VA (heavy chain 12, myoxin)	chr15q21	241966_at	NM_000259
3.63	4.30	0.67	1.04E-01	4.55E-01	SCRN3	secernin 3	chr2q31.1	222849_s_at	NM_024583
2.43	2.71	0.28	1.04E-01	4.55E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31 /// LOC100126583 /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant gamma 4 (G4m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical LOC100126583 /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	217236_x_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001724554 /// XM_941465
2.12	2.30	0.18	1.04E-01	4.55E-01	---	---	---	1561638_at	---
2.17	2.42	0.25	1.04E-01	4.55E-01	---	---	---	216861_at	---
3.30	3.87	0.57	1.04E-01	4.55E-01	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	chr8q22	205529_s_at	NM_004349 /// NM_175634 /// NM_175635 /// NM_175636
3.92	4.79	0.87	1.04E-01	4.55E-01	SYNE2	Spectrin repeat containing, nuclear envelope 2	chr14q23.2	240777_at	NM_015180 /// NM_182910 /// NM_182913 /// NM_182914
3.55	4.01	0.46	1.04E-01	4.55E-01	---	---	---	239876_at	---
4.78	5.14	0.36	1.04E-01	4.55E-01	MGC40489	Similar to pleckstrin homology domain containing, family M (with RUN domain) member 1; adapter protein 162	chr17q24	229747_x_at	XR_016048 /// XR_041390 /// XR_041391
4.59	4.83	0.24	1.04E-01	4.55E-01	---	---	---	216142_at	---
2.39	2.59	0.20	1.04E-01	4.55E-01	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	chr16q13	231634_at	NM_000339 /// NM_001126107 /// NM_001126108
4.25	4.56	0.32	1.04E-01	4.55E-01	FGF11	fibroblast growth factor 11	chr17p13.1	231803_at	NM_004112
3.80	4.30	0.50	1.04E-01	4.56E-01	CISH	cytokine inducible SH2-containing protein	chr3p21.3	223961_s_at	NM_013324 /// NM_145071
6.57	7.05	0.48	1.04E-01	4.56E-01	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	chr6p21.2-p21.1	201802_at	NM_001078174 /// NM_001078175 /// NM_001078176 /// NM_001078177 /// NM_004955
2.16	2.39	0.23	1.04E-01	4.56E-01	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	chr10q21.3	209910_at	NM_152707
2.06	2.31	0.25	1.05E-01	4.56E-01	---	---	---	243193_at	---
2.03	2.21	0.18	1.05E-01	4.56E-01	---	---	---	224487_at	---
2.81	3.08	0.26	1.05E-01	4.56E-01	ANTXR1	Anthrax toxin receptor 1	chr2p13.1	234430_at	NM_018153 /// NM_032208 /// NM_053034

4.95	5.23	0.28	1.05E-01	4.56E-01	LOC51057	hypothetical protein LOC51057	chr2p15	231770_x_at	NM_001042692 /// NM_015910
2.02	2.21	0.19	1.05E-01	4.56E-01	---	---	---	243327_at	---
5.30	5.73	0.43	1.05E-01	4.56E-01	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	chr3p22	207604_s_at	NM_003615
2.55	2.95	0.39	1.05E-01	4.56E-01	ATP11A	ATPase, class VI, type 11A	chr13q34	241604_at	NM_015205 /// NM_032189
2.83	3.18	0.35	1.05E-01	4.56E-01	ESR2	estrogen receptor 2 (ER beta)	chr14q23.2	210780_at	NM_001040275 /// NM_001040276 /// NM_001437
2.61	2.87	0.26	1.05E-01	4.56E-01	HMGCLL1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	chr6p12.1	1554872_a_at	NM_001042406 /// NM_019036
2.15	2.38	0.23	1.05E-01	4.56E-01	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	chr3p25.3	1563595_at	NM_001033117 /// NM_014850
1.89	2.07	0.19	1.05E-01	4.56E-01	FOXD3	forkhead box D3	chr1p32-p31	241612_at	NM_012183
2.84	3.21	0.37	1.05E-01	4.56E-01	---	---	---	236397_at	---
4.99	5.24	0.24	1.05E-01	4.56E-01	DCLK2	Doublecortin-like kinase 2	chr4q31.3	216725_at	NM_001040260 /// NM_001040261
6.27	7.55	1.28	1.05E-01	4.56E-01	---	---	---	213789_at	---
8.10	8.82	0.72	1.05E-01	4.56E-01	RAP2A	RAP2A, member of RAS oncogene family	chr13q34	221830_at	NM_021033
4.20	4.91	0.71	1.05E-01	4.56E-01	MPDZ	multiple PDZ domain protein	chr9p24-p22	205079_s_at	NM_003829
6.35	6.95	0.59	1.05E-01	4.56E-01	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	chr2q32.2	213374_x_at	NM_014362 /// NM_198047
2.84	3.28	0.45	1.05E-01	4.56E-01	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	chr12q12	1552695_a_at	NM_052885
2.89	3.33	0.44	1.05E-01	4.56E-01	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	chr4q13.3	220346_at	NM_001004346
3.37	3.71	0.34	1.05E-01	4.56E-01	NTN2L	netrin 2-like (chicken)	chr16p13.3	207640_x_at	NM_006181
2.55	2.88	0.33	1.05E-01	4.56E-01	IGHA1 /// IGHG1 /// IGHG3 /// IGHM /// LOC652494	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// similar to Ig heavy chain V-III region VH26 precursor	chr14q32.33	217360_x_at	XM_001717586 /// XM_001719484
2.31	2.62	0.31	1.05E-01	4.56E-01	---	---	---	1561237_at	---
1.99	2.30	0.30	1.05E-01	4.56E-01	---	---	---	235730_at	---
2.98	3.28	0.30	1.05E-01	4.56E-01	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	chr1p34.2	214058_at	NM_001033081 /// NM_001033082 /// NM_005376
3.18	3.45	0.26	1.05E-01	4.56E-01	C10orf59	chromosome 10 open reading frame 59	chr10q23.31	220564_at	NM_001031709 /// NM_018363
6.91	7.13	0.22	1.05E-01	4.56E-01	LOC100129975 /// LOC284393 /// LOC285176 /// LOC644937 /// RPL10	similar to ribosomal protein L10 /// similar to QM protein /// similar to ribosomal protein L10 /// similar to ribosomal protein L10 /// ribosomal protein L10	chr19p13.13 /// chr19p13.2 /// chr2q35 /// chr5q35.1 /// chrXq28	217680_x_at	NM_006013 /// XM_001715971 /// XM_001724324 /// XM_001725319 /// XM_001726591 /// XM_001726644 /// XM_001726646 /// XM_001726710 /// XM_001726716 /// XM_209178 /// XM_928025 /// XM_941010
4.49	5.35	0.86	1.05E-01	4.56E-01	IQGAP1	IQ motif containing GTPase activating protein 1	chr15q26.1	213446_s_at	NM_003870
2.12	2.39	0.27	1.05E-01	4.56E-01	---	---	---	231593_at	---
3.75	4.57	0.82	1.05E-01	4.56E-01	---	---	---	232565_at	---
3.51	3.79	0.28	1.05E-01	4.56E-01	CNKSR3	CNKSR family member 3	chr6q25.2	242394_at	NM_173515
2.64	2.94	0.30	1.05E-01	4.56E-01	---	---	---	240683_at	---
3.94	4.20	0.25	1.05E-01	4.56E-01	GJA3	gap junction protein, alpha 3, 46kDa	chr13q11-q12	208590_x_at	NM_021954
4.89	5.42	0.53	1.05E-01	4.56E-01	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	chr14q24.3-q31	202064_s_at	NM_005065
6.01	6.31	0.30	1.05E-01	4.56E-01	BTN3A1	butyrophilin, subfamily 3, member A1	chr6p22.1	207485_x_at	NM_007048

3.67	3.92	0.25	1.05E-01	4.56E-01	ODF3	outer dense fiber of sperm tails 3	chr11p15.5	1553051_s_at	NM_053280
2.07	2.30	0.24	1.05E-01	4.56E-01	SHANK2	SH3 and multiple ankyrin repeat domains 2	chr11q13.3	213307_at	NM_012309 /// NM_133266
2.96	3.26	0.30	1.05E-01	4.56E-01	GRK4	G protein-coupled receptor kinase 4	chr4p16.3	208365_s_at	NM_001004056 /// NM_001004057 /// NM_182982
7.60	8.11	0.51	1.05E-01	4.56E-01	CLIC4	chloride intracellular channel 4	chr1p36.11	201560_at	NM_013943
4.55	4.95	0.41	1.05E-01	4.56E-01	---	---	---	233812_at	---
3.59	4.52	0.93	1.05E-01	4.57E-01	C9orf150	chromosome 9 open reading frame 150	chr9p23	227443_at	NM_203403
6.56	7.19	0.63	1.05E-01	4.57E-01	ARMCX3	armadillo repeat containing, X-linked 3	chrXq21.33-q22.2	217858_s_at	NM_016607 /// NM_177947 /// NM_177948
2.17	2.51	0.34	1.05E-01	4.57E-01	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	1564443_at	NR_002612
2.84	3.13	0.30	1.05E-01	4.57E-01	---	---	---	231545_at	---
4.14	4.39	0.26	1.05E-01	4.57E-01	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	chr17q21.32	227377_at	NM_006546
3.43	3.76	0.33	1.05E-01	4.57E-01	---	---	---	1557421_at	---
4.16	4.43	0.27	1.05E-01	4.57E-01	---	---	---	215858_at	---
2.36	2.60	0.24	1.05E-01	4.57E-01	GRASPOS	GRP1-associated scaffold protein opposite strand	chr12q	1570186_at	---
3.73	3.97	0.24	1.05E-01	4.57E-01	RAE1	RAE1 RNA export 1 homolog (S. pombe)	chr20q13.31	211319_at	NM_001015885 /// NM_003610
2.04	2.27	0.23	1.05E-01	4.57E-01	---	---	---	240066_at	---
2.74	3.09	0.35	1.05E-01	4.57E-01	EVI1	ecotropic viral integration site 1	chr3q24-q28	221884_at	NM_001105077 /// NM_001105078 /// NM_005241
3.67	4.17	0.51	1.05E-01	4.57E-01	GAB1	GRB2-associated binding protein 1	chr4q31.21	207112_s_at	NM_002039 /// NM_207123
4.58	4.91	0.33	1.05E-01	4.57E-01	---	---	---	210161_at	---
5.19	5.45	0.26	1.05E-01	4.57E-01	CCDC64B	coiled-coil domain containing 64B	chr16p13.3	235095_at	NM_001103175
2.64	2.88	0.24	1.05E-01	4.57E-01	LOC730124	similar to hCG2041586	chr2q22.3	231337_at	XM_001127822 /// XM_001132529 /// XM_001717873
5.90	6.22	0.32	1.05E-01	4.57E-01	DHFRL1	dihydrofolate reductase-like 1	chr3q11.2	241727_x_at	NM_176815
2.35	2.57	0.22	1.05E-01	4.57E-01	---	---	---	240481_at	---
3.54	3.85	0.30	1.06E-01	4.57E-01	SLC4A9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	chr5q31	224053_s_at	NM_031467
2.76	3.16	0.40	1.06E-01	4.57E-01	---	---	---	1557038_s_at	---
2.27	2.50	0.24	1.06E-01	4.57E-01	TFEC	transcription factor EC	chr7q31.2	232383_at	NM_001018058 /// NM_012252
4.38	5.13	0.75	1.06E-01	4.57E-01	SFRS12IP1	SFRS12-interacting protein 1	chr5q12.3	235390_at	NM_173829
2.44	2.77	0.33	1.06E-01	4.57E-01	NHSL2	NHS-like 2	chrXq13.1	1569932_at	NM_001013627
1.89	2.38	0.49	1.06E-01	4.57E-01	SPOCK3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	chr4q32.3	235342_at	NM_001040159 /// NM_016950
6.71	7.00	0.28	1.06E-01	4.57E-01	NPFFR1	neuropeptide FF receptor 1	chr10q21-q22	221387_at	NM_022146
5.32	5.59	0.27	1.06E-01	4.57E-01	CENPO	centromere protein O	chr2p23.3	219472_at	NM_024322
3.78	4.05	0.27	1.06E-01	4.57E-01	KLK8	kallikrein-related peptidase 8	chr19q13.3-q13.4	206125_s_at	NM_007196 /// NM_144505 /// NM_144506 /// NM_144507
2.27	2.48	0.21	1.06E-01	4.57E-01	---	---	---	240874_at	---
5.85	6.11	0.26	1.06E-01	4.57E-01	CHMP4A	chromatin modifying protein 4A	chr14q12	218572_at	NM_014169
4.29	4.55	0.26	1.06E-01	4.57E-01	---	---	---	233646_at	---
2.19	2.44	0.25	1.06E-01	4.57E-01	---	---	---	1563219_at	---
3.18	3.38	0.20	1.06E-01	4.57E-01	---	---	---	1570541_s_at	---
1.92	2.10	0.18	1.06E-01	4.57E-01	PRO2949	hypothetical protein PRO2949	chr8q23.1	1553374_at	---
2.67	2.90	0.23	1.06E-01	4.57E-01	---	---	---	236602_at	---
2.26	2.53	0.27	1.06E-01	4.57E-01	---	---	---	237357_at	---
1.83	2.00	0.16	1.06E-01	4.57E-01	LOC286190	hypothetical protein LOC286190	chr8q13.2	1559264_at	---
5.57	5.82	0.25	1.06E-01	4.57E-01	PROX1	Prospero homeobox 1	chr1q32.2-q32.3	242119_at	NM_002763
4.19	4.52	0.33	1.06E-01	4.57E-01	FDFT1	Farnesyl-diphosphate farnesyltransferase 1	chr8p23.1-p22	241954_at	NM_004462
4.71	5.01	0.30	1.06E-01	4.58E-01	---	---	---	238570_at	---
2.33	2.61	0.28	1.06E-01	4.58E-01	LOC645591	hypothetical protein LOC645591	chr7q22.1	1554302_s_at	XM_934971
2.35	2.64	0.29	1.06E-01	4.58E-01	INSL5	insulin-like 5	chr1p31.1-p22.3	221091_at	NM_005478
2.42	2.68	0.26	1.06E-01	4.58E-01	ZNF567	zinc finger protein 567	chr19q13.12	238315_s_at	NM_152603
3.60	4.19	0.59	1.06E-01	4.58E-01	RABGAP1L	RAB GTPase activating protein 1-like	chr1q24	213982_s_at	NM_001035230 /// NM_014857
2.54	2.79	0.24	1.06E-01	4.58E-01	---	---	---	236720_at	---
2.34	2.55	0.21	1.06E-01	4.58E-01	---	---	---	1569603_at	---

2.12	2.62	0.51	1.06E-01	4.58E-01	MYO1B	myosin IB	chr2q12-q34	212364_at	NM_001130158 /// NM_012223
3.28	3.59	0.31	1.06E-01	4.58E-01	---	---	---	244715_at	---
1.97	2.21	0.24	1.06E-01	4.58E-01	---	---	---	234137_s_at	---
2.14	2.33	0.20	1.06E-01	4.58E-01	UBE3A	Ubiquitin protein ligase E3A	chr15q11-q13	234163_at	NM_000462 /// NM_130838 /// NM_130839
4.50	5.02	0.52	1.06E-01	4.58E-01	EGFLAM	EGF-like, fibronectin type III and laminin G domains	chr5p13.2-p13.1	226911_at	NM_152403 /// NM_182798 /// NM_182799 /// NM_182801
2.60	3.89	1.29	1.06E-01	4.58E-01	TH	tyrosine hydroxylase	chr11p15.5	208291_s_at	NM_000360 /// NM_199292 /// NM_199293
2.41	2.95	0.54	1.06E-01	4.58E-01	SHC4	SHC (Src homology 2 domain containing) family, member 4	chr15q21.1-q21.2	230538_at	NM_203349
4.34	4.70	0.36	1.06E-01	4.58E-01	---	---	---	1569443_s_at	---
5.98	6.27	0.29	1.06E-01	4.58E-01	GTSE1	G-2 and S-phase expressed 1	chr22q13.2-q13.3	229343_at	NM_016426
1.94	2.18	0.24	1.06E-01	4.58E-01	LOC100133303	hypothetical protein LOC100133303	chr6p21.33	216478_at	XM_001717921
4.08	4.32	0.24	1.06E-01	4.58E-01	---	---	---	240669_at	---
2.37	2.61	0.24	1.06E-01	4.58E-01	TRIM43	tripartite motif-containing 43	chr2q11.1	1553619_a_at	NM_138800
2.30	2.53	0.23	1.06E-01	4.58E-01	---	---	---	241073_at	---
2.83	3.02	0.19	1.06E-01	4.58E-01	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	chr1q32.1	201822_at	NM_006335
2.32	2.50	0.17	1.06E-01	4.58E-01	---	---	---	1561261_at	---
2.31	2.50	0.19	1.06E-01	4.58E-01	COBL	cordon-bleu homolog (mouse)	chr7p12.1	1552496_a_at	NM_015198
2.36	2.62	0.26	1.06E-01	4.58E-01	---	---	---	240879_x_at	---
2.07	2.28	0.21	1.06E-01	4.58E-01	LOC100129525	Hypothetical protein LOC100129525	chr8q24.21	243247_at	XM_001725349 /// XM_001725367 /// XM_001725397
7.44	7.76	0.32	1.06E-01	4.58E-01	PTGES2	prostaglandin E synthase 2	chr9q34.11	218083_at	NM_025072 /// NM_198938 /// NM_198940
2.24	2.46	0.22	1.06E-01	4.58E-01	MYO3A	myosin IIIA	chr10p11.1	221400_at	NM_017433
3.06	4.06	1.00	1.06E-01	4.58E-01	FAM162B	family with sequence similarity 162, member B	chr6q22.2	228875_at	NM_001085480
4.22	5.11	0.89	1.07E-01	4.58E-01	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	chr5q31	1558214_s_at	NM_001903
6.69	7.42	0.72	1.07E-01	4.58E-01	CLOCK	clock homolog (mouse)	chr4q12	204980_at	NM_004898
2.44	2.72	0.28	1.07E-01	4.58E-01	NPHP3	nephronophthisis 3 (adolescent)	chr3q22.1	1553389_at	NM_153240
2.48	2.76	0.28	1.07E-01	4.59E-01	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	chr1p33-p32	214530_x_at	NM_004437 /// NM_203342 /// NM_203343
2.94	3.23	0.29	1.07E-01	4.59E-01	DISC1	disrupted in schizophrenia 1	chr1q42.1	1563744_a_at	NM_001012957 /// NM_001012958 /// NM_001012959 /// NM_018662
2.10	2.42	0.32	1.07E-01	4.59E-01	GDA	guanine deaminase	chr9q21.13	224209_s_at	NM_004293
2.33	2.54	0.21	1.07E-01	4.59E-01	SETDB2	SET domain, bifurcated 2	chr13q14	238731_at	NM_031915
1.93	2.14	0.20	1.07E-01	4.59E-01	XKRY /// XKRY2	XK, Kell blood group complex subunit-related, Y-linked /// XK, Kell blood group complex subunit-related, Y-linked 2	chrYq11.221	208339_at	NM_001002906 /// NM_004677
3.13	3.42	0.29	1.07E-01	4.59E-01	ATAD3B	ATPase family, AAA domain containing 3B	chr1p36.33	233091_at	NM_031921
2.39	2.69	0.30	1.07E-01	4.59E-01	---	---	---	217616_at	---
5.55	6.29	0.74	1.07E-01	4.59E-01	---	---	---	1562836_at	---
6.62	7.31	0.69	1.07E-01	4.60E-01	RSL1D1	ribosomal L1 domain containing 1	chr16p13.13	212018_s_at	NM_015659
2.38	2.66	0.27	1.07E-01	4.60E-01	---	---	---	242874_at	---
3.73	3.98	0.26	1.07E-01	4.60E-01	---	---	---	233411_at	---
3.90	4.11	0.21	1.07E-01	4.60E-01	LMLN	leishmanolysin-like (metallopeptidase M8 family)	chr3q29	229611_at	NM_033029
2.39	2.80	0.41	1.07E-01	4.60E-01	PLCL1	phospholipase C-like 1	chr2q33	205934_at	NM_001114661 /// NM_006226
3.93	4.15	0.22	1.07E-01	4.60E-01	RGS6	regulator of G-protein signaling 6	chr14q24.3	214538_x_at	NM_004296
1.86	2.06	0.20	1.07E-01	4.60E-01	---	---	---	233238_s_at	---
2.58	2.77	0.19	1.07E-01	4.60E-01	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	chr18q11.2	235216_at	NM_052911
2.01	2.19	0.18	1.07E-01	4.60E-01	GRHL2	grainyhead-like 2 (Drosophila)	chr8q22.3	219388_at	NM_024915
2.77	2.99	0.23	1.07E-01	4.60E-01	LYG2	lysozyme G-like 2	chr2q11.2	1554398_at	NM_175735
2.98	3.29	0.31	1.07E-01	4.60E-01	XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	chrXq25	206484_s_at	NM_003399

1.99	2.21	0.22	1.07E-01	4.60E-01	HAPLN1	Hyaluronan and proteoglycan link protein 1	chr5q14.3	230204_at	NM_001884
6.56	6.97	0.40	1.07E-01	4.60E-01	GPSM3	G-protein signaling modulator 3 (AGS3-like, C. elegans)	chr6p21.3	204265_s_at	NM_022107
2.38	2.66	0.28	1.07E-01	4.60E-01	SFRS12	splicing factor, arginine/serine-rich 12	chr5q12.3	243361_at	NM_001077199 /// NM_139168
2.54	2.80	0.26	1.07E-01	4.60E-01	---	---	---	237809_at	---
2.02	2.26	0.25	1.07E-01	4.60E-01	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	chr13q32.1	1555560_at	NM_020121
2.35	2.56	0.21	1.07E-01	4.60E-01	PPP4R1L	protein phosphatase 4, regulatory subunit 1-like	chr20q13.32	1560175_at	NR_003505
1.84	2.08	0.24	1.07E-01	4.60E-01	LOC286154	Hypothetical protein LOC286154	chr8q22.3	1559030_a_at	---
2.63	2.88	0.25	1.07E-01	4.60E-01	---	---	---	233309_at	---
2.60	2.89	0.29	1.07E-01	4.60E-01	---	---	---	239724_at	---
2.23	2.57	0.34	1.07E-01	4.61E-01	NSL1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	chr1q41	209483_s_at	NM_001042549 /// NM_015471
3.20	3.45	0.25	1.08E-01	4.61E-01	C4orf17	chromosome 4 open reading frame 17	chr4q23	223990_at	NM_032149
2.90	3.57	0.67	1.08E-01	4.61E-01	PR47	platelet receptor for type III collagen, 47 kDa	---	1560526_at	---
4.57	5.44	0.87	1.08E-01	4.61E-01	SULF2	sulfatase 2	chr20q12-q13.2	224724_at	NM_018837 /// NM_198596
2.69	2.96	0.27	1.08E-01	4.61E-01	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	chr12q13	219956_at	NM_007210
5.08	5.44	0.36	1.08E-01	4.61E-01	SULT4A1	sulfotransferase family 4A, member 1	chr22q13.2-q13.31	219425_at	NM_014351
5.41	5.74	0.33	1.08E-01	4.61E-01	KIAA1618	KIAA1618	chr17q25.3	241347_at	NM_020954
3.54	3.79	0.25	1.08E-01	4.61E-01	HNF4A	hepatocyte nuclear factor 4, alpha	chr20q12-q13.1	214832_at	NM_000457 /// NM_001030003 /// NM_001030004 /// NM_175914 /// NM_178849 /// NM_178850
4.89	5.24	0.35	1.08E-01	4.61E-01	PEX11A	Peroxisomal biogenesis factor 11A	chr15q26.1	205160_at	NM_003847
2.02	2.19	0.17	1.08E-01	4.61E-01	RNF182	ring finger protein 182	chr6p23	230720_at	NM_152737
2.38	2.71	0.33	1.08E-01	4.61E-01	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	chr2q37.1	243628_at	NM_022730
2.66	2.88	0.22	1.08E-01	4.61E-01	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	211885_x_at	NM_000150 /// NM_001040701
4.47	4.88	0.41	1.08E-01	4.61E-01	DBN1	drebrin 1	chr5q35.3	217025_s_at	NM_004395 /// NM_080881
2.70	3.63	0.93	1.08E-01	4.61E-01	SGPP2	sphingosine-1-phosphate phosphotase 2	chr2q36.1	244780_at	NM_152386
6.21	6.53	0.32	1.08E-01	4.61E-01	GRWD1	glutamate-rich WD repeat containing 1	chr19q13.32	221549_at	NM_031485
1.87	2.12	0.25	1.08E-01	4.61E-01	---	---	---	1561926_at	---
4.99	5.97	0.97	1.08E-01	4.61E-01	LYRM2	LYR motif containing 2	chr6q14.2-q16.1	221311_x_at	NM_020466
2.50	2.82	0.32	1.08E-01	4.61E-01	---	---	---	236051_at	---
5.46	6.30	0.85	1.08E-01	4.61E-01	PCYOX1	prenylcysteine oxidase 1	chr2p13.3	203803_at	NM_016297
2.41	2.68	0.28	1.08E-01	4.61E-01	CENPI	centromere protein I	chrXq22.1	207590_s_at	NM_006733
2.24	2.46	0.22	1.08E-01	4.61E-01	LOC728153	similar to FAM133B protein	chr5q12.1	233204_at	XM_001128002 /// XM_001722995
1.91	2.11	0.20	1.08E-01	4.61E-01	FLG2	filaggrin family member 2	chr1q21.3	1569410_at	NM_001014342
3.01	3.28	0.27	1.08E-01	4.61E-01	WDR19	WD repeat domain 19	chr4p14	232163_at	NM_025132
5.35	6.03	0.68	1.08E-01	4.62E-01	ZC3H14	zinc finger CCCH-type containing 14	chr14q31.3	213064_at	NM_024824 /// NM_207660 /// NM_207661 /// NM_207662
7.15	8.22	1.07	1.08E-01	4.62E-01	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	chr5q13.3-q14	202539_s_at	NM_000859 /// NM_001130996
4.23	5.01	0.77	1.08E-01	4.62E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	212991_at	NM_012347 /// NM_033480 /// NM_033481
6.72	7.30	0.58	1.08E-01	4.62E-01	KIAA0182	KIAA0182	chr16q24.1	212057_at	NM_001134473 /// NM_014615
2.02	2.26	0.24	1.08E-01	4.62E-01	---	---	---	244117_at	---
4.53	4.86	0.32	1.08E-01	4.62E-01	---	---	---	222090_at	---
2.31	2.60	0.29	1.08E-01	4.62E-01	BCL2L14	BCL2-like 14 (apoptosis facilitator)	chr12p13-p12	234533_at	NM_030766 /// NM_138722 /// NM_138723 /// NM_138724
2.94	3.19	0.25	1.08E-01	4.62E-01	---	---	---	232351_at	---
5.46	6.03	0.56	1.08E-01	4.62E-01	---	---	---	228623_at	---

6.61	6.93	0.32	1.08E-01	4.62E-01	UNC93B1	unc-93 homolog B1 (C. elegans)	chr11q13	220998_s_at	NM_030930
1.98	2.20	0.23	1.08E-01	4.62E-01	ZNF391	zinc finger protein 391	chr6p22.1	215523_at	NM_001076781
5.88	6.65	0.78	1.08E-01	4.62E-01	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	---	223138_s_at	NM_001114397 /// NM_020865
3.04	4.52	1.48	1.08E-01	4.62E-01	---	---	---	211645_x_at	---
2.33	2.52	0.18	1.08E-01	4.62E-01	C3orf38	chromosome 3 open reading frame 38	chr3p11.2	1569128_at	NM_173824
4.77	5.73	0.95	1.08E-01	4.62E-01	---	---	---	1562235_s_at	---
4.48	5.42	0.95	1.08E-01	4.62E-01	NBN	nibrin	chr8q21	202906_s_at	NM_001024688 /// NM_002485
2.95	3.50	0.55	1.08E-01	4.62E-01	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	chr16q22	204130_at	NM_000196
4.07	4.50	0.43	1.08E-01	4.62E-01	RREB1	ras responsive element binding protein 1	chr6p25	242297_at	NM_001003698 /// NM_001003699 /// NM_002955
3.40	3.74	0.34	1.08E-01	4.62E-01	EPHB2	EPH receptor B2	chr1p36.1-p35	211165_x_at	NM_004442 /// NM_017449
3.98	4.27	0.29	1.08E-01	4.62E-01	LOC100129015	hypothetical protein LOC100129015	chr9q34.3	230034_x_at	XM_001715056 /// XM_001716341 /// XM_001716632
1.82	2.01	0.19	1.08E-01	4.62E-01	OR2L13	olfactory receptor, family 2, subfamily L, member 13	chr1q44	1554706_at	NM_175911
3.92	4.23	0.31	1.09E-01	4.62E-01	SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	chr16q22.1	220650_s_at	NM_004594
1.82	2.02	0.20	1.09E-01	4.62E-01	CA3	carbonic anhydrase III, muscle specific	chr8q13-q22	204865_at	NM_005181
3.20	3.44	0.24	1.09E-01	4.62E-01	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	chr17p13	206603_at	NM_001042
2.57	2.84	0.27	1.09E-01	4.63E-01	---	---	---	236723_at	---
2.20	2.52	0.32	1.09E-01	4.63E-01	---	---	---	238735_at	---
2.33	2.63	0.30	1.09E-01	4.63E-01	---	---	---	235363_at	---
2.83	3.12	0.29	1.09E-01	4.63E-01	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	chr6p21.3	234285_at	NM_001130066 /// NM_006772
3.02	3.23	0.21	1.09E-01	4.63E-01	---	---	---	1561506_at	---
2.22	2.46	0.24	1.09E-01	4.63E-01	---	---	---	241123_at	---
3.23	3.60	0.37	1.09E-01	4.63E-01	IL2RA	interleukin 2 receptor, alpha	chr10p15-p14	206341_at	NM_000417
2.81	3.12	0.30	1.09E-01	4.63E-01	---	---	---	220827_at	---
2.56	2.75	0.18	1.09E-01	4.63E-01	ABCA11	ATP-binding cassette, sub-family A (ABC1), member 11 (pseudogene)	chr4p16.3	220159_at	NR_002451
3.31	3.56	0.25	1.09E-01	4.63E-01	ADAM8	ADAM metallopeptidase domain 8	chr10q26.3	205179_s_at	NM_001109
2.03	2.25	0.22	1.09E-01	4.63E-01	---	---	---	243838_at	---
2.91	3.17	0.26	1.09E-01	4.63E-01	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	chr11q23	205456_at	NM_000733
3.09	3.40	0.31	1.09E-01	4.63E-01	---	---	---	230988_at	---
5.57	5.82	0.25	1.09E-01	4.63E-01	SLC31A1	solute carrier family 31 (copper transporters), member 1	chr9q31-q32	203971_at	NM_001859
6.59	7.39	0.80	1.09E-01	4.64E-01	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	chr5q13.3-q14	202540_s_at	NM_000859 /// NM_001130996
3.52	4.14	0.62	1.09E-01	4.64E-01	C11orf57	Chromosome 11 open reading frame 57	chr11q23.1	230724_s_at	NM_001082969 /// NM_001082970 /// NM_018195
4.07	4.54	0.47	1.09E-01	4.64E-01	BRWD1	bromodomain and WD repeat domain containing 1	chr21q22.2	231860_at	NM_001007246 /// NM_018963 /// NM_033656
3.07	3.36	0.29	1.09E-01	4.64E-01	CREBL1 /// TNXB	cAMP responsive element binding protein-like 1 /// tenascin XB	chr6p21.3	211611_s_at	NM_004381 /// NM_019105 /// NM_032470
4.92	5.35	0.44	1.09E-01	4.64E-01	DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1	chr3p22.3	217976_s_at	NM_016141
3.33	3.60	0.26	1.09E-01	4.64E-01	---	---	---	216656_at	---
6.11	6.53	0.42	1.09E-01	4.64E-01	SNPH	syntaphilin	chr20p13	205104_at	NM_014723
2.96	3.73	0.77	1.09E-01	4.64E-01	---	---	---	230387_at	---
7.34	8.06	0.73	1.09E-01	4.64E-01	---	---	---	213016_at	---
5.90	6.46	0.56	1.09E-01	4.64E-01	LPAR1	lysophosphatidic acid receptor 1	chr9q31.3	204037_at	NM_001401 /// NM_057159
3.61	3.97	0.37	1.09E-01	4.64E-01	PITX1	paired-like homeodomain 1	chr5q31	209587_at	NM_002653
3.85	4.21	0.36	1.09E-01	4.64E-01	---	---	---	239386_at	---
3.73	4.09	0.36	1.09E-01	4.64E-01	---	---	---	239886_at	---
1.96	2.29	0.33	1.09E-01	4.64E-01	---	---	---	235915_at	---
2.02	2.25	0.23	1.09E-01	4.64E-01	HCG11	HLA complex group 11	chr6p21	1557167_at	---
6.60	7.42	0.82	1.09E-01	4.64E-01	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	chr1p22.1	202776_at	NM_014597

3.54	4.55	1.01	1.09E-01	4.64E-01	EPRS	glutamyl-prolyl-tRNA synthetase	chr1q41-q42	200841_s_at	NM_004446
5.11	5.70	0.59	1.09E-01	4.64E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	225674_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844
6.42	6.83	0.41	1.09E-01	4.64E-01	ADNP	activity-dependent neuroprotector homeobox	chr20q13.13	226426_at	NM_015339 /// NM_181442
1.91	2.12	0.20	1.09E-01	4.64E-01	SCN9A	sodium channel, voltage-gated, type IX, alpha subunit	chr2q24	229199_at	NM_002977
2.54	2.85	0.31	1.09E-01	4.64E-01	SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	chr1p21	209865_at	NM_012243
2.70	2.96	0.26	1.09E-01	4.64E-01	PTBP1	Polypyrimidine tract binding protein 1	chr19p13.3	236819_at	NM_002819 /// NM_031990 /// NM_031991 /// NM_175847
3.04	3.33	0.29	1.09E-01	4.64E-01	U2AF2	U2 small nuclear RNA auxiliary factor 2	chr19q13.42	214171_s_at	NM_001012478 /// NM_007279
2.20	2.39	0.19	1.10E-01	4.64E-01	PI4K2B	Phosphatidylinositol 4-kinase type 2 beta	chr4p15.2	1559479_at	NM_018323
3.18	3.45	0.27	1.10E-01	4.65E-01	FLJ27352	hypothetical LOC145788	chr15q21.3	243309_at	XM_001722751 /// XM_001726239 /// XM_001726290
6.04	6.71	0.67	1.10E-01	4.65E-01	---	---	---	226941_at	---
5.76	6.32	0.55	1.10E-01	4.65E-01	PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2	chr6q21	219307_at	NM_020381
3.74	4.13	0.39	1.10E-01	4.65E-01	---	---	---	229219_s_at	---
2.97	3.34	0.37	1.10E-01	4.65E-01	NUDT4P1	Nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	chr1q21.1	229836_s_at	NR_002212
3.05	3.36	0.31	1.10E-01	4.65E-01	MAPK12	mitogen-activated protein kinase 12	chr22q13.33	206106_at	NM_002969
2.58	2.86	0.28	1.10E-01	4.65E-01	LOC100134119	similar to hCG2018924	---	230366_at	XM_001713939
2.95	3.22	0.27	1.10E-01	4.65E-01	---	---	---	1555994_at	---
2.86	3.12	0.27	1.10E-01	4.65E-01	---	---	---	240954_at	---
2.74	2.99	0.25	1.10E-01	4.65E-01	TMEM154	transmembrane protein 154	chr4q31.3	238063_at	NM_152680
2.46	2.71	0.25	1.10E-01	4.65E-01	C6orf206	chromosome 6 open reading frame 206	chr6p21.1	230695_s_at	NM_152732
3.13	3.36	0.24	1.10E-01	4.65E-01	CD200R1	CD200 receptor 1	chr3q13.2	1553395_a_at	NM_138806 /// NM_138939 /// NM_138940 /// NM_170780
2.42	2.64	0.22	1.10E-01	4.65E-01	FLJ33297	Hypothetical gene supported by AK090616	chr12p13.33	1569378_at	---
3.79	4.17	0.38	1.10E-01	4.65E-01	PKNOX2	PBX/knotted 1 homeobox 2	---	219046_s_at	NM_022062
4.78	5.11	0.33	1.10E-01	4.65E-01	---	---	---	242321_at	---
2.22	2.53	0.31	1.10E-01	4.65E-01	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	chr6q14.1	215086_at	NM_015525
2.39	2.88	0.48	1.10E-01	4.65E-01	---	---	---	240865_at	---
4.59	4.94	0.35	1.10E-01	4.65E-01	SNX24	sorting nexin 24	chr5q23.2	218705_s_at	NM_014035
4.23	4.58	0.35	1.10E-01	4.65E-01	PRSS3	protease, serine, 3	chr9p11.2	213421_x_at	NM_002771 /// NM_007343
2.12	2.35	0.24	1.10E-01	4.65E-01	RNF144B	ring finger 144B	chr6p22.3	235549_at	NM_182757
2.05	2.25	0.20	1.10E-01	4.65E-01	KIF2A	kinesin heavy chain member 2A	chr5q12-q13	220699_s_at	NM_001098511 /// NM_004520
2.00	2.20	0.20	1.10E-01	4.65E-01	FLJ12334	hypothetical gene supported by AK022396; AK097927	chr2p24.1	232664_at	XM_379079 /// XM_930836 /// XM_930854 /// XM_943793 /// XM_943797 /// XM_943801
2.68	2.88	0.20	1.10E-01	4.65E-01	ACHE	acetylcholinesterase (Yt blood group)	chr7q22	205377_s_at	NM_000665 /// NM_015831
2.19	2.41	0.22	1.10E-01	4.65E-01	LOC100129029	Hypothetical LOC100131270	chr2q24.1	1563120_at	XM_001719350 /// XM_001719351 /// XM_001724889
3.15	3.33	0.18	1.10E-01	4.65E-01	LOC339442	hypothetical protein LOC339442	chr1p34.3	1562510_at	---
2.54	2.79	0.25	1.10E-01	4.65E-01	ZNF780A	zinc finger protein 780A	chr19q13.2	239441_at	NM_001010880
7.26	7.61	0.35	1.10E-01	4.65E-01	SIRT2	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	chr19q13	220605_s_at	NM_012237 /// NM_030593

5.83	6.14	0.31	1.10E-01	4.65E-01	FBXO44	F-box protein 44	chr1p36.22	222861_x_at	NM_001014765 /// NM_033182 /// NM_183412 /// NM_183413
2.27	2.54	0.27	1.10E-01	4.65E-01	COL4A5	collagen, type IV, alpha 5	chrXq22	234387_at	NM_000495 /// NM_033380 /// NM_033381
2.18	2.45	0.28	1.10E-01	4.65E-01	---	---	---	235157_at	---
2.78	3.00	0.22	1.10E-01	4.65E-01	LOC440864	hypothetical gene supported by BC040724	chr2p16.3	1569034_a_at	XM_498902 /// XM_945185
1.85	2.06	0.20	1.10E-01	4.65E-01	LOC644213	Similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	chr1p12	222202_at	XR_016570 /// XR_018856 /// XR_040026
1.88	2.09	0.20	1.10E-01	4.65E-01	C12orf72	chromosome 12 open reading frame 72	chr12p11.21	1563474_at	NM_173802
2.04	2.35	0.31	1.10E-01	4.65E-01	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	chr17q11.2-q12|17q21.1	234354_x_at	NM_001005862 /// NM_004448
2.06	2.34	0.28	1.10E-01	4.65E-01	SLC25A27	solute carrier family 25, member 27	chr6p11.2-q12	231787_at	NM_004277
2.42	2.73	0.31	1.10E-01	4.66E-01	LOC100131317 /// POU4F1	similar to hCG1781072 /// POU class 4 homeobox 1	chr13q31.1	211341_at	NM_006237 /// XM_001722446
6.81	7.52	0.71	1.10E-01	4.66E-01	---	---	---	242558_at	---
5.61	6.03	0.42	1.10E-01	4.66E-01	PIAS2	protein inhibitor of activated STAT, 2	chr18q21.1	214442_s_at	NM_004671 /// NM_173206
3.80	4.09	0.28	1.10E-01	4.66E-01	HAPLN4 /// TM6SF2	hyaluronan and proteoglycan link protein 4 /// transmembrane 6 superfamily member 2	chr19p13.1 /// chr19p13.3-p12	233403_x_at	NM_001001524 /// NM_023002
4.72	5.11	0.39	1.10E-01	4.66E-01	STC2	stanniocalcin 2	chr5q35.2	203439_s_at	NM_003714
3.46	4.08	0.62	1.10E-01	4.66E-01	FRYL	FRY-like	chr4p12	1554260_a_at	NM_015030
3.14	3.42	0.29	1.10E-01	4.66E-01	---	---	---	1561102_at	---
2.68	2.96	0.28	1.10E-01	4.66E-01	PCNXL2	pecanex-like 2 (Drosophila)	chr1q42.2	1554256_a_at	NM_014801
1.96	2.23	0.27	1.10E-01	4.66E-01	---	---	---	239129_at	---
2.12	2.38	0.26	1.10E-01	4.66E-01	OMG	Oligodendrocyte myelin glycoprotein	chr17q11.2	238720_at	NM_002544
3.04	3.25	0.21	1.10E-01	4.66E-01	GPR110	G protein-coupled receptor 110	chr6p12.3	220907_at	NM_025048 /// NM_153840
4.43	4.76	0.33	1.10E-01	4.66E-01	BOLA2	bolA homolog 2 (E. coli)	chr16p11.2	241644_at	NM_001031827
5.05	5.46	0.41	1.10E-01	4.66E-01	---	---	---	229040_at	---
4.54	4.98	0.44	1.10E-01	4.66E-01	MSC	musculin (activated B-cell factor-1)	chr8q21	209928_s_at	NM_005098
4.49	4.97	0.49	1.11E-01	4.66E-01	LYRM2	LYR motif containing 2	chr6q14.2-q16.1	226919_at	NM_020466
6.07	6.71	0.64	1.11E-01	4.66E-01	KIAA1429	KIAA1429	chr8q22.1	223110_at	NM_015496 /// NM_183009
5.36	6.67	1.31	1.11E-01	4.66E-01	---	---	---	242384_at	---
3.91	4.80	0.90	1.11E-01	4.66E-01	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	chr7q31.33	204353_s_at	NM_001042594 /// NM_015450 /// NR_003102 /// NR_003103 /// NR_003104
5.83	6.53	0.70	1.11E-01	4.66E-01	TMEM181	transmembrane protein 181	chr6q25.3	225127_at	NM_020823
6.17	6.69	0.52	1.11E-01	4.66E-01	MRPS31	mitochondrial ribosomal protein S31	chr13q14.11	212604_at	NM_005830
3.81	4.26	0.45	1.11E-01	4.66E-01	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	chr1q32.1	205410_s_at	NM_001001396 /// NM_001684
2.57	2.99	0.42	1.11E-01	4.66E-01	SFRS15	splicing factor, arginine/serine-rich 15	chr21q22.1	222310_at	NM_020706
4.65	5.00	0.35	1.11E-01	4.66E-01	MAP3K7	Mitogen-activated protein kinase kinase kinase 7	chr6q16.1-q16.3	206853_s_at	NM_003188 /// NM_145331 /// NM_145332 /// NM_145333
5.71	6.03	0.32	1.11E-01	4.66E-01	---	---	---	243458_at	---
2.44	2.73	0.29	1.11E-01	4.66E-01	---	---	---	234869_at	---
2.83	3.10	0.27	1.11E-01	4.66E-01	---	---	---	239907_at	---
2.64	2.89	0.25	1.11E-01	4.66E-01	HPSE2 /// LOC100133895	heparanase 2 /// hypothetical protein LOC100133895	chr10q23-q24	220927_s_at	NM_021828 /// XM_001714212
2.39	2.63	0.24	1.11E-01	4.66E-01	TUBD1	tubulin, delta 1	chr17q23.1	221326_s_at	NM_016261
2.06	2.30	0.24	1.11E-01	4.66E-01	---	---	---	237278_x_at	---
1.89	2.09	0.20	1.11E-01	4.66E-01	---	---	---	238755_at	---
1.71	1.90	0.19	1.11E-01	4.66E-01	LOC729652	hypothetical protein LOC729652	chr16p13.3	1563637_at	XR_040488 /// XR_040489 /// XR_040490
1.99	2.16	0.18	1.11E-01	4.66E-01	---	---	---	240877_x_at	---
3.80	4.34	0.55	1.11E-01	4.66E-01	PDE1A	phosphodiesterase 1A, calmodulin-dependent	chr2q32.1	1558680_s_at	NM_001003683 /// NM_005019
1.91	2.14	0.23	1.11E-01	4.66E-01	---	---	---	216948_at	---

3.82	4.04	0.22	1.11E-01	4.66E-01	---	---	---	241637_at	---
2.12	2.31	0.19	1.11E-01	4.66E-01	---	---	---	1557402_at	---
2.08	2.26	0.19	1.11E-01	4.66E-01	---	---	---	238274_at	---
7.86	8.17	0.30	1.11E-01	4.66E-01	DUSP3	dual specificity phosphatase 3	chr17q21	201536_at	NM_004090
4.67	5.78	1.10	1.11E-01	4.66E-01	AIDA	axin interactor, dorsalization associated	chr1q41	220199_s_at	NM_022831
5.06	5.96	0.89	1.11E-01	4.66E-01	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	chr1q24-q25	223243_s_at	NM_025191
7.69	8.44	0.75	1.11E-01	4.66E-01	RAB18	RAB18, member RAS oncogene family	chr10p12.1	224377_s_at	NM_021252
3.18	3.69	0.51	1.11E-01	4.66E-01	---	---	---	236524_at	---
3.90	4.24	0.34	1.11E-01	4.66E-01	PGBD2	piggyBac transposable element derived 2	chr1q44	241490_s_at	NM_001017434 /// NM_170725
2.97	3.29	0.32	1.11E-01	4.66E-01	LOC170082	TFIIS central domain-containing protein 1	chrXp22.2	1553815_a_at	NM_152634
2.88	3.16	0.28	1.11E-01	4.66E-01	---	---	---	216448_at	---
2.78	3.11	0.33	1.11E-01	4.66E-01	RP11-114G1.1	Sp3 transcription factor pseudogene	chr13q31.3	216403_at	---
5.12	5.42	0.30	1.11E-01	4.66E-01	---	---	---	1569834_at	---
2.21	2.58	0.37	1.11E-01	4.66E-01	ZNF207	zinc finger protein 207	chr17q11.2	238772_at	NM_001032293 /// NM_001098507 /// NM_003457
5.21	5.84	0.63	1.11E-01	4.66E-01	ASCC3	activating signal cointegrator 1 complex subunit 3	chr6q16.1-q16.3	212815_at	NM_006828 /// NM_022091
2.03	2.23	0.20	1.11E-01	4.66E-01	---	---	---	1556763_at	---
6.30	6.81	0.51	1.11E-01	4.66E-01	ERBB2IP	erbb2 interacting protein	chr5q12.3	217941_s_at	NM_001006600 /// NM_018695
6.41	7.06	0.65	1.11E-01	4.66E-01	CFDP1	craniofacial development protein 1	chr16q22.2-q22.3	203166_at	NM_006324
4.00	4.25	0.25	1.11E-01	4.66E-01	LOC388503	similar to Complement C3 precursor	chr19p13.2	231691_at	NM_001013640
2.78	3.35	0.58	1.11E-01	4.66E-01	NCAM2	neural cell adhesion molecule 2	chr21q21.1	205669_at	NM_004540
4.29	4.59	0.30	1.11E-01	4.66E-01	---	---	---	243471_at	---
4.95	5.66	0.70	1.11E-01	4.67E-01	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	chr18q12.2	218209_s_at	NM_018170
2.80	3.07	0.27	1.11E-01	4.67E-01	MARVELD3	MARVEL domain containing 3	chr16q22.3	233634_at	NM_001017967 /// NM_052858
2.13	2.37	0.24	1.11E-01	4.67E-01	SIN3A	SIN3 homolog A, transcription regulator (yeast)	chr15q24.2	238189_at	NM_015477
4.50	4.88	0.38	1.11E-01	4.67E-01	LOC728353	hypothetical protein LOC728353	chr14q11.2	1559926_at	XR_041035 /// XR_041036 /// XR_041037
4.92	5.24	0.32	1.11E-01	4.67E-01	MIA	melanoma inhibitory activity	chr19q13.32-q13.33	206560_s_at	NM_006533
2.84	3.16	0.32	1.11E-01	4.67E-01	---	---	---	228609_at	---
2.54	2.83	0.29	1.11E-01	4.67E-01	PAK4	p21 protein (Cdc42/Rac)-activated kinase 4	chr19q13.2	215326_at	NM_001014831 /// NM_001014832 /// NM_001014834 /// NM_001014835 /// NM_005884
2.85	3.14	0.29	1.11E-01	4.67E-01	BSN	bassoon (presynaptic cytomatrix protein)	chr3p21.31	204586_at	NM_003458
2.09	2.36	0.27	1.11E-01	4.67E-01	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	chr14q11.2	230307_at	NM_030631
2.40	2.65	0.25	1.11E-01	4.67E-01	C1orf124	chromosome 1 open reading frame 124	chr1q42.12-q43	223511_at	NM_001010984 /// NM_032018
2.20	2.45	0.25	1.11E-01	4.67E-01	---	---	---	233627_at	---
2.55	2.76	0.21	1.11E-01	4.67E-01	---	---	---	230841_at	---
2.72	3.10	0.38	1.11E-01	4.67E-01	---	---	---	242233_at	---
4.68	5.03	0.34	1.11E-01	4.67E-01	IL4I1	interleukin 4 induced 1	chr19q13.3|19q13.3-q13.4	230966_at	NM_152899 /// NM_172374
2.96	3.17	0.21	1.11E-01	4.67E-01	RAB6A	RAB6A, member RAS oncogene family	chr11q13.3	1559174_at	NM_002869 /// NM_198896
2.33	2.65	0.32	1.11E-01	4.67E-01	FXYD7	FXYD domain containing ion transport regulator 7	chr19q13.12	220131_at	NM_022006
1.92	2.13	0.21	1.12E-01	4.67E-01	---	---	---	237822_at	---
2.07	2.28	0.20	1.12E-01	4.67E-01	---	---	---	221420_at	---
2.28	2.51	0.23	1.12E-01	4.67E-01	TRBV7-8	T cell receptor beta variable 7-8	chr7q34	234377_at	---
3.00	3.39	0.39	1.12E-01	4.67E-01	MTM1	myotubularin 1	chrXq28	36920_at	NM_000252
4.15	4.51	0.35	1.12E-01	4.67E-01	---	---	---	240443_at	---
2.82	3.15	0.33	1.12E-01	4.67E-01	MOGAT2	monoacylglycerol O-acyltransferase 2	chr11q13.5	207491_at	NM_025098
2.61	2.92	0.32	1.12E-01	4.67E-01	CNGA1	cyclic nucleotide gated channel alpha 1	chr4p12-cen	206417_at	NM_000087
2.79	3.10	0.31	1.12E-01	4.67E-01	ZNF296	zinc finger protein 296	chr19q13.32	238607_at	NM_145288
3.04	3.35	0.31	1.12E-01	4.67E-01	---	---	---	1566866_at	---
2.64	2.95	0.31	1.12E-01	4.67E-01	LEP	leptin	chr7q31.3	207092_at	NM_000230
4.51	4.81	0.30	1.12E-01	4.67E-01	TTL	tubulin tyrosine ligase	chr2q13	224908_s_at	NM_153712

3.14	3.39	0.26	1.12E-01	4.67E-01	CSAD	cysteine sulfinic acid decarboxylase	chr12q13.11-q14.3	238764_at	NM_015989
2.42	2.62	0.20	1.12E-01	4.67E-01	---	---	---	1569944_at	---
1.92	2.10	0.18	1.12E-01	4.67E-01	---	---	---	242964_at	---
2.31	2.47	0.17	1.12E-01	4.67E-01	PIWIL4	piwi-like 4 (Drosophila)	chr11q21	230480_at	NM_152431
4.60	4.80	0.20	1.12E-01	4.67E-01	MESP2	mesoderm posterior 2 homolog (mouse)	chr15q26.1	1556014_at	NM_001039958
13.16	13.35	0.19	1.12E-01	4.67E-01	---	---	---	AFFX-hum_alu_at	---
4.50	4.85	0.36	1.12E-01	4.67E-01	---	---	---	233473_x_at	---
8.53	9.28	0.75	1.12E-01	4.67E-01	PAIP2	poly(A) binding protein interacting protein 2	chr5q31.2	222983_s_at	NM_001033112 /// NM_016480
3.43	3.91	0.48	1.12E-01	4.67E-01	STRN3	striatin, calmodulin binding protein 3	chr14q13-q21	215505_s_at	NM_001083893 /// NM_014574
3.24	3.54	0.30	1.12E-01	4.67E-01	RBPMS	RNA binding protein with multiple splicing	chr8p12-p11	231961_at	NM_001008710 /// NM_001008711 /// NM_001008712 /// NM_006867
2.71	3.01	0.30	1.12E-01	4.67E-01	---	---	---	1561624_at	---
2.40	2.65	0.26	1.12E-01	4.67E-01	---	---	---	1559861_at	---
3.10	3.33	0.22	1.12E-01	4.67E-01	GLRA1	glycine receptor, alpha 1	chr5q32	207972_at	NM_000171
4.65	4.87	0.22	1.12E-01	4.67E-01	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	chr2q37.3	225791_at	NM_080678
2.09	2.30	0.20	1.12E-01	4.67E-01	---	---	---	241005_at	---
6.94	7.38	0.44	1.12E-01	4.67E-01	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	chr16q12.1	226994_at	NM_005880
3.04	3.29	0.24	1.12E-01	4.67E-01	DGCR5	DiGeorge syndrome critical region gene 5 (non-protein coding)	chr22q11	215244_at	NR_002733
2.22	2.44	0.22	1.12E-01	4.67E-01	---	---	---	215941_at	---
5.33	5.87	0.54	1.12E-01	4.67E-01	MAPK1	mitogen-activated protein kinase 1	chr22q11.2|22q11.21	208351_s_at	NM_002745 /// NM_138957
5.68	6.10	0.42	1.12E-01	4.67E-01	C20orf149	chromosome 20 open reading frame 149	chr20q13.33	227994_x_at	NM_024299
2.92	3.29	0.38	1.12E-01	4.68E-01	TTC37	tetratricopeptide repeat domain 37	chr5q15	1554029_a_at	NM_014639
2.14	2.37	0.23	1.12E-01	4.68E-01	DNA2	DNA replication helicase 2 homolog (yeast)	chr10q21.3-q22.1	213647_at	NM_001080449
2.00	2.20	0.20	1.12E-01	4.68E-01	---	---	---	1561256_at	---
1.84	2.02	0.18	1.12E-01	4.68E-01	---	---	---	1556212_x_at	---
3.34	3.68	0.33	1.12E-01	4.68E-01	KIAA0494	KIAA0494	chr1pter-p22.1	229524_at	NM_014774
5.02	5.24	0.23	1.12E-01	4.68E-01	INO80D	INO80 complex subunit D	chr2q33.3	220165_at	NM_017759
2.73	2.99	0.26	1.12E-01	4.68E-01	MAGIX	MAGI family member, X-linked	chrXp11.23	234927_s_at	NM_001099680 /// NM_001099681 /// NM_001099682 /// NM_024859
4.39	4.68	0.29	1.12E-01	4.68E-01	C2orf55	chromosome 2 open reading frame 55	chr2q11.2	229320_at	NM_207362
2.95	3.26	0.31	1.12E-01	4.68E-01	---	---	---	1559166_at	---
3.88	4.18	0.30	1.12E-01	4.68E-01	---	---	---	229681_at	---
2.25	2.54	0.28	1.12E-01	4.68E-01	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	chr2q35	1555116_s_at	NM_000578
2.18	2.43	0.25	1.12E-01	4.68E-01	---	---	---	1566622_at	---
2.63	2.86	0.23	1.12E-01	4.68E-01	---	---	---	235379_at	---
3.14	3.36	0.22	1.12E-01	4.68E-01	FANCM	Fanconi anemia, complementation group M	chr14q21.3	231971_at	NM_020937
1.94	2.17	0.24	1.12E-01	4.68E-01	DNAH3	dynein, axonemal, heavy chain 3	chr16p12.2	1560803_at	NM_017539
5.24	6.12	0.88	1.12E-01	4.68E-01	ZNF12	zinc finger protein 12	chr7p22.1	1554021_a_at	NM_006956 /// NM_016265
2.35	2.58	0.23	1.12E-01	4.68E-01	MFSD1	Major facilitator superfamily domain containing 1	chr3q25.33	240936_at	NM_022736
2.62	2.84	0.21	1.12E-01	4.68E-01	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	chr9p13-p12	1558115_at	NM_021111
2.29	2.50	0.21	1.12E-01	4.68E-01	GLCCI1	glucocorticoid induced transcript 1	chr7p21.3	225700_at	NM_138426
2.43	2.72	0.29	1.12E-01	4.68E-01	ITIH2	inter-alpha (globulin) inhibitor H2	chr10p15	204987_at	NM_002216
2.46	2.73	0.26	1.12E-01	4.68E-01	C21orf15	chromosome 21 open reading frame 15	chr21q11	1558589_at	---
2.94	3.96	1.02	1.12E-01	4.68E-01	ERAP2	endoplasmic reticulum aminopeptidase 2	chr5q15	219759_at	NM_001130140 /// NM_022350
2.72	3.03	0.31	1.13E-01	4.68E-01	---	---	---	240464_at	---
4.41	4.80	0.39	1.13E-01	4.68E-01	RTN2	reticulon 2	chr19q13.32	34408_at	NM_005619 /// NM_206900 /// NM_206901
3.27	3.59	0.32	1.13E-01	4.68E-01	KIF13A	kinesin family member 13A	chr6p23	232837_at	NM_001105566 /// NM_001105567 /// NM_001105568 /// NM_022113

4.52	4.89	0.37	1.13E-01	4.68E-01	---	---	---	242125_at	---
3.07	3.29	0.22	1.13E-01	4.68E-01	LOC284661	hypothetical protein LOC284661	chr1p36.32	1561384_a_at	---
1.93	2.23	0.30	1.13E-01	4.69E-01	KIF24	kinesin family member 24	chr9p13.3	220652_at	NM_194313
2.07	2.35	0.28	1.13E-01	4.69E-01	---	---	---	1561558_at	---
3.12	4.34	1.22	1.13E-01	4.69E-01	IGKC /// IGKV1-5 /// LOC647506 /// LOC652694	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5 /// similar to Ig kappa chain V-I region HK101 precursor /// similar to Ig kappa chain V-I region HK102 precursor	chr2p12	216576_x_at	XM_001713938 /// XM_942302
8.37	9.53	1.16	1.13E-01	4.69E-01	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	chr7q21.1	209993_at	NM_000927
5.69	6.20	0.51	1.13E-01	4.69E-01	SLC35B3	solute carrier family 35, member B3	chr6p24.3	222691_at	NM_015948
4.62	4.89	0.27	1.13E-01	4.69E-01	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	chr1p34.1	1555702_a_at	NM_006279 /// NM_174963 /// NM_174964 /// NM_174965 /// NM_174966 /// NM_174967 /// NM_174968 /// NM_174969 /// NM_174970 /// NM_174971
10.00	10.88	0.88	1.13E-01	4.69E-01	HSPA8	heat shock 70kDa protein 8	chr11q24.1	210338_s_at	NM_006597 /// NM_153201
2.48	2.72	0.23	1.13E-01	4.69E-01	---	---	---	244589_at	---
3.05	3.27	0.22	1.13E-01	4.69E-01	---	---	---	231685_at	---
4.30	4.75	0.45	1.13E-01	4.69E-01	ZNF44	zinc finger protein 44	chr19p13.2	215359_x_at	NM_016264 /// XM_001718561 /// XM_001719479 /// XM_001719639
6.06	6.80	0.74	1.13E-01	4.69E-01	---	---	---	236038_at	---
2.28	2.63	0.34	1.13E-01	4.69E-01	FLJ43080	hypothetical protein LOC642987	chr5q22.1	1568698_at	NM_001039763 /// XM_001718501 /// XM_001719018 /// XM_001724089
6.22	6.55	0.33	1.13E-01	4.69E-01	BTBD10	BTB (POZ) domain containing 10	chr11p15.2	223174_at	NM_032320
2.23	2.55	0.32	1.13E-01	4.69E-01	---	---	---	240671_at	---
4.20	4.52	0.31	1.13E-01	4.69E-01	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	chr15q22.3-q23	210083_at	NM_003612
4.01	4.29	0.28	1.13E-01	4.69E-01	---	---	---	240113_at	---
2.65	2.93	0.28	1.13E-01	4.69E-01	C21orf86	chromosome 21 open reading frame 86	chr21q22.3	1552819_at	XR_040463 /// XR_040464 /// XR_040465
2.17	2.42	0.26	1.13E-01	4.69E-01	---	---	---	235873_at	---
4.29	5.28	0.99	1.13E-01	4.69E-01	SMOC2	SPARC related modular calcium binding 2	chr6q27	223235_s_at	NM_022138
2.60	2.84	0.24	1.13E-01	4.69E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	1567377_at	NM_015512
2.14	2.33	0.19	1.13E-01	4.69E-01	---	---	---	233335_at	---
2.79	3.05	0.26	1.13E-01	4.69E-01	METTL8	methyltransferase like 8	chr2q31.1	232533_at	NM_024770
2.82	3.05	0.23	1.13E-01	4.69E-01	DKFZP434H168	hypothetical LOC26077	---	234905_at	---
5.89	6.51	0.61	1.13E-01	4.69E-01	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	chr10q24	209473_at	NM_001098175 /// NM_001776
4.69	5.09	0.40	1.13E-01	4.69E-01	LDB3	LIM domain binding 3	chr10q22.3-q23.2	216888_at	NM_001080114 /// NM_001080115 /// NM_001080116 /// NM_007078
5.43	5.74	0.31	1.13E-01	4.69E-01	ARHGAP23	Rho GTPase activating protein 23	chr17q12	230196_x_at	XM_001714948 /// XM_001716606 /// XM_290799
3.98	4.29	0.31	1.13E-01	4.69E-01	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	chr8p12	201374_x_at	NM_001009552 /// NM_004156
2.33	2.55	0.23	1.13E-01	4.69E-01	FNDC3A	Fibronectin type III domain containing 3A	chr13q14.2	238961_s_at	NM_001079673 /// NM_014923
8.69	9.59	0.90	1.13E-01	4.69E-01	COL1A2	collagen, type I, alpha 2	chr7q22.1	202403_s_at	NM_000089
2.28	2.85	0.57	1.13E-01	4.69E-01	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	chr2q32	209676_at	NM_001032281 /// NM_006287

2.23	2.60	0.38	1.13E-01	4.69E-01	---	---	---	238146_at	---
4.33	4.66	0.33	1.13E-01	4.69E-01	---	---	---	237641_at	---
2.83	3.14	0.30	1.13E-01	4.69E-01	ALDOB	aldolase B, fructose-bisphosphate	chr9q21.3-q22.2	217238_s_at	NM_000035
2.27	2.63	0.36	1.13E-01	4.69E-01	---	---	---	244340_x_at	---
2.28	2.53	0.25	1.13E-01	4.69E-01	GNA12	Guanine nucleotide binding protein (G protein) alpha 12	chr7p22.2	231309_at	NM_007353
2.15	2.43	0.28	1.13E-01	4.69E-01	SSTR2	somatostatin receptor 2	chr17q24	214597_at	NM_001050
7.13	7.55	0.42	1.13E-01	4.69E-01	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	chr11q12	219607_s_at	NM_024021 /// NM_148975
3.47	3.87	0.40	1.13E-01	4.69E-01	---	---	---	241877_at	---
2.24	2.43	0.19	1.13E-01	4.69E-01	---	---	---	231616_at	---
6.22	6.73	0.50	1.13E-01	4.70E-01	AP2B1	adaptor-related protein complex 2, beta 1 subunit	chr17q11.2-q12	200615_s_at	NM_001030006 /// NM_001282
3.25	3.71	0.46	1.13E-01	4.70E-01	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	chr12q13	228303_at	NM_007210
3.60	3.97	0.37	1.13E-01	4.70E-01	PHKG1	phosphorylase kinase, gamma 1 (muscle)	chr7p11.2	207312_at	NM_006213
2.17	2.43	0.26	1.13E-01	4.70E-01	OR2F1 /// OR2F2	olfactory receptor, family 2, subfamily F, member 1 /// olfactory receptor, family 2, subfamily F, member 2	chr7q35	208525_s_at	NM_001004685 /// NM_012369
2.62	3.04	0.42	1.13E-01	4.70E-01	HHIP	hedgehog interacting protein	chr4q28-q32	1556037_s_at	NM_022475
4.16	4.80	0.64	1.14E-01	4.70E-01	C12orf66	chromosome 12 open reading frame 66	chr12q14.2	235026_at	NM_152440
9.05	9.46	0.41	1.14E-01	4.70E-01	ATXN10	ataxin 10	chr22q13.31	208833_s_at	NM_013236
2.97	3.31	0.34	1.14E-01	4.70E-01	---	---	---	243085_at	---
3.81	4.13	0.32	1.14E-01	4.70E-01	R3HDM1	R3H domain containing 1	chr2q21.3	210714_at	NM_015361
1.89	2.16	0.26	1.14E-01	4.70E-01	CCDC121	coiled-coil domain containing 121	chr2p23.2	220321_s_at	NM_024584
1.91	2.11	0.20	1.14E-01	4.70E-01	LRRC2	leucine rich repeat containing 2	chr3p21.31	231781_s_at	NM_024512 /// NM_024750
6.14	7.38	1.24	1.14E-01	4.70E-01	SRP72	signal recognition particle 72kDa	chr4q11	208095_s_at	NM_006947
2.37	2.58	0.21	1.14E-01	4.70E-01	---	---	---	243185_at	---
1.93	2.11	0.19	1.14E-01	4.70E-01	---	---	---	234155_at	---
1.92	2.19	0.26	1.14E-01	4.70E-01	---	---	---	239605_x_at	---
3.81	4.06	0.25	1.14E-01	4.70E-01	ZNF37A	zinc finger protein 37A	chr10p11.2	228711_at	NM_001007094 /// NM_003421
3.33	3.56	0.24	1.14E-01	4.70E-01	---	---	---	230828_at	---
5.82	6.25	0.43	1.14E-01	4.70E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	225677_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844
2.07	2.28	0.20	1.14E-01	4.70E-01	LOC283027	hypothetical protein LOC283027	chr10q11.1	1562527_at	---
5.04	5.24	0.20	1.14E-01	4.70E-01	---	---	---	236682_at	---
2.16	2.42	0.26	1.14E-01	4.70E-01	---	---	---	243842_at	---
3.55	3.86	0.31	1.14E-01	4.71E-01	---	---	---	238225_at	---
5.13	5.44	0.31	1.14E-01	4.71E-01	---	---	---	236159_x_at	---
4.39	4.59	0.19	1.14E-01	4.71E-01	MEX3D	Mex-3 homolog D (C. elegans)	chr19p13.3	222042_x_at	NM_001085363 /// NM_203304
3.82	4.10	0.28	1.14E-01	4.71E-01	LOC100144602	hypothetical	---	238241_at	---
3.63	3.88	0.25	1.14E-01	4.71E-01	ZNF669	zinc finger protein 669	chr1q44	220215_at	NM_024804
2.32	2.55	0.22	1.14E-01	4.71E-01	JARID1B	jumonji, AT rich interactive domain 1B	chr1q32.1	201547_at	NM_006618
1.91	2.09	0.18	1.14E-01	4.71E-01	LCORL	ligand dependent nuclear receptor corepressor-like	chr4p15.32	235970_at	NM_153686
3.09	3.37	0.28	1.14E-01	4.71E-01	UBQLNL	ubiquilin-like	chr11p15.4	236965_at	NM_145053
5.38	5.84	0.45	1.14E-01	4.71E-01	RAP2A /// RAP2B	RAP2A, member of RAS oncogene family /// RAP2B, member of RAS oncogene family	chr13q34 /// chr3q25.2	214487_s_at	NM_002886 /// NM_021033
3.84	4.11	0.27	1.14E-01	4.71E-01	TET3	tet oncogene family member 3	chr2p13.1	1554641_a_at	NM_144993
2.64	2.86	0.22	1.14E-01	4.71E-01	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	chr14q31-q32.1	204635_at	NM_004755 /// NM_182398
3.01	3.21	0.20	1.14E-01	4.71E-01	---	---	---	243448_at	---
7.30	8.53	1.23	1.14E-01	4.71E-01	GSTM1	glutathione S-transferase M1	chr1p13.3	215333_x_at	NM_000561 /// NM_146421
2.77	3.03	0.26	1.14E-01	4.71E-01	H2BFXP /// LOC644328	H2B histone family, member X, pseudogene /// similar to Histone H2B type F-M (H2B.s) (H2B/s)	chrXq22.2	233963_at	NR_003238 /// XR_016511
4.25	4.51	0.26	1.14E-01	4.71E-01	---	---	---	241213_x_at	---
4.14	4.39	0.25	1.14E-01	4.71E-01	F11	coagulation factor XI	chr4q35	206610_s_at	NM_000128
2.90	3.14	0.23	1.14E-01	4.71E-01	---	---	---	224340_at	---
2.36	2.59	0.23	1.14E-01	4.71E-01	---	---	---	243810_at	---
2.33	2.53	0.20	1.14E-01	4.71E-01	---	---	---	214863_at	---
3.54	3.90	0.36	1.14E-01	4.71E-01	---	---	---	240501_at	---
8.54	9.07	0.53	1.14E-01	4.71E-01	PPAP2B	phosphatidic acid phosphatase type 2B	chr1pter-p22.1	212226_s_at	NM_003713 /// NM_177414
3.02	3.37	0.35	1.14E-01	4.71E-01	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	chr2q14	216275_at	NM_004336

2.97	3.29	0.31	1.14E-01	4.71E-01	RUFY2	RUN and FYVE domain containing 2	chr10q21.3	219957_at	NM_001042417 /// NM_017987
2.60	2.90	0.30	1.14E-01	4.71E-01	RAB11FIP4	RAB11 family interacting protein 4 (class II)	chr17q11.2	224482_s_at	NM_032932
3.09	3.51	0.42	1.14E-01	4.71E-01	HIC1	hypermethylated in cancer 1	chr17p13.3	208461_at	NM_001098202 /// NM_006497
3.58	3.87	0.29	1.14E-01	4.71E-01	BICD1	bicaudal D homolog 1 (Drosophila)	chr12p11.2-p11.1	1556051_a_at	NM_001003398 /// NM_001714
3.36	3.67	0.31	1.14E-01	4.71E-01	LOC646934	Similar to golgin-like protein	chr15q25.1	215572_at	XR_018310 /// XR_042348 /// XR_042482
13.34	13.50	0.16	1.14E-01	4.71E-01	COX2 /// ZFYVE20	cytochrome c oxidase II /// zinc finger, FYVE domain containing 20	chr3p24.3	1553570_x_at	NM_022340
5.84	6.19	0.35	1.15E-01	4.71E-01	TAOK2	TAO kinase 2	chr16p11.2	204878_s_at	NM_004783 /// NM_016151
2.61	2.96	0.35	1.15E-01	4.71E-01	CHD9	chromodomain helicase DNA binding protein 9	chr16q12.2	220586_at	NM_025134
4.56	4.75	0.20	1.15E-01	4.71E-01	FAM83A	family with sequence similarity 83, member A	chr8q24.13	242944_at	NM_032899 /// NM_207006
5.55	5.93	0.39	1.15E-01	4.72E-01	TNRC6B	trinucleotide repeat containing 6B	chr22q13.1	229036_at	NM_001024843 /// NM_015088
2.63	2.98	0.35	1.15E-01	4.72E-01	---	---	---	1555995_a_at	---
6.57	6.87	0.30	1.15E-01	4.72E-01	KIAA0841	KIAA0841	chr19q13.12	213053_at	NM_015302
2.55	2.84	0.29	1.15E-01	4.72E-01	MEIG1	meiosis expressed gene 1 homolog (mouse)	chr10p13	238158_at	NM_001080836
3.23	3.41	0.18	1.15E-01	4.72E-01	---	---	---	233383_at	---
2.44	3.79	1.35	1.15E-01	4.72E-01	PENK	proenkephalin	chr8q23-q24	213791_at	NM_006211
3.63	4.05	0.42	1.15E-01	4.72E-01	ARSK	arylsulfatase family, member K	chr5q15	239147_at	NM_198150
2.97	3.33	0.36	1.15E-01	4.72E-01	PRR15	proline rich 15	chr7p15.1	226961_at	NM_175887
5.43	6.17	0.74	1.15E-01	4.72E-01	GGNBP2	gametogenetin binding protein 2	chr17q12	233936_s_at	NM_024835
5.21	5.49	0.29	1.15E-01	4.72E-01	SURF2	surfeit 2	chr9q34.2	205224_at	NM_017503
3.01	3.27	0.26	1.15E-01	4.72E-01	WNT6	wingless-type MMTV integration site family, member 6	chr2q35	221609_s_at	NM_006522
6.04	6.52	0.48	1.15E-01	4.72E-01	BPTF	bromodomain PHD finger transcription factor	chr17q24.3	232909_s_at	NM_004459 /// NM_182641
1.75	1.94	0.19	1.15E-01	4.72E-01	ZNF560	zinc finger protein 560	chr19p13.2	1553276_at	NM_152476
7.55	8.83	1.27	1.15E-01	4.72E-01	GSTM2	glutathione S-transferase M2 (muscle)	chr1p13.3	204418_x_at	NM_000848
4.93	5.85	0.93	1.15E-01	4.72E-01	---	---	---	236322_at	---
6.33	7.18	0.85	1.15E-01	4.72E-01	LONRF2	LON peptidase N-terminal domain and ring finger 2	chr2q11.2	235977_at	NM_198461
5.58	6.40	0.82	1.15E-01	4.72E-01	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	chr7q21.3-q22.1	214670_at	NM_003439
8.36	8.89	0.52	1.15E-01	4.72E-01	PSMC1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	chr14q32.11	204219_s_at	NM_002802
4.14	4.61	0.47	1.15E-01	4.72E-01	THAP1	THAP domain containing, apoptosis associated protein 1	chr8p11.21	219292_at	NM_018105 /// NM_199003
5.83	6.30	0.47	1.15E-01	4.72E-01	KIAA0182	KIAA0182	chr16q24.1	212056_at	NM_001134473 /// NM_014615
6.31	6.70	0.39	1.15E-01	4.72E-01	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	chr10p11.22-p11.21	210094_s_at	NM_019619
11.78	12.15	0.36	1.15E-01	4.72E-01	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1q42.1	202017_at	NM_000120
4.56	4.92	0.36	1.15E-01	4.72E-01	ZNF93	zinc finger protein 93	chr19p12	215758_x_at	NM_031218
6.70	7.06	0.36	1.15E-01	4.72E-01	FAM109A	family with sequence similarity 109, member A	chr12q24.12	229690_at	NM_144671
4.15	4.50	0.35	1.15E-01	4.72E-01	TTC36	tetratricopeptide repeat domain 36	chr11q23.3	237350_at	NM_001080441
4.32	4.66	0.33	1.15E-01	4.72E-01	ZNF14	zinc finger protein 14	chr19p13.3-p13.2	219854_at	NM_021030
2.53	2.85	0.33	1.15E-01	4.72E-01	DNAH8	dynein, axonemal, heavy chain 8	chr6p21.31-p21.1	233052_at	NM_001371
2.47	2.79	0.32	1.15E-01	4.72E-01	ZNF483	zinc finger protein 483	chr9q31.3	243770_at	NM_001007169 /// NM_133464
2.71	3.02	0.31	1.15E-01	4.72E-01	FILIP1	filamin A interacting protein 1	chr6q14.1	231945_at	NM_015687
4.74	5.05	0.31	1.15E-01	4.72E-01	PARP10	poly (ADP-ribose) polymerase family, member 10	chr8q24.3	226401_at	NM_032789
4.26	4.56	0.30	1.15E-01	4.72E-01	---	---	---	220489_s_at	---
3.30	3.58	0.29	1.15E-01	4.72E-01	NEK10	NIMA (never in mitosis gene a)- related kinase 10	chr3p24.1	237227_at	NM_001031741 /// NM_152534
2.21	2.49	0.28	1.15E-01	4.72E-01	---	---	---	231098_at	---
8.09	8.35	0.26	1.15E-01	4.72E-01	SKP1	S-phase kinase-associated protein 1	chr5q31	200711_s_at	NM_006930 /// NM_170679
2.93	3.19	0.25	1.15E-01	4.72E-01	IL17RE	Interleukin 17 receptor E	chr3p25.3	229401_at	NM_153480 /// NM_153481 /// NM_153483
5.19	5.44	0.25	1.15E-01	4.72E-01	FAM148B	family with sequence similarity 148, member B	chr15q22.2	229727_x_at	NM_001007595
2.05	2.29	0.24	1.15E-01	4.72E-01	RICTOR	rapamycin-insensitive companion of mTOR	chr5p13.1	1552734_at	NM_152756
4.72	4.96	0.24	1.15E-01	4.72E-01	LOC100133461	hypothetical LOC100133461	---	1560911_at	XM_001715239

2.35	2.59	0.23	1.15E-01	4.72E-01	---	---	---	233154_at	---
5.37	5.60	0.23	1.15E-01	4.72E-01	---	---	---	216645_at	---
2.71	2.94	0.23	1.15E-01	4.72E-01	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	chr4q25	210868_s_at	NM_001130721 /// NM_024090
2.11	2.32	0.21	1.15E-01	4.72E-01	ADAM12	ADAM metallopeptidase domain 12	chr10q26.3	215613_at	NM_003474 /// NM_021641
2.09	2.29	0.20	1.15E-01	4.72E-01	---	---	---	240959_at	---
1.94	2.14	0.20	1.15E-01	4.72E-01	hCG_38480	potassium channel tetramerisation domain containing 1	chr18q11.2	1559276_at	XM_001127052 /// XM_001130247 /// XM_001722936
2.09	2.29	0.20	1.15E-01	4.72E-01	---	---	---	1560673_at	---
2.17	2.37	0.20	1.15E-01	4.72E-01	---	---	---	231528_at	---
4.94	5.38	0.44	1.15E-01	4.72E-01	---	---	---	244310_at	---
2.48	2.66	0.19	1.15E-01	4.72E-01	LOC219731	hypothetical protein LOC219731	chr10p14	1557208_at	---
6.93	7.28	0.35	1.15E-01	4.72E-01	HSF4	heat shock transcription factor 4	chr16q21	210977_s_at	NM_001040667 /// NM_001538
2.16	2.36	0.20	1.15E-01	4.72E-01	---	---	---	240004_at	---
5.27	5.57	0.31	1.15E-01	4.72E-01	---	---	---	227193_at	---
2.06	2.26	0.20	1.15E-01	4.72E-01	---	---	---	1560226_at	---
3.71	4.14	0.44	1.15E-01	4.72E-01	SRFBP1	serum response factor binding protein 1	chr5q23.1	241734_at	NM_152546
5.42	5.72	0.30	1.15E-01	4.72E-01	ZDHHC12	zinc finger, DHHC-type containing 12	chr9q34.11	226088_at	NM_032799
3.96	4.80	0.84	1.15E-01	4.72E-01	LAMA4	laminin, alpha 4	chr6q21	202202_s_at	NM_001105206 /// NM_001105207 /// NM_001105208 /// NM_001105209 /// NM_002290
2.91	3.57	0.66	1.15E-01	4.72E-01	CA8	carbonic anhydrase VIII	chr8q11-q12	220234_at	NM_004056
6.57	7.16	0.59	1.15E-01	4.72E-01	EXOC5	exocyst complex component 5	chr14q23.1	225084_at	NM_006544
5.16	5.42	0.25	1.16E-01	4.72E-01	C9orf46	chromosome 9 open reading frame 46	chr9p24.1	218992_at	NM_018465
2.62	2.90	0.28	1.16E-01	4.72E-01	KLHL18	kelch-like 18 (Drosophila)	chr3p21.31	207976_at	NM_025010
2.14	2.41	0.26	1.16E-01	4.72E-01	ZDHHC15	zinc finger, DHHC-type containing 15	chrXq13.3	1552557_a_at	NM_144969
5.43	6.47	1.04	1.16E-01	4.73E-01	C10orf58	chromosome 10 open reading frame 58	chr10q23.1	224435_at	NM_032333
2.90	3.63	0.73	1.16E-01	4.73E-01	---	---	---	233273_at	---
3.06	3.34	0.27	1.16E-01	4.73E-01	USH1C	Usher syndrome 1C (autosomal recessive, severe)	chr11p15.1-p14	211184_s_at	NM_005709 /// NM_153676
6.71	7.60	0.89	1.16E-01	4.73E-01	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	chr10q25-q26	203153_at	NM_001548
3.73	4.56	0.83	1.16E-01	4.73E-01	API5	apoptosis inhibitor 5	chr11p11.2	214959_s_at	NM_006595
1.93	2.12	0.19	1.16E-01	4.73E-01	LGI1	leucine-rich, glioma inactivated 1	chr10q24	206349_at	NM_005097
2.79	3.06	0.27	1.16E-01	4.73E-01	---	---	---	1556754_at	---
2.80	3.27	0.46	1.16E-01	4.73E-01	SYNGR3	synaptogyrin 3	chr16p13	205691_at	NM_004209
6.15	6.57	0.42	1.16E-01	4.73E-01	LOC388692	hypothetical gene supported by AK123662	chr1q21.1	235186_at	XR_039906 /// XR_039907 /// XR_039908
5.99	6.32	0.33	1.16E-01	4.73E-01	WNT10B	wingless-type MMTV integration site family, member 10B	chr12q13	206213_at	NM_003394
5.68	5.97	0.29	1.16E-01	4.73E-01	NOX5	NADPH oxidase, EF-hand calcium binding domain 5	chr15q23	220641_at	NM_024505
2.08	2.29	0.21	1.16E-01	4.73E-01	---	---	---	240013_at	---
5.49	5.93	0.44	1.16E-01	4.73E-01	LOC728153	similar to FAM133B protein	chr5q12.1	1560199_x_at	XM_001128002 /// XM_001722995
4.16	4.44	0.28	1.16E-01	4.73E-01	LOC100128155 /// VAV2	hypothetical protein LOC100128155 /// vav 2 guanine nucleotide exchange factor	chr9q34.1 /// chr9q34.2	205537_s_at	NM_001134398 /// NM_003371 /// XM_001719399 /// XM_001722275 /// XM_001722967
4.13	4.57	0.44	1.16E-01	4.73E-01	LOC728431	Hypothetical LOC728431	chr1p34.3	229678_at	XM_001127447 /// XM_001132105 /// XM_001716728
3.26	3.55	0.29	1.16E-01	4.73E-01	---	---	---	1558154_at	---
3.35	3.59	0.24	1.16E-01	4.73E-01	ALKBH7	AlkB, alkylation repair homolog 7 (E. coli)	chr19p13.3	227879_at	NM_032306
3.33	3.53	0.20	1.16E-01	4.73E-01	---	---	---	215344_at	---
2.46	2.87	0.41	1.16E-01	4.73E-01	HIST1H3E	histone cluster 1, H3e	chr6p21.3	236278_at	NM_003532

2.76	3.15	0.39	1.16E-01	4.73E-01	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	chr12q15	202971_s_at	NM_003583 /// NM_006482
2.61	2.90	0.29	1.16E-01	4.73E-01	ATF7IP	activating transcription factor 7 interacting protein	chr12p13.1	207728_at	NM_018179
3.54	3.83	0.29	1.16E-01	4.73E-01	NENF	Neuron derived neurotrophic factor	chr1q32.3	213673_x_at	NM_013349
6.57	7.09	0.52	1.16E-01	4.73E-01	SRPRB	signal recognition particle receptor, B subunit	chr3q22.1	222532_at	NM_021203
2.51	2.82	0.31	1.16E-01	4.73E-01	CCR7	chemokine (C-C motif) receptor 7	chr17q12-q21.2	206337_at	NM_001838
2.05	2.30	0.24	1.16E-01	4.73E-01	SLC39A14	solute carrier family 39 (zinc transporter), member 14	chr8p21.3	1555433_at	NM_001128431 /// NM_015359
2.74	2.95	0.21	1.16E-01	4.73E-01	---	---	---	1556374_s_at	---
2.81	2.98	0.18	1.16E-01	4.73E-01	MUC4	Mucin 4, cell surface associated	chr3q29	1561785_at	NM_004532 /// NM_018406 /// NM_138297
3.93	4.19	0.26	1.16E-01	4.73E-01	ARF1	ADP-ribosylation factor 1	chr1q42	1565651_at	NM_001024226 /// NM_001024227 /// NM_001024228 /// NM_001658
2.25	2.50	0.25	1.16E-01	4.73E-01	---	---	---	243114_at	---
3.09	3.35	0.26	1.16E-01	4.73E-01	---	---	---	241797_at	---
2.40	2.61	0.21	1.16E-01	4.73E-01	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	chr4p14-p13	216747_at	NM_173075
5.20	6.04	0.83	1.16E-01	4.73E-01	C20orf19	chromosome 20 open reading frame 19	chr20pter-q11.23	219961_s_at	NM_018474
6.81	7.50	0.70	1.16E-01	4.73E-01	MTDH	metadherin	chr8q22.1	212251_at	NM_178812
4.99	5.52	0.53	1.16E-01	4.73E-01	DLD	dihydrolipoamide dehydrogenase	chr7q31-q32	230426_at	NM_000108
6.54	6.93	0.39	1.16E-01	4.73E-01	YBX1 /// YBX1P2	Y box binding protein 1 /// Y box binding protein 1 pseudogene 2	chr1p34 /// chr7q22.2	216940_x_at	NM_004559
3.28	3.56	0.28	1.16E-01	4.73E-01	---	---	---	235187_s_at	---
5.42	6.58	1.16	1.16E-01	4.74E-01	ZNF12	zinc finger protein 12	chr7p22.1	1559881_s_at	NM_006956 /// NM_016265
3.04	3.58	0.54	1.16E-01	4.74E-01	ATF7IP	activating transcription factor 7 interacting protein	chr12p13.1	216197_at	NM_018179
7.07	7.45	0.38	1.16E-01	4.74E-01	GPC1	glypican 1	chr2q35-q37	202756_s_at	NM_002081
8.62	9.13	0.50	1.16E-01	4.74E-01	NUPR1	nuclear protein 1	chr16p11.2	209230_s_at	NM_001042483 /// NM_012385
2.88	3.21	0.33	1.16E-01	4.74E-01	---	---	---	237713_at	---
2.93	3.19	0.26	1.16E-01	4.74E-01	KRTAP8-1	keratin associated protein 8-1	chr21q22.1	1564974_at	NM_175857
2.78	3.03	0.25	1.16E-01	4.74E-01	---	---	---	243330_at	---
4.65	4.89	0.24	1.16E-01	4.74E-01	NCR3	natural cytotoxicity triggering receptor 3	chr6p21.3	210763_x_at	NM_147130
3.03	3.32	0.29	1.16E-01	4.74E-01	ITIH1	inter-alpha (globulin) inhibitor H1	chr3p21.2-p21.1	210888_s_at	NM_002215
2.44	3.06	0.62	1.16E-01	4.74E-01	PDE1A	phosphodiesterase 1A, calmodulin-dependent	chr2q32.1	233547_x_at	NM_001003683 /// NM_005019
2.45	2.74	0.29	1.16E-01	4.74E-01	---	---	---	238479_at	---
2.07	2.28	0.21	1.16E-01	4.74E-01	---	---	---	1563934_at	---
1.85	2.05	0.21	1.17E-01	4.74E-01	FBXL21	F-box and leucine-rich repeat protein 21	chr5q31	1555412_at	NM_012159
3.50	3.82	0.32	1.17E-01	4.74E-01	EIF5	eukaryotic translation initiation factor 5	chr14q32.32	208707_at	NM_001969 /// NM_183004
6.22	6.60	0.38	1.17E-01	4.74E-01	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	chr1q22	219259_at	NM_022367
2.92	3.22	0.29	1.17E-01	4.74E-01	SLC25A29	solute carrier family 25, member 29	chr14q32.2	231664_at	NM_001039355
2.01	2.26	0.25	1.17E-01	4.74E-01	GNRHR	gonadotropin-releasing hormone receptor	chr4q21.2	211522_s_at	NM_000406 /// NM_001012763
5.76	6.04	0.28	1.17E-01	4.74E-01	IQSEC2	IQ motif and Sec7 domain 2	chrXp11.22	214819_at	NM_001111125 /// NM_015075 /// XM_001714411
6.39	6.63	0.24	1.17E-01	4.74E-01	MINK1	misshapen-like kinase 1 (zebrafish)	chr17p13.2	215909_x_at	NM_001024937 /// NM_015716 /// NM_153827 /// NM_170663
7.07	7.72	0.65	1.17E-01	4.74E-01	LRPPRC	leucine-rich PPR-motif containing	chr2p21	211615_s_at	NM_133259
3.12	3.52	0.40	1.17E-01	4.74E-01	GNA14	guanine nucleotide binding protein (G protein), alpha 14	chr9q21	220108_at	NM_004297
2.31	2.64	0.33	1.17E-01	4.74E-01	TCP11L2	t-complex 11 (mouse)-like 2	chr12q23.3	1553861_at	NM_152772
1.75	1.91	0.16	1.17E-01	4.74E-01	LOC401134	hypothetical gene supported by BC040544	chr4q13.1	1557822_at	---
5.00	5.30	0.30	1.17E-01	4.74E-01	USHBP1	Usher syndrome 1C binding protein 1	chr19p13	235510_at	NM_031941
3.64	3.91	0.27	1.17E-01	4.74E-01	MMP24	matrix metallopeptidase 24 (membrane-inserted)	chr20q11.2	213171_s_at	NM_006690

2.91	3.18	0.27	1.17E-01	4.74E-01	CSH2	chorionic somatomammotropin hormone 2	chr17q24.2	207770_x_at	NM_020991 /// NM_022644 /// NM_022645																				
2.35	2.54	0.19	1.17E-01	4.74E-01	LOC642924	hypothetical protein LOC642924	chr8q22.1	1561423_at	XM_931168																				
3.82	4.20	0.38	1.17E-01	4.74E-01	---	---	---	239220_at	---																				
2.50	2.79	0.29	1.17E-01	4.75E-01	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	chr2q33.3-q34	206794_at	NM_001042599 /// NM_005235																				
9.65	9.89	0.23	1.17E-01	4.75E-01	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	chr1p36.23	201336_at	NM_004781																				
2.28	2.48	0.20	1.17E-01	4.75E-01	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	chr10p13	235478_at	NM_001033855 /// NM_001033857 /// NM_001033858 /// NM_022487																				
6.24	6.58	0.34	1.17E-01	4.75E-01	CLCN7	chloride channel 7	chr16p13	209235_at	NM_001114331 /// NM_001287																				
4.02	4.34	0.32	1.17E-01	4.75E-01	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)	chr17q25.3	224138_at	NM_005189 /// NM_032647																				
2.38	2.58	0.20	1.17E-01	4.75E-01	LOC641364	hypothetical protein LOC641364	chr4q28-q31	1562253_at	---																				
2.04	2.22	0.18	1.17E-01	4.75E-01	CLEC12B	C-type lectin domain family 12, member B	chr12p13.2	231357_at	NM_001129998 /// NM_205852																				
2.84	4.42	1.58	1.17E-01	4.75E-01	CCL19	chemokine (C-C motif) ligand 19	chr9p13	210072_at	NM_006274																				
2.18	2.45	0.27	1.17E-01	4.75E-01	SLC30A10	solute carrier family 30, member 10	chr1q41	220435_at	NM_018713																				
2.13	2.37	0.24	1.17E-01	4.75E-01	---	---	---	1558624_at	---																				
9.70	10.88	1.18	1.17E-01	4.75E-01	HSPD1	heat shock 60kDa protein 1 (chaperonin)	chr2q33.1	200806_s_at	NM_002156 /// NM_199440																				
3.96	4.29	0.33	1.17E-01	4.75E-01	C8orf44	chromosome 8 open reading frame 44	chr8q13.1	220216_at	NM_019607																				
1.78	1.95	0.17	1.17E-01	4.75E-01	IMPG1	interphotoreceptor matrix proteoglycan 1	chr6q14.2-q15	207054_at	NM_001563																				
5.90	6.43	0.53	1.17E-01	4.75E-01	---	---	---	226779_at	---																				
5.18	5.56	0.38	1.17E-01	4.75E-01	EML4	echinoderm microtubule associated protein like 4	chr2p22-p21	228674_s_at	NM_019063																				
5.11	5.46	0.35	1.17E-01	4.75E-01	SPTBN2	spectrin, beta, non-erythrocytic 2	chr11q13	205155_s_at	NM_006946																				
1.78	1.96	0.18	1.17E-01	4.75E-01	---	---	---	240599_x_at	---																				
3.65	4.28	0.63	1.17E-01	4.75E-01	KIAA1826	KIAA1826	chr11q22	223799_at	NM_032424																				
2.09	2.29	0.20	1.17E-01	4.75E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	236416_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735																				
5.00	5.32	0.33	1.17E-01	4.75E-01	GLP1R	glucagon-like peptide 1 receptor	chr6p21	208390_s_at	NM_002062																				
3.58	3.88	0.29	1.17E-01	4.75E-01	---	---	---	244326_at	---																				
3.09	3.38	0.29	1.17E-01	4.75E-01	CSNK1G3	casein kinase 1, gamma 3	chr5q23	229702_at	NM_001031812 /// NM_001044722 /// NM_001044723 /// NM_004384																				
2.19	2.45	0.26	1.17E-01	4.75E-01	LOC388456	hypothetical gene supported by BC039671	chr18p11.32	1563117_at	---																				
1.86	2.13	0.27	1.17E-01	4.75E-01	CLCA2	CLCA family member 2, chloride channel regulator	chr1p31-p22	217528_at	NM_006536																				
3.60	4.29	0.68	1.17E-01	4.75E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	223578_x_at	NR_002819																				
4.65	5.04	0.39	1.17E-01	4.75E-01	ADA	adenosine deaminase	chr20q12-q13.11	216705_s_at	NM_000022																				
2.08	2.29	0.21	1.17E-01	4.75E-01	---	---	---	239095_at	---																				
3.92	4.78	0.87	1.17E-01	4.75E-01	IGHM /// LOC100133862	immunoglobulin heavy constant mu /// similar to hCG1773549	chr14q32.33	211634_x_at	XM_001720441																				
2.95	3.26	0.31	1.18E-01	4.75E-01	---	---	---	231445_at	---																				
4.10	4.79	0.69	1.18E-01	4.75E-01	LARP4	La ribonucleoprotein domain family, member 4	chr12q13.13	1555384_a_at	NM_052879 /// NM_199188 /// NM_199190																				
8.89	9.41	0.51	1.18E-01	4.75E-01	hCG_1781062 /// SRP9	hCG1781062 /// signal recognition particle 9kDa	chr10q23.32 /// chr1q42.12	201273_s_at	NM_001130440 /// NM_003133 /// XM_001720126 /// XM_927451 /// XM_938116																				

2.48	2.74	0.26	1.18E-01	4.75E-01	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	chr5q31-q32	205643_s_at	NM_001127381 /// NM_004576 /// NM_181674 /// NM_181675 /// NM_181676 /// NM_181677 /// NM_181678																					
2.78	3.01	0.24	1.18E-01	4.75E-01	GYPB	glycophorin B (MNS blood group)	chr4q28-q31	214407_x_at	NM_002100																					
2.30	2.52	0.23	1.18E-01	4.75E-01	LYPD6	LY6/PLAUR domain containing 6	chr2q23.2	227764_at	NM_194317																					
2.41	2.62	0.21	1.18E-01	4.75E-01	LOC100128139	hypothetical protein LOC100128139	chr19p12	236768_at	XM_001714998 /// XM_001718929 /// XM_001719779																					
3.68	3.97	0.30	1.18E-01	4.75E-01	---	---	---	232665_x_at	---																					
1.88	2.08	0.19	1.18E-01	4.75E-01	SLC17A8	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8	chr12q23.1	1553415_at	NM_139319																					
9.60	9.97	0.37	1.18E-01	4.75E-01	MYL9	myosin, light chain 9, regulatory	chr20q11.23	201058_s_at	NM_006097 /// NM_181526																					
1.99	2.31	0.32	1.18E-01	4.75E-01	GRK4	G protein-coupled receptor kinase 4	chr4p16.3	210600_s_at	NM_001004056 /// NM_001004057 /// NM_182982																					
1.96	2.15	0.19	1.18E-01	4.76E-01	LOC643194	similar to hCG2039888	chr2q24.2	237610_at	XM_001714455 /// XM_931396 /// XM_943830																					
2.52	2.72	0.20	1.18E-01	4.76E-01	C4orf27	chromosome 4 open reading frame 27	chr4q33	1556086_at	NM_017867																					
7.55	7.77	0.22	1.18E-01	4.76E-01	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	chr14q24.1	209452_s_at	NM_006370																					
3.03	3.25	0.22	1.18E-01	4.76E-01	---	---	---	243055_at	---																					
4.47	5.12	0.64	1.18E-01	4.76E-01	---	---	---	235601_at	---																					
6.16	6.41	0.25	1.18E-01	4.76E-01	GPR153	G protein-coupled receptor 153	chr1p36.31	64942_at	NM_207370																					
1.94	2.17	0.23	1.18E-01	4.76E-01	STXBP6	syntaxin binding protein 6 (amisyn)	chr14q12	230560_at	NM_014178																					
2.28	2.47	0.19	1.18E-01	4.76E-01	ATAD2B	ATPase family, AAA domain containing 2B	chr2p24.1-p23.3	1558807_at	NM_017552																					
3.24	3.53	0.29	1.18E-01	4.76E-01	NF1	neurofibromin 1	chr17q11.2	204323_x_at	NM_000267 /// NM_001042492 /// NM_001128147																					
5.18	5.76	0.58	1.18E-01	4.76E-01	---	---	---	232527_at	---																					
2.23	2.53	0.30	1.18E-01	4.76E-01	THBS1	Thrombospondin 1	chr15q15	239336_at	NM_003246																					
5.15	5.63	0.48	1.18E-01	4.76E-01	DPYD	dihydropyrimidine dehydrogenase	chr1p22	204646_at	NM_000110																					
3.20	3.46	0.26	1.18E-01	4.76E-01	---	---	---	1556951_at	---																					
2.09	2.28	0.18	1.18E-01	4.76E-01	---	---	---	240714_at	---																					
6.92	7.90	0.98	1.18E-01	4.76E-01	TARS	threonyl-tRNA synthetase	chr5p13.2	201263_at	NM_152295																					
3.89	4.59	0.70	1.18E-01	4.76E-01	SDCCAG1	serologically defined colon cancer antigen 1	chr14q22	1557950_at	NM_004713																					
4.69	5.23	0.54	1.18E-01	4.76E-01	ARP11	actin-related Arp11	chr7q36.1	223874_at	XR_041997 /// XR_041998 /// XR_041999 /// XR_042000																					
2.27	2.69	0.42	1.18E-01	4.76E-01	---	---	---	1561690_at	---																					
6.45	6.80	0.35	1.18E-01	4.76E-01	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	chr16p12.3	228074_at	NM_001034841																					
4.98	5.32	0.34	1.18E-01	4.76E-01	---	---	---	235293_at	---																					
2.70	3.01	0.31	1.18E-01	4.76E-01	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	chr20q13.3	210508_s_at	NM_004518 /// NM_172106 /// NM_172107 /// NM_172108 /// NM_172109																					
2.90	3.19	0.29	1.18E-01	4.76E-01	ADPRH	ADP-ribosylarginine hydrolase	chr3q13.31-q13.33	207863_at	NM_001125																					
2.40	2.67	0.27	1.18E-01	4.76E-01	EHD4	EH-domain containing 4	chr15q11.1	1556607_at	NM_139265																					
1.89	2.16	0.27	1.18E-01	4.76E-01	KRTAP3-3 /// LOC100132276	keratin associated protein 3-3 /// hypothetical protein LOC100132276	chr17q12-q21	233681_at	NM_033185 /// XM_001722601																					
2.49	2.74	0.25	1.18E-01	4.76E-01	---	---	---	234077_at	---																					
3.05	3.29	0.24	1.18E-01	4.76E-01	LOC151171	hypothetical protein LOC151171	chr2q37.3	1562214_at	---																					
2.47	2.70	0.22	1.18E-01	4.76E-01	CYP2C9	Cytochrome P450, family 2, subfamily C, polypeptide 9	chr10q24	216661_x_at	NM_000771																					
1.94	2.10	0.16	1.18E-01	4.76E-01	STXBP5L	syntaxin binding protein 5-like	chr3q13.33	1568896_at	NM_014980																					
1.80	1.99	0.19	1.18E-01	4.77E-01	BRIP1	BRCA1 interacting protein C-terminal helicase 1	chr17q22-q24	221703_at	NM_032043																					
7.44	8.06	0.62	1.18E-01	4.77E-01	SCCPDH	saccharopine dehydrogenase (putative)	chr1q44	201825_s_at	NM_016002																					

3.08	3.32	0.23	1.19E-01	4.77E-01	CMTM1	CKLF-like MARVEL transmembrane domain containing 1	chr16q21	1555738_at	NM_052999 /// NM_181268 /// NM_181269 /// NM_181270 /// NM_181271 /// NM_181272 /// NM_181283 /// NM_181296																				
2.40	2.63	0.23	1.19E-01	4.77E-01	ZNF362	Zinc finger protein 362	chr1p35.1	214915_at	NM_152493																				
2.59	2.82	0.23	1.19E-01	4.77E-01	GPR55	G protein-coupled receptor 55	chr2q37	237559_at	NM_005683																				
4.31	4.51	0.20	1.19E-01	4.77E-01	PRKCG	protein kinase C, gamma	chr19q13.4	236195_x_at	NM_002739																				
2.82	3.10	0.28	1.19E-01	4.77E-01	LOC100130740	similar to hCG2042068	chr17q21.32	236893_at	XM_001722876 /// XM_001725076 /// XM_001726544																				
3.13	3.40	0.27	1.19E-01	4.77E-01	NDFIP2	Nedd4 family interacting protein 2	chr13q31.1	230190_at	NM_019080																				
2.62	2.87	0.25	1.19E-01	4.77E-01	---	---	---	234059_at	---																				
4.19	4.48	0.29	1.19E-01	4.77E-01	---	---	---	233802_at	---																				
6.36	6.79	0.43	1.19E-01	4.77E-01	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	chr19q13.2	225418_at	NM_001042724 /// NM_002856																				
3.49	3.82	0.33	1.19E-01	4.77E-01	---	---	---	242885_at	---																				
4.48	4.80	0.32	1.19E-01	4.77E-01	---	---	---	243117_at	---																				
3.33	3.62	0.29	1.19E-01	4.77E-01	---	---	---	239758_at	---																				
5.58	5.83	0.26	1.19E-01	4.77E-01	SEMA6C	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	chr1q21.2	208100_x_at	NM_030913																				
4.11	4.55	0.44	1.19E-01	4.77E-01	GPR107	G protein-coupled receptor 107	chr9q34.11	211977_at	NM_020960																				
2.00	2.24	0.24	1.19E-01	4.77E-01	LOC100132735	hypothetical protein LOC100132735	chr6q24.1	1557161_at	XM_001717182 /// XM_001717916 /// XM_001719742																				
2.41	2.59	0.18	1.19E-01	4.77E-01	EMX1	empty spiracles homeobox 1	chr2p14-p13	215264_at	NM_004097																				
4.50	5.00	0.50	1.19E-01	4.77E-01	ZNF280B	zinc finger protein 280B	chr22q11.22	229360_at	NM_080764																				
2.81	3.08	0.27	1.19E-01	4.77E-01	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	chr8q21.3	207386_at	NM_004820																				
3.97	4.19	0.22	1.19E-01	4.77E-01	LILRA3	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	chr19q13.4	206881_s_at	NM_006865																				
2.14	2.32	0.19	1.19E-01	4.77E-01	C6orf199	chromosome 6 open reading frame 199	chr6q21	1552299_at	NM_145025																				
3.00	3.29	0.28	1.19E-01	4.77E-01	---	---	---	1562324_a_at	---																				
3.36	3.64	0.28	1.19E-01	4.77E-01	C21orf84	chromosome 21 open reading frame 84	chr21q22.3	240589_at	XR_040120 /// XR_040121 /// XR_040122																				
4.34	4.92	0.58	1.19E-01	4.78E-01	IL1R2	interleukin 1 receptor, type II	chr2q12-q22	211372_s_at	NM_004633 /// NM_173343																				
4.37	5.66	1.28	1.19E-01	4.78E-01	USP47	ubiquitin specific peptidase 47	chr11p15.3	223701_s_at	NM_017944																				
2.48	3.12	0.64	1.19E-01	4.78E-01	SST	somatostatin	chr3q28	213921_at	NM_001048																				
4.13	4.72	0.59	1.19E-01	4.78E-01	ZNF805	zinc finger protein 805	chr19q13.43	238436_s_at	XM_001718504 /// XM_001718548 /// XM_001719150																				
5.60	6.00	0.40	1.19E-01	4.78E-01	FZD4	frizzled homolog 4 (Drosophila)	chr11q14.2	218665_at	NM_012193																				
5.13	5.52	0.39	1.19E-01	4.78E-01	PPID	peptidylprolyl isomerase D (cyclophilin D)	chr4q31.3	204186_s_at	NM_005038																				
3.15	3.54	0.38	1.19E-01	4.78E-01	PLG	plasminogen	chr6q26	240033_at	NM_000301																				
2.98	3.26	0.28	1.19E-01	4.78E-01	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	chr15q21.1	240705_at	NM_000103 /// NM_031226																				
2.69	2.96	0.27	1.19E-01	4.78E-01	AXIN2	axin 2	chr17q23-q24	224498_x_at	NM_004655																				
4.56	4.83	0.27	1.19E-01	4.78E-01	C17orf93	chromosome 17 open reading frame 93	chr17q21.3	230845_at	NR_024103																				
2.60	2.86	0.26	1.19E-01	4.78E-01	TEX11	testis expressed 11	chrXq13.1	221259_s_at	NM_001003811 /// NM_031276																				
4.04	4.29	0.26	1.19E-01	4.78E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	217197_x_at	NM_001079691 /// NM_052818																				
2.36	2.61	0.25	1.19E-01	4.78E-01	TMEM162	transmembrane protein 162	chr19q13.12	242259_at	NM_152481																				
2.44	2.68	0.24	1.19E-01	4.78E-01	---	---	---	235285_at	---																				
3.16	3.40	0.24	1.19E-01	4.78E-01	---	---	---	241237_at	---																				
2.47	2.71	0.24	1.19E-01	4.78E-01	EFNB3	ephrin-B3	chr17p13.1-p11.2	205031_at	NM_001406																				
2.32	2.52	0.20	1.19E-01	4.78E-01	---	---	---	244069_at	---																				
2.03	2.23	0.20	1.19E-01	4.78E-01	VPS8	vacuolar protein sorting 8 homolog (S. cerevisiae)	chr3q27.2	1559500_at	NM_001009921 /// NM_015303																				
2.27	2.47	0.19	1.19E-01	4.78E-01	CDSN	corneodesmosin	chr6p21.3	206193_s_at	NM_001264																				
3.68	3.93	0.25	1.19E-01	4.78E-01	SLC30A2	solute carrier family 30 (zinc transporter), member 2	chr1p35.3	224485_s_at	NM_001004434 /// NM_032513																				

5.11	5.53	0.42	1.20E-01	4.78E-01	OSBP2	oxysterol binding protein 2	chr22q12.2	221237_s_at	NM_030758
7.87	8.50	0.63	1.20E-01	4.78E-01	CAT	catalase	chr11p13	211922_s_at	NM_001752
6.29	6.75	0.45	1.20E-01	4.78E-01	ANKHD1 /// ANKHD1-EIF4EBP3 /// EIF4EBP3	ankyrin repeat and KH domain containing 1 /// ANKHD1-EIF4EBP3 /// eukaryotic translation initiation factor 4E binding protein 3	chr5q31.3	208773_s_at	NM_003732 /// NM_017747 /// NM_017978 /// NM_020690 /// NM_024668
3.04	3.39	0.35	1.20E-01	4.78E-01	RERE	arginine-glutamic acid dipeptide (RE) repeats	chr1p36.2-p36.1	200938_s_at	NM_001042681 /// NM_001042682 /// NM_012102
4.35	4.72	0.37	1.20E-01	4.78E-01	BMP1	bone morphogenetic protein 1	chr8p21.3	1569002_x_at	NM_001199 /// NM_006128 /// NM_006129
3.97	4.31	0.34	1.20E-01	4.78E-01	GON4L	gon-4-like (C. elegans)	chr1q22	1555913_at	NM_001037533 /// NM_032292
4.00	4.47	0.47	1.20E-01	4.78E-01	---	---	---	228008_at	---
3.76	4.15	0.39	1.20E-01	4.78E-01	PRDM14	PR domain containing 14	chr8q13.3	220714_at	NM_024504
3.79	4.14	0.35	1.20E-01	4.78E-01	C12orf30	chromosome 12 open reading frame 30	chr12q24.13	227245_at	NM_024953
3.27	3.50	0.23	1.20E-01	4.78E-01	---	---	---	239048_at	---
1.97	2.18	0.21	1.20E-01	4.78E-01	ANKRD43	ankyrin repeat domain 43	chr5q31.1	230238_at	NM_175873
5.99	6.52	0.52	1.20E-01	4.78E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	223437_at	NM_001001928 /// NM_005036
2.93	3.24	0.31	1.20E-01	4.78E-01	LOC729940	similar to hCG2036908	chr2q37.1	233486_at	XM_001134157 /// XM_001720637
2.96	3.31	0.35	1.20E-01	4.78E-01	CDC2	cell division cycle 2, G1 to S and G2 to M	chr10q21.1	203214_x_at	NM_001130829 /// NM_001786 /// NM_033379
2.13	2.34	0.21	1.20E-01	4.78E-01	FERMT1	fermitin family homolog 1 (Drosophila)	chr20p12.3	1557334_a_at	NM_017671
3.08	3.35	0.28	1.20E-01	4.78E-01	CYP4F22	cytochrome P450, family 4, subfamily F, polypeptide 22	chr19p13.12	244692_at	NM_173483
3.57	3.90	0.32	1.20E-01	4.78E-01	---	---	---	243006_at	---
13.16	13.32	0.17	1.20E-01	4.78E-01	COX2 /// ZFYVE20	cytochrome c oxidase II /// zinc finger, FYVE domain containing 20	chr3p24.3	1553569_at	NM_022340
2.49	2.94	0.45	1.20E-01	4.78E-01	KIAA0754	hypothetical LOC643314	chr1p34.2	215268_at	NM_015038
2.83	3.14	0.31	1.20E-01	4.78E-01	SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	chr1p32-p31	209713_s_at	NM_015139
4.13	5.60	1.47	1.20E-01	4.78E-01	LOC100130100	similar to hCG26659	chr2q14.1	217378_x_at	XM_001716310 /// XM_001716615
2.73	3.12	0.39	1.20E-01	4.78E-01	TMEM33	transmembrane protein 33	chr4p13	238831_at	NM_018126
2.68	2.98	0.30	1.20E-01	4.78E-01	---	---	---	1562453_at	---
3.14	3.36	0.22	1.20E-01	4.78E-01	---	---	---	1569738_at	---
5.34	5.77	0.44	1.20E-01	4.79E-01	SAR1B	SAR1 gene homolog B (S. cerevisiae)	chr5q31.1	223512_at	NM_001033503 /// NM_016103
3.74	4.02	0.28	1.20E-01	4.79E-01	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	chr7q35-q36	231144_at	NM_001003801 /// NM_001003802 /// NM_003078
2.21	2.54	0.32	1.20E-01	4.79E-01	PRDM2	PR domain containing 2, with ZNF domain	chr1p36.21	216445_at	NM_001007257 /// NM_012231 /// NM_015866
2.90	3.09	0.19	1.20E-01	4.79E-01	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	chr22q13.3	41660_at	NM_014246
3.07	3.32	0.25	1.20E-01	4.79E-01	---	---	---	240817_at	---
5.95	6.27	0.32	1.20E-01	4.79E-01	SLC35E1	solute carrier family 35, member E1	chr19p13.11	235035_at	NM_024881
5.87	7.76	1.89	1.20E-01	4.79E-01	IGKC	Netrin 2-like (chicken)	chr2p12	214669_x_at	---
2.24	2.47	0.23	1.20E-01	4.79E-01	---	---	---	240790_at	---
3.35	3.80	0.45	1.20E-01	4.79E-01	---	---	---	241102_at	---
2.33	2.62	0.28	1.20E-01	4.79E-01	ZNF483	zinc finger protein 483	chr9q31.3	1570534_a_at	NM_001007169 /// NM_133464
2.64	2.87	0.23	1.20E-01	4.79E-01	LOC100129296 /// MYCNOS	hypothetical protein LOC100129296 /// v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) opposite strand	chr2p24.1 /// chr2p24.3	207028_at	XM_001715416 /// XR_039828 /// XR_039829 /// XR_039830
2.04	2.26	0.23	1.20E-01	4.79E-01	---	---	---	1560483_at	---

2.29	2.48	0.18	1.20E-01	4.79E-01	SUZ12	Suppressor of zeste 12 homolog (Drosophila)	chr17q11.2	1566191_at	NM_015355
2.10	2.28	0.18	1.20E-01	4.80E-01	CAPZB	capping protein (actin filament) muscle Z-line, beta	chr1p36.1	215097_at	NM_004930
5.21	5.84	0.63	1.20E-01	4.80E-01	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	chr4q12	228584_at	NM_000232
4.96	5.29	0.33	1.20E-01	4.80E-01	C20orf10	chromosome 20 open reading frame 10	chr20q12-q13.12	207482_at	NM_014477
2.93	3.26	0.33	1.20E-01	4.80E-01	C16orf42	Chromosome 16 open reading frame 42	chr16p13.3	221993_s_at	NM_001001410
1.93	2.11	0.18	1.20E-01	4.80E-01	DKFZP434B061	DKFZP434B061 protein	chr13p13	237047_at	XR_015528 /// XR_040812
6.07	6.57	0.50	1.21E-01	4.80E-01	LAMC1	laminin, gamma 1 (formerly LAMB2)	chr1q31	200770_s_at	NM_002293
2.63	2.96	0.33	1.21E-01	4.80E-01	CTGLF1	Centaurin, gamma-like family, member 1	chr10q11.21	1565620_at	NM_133446
3.59	3.85	0.27	1.21E-01	4.80E-01	LGI4	leucine-rich repeat LGI family, member 4	chr19q13.12|19q13.11	227821_at	NM_139284
4.03	4.81	0.78	1.21E-01	4.80E-01	ATM	ataxia telangiectasia mutated	chr11q22-q23	208442_s_at	NM_000051 /// NM_138292
3.37	3.97	0.59	1.21E-01	4.80E-01	NET1	neuroepithelial cell transforming gene 1	chr10p15	201830_s_at	NM_001047160 /// NM_005863
5.09	5.53	0.45	1.21E-01	4.80E-01	STAT1	signal transducer and activator of transcription 1, 91kDa	chr2q32.2	209969_s_at	NM_007315 /// NM_139266
2.98	3.27	0.29	1.21E-01	4.80E-01	GPR25	G protein-coupled receptor 25	chr1q32.1	221363_x_at	NM_005298
2.61	2.89	0.29	1.21E-01	4.80E-01	---	---	---	1557275_a_at	---
1.88	2.08	0.19	1.21E-01	4.80E-01	CCDC65	coiled-coil domain containing 65	chr12q13.12	1552320_a_at	NM_033124
1.82	2.00	0.17	1.21E-01	4.80E-01	KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	chr2q37	211427_s_at	NM_002242
3.69	3.92	0.23	1.21E-01	4.80E-01	EP400NL	EP400 N-terminal like	chr12q24.33	241437_s_at	NR_003290
5.22	5.56	0.34	1.21E-01	4.80E-01	ZNF260	zinc finger protein 260	chr19q13.12	228920_at	NM_001012756
2.45	2.72	0.27	1.21E-01	4.80E-01	DLG1	discs, large homolog 1 (Drosophila)	chr3q29	215988_s_at	NM_001098424 /// NM_004087
4.08	4.33	0.25	1.21E-01	4.80E-01	C19orf6	Chromosome 19 open reading frame 6	chr19p13.3	230089_s_at	NM_001033026 /// NM_033420
5.98	6.31	0.34	1.21E-01	4.80E-01	MYO7B	myosin VIIB	chr2q21.1	235383_at	NM_001080527
3.12	3.37	0.25	1.21E-01	4.80E-01	DKFZP434L187	hypothetical LOC26082	chr15q13.2	216596_at	XM_496054
4.34	4.59	0.26	1.21E-01	4.80E-01	MYH14	myosin, heavy chain 14	chr19q13.33	217660_at	NM_001077186 /// NM_024729
5.94	6.23	0.29	1.21E-01	4.80E-01	PPID	peptidylprolyl isomerase D (cyclophilin D)	chr4q31.3	204185_x_at	NM_005038
1.89	2.08	0.19	1.21E-01	4.80E-01	---	---	---	239520_at	---
3.61	4.03	0.41	1.21E-01	4.80E-01	PHF3	PHD finger protein 3	chr6q12	217951_s_at	NM_015153
2.23	2.44	0.22	1.21E-01	4.80E-01	---	---	---	233629_at	---
3.97	4.34	0.37	1.21E-01	4.80E-01	---	---	---	238595_at	---
2.53	2.77	0.24	1.21E-01	4.80E-01	---	---	---	239075_at	---
2.19	2.40	0.21	1.21E-01	4.80E-01	CDH26	cadherin-like 26	chr20q13.2-q13.33	233663_s_at	NM_021810 /// NM_177980
8.63	9.04	0.41	1.21E-01	4.80E-01	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	chr4q24	200667_at	NM_003340 /// NM_181886 /// NM_181887 /// NM_181888 /// NM_181889 /// NM_181890 /// NM_181891 /// NM_181892 /// NM_181893
2.04	2.25	0.21	1.21E-01	4.80E-01	DNMBP	dynamin binding protein	chr10q24.2	1562969_at	NM_015221
5.12	5.36	0.24	1.21E-01	4.80E-01	JTV1	JTV1 gene	chr7p22	209972_s_at	NM_006303
3.19	3.63	0.45	1.21E-01	4.80E-01	ICA1L	islet cell autoantigen 1,69kDa-like	chr2q33.1	230454_at	NM_138468 /// NM_178231
5.36	5.63	0.27	1.21E-01	4.81E-01	STK32C	serine/threonine kinase 32C	chr10q26.3	230934_at	NM_173575
3.91	4.21	0.30	1.21E-01	4.81E-01	---	---	---	217721_at	---
3.92	4.23	0.31	1.21E-01	4.81E-01	CTBP1	C-terminal binding protein 1	chr4p16	1557714_at	NM_001012614 /// NM_001328
3.01	3.29	0.28	1.21E-01	4.81E-01	TMEM17	Transmembrane protein 17	chr2p15	244448_at	NM_198276
3.57	5.11	1.54	1.21E-01	4.81E-01	LOC100130100	similar to hCG26659	chr2q14.1	215176_x_at	XM_001716310 /// XM_001716615
4.01	4.47	0.46	1.21E-01	4.81E-01	FLJ21767 /// RASA4	RAS p21 protein activator 4 pseudogene /// RAS p21 protein activator 4	chr7p13 /// chr7q22	208534_s_at	NM_001079877 /// NM_006989 /// NR_024116 /// XM_001713977 /// XM_001724280

2.37	2.66	0.29	1.21E-01	4.81E-01	HTR4	5-hydroxytryptamine (serotonin) receptor 4	chr5q31-q33	207577_at	NM_000870 /// NM_001040169 /// NM_001040171 /// NM_001040172 /// NM_001040173 /// NM_001040174 /// NM_199453
3.69	4.51	0.81	1.21E-01	4.81E-01	---	---	---	1565776_at	---
5.33	6.14	0.81	1.21E-01	4.81E-01	---	---	---	238544_at	---
4.10	4.79	0.69	1.21E-01	4.81E-01	RABL3	RAB, member of RAS oncogene family-like 3	chr3q13.33	226089_at	NM_173825
2.75	3.10	0.35	1.21E-01	4.81E-01	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	chr5q13	228109_at	NM_006909
3.94	4.28	0.34	1.21E-01	4.81E-01	CLCNKB	chloride channel Kb	chr1p36	205985_x_at	NM_000085
2.40	2.73	0.33	1.21E-01	4.81E-01	PDPN	podoplanin	chr1p36.21	221898_at	NM_001006624 /// NM_001006625 /// NM_006474 /// NM_198389
2.46	2.79	0.32	1.21E-01	4.81E-01	TBL1X	Transducin (beta)-like 1X-linked	chrXp22.3	213401_s_at	NM_005647
3.06	3.37	0.31	1.21E-01	4.81E-01	LOC100131067	Hypothetical protein LOC100131067	chr5q14.1	242585_at	XM_001720191 /// XM_001722264 /// XM_001723049
4.17	4.46	0.29	1.21E-01	4.81E-01	---	---	---	240306_at	---
4.86	5.14	0.27	1.21E-01	4.81E-01	C3orf58	chromosome 3 open reading frame 58	chr3q24	228079_at	NM_001134470 /// NM_173552
1.99	2.25	0.27	1.21E-01	4.81E-01	PRKD3	protein kinase D3	chr2p21	1554910_at	NM_005813
2.93	3.17	0.24	1.21E-01	4.81E-01	---	---	---	230286_at	---
3.26	3.49	0.23	1.21E-01	4.81E-01	WNK1	WNK lysine deficient protein kinase 1	chr12p13.3	211993_at	NM_018979
2.37	2.60	0.23	1.21E-01	4.81E-01	CSMD1	CUB and Sushi multiple domains 1	chr8p23.2	241960_at	NM_033225
7.98	8.20	0.21	1.21E-01	4.81E-01	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	chr1p36.1	208728_s_at	NM_001039802 /// NM_001791 /// NM_044472
2.30	2.49	0.19	1.21E-01	4.81E-01	---	---	---	234693_at	---
4.82	5.29	0.47	1.21E-01	4.81E-01	---	---	---	237018_at	---
4.51	5.35	0.85	1.22E-01	4.81E-01	LOXL1	lysyl oxidase-like 1	chr15q24-q25|15q22	203570_at	NM_005576
2.48	2.75	0.27	1.22E-01	4.81E-01	LOC401320	Hypothetical LOC401320	chr7p15.1	239640_at	XM_379482 /// XM_380098 /// XM_938539
1.95	2.18	0.23	1.22E-01	4.81E-01	---	---	---	243183_at	---
2.27	2.50	0.23	1.22E-01	4.81E-01	KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	chr2q37	210179_at	NM_002242
2.44	2.70	0.26	1.22E-01	4.81E-01	---	---	---	1559037_a_at	---
2.12	2.30	0.18	1.22E-01	4.81E-01	---	---	---	243375_at	---
7.33	7.90	0.57	1.22E-01	4.81E-01	TRIM44	tripartite motif-containing 44	chr11p13	217759_at	NM_017583
2.42	2.67	0.25	1.22E-01	4.81E-01	CXCL2	Chemokine (C-X-C motif) ligand 2	chr4q21	230101_at	NM_002089
2.08	2.31	0.23	1.22E-01	4.81E-01	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	chr4q13.3	1554841_at	NM_001004346
6.27	6.71	0.44	1.22E-01	4.81E-01	NBN	nibrin	chr8q21	202907_s_at	NM_001024688 /// NM_002485
4.90	5.21	0.32	1.22E-01	4.81E-01	C20orf59	chromosome 20 open reading frame 59	chr20q13.33	232922_s_at	NM_022082
4.72	4.95	0.23	1.22E-01	4.81E-01	PODNL1	podocan-like 1	chr19p13.12	220411_x_at	NM_024825
5.65	5.98	0.33	1.22E-01	4.81E-01	SLC29A4	solute carrier family 29 (nucleoside transporters), member 4	chr7p22.1	227281_at	NM_001040661 /// NM_153247
2.05	2.32	0.28	1.22E-01	4.81E-01	SLC25A43	solute carrier family 25, member 43	chrXq24	1557411_s_at	NM_145305
1.74	1.94	0.20	1.22E-01	4.81E-01	---	---	---	242296_x_at	---
4.77	5.45	0.68	1.22E-01	4.81E-01	HSPA4	Heat shock 70kDa protein 4	chr5q31.1-q31.2	208814_at	NM_002154
6.84	7.17	0.34	1.22E-01	4.81E-01	hCG_20426	HCG20426	chr1p36.33	230160_x_at	XR_040433 /// XR_040434 /// XR_040435

2.40	2.68	0.27	1.22E-01	4.81E-01	TRIM14	tripartite motif-containing 14	chr9q22.33	210846_x_at	NM_014788 /// NM_033219 /// NM_033220 /// NM_033221
4.08	4.30	0.22	1.22E-01	4.81E-01	LOC100130426	hypothetical protein LOC100130426	chr9q21.13	240767_x_at	XM_001714694 /// XM_001715049 /// XM_001715806
2.24	2.44	0.20	1.22E-01	4.81E-01	C14orf43	chromosome 14 open reading frame 43	chr14q24.3	235430_at	NM_001043318 /// NM_194278
2.35	2.60	0.25	1.22E-01	4.81E-01	GLMN	glomulin, FKBP associated protein	chr1p22.1	237388_at	NM_053274
2.53	2.75	0.22	1.22E-01	4.81E-01	PDE11A	phosphodiesterase 11A	chr2q31.2	224223_s_at	NM_001077196 /// NM_001077197 /// NM_001077358 /// NM_016953
2.02	2.28	0.26	1.22E-01	4.81E-01	BCL2L13	BCL2-like 13 (apoptosis facilitator)	chr22q11.1	1560977_a_at	NM_015367
4.86	5.24	0.38	1.22E-01	4.81E-01	LOC286437	hypothetical protein LOC286437	chrXq22.2	239762_at	---
3.86	4.23	0.37	1.22E-01	4.81E-01	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	chr12q12-q13	204997_at	NM_005276
2.47	2.81	0.34	1.22E-01	4.81E-01	---	---	---	215212_at	---
2.00	2.33	0.33	1.22E-01	4.81E-01	MYH1	myosin, heavy chain 1, skeletal muscle, adult	chr17p13.1	205951_at	NM_005963
3.13	3.42	0.29	1.22E-01	4.81E-01	EFNA2	ephrin-A2	chr19p13.3	1553573_s_at	NM_001405
3.86	4.14	0.28	1.22E-01	4.81E-01	TMEM190	transmembrane protein 190	chr19q13.42	1552594_at	NM_139172
4.85	5.12	0.27	1.22E-01	4.81E-01	DTNB	dystrobrevin, beta	chr2p24	214253_s_at	NM_021907 /// NM_033147 /// NM_033148 /// NM_183360 /// NM_183361
2.50	2.76	0.26	1.22E-01	4.81E-01	IL21	interleukin 21	chr4q26-q27	221271_at	NM_021803
1.97	2.20	0.23	1.22E-01	4.81E-01	ACTN2	actinin, alpha 2	chr1q42-q43	203863_at	NM_001103
3.00	3.22	0.22	1.22E-01	4.81E-01	PODN	podocan	chr1p32.3	233148_at	NM_153703
1.89	2.11	0.22	1.22E-01	4.81E-01	MGC40069	T cell receptor alpha variable 8-3	chr14q11.2	243602_at	XR_017974
1.97	2.15	0.18	1.22E-01	4.81E-01	LOC286087	hypothetical protein LOC286087	chr8p23.2	1556842_at	---
4.12	4.38	0.27	1.22E-01	4.81E-01	HCFC1	host cell factor C1 (VP16-accessory protein)	chrXq28	202473_x_at	NM_005334
2.99	3.33	0.34	1.22E-01	4.81E-01	---	---	---	239449_at	---
4.25	4.50	0.25	1.22E-01	4.81E-01	---	---	---	240644_at	---
2.61	2.83	0.23	1.22E-01	4.81E-01	POLH	polymerase (DNA directed), eta	chr6p21.1	1557701_s_at	NM_006502
2.20	2.42	0.21	1.22E-01	4.81E-01	---	---	---	244141_at	---
5.61	6.71	1.11	1.22E-01	4.81E-01	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	chr10q25.2	225420_at	NM_020918
6.73	7.34	0.60	1.22E-01	4.81E-01	C6orf89	chromosome 6 open reading frame 89	chr6p21.2	224977_at	NM_152734
4.12	4.76	0.65	1.22E-01	4.82E-01	GLS	glutaminase	chr2q32-q34	203158_s_at	NM_014905
7.57	8.24	0.68	1.22E-01	4.82E-01	TMED2	transmembrane emp24 domain trafficking protein 2	chr12q24.31	204426_at	NM_006815
5.96	6.71	0.74	1.22E-01	4.82E-01	MRPL1	mitochondrial ribosomal protein L1	chr4q21.1	223154_at	NM_020236
2.83	3.15	0.33	1.22E-01	4.82E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	224343_x_at	---
4.45	4.69	0.24	1.22E-01	4.82E-01	CABP1	calcium binding protein 1	chr12q24.31	208321_s_at	NM_001033677 /// NM_004276 /// NM_031205
2.09	2.32	0.23	1.22E-01	4.82E-01	COL12A1	Collagen, type XII, alpha 1	chr6q12-q13	233109_at	NM_004370 /// NM_080645
3.24	3.50	0.26	1.22E-01	4.82E-01	LOC100129122	Hypothetical protein LOC100129122	chr13q32.3	239356_at	XM_001714405 /// XM_001714912 /// XM_001715622
3.97	4.22	0.24	1.22E-01	4.82E-01	HUNK	hormonally up-regulated Neu-associated kinase	chr21q22.1	219535_at	NM_014586
4.55	4.85	0.30	1.23E-01	4.82E-01	PTPRU	protein tyrosine phosphatase, receptor type, U	chr1p35.3-p35.1	211320_s_at	NM_005704 /// NM_133177 /// NM_133178
3.31	3.59	0.28	1.23E-01	4.82E-01	---	---	---	234506_at	---
2.28	2.55	0.27	1.23E-01	4.82E-01	---	---	---	241226_at	---
4.38	4.62	0.24	1.23E-01	4.82E-01	---	---	---	237736_at	---
1.99	2.21	0.22	1.23E-01	4.82E-01	INTS7	integrator complex subunit 7	chr1p36.13-q42.3	1570173_at	NM_015434
5.22	5.44	0.22	1.23E-01	4.82E-01	PANX2	Pannexin 2	chr22q13.33	244471_x_at	NM_052839
1.93	2.13	0.19	1.23E-01	4.82E-01	POLE4	Polymerase (DNA-directed), epsilon 4 (p12 subunit)	chr2p12	1565329_at	NM_019896
2.36	2.66	0.30	1.23E-01	4.82E-01	EIF3M	eukaryotic translation initiation factor 3, subunit M	chr11p13	215190_at	NM_006360
4.81	5.09	0.29	1.23E-01	4.82E-01	---	---	---	242383_at	---
2.61	2.85	0.24	1.23E-01	4.82E-01	---	---	---	236974_at	---
3.61	4.10	0.49	1.23E-01	4.82E-01	LOC149086	hypothetical protein LOC149086	chr1p35.2	1566646_at	XR_017808 /// XR_041107 /// XR_041108

3.31	3.59	0.28	1.23E-01	4.82E-01	TUG1	taurine upregulated gene 1	chr22q12.2	230635_at	NR_002323
3.17	3.59	0.42	1.23E-01	4.82E-01	FRMD4A	FERM domain containing 4A	chr10p13	225163_at	NM_018027
3.53	3.85	0.32	1.23E-01	4.82E-01	P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	chr12q24.33	224069_x_at	NM_012226 /// NM_016318 /// NM_170682 /// NM_170683 /// NM_174872 /// NM_174873
4.41	4.97	0.56	1.23E-01	4.82E-01	GPSM2	G-protein signaling modulator 2 (AGS3-like, C. elegans)	chr1p13.3	221922_at	NM_013296
8.06	8.46	0.40	1.23E-01	4.82E-01	ADFP	adipose differentiation-related protein	chr9p22.1	209122_at	NM_001122
3.36	3.74	0.38	1.23E-01	4.82E-01	KLHDC5	kelch domain containing 5	chr12p11.22	225961_at	NM_020782
2.36	2.65	0.28	1.23E-01	4.82E-01	---	---	---	1564077_at	---
5.02	5.30	0.28	1.23E-01	4.82E-01	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	chr19q13.32	239362_at	NM_003827
1.97	2.25	0.27	1.23E-01	4.82E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	220704_at	NM_006060
2.60	2.87	0.26	1.23E-01	4.82E-01	PAX9	paired box 9	chr14q12-q13	207059_at	NM_006194
3.74	4.00	0.26	1.23E-01	4.82E-01	TBC1D29	TBC1 domain family, member 29	chr17q11.2	208008_at	NM_015594
2.18	2.43	0.25	1.23E-01	4.82E-01	SP4	Sp4 transcription factor	chr7p15.3	206663_at	NM_003112
4.16	4.41	0.25	1.23E-01	4.82E-01	SLC22A23	solute carrier family 22, member 23	chr6p25.2	233206_at	NM_015482 /// NM_021945
3.56	3.81	0.25	1.23E-01	4.82E-01	LGALS7 /// LGALS7B	lectin, galactoside-binding, soluble, 7 /// lectin, galactoside-binding, soluble, 7B	chr19q13.2	206400_at	NM_001042507 /// NM_002307 /// XM_001720971
3.23	3.45	0.23	1.23E-01	4.82E-01	---	---	---	237454_at	---
2.70	2.92	0.22	1.23E-01	4.82E-01	---	---	---	213393_at	---
2.85	3.07	0.22	1.23E-01	4.82E-01	RNASEH2B	Ribonuclease H2, subunit B	chr13q14.3	215040_at	NM_024570
1.99	2.19	0.20	1.23E-01	4.82E-01	---	---	---	236391_at	---
4.45	5.29	0.84	1.23E-01	4.82E-01	SDAD1	SDA1 domain containing 1	chr4q21.1	228408_s_at	NM_018115
8.21	8.67	0.46	1.23E-01	4.82E-01	FADS1 /// FADS3	fatty acid desaturase 1 /// fatty acid desaturase 3	chr11q12-q13.1 /// chr11q12.2-q13.1	208964_s_at	NM_013402 /// NM_021727
2.42	2.68	0.26	1.23E-01	4.82E-01	ARL17	ADP-ribosylation factor-like 17	chr17q21.31	232987_at	NM_001039083 /// NM_001103154
3.49	3.71	0.23	1.23E-01	4.82E-01	---	---	---	244263_at	---
4.07	4.28	0.21	1.23E-01	4.82E-01	EPHA8	EPH receptor A8	chr1p36.12	231796_at	NM_001006943 /// NM_020526
2.05	2.26	0.21	1.23E-01	4.82E-01	SOX6	SRY (sex determining region Y)-box 6	chr11p15.3	1570486_at	NM_017508 /// NM_033326
8.59	9.06	0.48	1.23E-01	4.82E-01	GPD1L	glycerol-3-phosphate dehydrogenase 1-like	chr3p22.3	212510_at	NM_015141
2.59	2.83	0.25	1.23E-01	4.82E-01	HEY2	hairy/enhancer-of-split related with YRPW motif 2	chr6q21	219743_at	NM_012259
2.05	2.27	0.22	1.23E-01	4.82E-01	---	---	---	1565282_at	---
2.17	2.38	0.21	1.23E-01	4.82E-01	HEMGN	hemogen	chr9q22.33	223670_s_at	NM_018437 /// NM_197978
6.84	7.60	0.77	1.23E-01	4.82E-01	ADD3	adducin 3 (gamma)	chr10q24.2-q24.3	201753_s_at	NM_001121 /// NM_016824 /// NM_019903
5.93	6.29	0.36	1.23E-01	4.82E-01	PCDH12	protocadherin 12	chr5q31	219656_at	NM_016580
4.89	5.25	0.35	1.23E-01	4.82E-01	41519	septin 2	chr2q37	1559038_at	NM_001008491 /// NM_001008492 /// NM_004404 /// NM_006155
3.27	3.62	0.35	1.23E-01	4.82E-01	ZNF473	zinc finger protein 473	chr19q13.33	213124_at	NM_001006656 /// NM_015428
3.30	3.63	0.34	1.23E-01	4.82E-01	FLJ40125	Hypothetical protein FLJ40125	chr19q13.32	238930_at	NM_001080401
2.60	2.93	0.32	1.23E-01	4.82E-01	HYDIN /// HYDIN2 /// LOC100133820	hydrocephalus inducing homolog (mouse) /// hydrocephalus inducing homolog 2 (mouse) /// hypothetical protein LOC100133820	chr16q22.1-q22.3 /// chr1q21.1	232984_at	NM_017558 /// NM_032821 /// XM_001717308 /// XM_001717859
3.37	3.65	0.28	1.23E-01	4.82E-01	SP140L	SP140 nuclear body protein-like	chr2q37.1	223934_at	NM_138402
3.18	3.44	0.26	1.23E-01	4.82E-01	---	---	---	1563344_at	---
3.72	3.97	0.24	1.23E-01	4.82E-01	---	---	---	1556985_at	---
4.75	5.11	0.37	1.23E-01	4.82E-01	LOC730098	similar to chemokine (C-C motif) ligand 27	chr9p13.3	230327_at	XR_041278 /// XR_041279 /// XR_041280
3.11	3.32	0.21	1.23E-01	4.82E-01	---	---	---	217180_at	---
2.20	2.48	0.28	1.23E-01	4.82E-01	RNF8	ring finger protein 8	chr6p21.3	203161_s_at	NM_003958 /// NM_183078
3.67	3.93	0.26	1.23E-01	4.82E-01	---	---	---	243186_at	---
2.87	3.45	0.58	1.23E-01	4.83E-01	FAIM2	Fas apoptotic inhibitory molecule 2	chr12q13	203619_s_at	NM_012306

2.47	2.72	0.25	1.23E-01	4.83E-01	GRIP1	glutamate receptor interacting protein 1	chr12q14.3	214018_at	NM_021150
2.09	2.28	0.19	1.23E-01	4.83E-01	KRTAP4-4	keratin associated protein 4-4	chr17q12-q21	234684_s_at	NM_032524
3.92	4.81	0.89	1.24E-01	4.83E-01	MYO1B	myosin IB	chr2q12-q34	212365_at	NM_001130158 /// NM_012223
5.45	5.79	0.34	1.24E-01	4.83E-01	SCAF1	SR-related CTD-associated factor 1	chr19q13.3-q13.4	225500_x_at	NM_021228
3.28	3.55	0.26	1.24E-01	4.83E-01	OR10D3P	olfactory receptor, family 10, subfamily D, member 3 pseudogene	chr11q24.2	1567253_at	---
2.52	2.70	0.19	1.24E-01	4.83E-01	CASC2	cancer susceptibility candidate 2	chr10q26.11	1562336_at	XR_041332 /// XR_041333 /// XR_041334
3.31	3.59	0.28	1.24E-01	4.83E-01	C17orf53	chromosome 17 open reading frame 53	chr17q21.31	219879_s_at	NM_024032
2.76	3.07	0.31	1.24E-01	4.83E-01	DMXL2	Dmx-like 2	chr15q21.2	215761_at	NM_015263
3.02	3.24	0.23	1.24E-01	4.83E-01	---	---	---	239972_at	---
6.70	7.28	0.58	1.24E-01	4.84E-01	RNF13	ring finger protein 13	chr3q25.1	201780_s_at	NM_007282 /// NM_183381 /// NM_183383 /// NM_183384
2.88	3.10	0.22	1.24E-01	4.84E-01	A4GNT	alpha-1,4-N-acetylglucosaminyltransferase	chr3p14.3	221131_at	NM_016161
6.52	7.97	1.45	1.24E-01	4.84E-01	COL1A1	collagen, type I, alpha 1	chr17q21.33	202310_s_at	NM_000088
7.20	7.96	0.76	1.24E-01	4.84E-01	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	chr2q14.1	208895_s_at	NM_006773
5.49	6.20	0.71	1.24E-01	4.84E-01	FAM171B	family with sequence similarity 171, member B	chr2q32.1	227370_at	NM_177454
5.43	5.91	0.48	1.24E-01	4.84E-01	FBXO28	F-box protein 28	chr1q42.11	202271_at	NM_015176
2.60	3.04	0.44	1.24E-01	4.84E-01	---	---	---	1569311_at	---
8.85	9.20	0.35	1.24E-01	4.84E-01	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	chr11q23.1-q23.2	218194_at	NM_015523
4.84	5.20	0.35	1.24E-01	4.84E-01	CSNK2A1 /// CSNK2A1P	casein kinase 2, alpha 1 polypeptide /// casein kinase 2, alpha 1 polypeptide pseudogene	chr11p15.3 /// chr20p13	212073_at	NM_001895 /// NM_177559 /// NM_177560 /// NR_002207
6.50	6.81	0.31	1.24E-01	4.84E-01	METRN	meteorin, glial cell differentiation regulator	chr16p13.3	219051_x_at	NM_024042
3.86	4.16	0.30	1.24E-01	4.84E-01	MPP2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	chr17q12-q21	213270_at	NM_005374
2.60	2.90	0.29	1.24E-01	4.84E-01	AGXT	alanine-glyoxylate aminotransferase	chr2q36-q37	210326_at	NM_000030
4.39	4.66	0.27	1.24E-01	4.84E-01	LOC157627	hypothetical LOC157627	chr8p23.1	1556046_a_at	---
4.59	4.83	0.25	1.24E-01	4.84E-01	---	---	---	240305_at	---
2.53	2.78	0.24	1.24E-01	4.84E-01	FMN1	formin 1	chr15q13.3	1563559_at	NM_001103184
3.91	4.16	0.24	1.24E-01	4.84E-01	PARC	p53-associated parkin-like cytoplasmic protein	chr6p21.1	236392_at	NM_015089
2.50	2.74	0.23	1.24E-01	4.84E-01	---	---	---	236868_at	---
5.90	6.13	0.22	1.24E-01	4.84E-01	---	---	---	215628_x_at	---
5.40	5.61	0.22	1.24E-01	4.84E-01	---	---	---	240813_at	---
4.14	4.44	0.30	1.24E-01	4.84E-01	---	---	---	224087_at	---
2.53	2.78	0.25	1.24E-01	4.84E-01	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	1557737_s_at	NM_005385
5.01	5.64	0.62	1.24E-01	4.84E-01	MCAM	melanoma cell adhesion molecule	chr11q23.3	209087_x_at	NM_006500
3.23	3.70	0.47	1.24E-01	4.84E-01	RPL39L	ribosomal protein L39-like	chr3q27	210115_at	NM_052969
3.28	3.74	0.46	1.24E-01	4.84E-01	IKIP	IKK interacting protein	chr12q23.1	227295_at	NM_153687 /// NM_201612 /// NM_201613
2.12	2.34	0.23	1.24E-01	4.84E-01	ARL17 /// ARL17P1	ADP-ribosylation factor-like 17 /// ADP-ribosylation factor-like 17 pseudogene 1	chr17q21.31 /// chr17q21.32	210435_at	NM_001039083 /// NM_001103154 /// NM_001113738 /// NM_016632
3.05	3.31	0.25	1.24E-01	4.84E-01	DOK6	docking protein 6	chr18q22.2	236290_at	NM_152721
3.24	3.50	0.25	1.24E-01	4.84E-01	ODF4	outer dense fiber of sperm tails 4	chr17p13.1	1552409_a_at	NM_153007
2.63	3.09	0.46	1.24E-01	4.84E-01	IL33	interleukin 33	chr9p24.1	209821_at	NM_033439
2.49	2.69	0.20	1.24E-01	4.84E-01	CEP110	centrosomal protein 110kDa	chr9q33-q34	242916_at	NM_007018
1.74	1.90	0.16	1.24E-01	4.84E-01	---	---	---	1560721_at	---
2.96	3.19	0.23	1.24E-01	4.84E-01	---	---	---	240638_at	---
4.52	5.41	0.89	1.24E-01	4.84E-01	UBA6	ubiquitin-like modifier activating enzyme 6	chr4q13.2	222600_s_at	NM_018227
4.93	5.62	0.69	1.24E-01	4.84E-01	DENND4A	DENN/MADD domain containing 4A	chr15q22.31	1554352_s_at	NM_005848
8.26	8.93	0.67	1.24E-01	4.84E-01	LOC100132235 /// PNRC2	hypothetical protein LOC100132235 /// proline-rich nuclear receptor coactivator 2	chr1p36.11	217779_s_at	NM_017761 /// XM_001713881
5.59	6.03	0.44	1.24E-01	4.84E-01	ZNF182	zinc finger protein 182	chrXp22.11-p11.23	244024_at	NM_001007088 /// NM_006962
2.64	2.98	0.34	1.24E-01	4.84E-01	MED17	mediator complex subunit 17	chr11q14	232483_at	NM_004268
3.28	3.60	0.32	1.24E-01	4.84E-01	DGCR14	DiGeorge syndrome critical region gene 14	chr22q11.21|22q11.2	216285_at	NM_022719
1.78	2.00	0.22	1.24E-01	4.84E-01	---	---	---	238384_x_at	---
2.12	2.34	0.22	1.24E-01	4.84E-01	---	---	---	1566043_at	---
4.84	5.86	1.01	1.25E-01	4.84E-01	ACAT2	acetyl-Coenzyme A acetyltransferase 2	chr6q25.3	209608_s_at	NM_005891
2.85	3.10	0.24	1.25E-01	4.84E-01	ZP4	zona pellucida glycoprotein 4	chr1q43	231756_at	NM_021186
1.99	2.20	0.22	1.24E-01	4.84E-01	---	---	---	1560257_at	---
2.42	2.69	0.27	1.25E-01	4.85E-01	LOC440863	hypothetical gene supported by AK026773	chr2p16.3	234478_at	---
2.25	2.51	0.26	1.25E-01	4.85E-01	---	---	---	235922_at	---

2.14	2.44	0.30	1.25E-01	4.85E-01	---	---	---	235183_at	---
2.72	2.96	0.24	1.25E-01	4.85E-01	MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	chr17q21.31	206186_at	NM_001932 /// NR_003562
5.56	6.09	0.53	1.25E-01	4.85E-01	SON	SON DNA binding protein	chr21q22.1-q22.2|21q22.11	201085_s_at	NM_032195 /// NM_138927
5.00	5.43	0.43	1.25E-01	4.85E-01	PEX6	peroxisomal biogenesis factor 6	chr6p21.1	204545_at	NM_000287
3.27	3.57	0.30	1.25E-01	4.85E-01	LOC442421 /// LOC728683	hypothetical LOC442421 /// similar to LOC442421 protein	chr9q12	217158_at	XM_001128151 /// XM_001732880 /// XM_001732881 /// XR_015311
2.93	3.17	0.24	1.25E-01	4.85E-01	C10orf72	Chromosome 10 open reading frame 72	chr10q11.22	230103_at	NM_001031746 /// NM_144984
2.44	2.66	0.22	1.25E-01	4.85E-01	SPIN2A	spindlin family, member 2A	chrXp11.1	207841_at	NM_019003
3.26	3.46	0.19	1.25E-01	4.85E-01	GGTLC1	gamma-glutamyltransferase light chain 1	chr20p11.1	211416_x_at	NM_080920 /// NM_178311 /// NM_178312
6.08	6.60	0.53	1.25E-01	4.85E-01	UTP23	UTP23, small subunit (SSU) processome component, homolog (yeast)	chr8q24.11	227402_s_at	NM_032334
3.82	4.02	0.20	1.25E-01	4.85E-01	C3orf27	chromosome 3 open reading frame 27	chr3q21	208440_at	NM_007354
5.05	5.39	0.34	1.25E-01	4.85E-01	---	---	---	1557814_a_at	---
2.46	2.69	0.22	1.25E-01	4.85E-01	LOC439990	hypothetical gene supported by BC009626; BC048265	chr10q22.3	1569322_at	---
4.91	5.12	0.21	1.25E-01	4.85E-01	---	---	---	1570362_at	---
2.66	2.91	0.25	1.25E-01	4.85E-01	C14orf106	Chromosome 14 open reading frame 106	chr14q21.3	241816_at	NM_018353
2.09	2.30	0.21	1.25E-01	4.85E-01	LOC285419	hypothetical protein LOC285419	chr4q28.1	1561096_at	---
2.04	2.25	0.21	1.25E-01	4.85E-01	---	---	---	1564358_at	---
2.79	3.14	0.34	1.25E-01	4.86E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	243843_at	NM_001079691 /// NM_052818
5.69	5.98	0.29	1.25E-01	4.86E-01	---	---	---	224346_at	---
8.43	8.81	0.38	1.25E-01	4.86E-01	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	chr19q13.1	204570_at	NM_001864
11.56	11.88	0.33	1.25E-01	4.86E-01	DHCR24	24-dehydrocholesterol reductase	chr1p33-p31.1	200862_at	NM_014762
2.13	2.36	0.23	1.25E-01	4.86E-01	LHFPL1	lipoma HMGIC fusion partner-like 1	chrXq23	236048_at	NM_178175
1.80	1.98	0.17	1.25E-01	4.86E-01	---	---	---	1568660_a_at	---
4.40	4.99	0.59	1.25E-01	4.86E-01	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	chr19q13.2	232079_s_at	NM_001042724 /// NM_002856
3.62	3.93	0.31	1.25E-01	4.86E-01	VPS29	vacuolar protein sorting 29 homolog (S. cerevisiae)	chr12q24	1554388_at	NM_016226 /// NM_057180
3.63	3.89	0.25	1.25E-01	4.86E-01	SYT9	synaptotagmin IX	chr11p15.4	232445_at	NM_175733
5.91	6.51	0.60	1.25E-01	4.86E-01	SSR1	signal sequence receptor, alpha	chr6p24.3	200889_s_at	NM_003144
4.07	4.31	0.24	1.25E-01	4.86E-01	---	---	---	243891_at	---
2.96	3.22	0.26	1.25E-01	4.86E-01	KIR2DS3	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 3	chr19q13.4	208122_x_at	NM_012313
3.37	3.63	0.25	1.25E-01	4.86E-01	TMEM165	Transmembrane protein 165	chr4q12	226827_at	NM_018475
5.02	5.93	0.91	1.25E-01	4.86E-01	CLCN3	chloride channel 3	chr4q33	201732_s_at	NM_001829 /// NM_173872
3.08	3.40	0.33	1.25E-01	4.86E-01	---	---	---	237136_at	---
3.66	4.05	0.39	1.25E-01	4.86E-01	---	---	---	230171_at	---
1.99	2.22	0.23	1.25E-01	4.86E-01	PCDH20	protocadherin 20	chr13q21	232054_at	NM_022843
5.77	6.03	0.26	1.26E-01	4.86E-01	PARP10	Poly (ADP-ribose) polymerase family, member 10	chr8q24.3	228669_x_at	NM_032789
2.98	3.31	0.33	1.26E-01	4.86E-01	---	---	---	231459_at	---
2.68	2.97	0.30	1.26E-01	4.86E-01	---	---	---	243482_at	---

2.47	2.71	0.24	1.26E-01	4.86E-01	NR1I3	nuclear receptor subfamily 1, group I, member 3	chr1q23.3	207007_at	NM_001077469 /// NM_001077470 /// NM_001077471 /// NM_001077472 /// NM_001077473 /// NM_001077474 /// NM_001077475 /// NM_001077476 /// NM_001077477 /// NM_001077478 /// NM_001077479 /// NM_001077480 /// NM_001077481 /// NM_001077482 /// NM_005122
4.55	4.90	0.35	1.26E-01	4.86E-01	---	---	---	241154_x_at	---
2.95	3.15	0.20	1.26E-01	4.87E-01	C10orf68	chromosome 10 open reading frame 68	chr10p11.22	220749_at	NM_024688
3.09	3.44	0.35	1.26E-01	4.87E-01	---	---	---	232906_at	---
3.49	3.80	0.31	1.26E-01	4.87E-01	DCHS1	dachsous 1 (Drosophila)	chr11p15.4	218892_at	NM_003737
3.05	3.26	0.21	1.26E-01	4.87E-01	KCNQ1OT1	KCNQ1 overlapping transcript 1 (non-protein coding)	chr11p15	244727_at	NR_002728
3.03	3.21	0.19	1.26E-01	4.87E-01	CAMP	cathelicidin antimicrobial peptide	chr3p21.3	210244_at	NM_004345
2.68	3.08	0.40	1.26E-01	4.87E-01	ARHGEF4	Rho guanine nucleotide exchange factor (GEF) 4	chr2q22	205109_s_at	NM_015320 /// NM_032995
5.07	5.40	0.33	1.26E-01	4.87E-01	IFT88	intraflagellar transport 88 homolog (Chlamydomonas)	chr13q12.1	204703_at	NM_006531 /// NM_175605
6.24	6.51	0.28	1.26E-01	4.87E-01	CRKRS	Cdc2-related kinase, arginine/serine-rich	chr17q12	225697_at	NM_015083 /// NM_016507
2.63	2.90	0.27	1.26E-01	4.87E-01	LOC731109	similar to ring finger protein 187	---	228470_at	XM_001131982 /// XM_001722245
2.46	2.69	0.23	1.26E-01	4.87E-01	---	---	---	239885_at	---
7.12	7.86	0.75	1.26E-01	4.87E-01	KPNB1	karyopherin (importin) beta 1	chr17q21.32	208974_x_at	NM_002265
5.43	6.00	0.57	1.26E-01	4.87E-01	ZNF302	zinc finger protein 302	chr19q13.11	218490_s_at	NM_001012320 /// NM_018443
2.01	2.26	0.25	1.26E-01	4.87E-01	---	---	---	1570031_at	---
2.41	2.62	0.21	1.26E-01	4.87E-01	RBM22	RNA binding motif protein 22	chr5q33.1	236872_at	NM_018047
5.47	6.60	1.13	1.26E-01	4.87E-01	CHURC1	churchill domain containing 1	chr14q23.3	226736_at	NM_145165
5.31	6.22	0.91	1.26E-01	4.87E-01	DKFZP586I1420	hypothetical protein DKFZp586I1420	chr7p15.1	213546_at	NR_002186
5.34	5.99	0.65	1.26E-01	4.87E-01	PSEN1	presenilin 1	chr14q24.3	207782_s_at	NM_000021 /// NM_007318
7.41	7.93	0.52	1.26E-01	4.87E-01	ZCRB1	zinc finger CCHC-type and RNA binding motif 1	chr12q12	225394_s_at	NM_033114
2.93	3.32	0.39	1.26E-01	4.87E-01	DOK5	docking protein 5	chr20q13.2	1554863_s_at	NM_018431
3.99	4.32	0.33	1.26E-01	4.87E-01	IL12RB1	interleukin 12 receptor, beta 1	chr19p13.1	239522_at	NM_005535 /// NM_153701
2.64	2.97	0.32	1.26E-01	4.87E-01	CABP1	calcium binding protein 1	chr12q24.31	210181_s_at	NM_001033677 /// NM_004276 /// NM_031205
3.93	4.18	0.25	1.26E-01	4.87E-01	---	---	---	227906_s_at	---
3.12	3.37	0.25	1.26E-01	4.87E-01	PARK2	Parkinson disease (autosomal recessive, juvenile) 2, parkin	chr6q25.2-q27	207058_s_at	NM_004562 /// NM_013987 /// NM_013988
2.10	2.33	0.23	1.26E-01	4.87E-01	---	---	---	244047_at	---
2.24	2.46	0.22	1.26E-01	4.87E-01	IGHMBP2	immunoglobulin mu binding protein 2	chr11q13.3	243746_at	NM_002180
2.26	2.48	0.22	1.26E-01	4.87E-01	ABCC11	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	chr16q12.1	224146_s_at	NM_032583 /// NM_033151 /// NM_145186
2.42	2.63	0.21	1.26E-01	4.87E-01	---	---	---	240047_at	---
1.92	2.11	0.18	1.26E-01	4.87E-01	LOC158381	ATPase, Class I, type 8B family pseudogene	chr9p13.3	1568687_s_at	NR_003581 /// NR_003582

6.35	7.40	1.04	1.26E-01	4.87E-01	ADD3	adducin 3 (gamma)	chr10q24.2-q24.3	205882_x_at	NM_001121 /// NM_016824 /// NM_019903
4.98	5.63	0.64	1.26E-01	4.87E-01	ZNF136	zinc finger protein 136	chr19p13.2-p13.12	206240_s_at	NM_003437
2.27	2.88	0.61	1.26E-01	4.87E-01	DUOX1	dual oxidase 1	chr15q15.3	215800_at	NM_017434 /// NM_175940
8.20	8.75	0.54	1.26E-01	4.87E-01	---	---	---	225239_at	---
4.31	4.59	0.29	1.26E-01	4.87E-01	TRAF3	TNF receptor-associated factor 3	chr14q32.32	208315_x_at	NM_003300 /// NM_145725 /// NM_145726
2.53	2.81	0.27	1.26E-01	4.87E-01	---	---	---	239425_at	---
2.64	2.91	0.27	1.26E-01	4.87E-01	LOC100128126	hypothetical protein LOC100128126	chr8q21.11	1561391_at	XM_001721269 /// XM_001721290 /// XM_001721327
2.05	2.31	0.26	1.26E-01	4.87E-01	---	---	---	1557174_a_at	---
2.51	2.77	0.26	1.26E-01	4.87E-01	GPR55	G protein-coupled receptor 55	chr2q37	231745_at	NM_005683
2.12	2.36	0.24	1.26E-01	4.87E-01	---	---	---	233020_at	---
3.74	3.97	0.23	1.26E-01	4.87E-01	ST18	Suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	chr8q11.23	1570307_s_at	NM_014682
3.81	4.04	0.23	1.26E-01	4.87E-01	---	---	---	234423_x_at	---
2.56	2.78	0.23	1.26E-01	4.87E-01	---	---	---	237935_at	---
7.03	7.72	0.69	1.26E-01	4.87E-01	RUNDC3B	RUN domain containing 3B	chr7q21.12	215321_at	NM_001134405 /// NM_001134406 /// NM_138290
4.30	4.55	0.25	1.26E-01	4.87E-01	FLJ32224	hypothetical gene supported by AK056786	chr1p34.2	1558832_at	---
4.26	4.86	0.60	1.26E-01	4.87E-01	BNC2	basonuclin 2	chr9p22.3-p22.2	220272_at	NM_017637
3.41	3.66	0.25	1.26E-01	4.87E-01	---	---	---	230834_at	---
7.64	8.34	0.70	1.26E-01	4.87E-01	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	chr16q12	217727_x_at	NM_018206
4.06	4.40	0.34	1.26E-01	4.87E-01	PCM1	pericentriolar material 1	chr8p22-p21.3	209997_x_at	NM_006197
2.14	2.42	0.28	1.26E-01	4.87E-01	FAM134B	family with sequence similarity 134, member B	chr5p15.1	218532_s_at	NM_001034850 /// NM_019000
2.73	2.96	0.23	1.26E-01	4.87E-01	---	---	---	241203_at	---
2.15	2.46	0.31	1.27E-01	4.87E-01	---	---	---	239371_at	---
2.68	2.94	0.26	1.27E-01	4.87E-01	HIST1H1T	histone cluster 1, H1t	chr6p21.3	207982_at	NM_005323
2.80	3.12	0.32	1.27E-01	4.88E-01	FOXA3	forkhead box A3	chr19q13.2-q13.4	228463_at	NM_004497
3.69	4.12	0.43	1.27E-01	4.88E-01	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	chr11p12-p11.12	235734_at	NM_016223
3.71	4.43	0.72	1.27E-01	4.88E-01	CD2	CD2 molecule	chr1p13	205831_at	NM_001767
3.04	3.66	0.61	1.27E-01	4.88E-01	---	---	---	243736_at	---
2.76	3.21	0.46	1.27E-01	4.88E-01	---	---	---	228507_at	---
3.54	3.99	0.45	1.27E-01	4.88E-01	ATPAF2	ATP synthase mitochondrial F1 complex assembly factor 2	chr17p11.2	214330_at	NM_145691
4.51	4.87	0.36	1.27E-01	4.88E-01	IBSP	integrin-binding sialoprotein	chr4q21-q25	207370_at	NM_004967
2.77	3.10	0.33	1.27E-01	4.88E-01	---	---	---	240264_at	---
3.41	3.74	0.32	1.27E-01	4.88E-01	HM13	histocompatibility (minor) 13	chr20q11.21	1558561_at	NM_030789 /// NM_178580 /// NM_178581 /// NM_178582
2.11	2.40	0.29	1.27E-01	4.88E-01	MET	met proto-oncogene (hepatocyte growth factor receptor)	chr7q31	213816_s_at	NM_000245 /// NM_001127500
2.18	2.43	0.25	1.27E-01	4.88E-01	UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A9	chr2q37	232655_at	NM_000463
2.51	2.74	0.23	1.27E-01	4.88E-01	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	chr18q11.2	235645_at	NM_052911
3.24	3.46	0.22	1.27E-01	4.88E-01	CRLS1	Cardiolipin synthase 1	chr20p13-p12.3	226937_at	NM_001127458 /// NM_019095
4.33	4.52	0.19	1.27E-01	4.88E-01	GJB1	gap junction protein, beta 1, 32kDa	chrXq13.1	204973_at	NM_000166 /// NM_001097642
3.14	3.39	0.25	1.27E-01	4.88E-01	---	---	---	233416_at	---
2.40	2.63	0.23	1.27E-01	4.88E-01	DIAPH2	diaphanous homolog 2 (Drosophila)	chrXq21.33	217246_s_at	NM_006729 /// NM_007309
2.01	2.23	0.22	1.27E-01	4.88E-01	---	---	---	241051_at	---
3.22	3.69	0.47	1.27E-01	4.88E-01	---	---	---	229261_at	---
5.04	5.37	0.33	1.27E-01	4.88E-01	CDH23	cadherin-like 23	chr10q21-q22	232845_at	NM_022124 /// NM_052836
4.24	4.68	0.44	1.27E-01	4.88E-01	MYO5A	myosin VA (heavy chain 12, myoxin)	chr15q21	204527_at	NM_000259
2.61	2.86	0.25	1.27E-01	4.88E-01	PDZD2	PDZ domain containing 2	chr5p13.3	233026_s_at	NM_178140
2.63	2.85	0.22	1.27E-01	4.88E-01	---	---	---	239612_at	---

3.74	4.06	0.32	1.27E-01	4.88E-01	CPLX2	complexin 2	chr5q35.2	225815_at	NM_001008220 /// NM_006650
6.44	6.73	0.29	1.27E-01	4.88E-01	---	---	---	214002_at	---
1.95	2.17	0.22	1.27E-01	4.88E-01	---	---	---	240622_at	---
3.57	3.94	0.37	1.27E-01	4.88E-01	---	---	---	239865_at	---
4.06	4.68	0.61	1.27E-01	4.88E-01	CDC27	cell division cycle 27 homolog (S. cerevisiae)	chr17q12-q23.2	217879_at	NM_001114091 /// NM_001256
3.12	3.29	0.18	1.27E-01	4.88E-01	FLJ11827	hypothetical protein FLJ11827	chr3q23	220912_at	XR_040865 /// XR_040866 /// XR_040867
2.30	2.49	0.18	1.27E-01	4.88E-01	NALCN	sodium leak channel, non-selective	chr13q32.3	242880_at	NM_052867
3.46	3.75	0.29	1.27E-01	4.88E-01	MKL1	megakaryoblastic leukemia (translocation) 1	chr22q13	215291_at	NM_020831
8.24	8.86	0.63	1.27E-01	4.89E-01	KPNB1	karyopherin (importin) beta 1	chr17q21.32	213507_s_at	NM_002265
4.06	4.48	0.42	1.27E-01	4.89E-01	NUP210	nucleoporin 210kDa	chr3p25.1	220035_at	NM_024923
2.57	2.85	0.29	1.27E-01	4.89E-01	---	---	---	232595_at	---
2.60	2.85	0.25	1.27E-01	4.89E-01	---	---	---	230451_at	---
2.32	2.53	0.21	1.27E-01	4.89E-01	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	chr19p13.2	211591_s_at	NM_001111307 /// NM_001111308 /// NM_001111309 /// NM_006202
2.54	2.73	0.19	1.27E-01	4.89E-01	---	---	---	1559347_at	---
5.43	5.70	0.27	1.27E-01	4.89E-01	PTPRA	Protein tyrosine phosphatase, receptor type, A	chr20p13	233776_at	NM_002836 /// NM_080840 /// NM_080841
4.01	4.77	0.76	1.28E-01	4.89E-01	CLEC10A	C-type lectin domain family 10, member A	chr17p13.1	206682_at	NM_006344 /// NM_182906
3.44	4.12	0.67	1.28E-01	4.89E-01	BBS12	Bardet-Biedl syndrome 12	chr4q27	229603_at	NM_152618
4.12	4.43	0.32	1.28E-01	4.89E-01	C1orf68	chromosome 1 open reading frame 68	chr1q21.3	216701_at	NM_001024679 /// XM_001721554 /// XM_001724444 /// XM_001724465
2.84	3.12	0.27	1.27E-01	4.89E-01	MATR3	Matrin 3	chr5q31.2	238993_at	NM_018834 /// NM_199189
2.51	2.77	0.27	1.28E-01	4.89E-01	NAV2	neuron navigator 2	chr11p15.1	1556606_at	NM_001111018 /// NM_001111019 /// NM_145117 /// NM_182964
2.35	2.57	0.22	1.28E-01	4.89E-01	PPP3CC	Protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	chr8p21.3	213950_s_at	NM_005605
1.97	2.12	0.15	1.28E-01	4.89E-01	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	chr5p13.2	238336_s_at	NM_001012339 /// NM_194283
4.24	4.84	0.61	1.28E-01	4.89E-01	GLT8D2	glycosyltransferase 8 domain containing 2	chr12q	227070_at	NM_031302
2.87	3.20	0.32	1.28E-01	4.89E-01	---	---	---	220855_at	---
3.08	3.32	0.24	1.28E-01	4.89E-01	BLK	B lymphoid tyrosine kinase	chr8p23-p22	206255_at	NM_001715
3.10	3.27	0.17	1.28E-01	4.89E-01	MAP6	microtubule-associated protein 6	chr11q13.5	241980_at	NM_033063 /// NM_207577
2.42	2.82	0.41	1.28E-01	4.89E-01	SUSD4	sushi domain containing 4	chr1q41	223822_at	NM_001037175 /// NM_017982
2.57	2.83	0.26	1.28E-01	4.89E-01	---	---	---	244368_x_at	---
4.10	5.00	0.91	1.28E-01	4.89E-01	SKAP1	src kinase associated phosphoprotein 1	chr17q21.32	205790_at	NM_001075099 /// NM_003726
2.83	3.03	0.20	1.28E-01	4.89E-01	LOC652147	similar to U5 snRNP-specific protein, 200 kDa	---	217114_at	XM_941485
2.54	3.27	0.73	1.28E-01	4.89E-01	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	chr1q23	211734_s_at	NM_002001
2.42	2.76	0.34	1.28E-01	4.89E-01	LOC730125	Hypothetical LOC730125	chr14q32.2	232111_at	XM_001133650 /// XM_001134301 /// XM_001724190
2.14	2.45	0.31	1.28E-01	4.89E-01	---	---	---	234508_at	---
3.13	3.43	0.30	1.28E-01	4.89E-01	ALMS1	Alstrom syndrome 1	chr2p13	214221_at	NM_015120
6.47	6.76	0.29	1.28E-01	4.89E-01	FBXW5	F-box and WD repeat domain containing 5	chr9q34.3	223050_s_at	NM_018998
5.36	5.64	0.28	1.28E-01	4.89E-01	C17orf56	chromosome 17 open reading frame 56	chr17q25.3	236737_at	NM_144679
3.89	4.16	0.27	1.28E-01	4.89E-01	---	---	---	1556584_at	---

2.55	2.81	0.26	1.28E-01	4.89E-01	---	---	---	1568905_at	---
3.75	4.01	0.26	1.28E-01	4.89E-01	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	chr17q21.32	204626_s_at	NM_000212
2.18	2.44	0.26	1.28E-01	4.89E-01	CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22	chr1p33	217319_x_at	NM_001010969
3.09	3.46	0.37	1.28E-01	4.89E-01	LOC390561 /// LOC730909	similar to hect domain and RLD 2 /// similar to hect domain and RLD 2	chr15q13.2	216830_at	XM_001127692 /// XM_001716926 /// XM_001716930 /// XM_001718721 /// XM_001726958 /// XM_001726963
5.45	6.46	1.01	1.28E-01	4.89E-01	IGKC	immunoglobulin kappa constant	chr2p12	214836_x_at	---
2.72	3.20	0.48	1.28E-01	4.89E-01	---	---	---	242699_at	---
2.30	2.53	0.23	1.28E-01	4.89E-01	PHKB	phosphorylase kinase, beta	chr16q12-q13	242248_at	NM_000293 /// NM_001031835
3.39	3.58	0.19	1.28E-01	4.89E-01	LYZL4	lysozyme-like 4	chr3p22.1	231306_at	NM_144634
2.15	2.32	0.17	1.28E-01	4.89E-01	---	---	---	237114_at	---
5.86	6.89	1.03	1.28E-01	4.89E-01	---	---	---	227082_at	---
4.53	5.36	0.83	1.28E-01	4.89E-01	MAP3K2	mitogen-activated protein kinase kinase kinase 2	chr2q14.3	221695_s_at	NM_006609
9.42	10.12	0.70	1.28E-01	4.89E-01	NCOA4	nuclear receptor coactivator 4	chr10q11.2	210774_s_at	NM_005437
3.91	4.57	0.66	1.28E-01	4.89E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	217227_x_at	---
4.84	5.45	0.60	1.28E-01	4.89E-01	SFRS12IP1	SFRS12-interacting protein 1	chr5q12.3	217608_at	NM_173829
5.35	5.89	0.54	1.28E-01	4.89E-01	PLAA	phospholipase A2-activating protein	chr9p21	209533_s_at	NM_001031689 /// NM_004253
4.46	4.87	0.41	1.28E-01	4.89E-01	PAK7	p21 protein (Cdc42/Rac)-activated kinase 7	chr20p12	213990_s_at	NM_020341 /// NM_177990
9.20	9.60	0.40	1.28E-01	4.89E-01	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	chr2q36.1	208679_s_at	NM_005731 /// NM_152862
4.69	5.03	0.34	1.28E-01	4.89E-01	---	---	---	216729_at	---
3.38	3.70	0.33	1.28E-01	4.89E-01	KIAA1632	KIAA1632	chr18q12.3-q21.1	1563471_at	NM_020964
2.46	2.78	0.32	1.28E-01	4.89E-01	---	---	---	239262_at	---
1.97	2.26	0.30	1.28E-01	4.89E-01	TRIO	Triple functional domain (PTPRF interacting)	chr5p15.2	216697_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929
2.80	3.07	0.27	1.28E-01	4.89E-01	MYLK	myosin light chain kinase	chr3q21	1563466_at	NM_053025 /// NM_053026 /// NM_053027 /// NM_053028 /// NM_053031 /// NM_053032
4.61	4.88	0.27	1.28E-01	4.89E-01	HES7	hairy and enhancer of split 7 (Drosophila)	chr17p13.1	224548_at	NM_032580
4.46	4.73	0.27	1.28E-01	4.89E-01	POLR2D	Polymerase (RNA) II (DNA directed) polypeptide D	chr2q21	214144_at	NM_004805
4.27	4.54	0.26	1.28E-01	4.89E-01	---	---	---	242485_at	---
2.86	3.10	0.24	1.28E-01	4.89E-01	---	---	---	1556383_at	---
2.15	2.38	0.23	1.28E-01	4.89E-01	TSSK1A /// TSSK1B	testis-specific serine kinase 1A pseudogene /// testis-specific serine kinase 1B	chr22q11.21 /// chr5q22.2	211694_at	NM_032028
2.92	3.15	0.23	1.28E-01	4.89E-01	---	---	---	236490_at	---
2.52	2.74	0.22	1.28E-01	4.89E-01	KLK5	kallikrein-related peptidase 5	chr19q13.3-q13.4	222242_s_at	NM_001077491 /// NM_001077492 /// NM_012427
2.38	2.56	0.18	1.28E-01	4.89E-01	---	---	---	240136_at	---
4.36	4.97	0.61	1.28E-01	4.89E-01	FAM102B	family with sequence similarity 102, member B	chr1p13.3	226568_at	NM_001010883
3.91	4.46	0.55	1.28E-01	4.89E-01	---	---	---	244456_at	---
5.92	6.32	0.40	1.28E-01	4.89E-01	LOC100134190 /// LRP1	similar to low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) /// low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	chr12q13-q14	200784_s_at	NM_002332 /// XR_037669

3.69	4.06	0.37	1.28E-01	4.89E-01	TOM1L1	target of myb1 (chicken)-like 1	chr17q23.2	240261_at	NM_005486 /// XM_001723684 /// XM_001725529 /// XM_001726674																				
2.68	2.96	0.28	1.28E-01	4.89E-01	CFC1 /// CFC1B	cripto, FRL-1, cryptic family 1 /// cripto, FRL-1, cryptic family 1B	chr2q21.1	223753_s_at	NM_001079530 /// NM_032545																				
10.43	10.71	0.27	1.28E-01	4.89E-01	SKP1	S-phase kinase-associated protein 1	chr5q31	200718_s_at	NM_006930 /// NM_170679																				
2.51	2.77	0.26	1.28E-01	4.89E-01	ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	chr7p14	226690_at	NM_001118																				
4.78	5.10	0.32	1.28E-01	4.89E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	205039_s_at	NM_006060																				
2.18	2.43	0.24	1.28E-01	4.89E-01	OLIG2	oligodendrocyte lineage transcription factor 2	chr21q22.11	213825_at	NM_005806																				
5.81	6.84	1.03	1.28E-01	4.89E-01	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	chr3q23-q24	202619_s_at	NM_000935 /// NM_182943																				
3.76	4.35	0.59	1.28E-01	4.89E-01	NFYB	nuclear transcription factor Y, beta	chr12q22-q23	218129_s_at	NM_006166																				
1.72	1.89	0.17	1.28E-01	4.89E-01	CLEC7A	C-type lectin domain family 7, member A	chr12p13.2	241098_at	NM_022570 /// NM_197947 /// NM_197948 /// NM_197949 /// NM_197950 /// NM_197954																				
3.60	3.83	0.23	1.29E-01	4.90E-01	---	---	---	216043_x_at	---																				
3.51	3.74	0.23	1.29E-01	4.90E-01	NOS2A	nitric oxide synthase 2A (inducible, hepatocytes)	chr17q11.2-q12	210037_s_at	NM_000625																				
2.29	2.51	0.22	1.29E-01	4.90E-01	FPR1	formyl peptide receptor 1	chr19q13.4	205118_at	NM_002029																				
3.66	3.87	0.21	1.29E-01	4.90E-01	KLK4	kallikrein-related peptidase 4	chr19q13.41	233854_x_at	NM_004917																				
7.16	7.95	0.79	1.29E-01	4.90E-01	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	chr12q13.13	226085_at	NM_001127321 /// NM_001127322 /// NM_012117																				
2.03	2.24	0.21	1.29E-01	4.90E-01	CRYBA1	crystallin, beta A1	chr17q11.2	206982_at	NM_005208																				
2.04	2.22	0.18	1.29E-01	4.90E-01	CNKSR2	connector enhancer of kinase suppressor of Ras 2	chrXp22.12	206731_at	NM_014927																				
5.59	6.72	1.13	1.29E-01	4.90E-01	INSIG1	insulin induced gene 1	chr7q36	201627_s_at	NM_005542 /// NM_198336 /// NM_198337																				
4.85	5.69	0.83	1.29E-01	4.90E-01	BAG2	BCL2-associated athanogene 2	chr6p12.3-p11.2	209406_at	NM_004282																				
8.10	8.53	0.43	1.29E-01	4.90E-01	NSFL1C	NSFL1 (p97) cofactor (p47)	chr20p13	220248_x_at	NM_016143 /// NM_018839 /// NM_182483																				
4.84	5.10	0.26	1.29E-01	4.90E-01	---	---	---	244491_at	---																				
3.03	3.27	0.24	1.29E-01	4.90E-01	C7orf61	chromosome 7 open reading frame 61	chr7q22.1	229913_at	NM_001004323																				

2.28	2.51	0.24	1.29E-01	4.90E-01	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	chr12p13.3	211592_s_at	NM_000719 /// NM_001129827 /// NM_001129829 /// NM_001129830 /// NM_001129831 /// NM_001129832 /// NM_001129833 /// NM_001129834 /// NM_001129835 /// NM_001129836 /// NM_001129837 /// NM_001129838 /// NM_001129839 /// NM_001129840 /// NM_001129841 /// NM_001129842 /// NM_001129843 /// NM_001129844 /// NM_001129846 /// NM_199460																			
3.48	3.71	0.23	1.29E-01	4.90E-01	PWWP2A	PWWP domain containing 2A	chr5q33.3	228337_at	NM_001130864 /// NM_052927																				
5.15	5.46	0.31	1.29E-01	4.90E-01	CSDA	Cold shock domain protein A	chr12p13.1	213319_s_at	NM_003651																				
2.92	3.18	0.26	1.29E-01	4.90E-01	---	---	---	217311_at	---																				
4.38	4.64	0.26	1.29E-01	4.90E-01	CSNK1G1	casein kinase 1, gamma 1	chr15q22.1-q22.31	220640_at	NM_022048																				
3.10	3.33	0.23	1.29E-01	4.90E-01	---	---	---	231193_s_at	---																				
1.84	2.05	0.21	1.29E-01	4.90E-01	TOR1AIP2	torsin A interacting protein 2	chr1q25.2	235453_at	NM_145034																				
2.11	2.31	0.20	1.29E-01	4.90E-01	---	---	---	230357_at	---																				
4.62	4.94	0.32	1.29E-01	4.90E-01	ZNF174	zinc finger protein 174	chr16p13.3	210291_s_at	NM_001032292 /// NM_003450																				
2.08	2.28	0.20	1.29E-01	4.90E-01	RP4-692D3.1	hypothetical protein LOC728621	chr1p34.2	243036_at	NM_001080850																				
3.15	3.48	0.33	1.29E-01	4.90E-01	---	---	---	236105_at	---																				
5.74	6.42	0.68	1.29E-01	4.90E-01	MRPL13	mitochondrial ribosomal protein L13	chr8q22.1-q22.3	218049_s_at	NM_014078																				
3.21	3.63	0.41	1.29E-01	4.90E-01	---	---	---	235419_at	---																				
5.45	5.76	0.31	1.29E-01	4.90E-01	BAI1	brain-specific angiogenesis inhibitor 1	chr8q24	206083_at	NM_001702																				
3.90	4.21	0.30	1.29E-01	4.90E-01	---	---	---	244212_at	---																				
2.81	3.08	0.27	1.29E-01	4.90E-01	---	---	---	227191_at	---																				
4.81	5.08	0.26	1.29E-01	4.90E-01	---	---	---	213100_at	---																				
1.84	2.02	0.18	1.29E-01	4.90E-01	---	---	---	240750_at	---																				
3.49	3.77	0.28	1.29E-01	4.90E-01	---	---	---	217115_at	---																				
2.47	2.92	0.45	1.29E-01	4.90E-01	CD300LG	CD300 molecule-like family member g	chr17q21.31	1552509_a_at	NM_145273																				
5.50	5.90	0.40	1.29E-01	4.90E-01	LOC153684	hypothetical LOC153684	chr5p12	232645_at	XR_018004 /// XR_040067 /// XR_040068																				
5.89	6.17	0.28	1.29E-01	4.90E-01	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	chr19q12-q13.1	204954_s_at	NM_004714 /// NM_006483 /// NM_006484																				
4.65	4.91	0.26	1.29E-01	4.90E-01	LDB3	LIM domain binding 3	chr10q22.3-q23.2	213717_at	NM_001080114 /// NM_001080115 /// NM_001080116 /// NM_007078																				

4.02	4.28	0.26	1.29E-01	4.90E-01	C1orf222	chromosome 1 open reading frame 222	chr1p36.33	215788_at	NM_001003808
4.47	4.72	0.26	1.29E-01	4.90E-01	DUSP9	dual specificity phosphatase 9	chrXq28	205777_at	NM_001395
2.41	2.65	0.24	1.29E-01	4.90E-01	SIX2	SIX homeobox 2	chr2p16-p15	206511_s_at	NM_016932
2.00	2.22	0.23	1.29E-01	4.90E-01	SPATA9	spermatogenesis associated 9	chr5q15	223841_s_at	NM_031952
1.84	2.01	0.17	1.29E-01	4.90E-01	---	---	---	238264_at	---
3.43	3.64	0.21	1.29E-01	4.90E-01	---	---	---	1558740_s_at	---
2.14	3.68	1.54	1.29E-01	4.90E-01	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	chr4q21	212592_at	NM_144646
1.85	2.07	0.21	1.29E-01	4.91E-01	---	---	---	234228_at	---
2.21	2.40	0.19	1.29E-01	4.91E-01	LIN9	lin-9 homolog (C. elegans)	chr1q42.12	235039_x_at	NM_173083
2.28	2.54	0.26	1.29E-01	4.91E-01	LOC100132686	hypothetical LOC100132686	chr11q23.1	1555180_at	XM_001725713 /// XM_001725819 /// XM_001725878
3.02	3.25	0.23	1.29E-01	4.91E-01	---	---	---	240358_at	---
3.45	3.75	0.30	1.30E-01	4.91E-01	RSPO1	R-spondin homolog (Xenopus laevis)	chr1p34.3	241450_at	NM_001038633
5.10	5.62	0.52	1.30E-01	4.91E-01	---	---	---	235094_at	---
4.89	5.24	0.35	1.30E-01	4.91E-01	SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	chr1p35.3	1554050_at	NM_001009568 /// NM_014474
4.03	4.38	0.34	1.30E-01	4.91E-01	ZNF419	zinc finger protein 419	chr19q13.43	219826_at	NM_001098491 /// NM_001098492 /// NM_001098493 /// NM_001098494 /// NM_001098495 /// NM_001098496 /// NM_024691
2.98	3.21	0.22	1.30E-01	4.91E-01	LOC284260	hypothetical gene supported by BC011527; BC021928; BC011527; BC021928	chr18q12.3	1561587_at	XM_001720683 /// XM_001721958 /// XM_001723622
2.10	2.29	0.19	1.30E-01	4.91E-01	---	---	---	244446_at	---
1.84	2.02	0.18	1.30E-01	4.91E-01	LOC285045	hypothetical LOC285045	chr2p22.3	1563083_s_at	---
3.59	4.62	1.02	1.30E-01	4.91E-01	---	---	---	1560813_at	---
3.36	4.24	0.89	1.30E-01	4.91E-01	RORB	RAR-related orphan receptor B	chr9q22	242385_at	NM_006914
3.21	3.75	0.54	1.30E-01	4.91E-01	---	---	---	234151_at	---
4.87	5.28	0.41	1.30E-01	4.91E-01	TAF2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	chr8q24.12	1554721_a_at	NM_003184
4.27	4.57	0.30	1.30E-01	4.91E-01	---	---	---	231682_at	---
2.76	3.02	0.26	1.30E-01	4.91E-01	KIAA1333	KIAA1333	chr14q12	223254_s_at	NM_017769
2.09	2.29	0.21	1.30E-01	4.91E-01	PHC3	polyhomeotic homolog 3 (Drosophila)	chr3q26.2	220328_at	NM_024947
2.71	3.02	0.31	1.30E-01	4.91E-01	ZNF114	zinc finger protein 114	chr19q13.32	1552947_x_at	NM_153608
2.71	2.93	0.22	1.30E-01	4.91E-01	GJC1	gap junction protein, gamma 1, 45kDa	chr17q21.31	208460_at	NM_001080383 /// NM_005497
4.07	4.63	0.56	1.30E-01	4.91E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM /// IGHV4-31 /// IGHV@ /// LOC100126583 /// LOC100133739	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable group /// hypothetical LOC100126583 /// similar to hCG2038920	chr14q32.33	214916_x_at	XM_001718220
3.23	3.55	0.32	1.30E-01	4.91E-01	LOC730184	hypothetical LOC730184	chr2p14	241053_at	XM_001132826 /// XM_001132908 /// XM_001719167
2.60	2.91	0.31	1.30E-01	4.91E-01	MRPL38	Mitochondrial ribosomal protein L38	chr17q25.3	230726_at	NM_032478
5.31	5.60	0.30	1.30E-01	4.91E-01	LRRC61	leucine rich repeat containing 61	chr7q31-q35	218907_s_at	NM_023942
4.07	4.31	0.24	1.30E-01	4.91E-01	ANXA2P3	annexin A2 pseudogene 3	chr10q21-q22	211241_at	NR_001446
2.45	2.64	0.19	1.30E-01	4.91E-01	---	---	---	225518_x_at	---
4.79	5.52	0.73	1.30E-01	4.91E-01	KIF5B	kinesin family member 5B	chr10pter-q22.1	201992_s_at	NM_004521

3.13	3.54	0.41	1.30E-01	4.91E-01	LOC283143	hypothetical protein LOC283143	chr11q23.2	239675_at	XR_039943 /// XR_039944 /// XR_039945																					
3.95	4.29	0.34	1.30E-01	4.91E-01	SCAPER	S phase cyclin A-associated protein in the ER	chr15q24	209741_x_at	NM_020843																					
2.43	2.67	0.24	1.30E-01	4.91E-01	---	---	---	233865_at	---																					
4.82	5.29	0.47	1.30E-01	4.91E-01	GRLF1	glucocorticoid receptor DNA binding factor 1	chr19q13.3	202045_s_at	NM_004491																					
9.79	10.22	0.43	1.30E-01	4.91E-01	SET	SET nuclear oncogene	chr9q34	200630_x_at	NM_001122821 /// NM_003011																					
2.68	3.08	0.40	1.30E-01	4.91E-01	PLAU	plasminogen activator, urokinase	chr10q24	211668_s_at	NM_002658																					
3.07	3.43	0.36	1.30E-01	4.91E-01	IRF5	interferon regulatory factor 5	chr7q32	205468_s_at	NM_001098627 /// NM_001098628 /// NM_001098629 /// NM_001098630 /// NM_001098631 /// NM_002200 /// NM_032643																					
6.38	6.70	0.33	1.30E-01	4.91E-01	KCTD1	potassium channel tetramerisation domain containing 1	chr18q11.2	226246_at	NM_198991																					
2.80	3.11	0.32	1.30E-01	4.91E-01	ZNF394	Zinc finger protein 394	chr7q22.1	243024_at	NM_032164																					
2.87	3.18	0.31	1.30E-01	4.91E-01	LOC401913	hypothetical LOC401913	chr19q13.11	244176_at	XR_016508 /// XR_018932 /// XR_038711																					
3.99	4.29	0.31	1.30E-01	4.91E-01	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	chr6p21.1-p11.2	1553977_a_at	NM_016593																					
6.58	6.85	0.28	1.30E-01	4.91E-01	CD82	CD82 molecule	chr11p11.2	203904_x_at	NM_001024844 /// NM_002231																					
4.25	4.51	0.25	1.30E-01	4.91E-01	MYOD1	myogenic differentiation 1	chr11p15.4	206657_s_at	NM_002478																					
3.12	3.37	0.25	1.30E-01	4.91E-01	RYR2	ryanodine receptor 2 (cardiac)	chr1q42.1-q43	207557_s_at	NM_001035																					
2.18	2.43	0.24	1.30E-01	4.91E-01	---	---	---	1562965_at	---																					
2.07	2.32	0.24	1.30E-01	4.91E-01	---	---	---	1557874_at	---																					
2.86	3.09	0.23	1.30E-01	4.91E-01	MGC12935	hypothetical LOC84780	chr6p21.32	223932_at	---																					
3.73	3.96	0.23	1.30E-01	4.91E-01	PDE7B	phosphodiesterase 7B	chr6q23-q24	243438_at	NM_018945																					
2.14	2.35	0.21	1.30E-01	4.91E-01	---	---	---	243756_at	---																					
2.27	2.47	0.21	1.30E-01	4.91E-01	---	---	---	237523_at	---																					
2.16	2.37	0.21	1.30E-01	4.91E-01	---	---	---	1570271_at	---																					
1.91	2.10	0.19	1.30E-01	4.91E-01	MGC40069	hypothetical protein MGC40069	chr14q11.2	1555073_at	XR_017974																					
4.54	4.84	0.30	1.30E-01	4.91E-01	---	---	---	243895_x_at	---																					
2.38	2.66	0.28	1.30E-01	4.91E-01	---	---	---	1564822_at	---																					
4.37	4.63	0.27	1.30E-01	4.91E-01	FKSG43 /// FRMD8	FKSG43 gene /// FERM domain containing 8	chr11q13 /// chrXq11.1	224271_x_at	NM_031904																					
4.25	4.48	0.23	1.30E-01	4.91E-01	EVI5	ecotropic viral integration site 5	chr1p22.1	208297_s_at	NM_005665																					
1.91	2.13	0.23	1.30E-01	4.91E-01	C15orf32	chromosome 15 open reading frame 32	chr15q26.1	1553482_at	NM_153040																					
3.20	3.60	0.40	1.30E-01	4.91E-01	---	---	---	240538_at	---																					
3.74	4.08	0.34	1.30E-01	4.91E-01	EIF2C1	eukaryotic translation initiation factor 2C, 1	chr1p35-p34	222576_s_at	NM_012199																					
3.59	3.87	0.29	1.30E-01	4.91E-01	PDE3A	phosphodiesterase 3A, cGMP-inhibited	chr12p12	206388_at	NM_000921																					
3.36	3.63	0.28	1.30E-01	4.91E-01	---	---	---	236752_at	---																					
2.29	2.53	0.24	1.30E-01	4.91E-01	ARG1	arginase, liver	chr6q23	206177_s_at	NM_000045																					
2.61	2.83	0.22	1.30E-01	4.91E-01	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	chr16p	206353_at	NM_005205																					
2.08	2.28	0.20	1.30E-01	4.91E-01	---	---	---	1566995_at	---																					
1.94	2.17	0.22	1.31E-01	4.92E-01	LRRC39	leucine rich repeat containing 39	chr1p21.2	1559580_at	NM_144620																					
2.84	3.59	0.76	1.31E-01	4.92E-01	PCDH21	protocadherin 21	chr10q22.1-q22.3	213369_at	NM_033100																					
5.68	6.14	0.46	1.31E-01	4.92E-01	ENOX2	ecto-NOX disulfide-thiol exchanger 2	chrXq25-q26.2	204643_s_at	NM_006375 /// NM_182314																					
2.20	2.41	0.22	1.31E-01	4.92E-01	RETNLB	resistin like beta	chr3q13.1	223970_at	NM_032579																					
3.78	4.07	0.29	1.31E-01	4.92E-01	LOC285095	similar to mCG14474	chr2q37.3	238196_at	XM_001722643 /// XM_211764																					
2.43	2.61	0.18	1.31E-01	4.92E-01	IRX5	iroquois homeobox 5	chr16q11.2-q13	210239_at	NM_005853																					
4.02	4.81	0.79	1.31E-01	4.92E-01	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	chr2p22-p21	209421_at	NM_000251																					
3.06	3.30	0.24	1.31E-01	4.92E-01	VIL1	villin 1	chr2q35-q36	228912_at	NM_007127																					
1.96	2.15	0.19	1.31E-01	4.92E-01	---	---	---	244775_at	---																					
2.93	3.22	0.29	1.31E-01	4.92E-01	---	---	---	1556753_s_at	---																					
4.01	4.33	0.32	1.31E-01	4.92E-01	SOLH	small optic lobes homolog (Drosophila)	chr16p13.3	230295_at	NM_005632																					
4.22	4.50	0.28	1.31E-01	4.92E-01	SARDH	sarcosine dehydrogenase	chr9q33-q34	211322_s_at	NM_001134707 /// NM_007101																					
5.08	5.59	0.51	1.31E-01	4.92E-01	---	---	---	233270_x_at	---																					
2.33	2.67	0.34	1.31E-01	4.92E-01	---	---	---	233770_at	---																					
6.06	6.91	0.85	1.31E-01	4.92E-01	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	chrXp22.2	203300_x_at	NM_003916																					
8.28	8.87	0.59	1.31E-01	4.92E-01	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	chr7q22.1-q22.3	201068_s_at	NM_002803																					

2.58	2.92	0.34	1.31E-01	4.92E-01	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	chr3p24.2	228716_at	NM_000461 /// NM_001128176 /// NM_001128177
1.89	2.13	0.24	1.31E-01	4.92E-01	---	---	---	1559275_x_at	---
3.63	4.04	0.41	1.31E-01	4.93E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	205872_x_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359
5.33	5.84	0.50	1.31E-01	4.93E-01	SYNJ2BP	synaptojanin 2 binding protein	chr14q24.2	219156_at	NM_018373
2.12	2.38	0.26	1.31E-01	4.93E-01	---	---	---	244392_at	---
2.71	2.94	0.23	1.31E-01	4.93E-01	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	chr14q24.3-q31	202063_s_at	NM_005065
1.94	2.17	0.22	1.31E-01	4.93E-01	DEPDC1	DEP domain containing 1	chr1p31.2	235545_at	NM_001114120 /// NM_017779
2.21	2.50	0.29	1.31E-01	4.93E-01	FOXP2	forkhead box P2	chr7q31	243278_at	NM_014491 /// NM_148898 /// NM_148899
1.98	2.17	0.19	1.31E-01	4.93E-01	---	---	---	1560864_at	---
2.61	2.84	0.23	1.31E-01	4.93E-01	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	chr20q13.33	237179_at	NM_001104925 /// NM_018257
3.01	3.21	0.20	1.31E-01	4.93E-01	SLC28A2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	chr15q15	207249_s_at	NM_004212
1.95	2.13	0.18	1.31E-01	4.93E-01	ZNF28	zinc finger protein 28	chr19q	1567853_at	NM_006969
7.41	8.01	0.60	1.31E-01	4.93E-01	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	chr14q23	201532_at	NM_002788 /// NM_152132
6.62	6.85	0.23	1.31E-01	4.93E-01	---	---	---	242145_at	---
2.02	2.23	0.21	1.31E-01	4.93E-01	KIAA0408	KIAA0408	chr6q22.33	205496_at	NM_014702
5.09	5.33	0.24	1.31E-01	4.93E-01	BCL2L13	BCL2-like 13 (apoptosis facilitator)	chr22q11.1	226798_at	NM_015367
3.93	4.23	0.30	1.31E-01	4.93E-01	XRRA1	X-ray radiation resistance associated 1	chr11q13.4	230557_at	NM_182969
2.05	2.25	0.20	1.31E-01	4.93E-01	BAGE	B melanoma antigen	chr21p11.1	1555603_at	NM_001187
2.52	2.75	0.23	1.31E-01	4.93E-01	MCM10	minichromosome maintenance complex component 10	chr10p13	223570_at	NM_018518 /// NM_182751
2.06	2.32	0.26	1.31E-01	4.93E-01	---	---	---	215981_at	---
3.68	4.21	0.53	1.31E-01	4.93E-01	---	---	---	215304_at	---
3.27	3.51	0.25	1.31E-01	4.93E-01	---	---	---	240797_at	---
2.60	2.81	0.21	1.31E-01	4.93E-01	LOC100129936	hypothetical LOC100129936	chr22q12.1	232310_at	XM_001720726 /// XM_001723247 /// XM_001726281
4.37	4.91	0.54	1.31E-01	4.93E-01	SMAD5	SMAD family member 5	chr5q31	205188_s_at	NM_001001419 /// NM_001001420 /// NM_005903
6.54	6.83	0.30	1.31E-01	4.93E-01	BACE1	beta-site APP-cleaving enzyme 1	chr11q23.2-q23.3	222462_s_at	NM_012104 /// NM_138971 /// NM_138972 /// NM_138973
2.37	2.58	0.21	1.32E-01	4.93E-01	---	---	---	236025_at	---
3.57	3.90	0.32	1.32E-01	4.93E-01	---	---	---	236776_at	---
4.34	4.59	0.26	1.32E-01	4.93E-01	PGC	progastricsin (pepsinogen C)	chr6p21.3-p21.1	205261_at	NM_002630
1.99	2.21	0.22	1.32E-01	4.93E-01	UTS2D	urotensin 2 domain containing	chr3q28	243175_at	NM_198152
2.34	2.58	0.24	1.32E-01	4.93E-01	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	chr4p16.1	228137_s_at	NM_020416 /// NM_181876
2.28	2.46	0.19	1.32E-01	4.93E-01	---	---	---	238302_at	---
4.54	4.96	0.42	1.32E-01	4.94E-01	ZNF844	zinc finger protein 844	chr19p13.2	228346_at	XR_015205 /// XR_015644 /// XR_041446
4.28	4.95	0.67	1.32E-01	4.94E-01	---	---	---	242673_at	---
2.28	2.50	0.22	1.32E-01	4.94E-01	PCDHA6	protocadherin alpha 6	chr5q31	211811_s_at	NM_018909 /// NM_031848 /// NM_031849
3.26	3.50	0.24	1.32E-01	4.94E-01	---	---	---	1569009_s_at	---
4.25	4.95	0.70	1.32E-01	4.94E-01	API5	apoptosis inhibitor 5	chr11p11.2	201686_x_at	NM_006595
4.40	4.78	0.39	1.32E-01	4.94E-01	---	---	---	229994_at	---
3.86	4.18	0.32	1.32E-01	4.94E-01	KLF9	Kruppel-like factor 9	chr9q13	228474_s_at	NM_001206
4.49	4.80	0.31	1.32E-01	4.94E-01	KIAA1128	KIAA1128	chr10q23.1	209378_s_at	NM_018999
4.10	4.41	0.30	1.32E-01	4.94E-01	NXPH3	neurexophilin 3	chr17q21.33	221991_at	NM_007225
2.33	2.60	0.27	1.32E-01	4.94E-01	---	---	---	233727_at	---

4.19	4.74	0.55	1.32E-01	4.94E-01	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	chr8q22.1	222699_s_at	NM_024613
4.64	4.99	0.35	1.32E-01	4.94E-01	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	chr22q13.31-q13.33	220020_at	NM_022098
2.07	2.31	0.25	1.32E-01	4.94E-01	---	---	---	233716_at	---
2.08	2.29	0.20	1.32E-01	4.94E-01	---	---	---	242901_at	---
2.58	2.76	0.18	1.32E-01	4.94E-01	S100Z	S100 calcium binding protein Z	chr5q13.3	1554876_a_at	NM_130772
2.17	2.35	0.18	1.32E-01	4.94E-01	---	---	---	237448_at	---
2.80	3.08	0.28	1.32E-01	4.94E-01	---	---	---	243698_at	---
2.73	2.98	0.26	1.32E-01	4.94E-01	LOC401052	hypothetical LOC401052	chr3p25.3	232812_at	NM_001008737
5.91	6.77	0.86	1.32E-01	4.94E-01	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	chr17p13.3	200813_s_at	NM_000430
3.75	4.08	0.33	1.32E-01	4.94E-01	MFSD7	major facilitator superfamily domain containing 7	chr4p16.3	214269_at	NM_032219
3.78	4.09	0.32	1.32E-01	4.94E-01	H1FX	H1 histone family, member X	chr3q21.3	231004_s_at	NM_006026
2.63	2.89	0.27	1.32E-01	4.94E-01	FAM55D	family with sequence similarity 55, member D	chr11q23.2	220645_at	NM_001077639 /// NM_017678
2.58	2.82	0.23	1.32E-01	4.94E-01	KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6	chr21q22.1|21q22.13-q22.2	210454_s_at	NM_002240
2.60	2.80	0.20	1.32E-01	4.94E-01	GLP2R	glucagon-like peptide 2 receptor	chr17p13.3	221312_at	NM_004246
6.08	6.45	0.36	1.32E-01	4.94E-01	CNN2	calponin 2	chr19p13.3	201605_x_at	NM_004368 /// NM_201277
2.52	2.75	0.23	1.32E-01	4.94E-01	SP100	SP100 nuclear antigen	chr2q37.1	237426_at	NM_001080391 /// NM_003113
2.69	3.00	0.31	1.32E-01	4.94E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	214130_s_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359
4.24	4.51	0.27	1.32E-01	4.94E-01	TMCO7	transmembrane and coiled-coil domains 7	chr16q22.1	226467_at	NM_024562
2.05	2.28	0.23	1.32E-01	4.94E-01	C10orf119	chromosome 10 open reading frame 119	chr10q26.11	233028_at	NM_024834
1.82	2.03	0.20	1.32E-01	4.94E-01	LOC401463	hypothetical gene supported by BC022555; BC050012	chr8q12.3	1563927_a_at	NR_015374
2.62	2.95	0.33	1.32E-01	4.94E-01	LOC26010	Viral DNA polymerase-transactivated protein 6	chr2q33.1	244597_at	NM_001100422 /// NM_001100423 /// NM_001100424 /// NM_015535
4.01	4.28	0.27	1.32E-01	4.94E-01	DAGLA	diacylglycerol lipase, alpha	chr11q12.2	214128_at	NM_006133
4.44	4.71	0.27	1.32E-01	4.94E-01	HFE	hemochromatosis	chr6p21.3	211328_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
2.72	2.99	0.26	1.32E-01	4.94E-01	SLC39A8	Solute carrier family 39 (zinc transporter), member 8	chr4q22-q24	228945_s_at	NM_022154
1.90	2.10	0.20	1.32E-01	4.94E-01	---	---	---	240957_at	---
3.24	3.56	0.32	1.32E-01	4.94E-01	---	---	---	244666_at	---
2.53	2.78	0.25	1.32E-01	4.94E-01	SPTBN1	spectrin, beta, non-erythrocytic 1	chr2p21	214856_at	NM_003128 /// NM_178313
2.26	2.42	0.17	1.32E-01	4.94E-01	---	---	---	237908_at	---
3.62	3.87	0.26	1.33E-01	4.95E-01	IVD	Isovaleryl Coenzyme A dehydrogenase	chr15q14-q15	217251_x_at	NM_002225
3.03	3.34	0.31	1.33E-01	4.95E-01	ATAD2	ATPase family, AAA domain containing 2	chr8q24.13	235266_at	NM_014109
3.39	3.69	0.30	1.33E-01	4.95E-01	SHH	sonic hedgehog homolog (Drosophila)	chr7q36	207586_at	NM_000193
3.77	4.06	0.29	1.33E-01	4.95E-01	SFTPC	surfactant protein C	chr8p21	205982_x_at	NM_003018
2.21	2.46	0.26	1.33E-01	4.95E-01	PCDHB16	protocadherin beta 16	chr5q31	232099_at	NM_020957
2.78	3.01	0.22	1.33E-01	4.95E-01	---	---	---	244778_x_at	---
2.03	2.25	0.22	1.33E-01	4.95E-01	SYT7	synaptotagmin VII	chr11q12-q13.1	1559956_at	NM_004200
2.23	2.43	0.20	1.33E-01	4.95E-01	---	---	---	240533_at	---
2.53	2.72	0.19	1.33E-01	4.95E-01	---	---	---	238360_s_at	---
4.71	5.64	0.93	1.33E-01	4.95E-01	PLN	phospholamban	chr6q22.1	204939_s_at	NM_002667
3.27	3.53	0.26	1.33E-01	4.95E-01	---	---	---	244202_at	---
2.99	3.28	0.29	1.33E-01	4.95E-01	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	chr2p21	202434_s_at	NM_000104
3.58	4.01	0.43	1.33E-01	4.95E-01	---	---	---	1559795_at	---

3.12	3.75	0.62	1.33E-01	4.95E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	211681_s_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257
4.03	4.51	0.48	1.33E-01	4.95E-01	CLASP2	cytoplasmic linker associated protein 2	chr3p22.3	1555469_a_at	NM_015097
2.94	3.35	0.40	1.33E-01	4.95E-01	LOC63920	transposon-derived Buster3 transposase-like	chr5q33.3	220770_s_at	NM_022090
4.11	4.83	0.72	1.33E-01	4.95E-01	---	---	---	233303_at	---
4.44	4.69	0.25	1.33E-01	4.95E-01	BOC	Boc homolog (mouse)	chr3q13.2	230035_at	NM_033254
5.53	6.04	0.51	1.33E-01	4.95E-01	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	chr2p11.2	1566472_s_at	NM_017750
9.27	9.75	0.48	1.33E-01	4.95E-01	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	217802_s_at	NM_022731
3.56	4.00	0.44	1.33E-01	4.95E-01	PCDH17	protocadherin 17	chr13q21.1	227289_at	NM_001040429
4.97	5.31	0.34	1.33E-01	4.95E-01	PRODH2	proline dehydrogenase (oxidase) 2	chr19q13.1	216696_s_at	NM_021232
2.03	2.24	0.20	1.33E-01	4.95E-01	FLJ26850	FLJ26850 protein	chr19q13.33	237298_at	XR_040269 /// XR_040270 /// XR_040271
4.02	4.39	0.38	1.33E-01	4.95E-01	ZBTB43	zinc finger and BTB domain containing 43	chr9q33-q34	204181_s_at	NM_014007
2.50	2.75	0.25	1.33E-01	4.95E-01	---	---	---	1567374_at	---
4.77	5.00	0.23	1.33E-01	4.95E-01	LOC100129503	hypothetical protein LOC100129503	chr17q25.3	216107_at	XM_001716524 /// XM_001721698 /// XM_001727002
3.08	3.39	0.30	1.33E-01	4.95E-01	MYCT1	myc target 1	chr6q25.2	220471_s_at	NM_025107
5.69	6.35	0.66	1.33E-01	4.95E-01	FAM82B	family with sequence similarity 82, member B	chr8q21.3	218549_s_at	NM_016033
2.20	2.38	0.18	1.33E-01	4.95E-01	RGS20	regulator of G-protein signaling 20	chr8q	210138_at	NM_003702 /// NM_170587
1.77	1.92	0.15	1.33E-01	4.95E-01	---	---	---	241306_at	---
5.45	5.70	0.25	1.33E-01	4.95E-01	---	---	---	240205_x_at	---
6.00	6.49	0.49	1.33E-01	4.96E-01	ANXA4	annexin A4	chr2p13	201302_at	NM_001153
4.52	5.34	0.81	1.33E-01	4.96E-01	TTC14	tetratricopeptide repeat domain 14	chr3q26.33	225178_at	NM_001042601 /// NM_133462
6.47	6.78	0.31	1.33E-01	4.96E-01	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	chr12q24.3-qter	201354_s_at	NM_013449
3.50	3.83	0.33	1.33E-01	4.96E-01	C21orf67	chromosome 21 open reading frame 67	chr21q22.3	1555393_s_at	XR_039924 /// XR_039925 /// XR_039926
5.74	6.46	0.72	1.33E-01	4.96E-01	RSBN1	round spermatid basic protein 1	chr1p13.2	222791_at	NM_018364
3.00	3.55	0.55	1.33E-01	4.96E-01	ZNF385B	zinc finger protein 385B	chr2q31.2-q31.3	229019_at	NM_001113397 /// NM_001113398 /// NM_152520
5.83	6.33	0.50	1.33E-01	4.96E-01	CD248	CD248 molecule, endosialin	chr11q13	219025_at	NM_020404
2.43	2.70	0.27	1.33E-01	4.96E-01	---	---	---	236089_at	---
2.89	3.16	0.27	1.33E-01	4.96E-01	---	---	---	234415_x_at	---
2.05	2.31	0.26	1.33E-01	4.96E-01	---	---	---	221153_s_at	---
3.90	4.12	0.22	1.33E-01	4.96E-01	ADIG	adipogenin	chr20q11.23	1554129_a_at	NM_001018082
3.04	3.31	0.26	1.33E-01	4.96E-01	---	---	---	242514_at	---
2.16	2.36	0.20	1.33E-01	4.96E-01	LOC643449	similar to hCG2041756	chr4p12	241594_at	XM_001714546 /// XM_931553 /// XM_945026
2.86	3.10	0.23	1.33E-01	4.96E-01	---	---	---	237440_at	---
1.92	2.12	0.21	1.34E-01	4.96E-01	PCCA	Propionyl Coenzyme A carboxylase, alpha polypeptide	chr13q32	216533_at	NM_000282 /// NM_001127692
5.51	6.36	0.85	1.34E-01	4.96E-01	KIAA1627	KIAA1627 protein	chr4q26	227601_at	NM_020961
2.51	3.16	0.65	1.34E-01	4.96E-01	GJC1	gap junction protein, gamma 1, 45kDa	chr17q21.31	228776_at	NM_001080383 /// NM_005497
3.33	3.65	0.33	1.34E-01	4.96E-01	CHRNA3	cholinergic receptor, nicotinic, alpha 3	chr15q24	211587_x_at	NM_000743
2.56	2.82	0.26	1.34E-01	4.96E-01	TNNT1	troponin T type 1 (skeletal, slow)	chr19q13.4	213201_s_at	NM_001126132 /// NM_001126133 /// NM_003283
2.09	2.33	0.25	1.34E-01	4.96E-01	---	---	---	1561872_at	---
3.30	3.54	0.24	1.34E-01	4.96E-01	GSX2	GS homeobox 2	chr4q11-q12	230338_x_at	NM_133267

2.77	3.01	0.24	1.34E-01	4.96E-01	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	chr13q32	216512_s_at	NM_001129889 /// NM_001922
2.27	2.49	0.22	1.34E-01	4.96E-01	---	---	---	230324_at	---
3.66	3.90	0.24	1.34E-01	4.96E-01	---	---	---	236676_at	---
1.84	2.04	0.20	1.34E-01	4.96E-01	AGBL3	ATP/GTP binding protein-like 3	chr7q33	220649_at	XM_001723112 /// XM_001723784 /// XM_001726535 /// XM_001726650
3.17	3.49	0.32	1.34E-01	4.96E-01	---	---	---	239659_at	---
5.83	6.03	0.21	1.34E-01	4.96E-01	ZNF611	zinc finger protein 611	chr19q13.41	208137_x_at	NM_030972
2.06	2.24	0.18	1.34E-01	4.97E-01	ST18	Suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	chr8q11.23	1557583_at	NM_014682
2.59	2.86	0.27	1.34E-01	4.97E-01	KLF1	Kruppel-like factor 1 (erythroid)	chr19p13.13-p13.12	210504_at	NM_006563
3.40	3.79	0.39	1.34E-01	4.97E-01	GJD3	gap junction protein, delta 3, 31.9kDa	chr17q21.2	230025_at	NM_152219
2.22	2.48	0.26	1.34E-01	4.97E-01	DOCK11	dedicator of cytokinesis 11	chrXq24	238356_at	NM_144658
2.35	2.55	0.20	1.34E-01	4.97E-01	LOC643783	hypothetical LOC643783	chr4q12	235667_at	XM_001720472 /// XM_931798 /// XM_942784
2.68	2.88	0.19	1.34E-01	4.97E-01	PRAMEF10	PRAME family member 10	chr1p36.21	217273_at	NM_001039361
2.54	2.75	0.21	1.34E-01	4.97E-01	TRPM6	transient receptor potential cation channel, subfamily M, member 6	chr9q21.13	234864_s_at	NM_017662
2.97	3.16	0.20	1.34E-01	4.97E-01	MUSK	muscle, skeletal, receptor tyrosine kinase	chr9q31.3-q32	207632_at	NM_005592
3.21	3.50	0.29	1.34E-01	4.97E-01	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	chrXp22.11	210456_at	NM_004845
2.31	2.56	0.25	1.34E-01	4.97E-01	---	---	---	234086_at	---
3.93	4.24	0.30	1.34E-01	4.97E-01	---	---	---	239453_at	---
3.44	3.67	0.23	1.34E-01	4.97E-01	---	---	---	233359_at	---
2.02	2.23	0.21	1.34E-01	4.97E-01	---	---	---	243657_at	---
6.03	6.68	0.65	1.34E-01	4.97E-01	KPNA1	karyopherin alpha 1 (importin alpha 5)	chr3q21	202055_at	NM_002264
3.44	3.80	0.36	1.34E-01	4.98E-01	FBXO3	F-box protein 3	chr11p13	229955_at	NM_012175 /// NM_033406
8.45	8.93	0.47	1.34E-01	4.98E-01	PPT1	palmitoyl-protein thioesterase 1	chr1p32	200975_at	NM_000310
3.11	3.41	0.29	1.34E-01	4.98E-01	RPL37	Ribosomal protein L37	chr5p13	224766_at	NM_000997
5.83	6.69	0.86	1.34E-01	4.98E-01	NAMPT	nicotinamide phosphoribosyltransferase	chr7q22.2	217738_at	NM_005746
12.15	12.42	0.26	1.35E-01	4.98E-01	---	---	---	AFFX-r2-P1-cre-3_at	---
9.99	10.25	0.25	1.35E-01	4.98E-01	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	chr7p22	208640_at	NM_006908 /// NM_018890 /// NM_198829
2.73	2.94	0.22	1.35E-01	4.98E-01	KIAA1324	KIAA1324	chr1p13.3	243349_at	NM_020775
4.47	4.86	0.40	1.35E-01	4.98E-01	ICOSLG	inducible T-cell co-stimulator ligand	chr21q22.3	211198_s_at	NM_015259
7.09	7.36	0.28	1.35E-01	4.98E-01	PNPLA2	patatin-like phospholipase domain containing 2	chr11p15.5	212705_x_at	NM_020376
3.44	3.63	0.19	1.35E-01	4.98E-01	SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	chr5q31-q32	208494_at	NM_014228
4.78	5.30	0.52	1.35E-01	4.98E-01	SLC44A1	solute carrier family 44, member 1	chr9q31.2	224595_at	NM_080546
5.78	6.09	0.31	1.35E-01	4.98E-01	---	---	---	AFFX-BioB-5_at	---
3.29	3.49	0.20	1.35E-01	4.98E-01	---	---	---	240920_at	---
4.96	5.32	0.36	1.35E-01	4.98E-01	HLX	H2.0-like homeobox	chr1q41-q42.1	214438_at	NM_021958
5.76	6.06	0.30	1.35E-01	4.98E-01	SNX27	sorting nexin family member 27	chr1q21.3	221006_s_at	NM_030918
6.60	7.31	0.71	1.35E-01	4.98E-01	RRM1	ribonucleotide reductase M1	chr11p15.5	201477_s_at	NM_001033
3.62	4.19	0.57	1.35E-01	4.98E-01	---	---	---	230201_at	---
4.36	4.91	0.54	1.35E-01	4.98E-01	---	---	---	227273_at	---
3.08	3.49	0.41	1.35E-01	4.98E-01	TSPAN5	tetraspanin 5	chr4q23	225387_at	NM_005723
4.36	4.70	0.33	1.35E-01	4.98E-01	---	---	---	238936_at	---
3.76	4.08	0.32	1.35E-01	4.98E-01	C9orf58	chromosome 9 open reading frame 58	chr9q34.13-q34.3	223074_s_at	NM_031426
8.79	9.09	0.30	1.35E-01	4.98E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	200655_s_at	NM_001743 /// NM_005184 /// NM_006888
2.04	2.24	0.21	1.35E-01	4.98E-01	CNTN3	contactin 3 (plasmacytoma associated)	chr3p26	229831_at	NM_020872
2.30	2.49	0.19	1.35E-01	4.98E-01	hCG_1814936	hCG1814936	chr4q32.1	243892_at	XM_001131500 /// XM_001722027 /// XM_933981
2.14	2.32	0.18	1.35E-01	4.98E-01	---	---	---	231696_x_at	---
4.98	5.72	0.74	1.35E-01	4.98E-01	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	chr14q24.3-q31	202062_s_at	NM_005065
4.73	5.00	0.27	1.35E-01	4.98E-01	LOC91450	hypothetical protein LOC91450	chr15q24.1	233418_at	---

2.79	3.10	0.31	1.35E-01	4.98E-01	DPCR1	diffuse panbronchiolitis critical region 1	chr6p21.33	231646_at	NM_080870
2.22	2.43	0.21	1.35E-01	4.98E-01	---	---	---	1566486_at	---
4.82	5.71	0.89	1.35E-01	4.98E-01	ZNF638	Zinc finger protein 638	chr2p13.2-p13.1	239243_at	NM_001014972 /// NM_014497
2.56	2.90	0.34	1.35E-01	4.98E-01	SNX13	sorting nexin 13	chr7p21.1	215820_x_at	NM_015132
2.76	3.03	0.27	1.35E-01	4.98E-01	---	---	---	1563106_at	---
2.99	3.21	0.22	1.35E-01	4.98E-01	LOC285638	hypothetical protein LOC285638	chr5q21.3	1563489_at	---
2.91	3.23	0.32	1.35E-01	4.99E-01	---	---	---	240775_at	---
3.83	4.09	0.26	1.35E-01	4.99E-01	STRBP	spermatid perinuclear RNA binding protein	chr9q33.3	223245_at	NM_018387
2.52	2.76	0.25	1.35E-01	4.99E-01	---	---	---	239174_at	---
1.93	2.12	0.18	1.35E-01	4.99E-01	TTN	titin	chr2q31	244839_at	NM_003319 /// NM_133378 /// NM_133379 /// NM_133432 /// NM_133437
4.27	4.52	0.25	1.35E-01	4.99E-01	UNC5A	Unc-5 homolog A (C. elegans)	chr5q35.2	243833_at	NM_133369
2.88	3.19	0.32	1.35E-01	4.99E-01	USP25	ubiquitin specific peptidase 25	chr21q11.2	1555559_s_at	NM_013396
2.17	2.42	0.25	1.35E-01	4.99E-01	TRIM63	tripartite motif-containing 63	chr1p34-p33	236972_at	NM_032588
6.85	7.50	0.65	1.35E-01	4.99E-01	PHF17	PHD finger protein 17	chr4q26-q27	218517_at	NM_024900 /// NM_199320
2.80	3.30	0.51	1.35E-01	4.99E-01	PCLO	piccolo (presynaptic cytomatrix protein)	chr7q11.23-q21.3	213558_at	NM_014510 /// NM_033026
3.69	3.98	0.29	1.35E-01	4.99E-01	---	---	---	236137_at	---
2.94	3.21	0.26	1.35E-01	4.99E-01	---	---	---	231414_at	---
4.84	5.12	0.28	1.35E-01	4.99E-01	HNF1A	HNF1 homeobox A	chr12q22-qter|12q24.2	210515_at	NM_000545
4.00	4.34	0.33	1.35E-01	4.99E-01	CD99L2	CD99 molecule-like 2	chrXq28	1554758_a_at	NM_031462 /// NM_134445 /// NM_134446
3.49	3.80	0.31	1.35E-01	4.99E-01	PRPH	peripherin	chr12q12-q13	213847_at	NM_006262
2.35	2.65	0.30	1.35E-01	4.99E-01	S100A12	S100 calcium binding protein A12	chr1q21	205863_at	NM_005621
4.52	4.73	0.21	1.35E-01	4.99E-01	---	---	---	237455_at	---
1.78	1.96	0.18	1.36E-01	4.99E-01	---	---	---	237391_at	---
2.92	3.35	0.43	1.36E-01	4.99E-01	---	---	---	240154_at	---
5.23	5.43	0.20	1.36E-01	4.99E-01	---	---	---	231298_at	---
7.52	8.16	0.64	1.36E-01	4.99E-01	AGTR1	angiotensin II receptor, type 1	chr3q21-q25	205357_s_at	NM_000685 /// NM_004835 /// NM_009585 /// NM_031850 /// NM_032049
2.72	2.99	0.27	1.36E-01	4.99E-01	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	chrXp22.1-p21.3	220663_at	NM_014271
2.06	2.32	0.26	1.36E-01	4.99E-01	---	---	---	1560742_at	---
2.29	2.54	0.26	1.36E-01	4.99E-01	PPBPL2	pro-platelet basic protein-like 2	chr4q13.3	208346_at	XR_040069 /// XR_040070 /// XR_040071
5.70	5.95	0.25	1.36E-01	4.99E-01	---	---	---	210679_x_at	---
4.06	4.30	0.24	1.36E-01	4.99E-01	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	chr1p34.2	215491_at	NM_001033081 /// NM_001033082 /// NM_005376
3.48	3.72	0.23	1.36E-01	4.99E-01	APCDD1L	adenomatosis polyposis coli down-regulated 1-like	chr20q13.32	235548_at	NM_153360
3.56	3.79	0.23	1.36E-01	4.99E-01	---	---	---	241570_at	---
2.12	2.41	0.29	1.36E-01	4.99E-01	---	---	---	244244_at	---
3.64	4.08	0.43	1.36E-01	4.99E-01	KIAA1217	KIAA1217	chr10p12.2-p12.1	232762_at	NM_001098500 /// NM_001098501 /// NM_019590
2.54	2.73	0.19	1.36E-01	4.99E-01	---	---	---	237952_at	---
3.13	3.42	0.29	1.36E-01	4.99E-01	LOC100131017	Similar to zinc finger protein 316	chr7p22.1	243075_at	XM_001721918 /// XM_001721974
2.09	2.31	0.22	1.36E-01	4.99E-01	MRPS22	mitochondrial ribosomal protein S22	chr3q23	226256_at	NM_020191
2.28	2.49	0.21	1.36E-01	4.99E-01	---	---	---	237290_at	---
2.73	2.93	0.20	1.36E-01	4.99E-01	---	---	---	242075_at	---
4.49	5.18	0.70	1.36E-01	4.99E-01	TSHZ2	Teashirt zinc finger homeobox 2	chr20q13.2	238577_s_at	NM_173485
4.00	4.30	0.29	1.36E-01	4.99E-01	---	---	---	232447_at	---
5.20	5.45	0.26	1.36E-01	4.99E-01	TSPAN16	tetraspanin 16	chr19p13.2	233236_at	NM_012466
3.70	4.32	0.62	1.36E-01	4.99E-01	ACSL4	Acyl-CoA synthetase long-chain family member 4	chrXq22.3-q23	1557418_at	NM_004458 /// NM_022977
2.69	2.94	0.26	1.36E-01	4.99E-01	LRTM1	leucine-rich repeats and transmembrane domains 1	chr3p14.3	221612_at	NM_020678
2.17	2.43	0.26	1.36E-01	4.99E-01	FAM126A	family with sequence similarity 126, member A	chr7p15.3	231396_s_at	NM_032581

3.22	3.44	0.23	1.36E-01	4.99E-01	ZNF777	Zinc finger protein 777	chr7q36.1	228687_at	NM_015694
6.19	7.11	0.92	1.36E-01	4.99E-01	RARS2	arginyl-tRNA synthetase 2, mitochondrial	chr6q16.1	232902_s_at	NM_020320
6.07	6.61	0.53	1.36E-01	4.99E-01	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	chr11q23	204070_at	NM_004585
6.41	6.90	0.49	1.36E-01	4.99E-01	SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	chr9p22.3	210465_s_at	NM_001039697
3.44	3.88	0.45	1.36E-01	4.99E-01	---	---	---	1556185_a_at	---
3.12	3.48	0.36	1.36E-01	4.99E-01	FANCD2	Fanconi anemia, complementation group D2	chr3p26	223545_at	NM_001018115 /// NM_033084
4.33	4.65	0.31	1.36E-01	4.99E-01	NT5DC2	5'-nucleotidase domain containing 2	chr3p21.1	1556894_at	NM_001134231 /// NM_022908
3.76	4.04	0.28	1.36E-01	4.99E-01	ANKH	ankylosis, progressive homolog (mouse)	chr5p15.1	223094_s_at	NM_054027
2.44	2.72	0.28	1.36E-01	4.99E-01	NCAPG	non-SMC condensin I complex, subunit G	chr4p15.33	218662_s_at	NM_022346
4.18	4.73	0.55	1.36E-01	4.99E-01	FBXO45	F-box protein 45	chr3q29	225099_at	NM_001105573
3.89	4.33	0.44	1.36E-01	4.99E-01	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	chr2p21	209287_s_at	NM_006449
6.90	7.23	0.33	1.36E-01	4.99E-01	GSK3A	glycogen synthase kinase 3 alpha	chr19q13.2	202210_x_at	NM_019884
2.30	2.61	0.32	1.36E-01	4.99E-01	CCDC48	EF-hand domain-containing protein ENSP00000381169	chr3q21.3	233259_at	NM_024768
2.19	2.46	0.27	1.36E-01	4.99E-01	---	---	---	236955_at	---
4.90	5.14	0.24	1.36E-01	4.99E-01	LOC729683	hypothetical protein LOC729683	chr17q23.3	236614_at	XR_040516 /// XR_040517 /// XR_040518
3.50	3.73	0.23	1.36E-01	4.99E-01	---	---	---	237901_at	---
3.76	3.97	0.21	1.36E-01	4.99E-01	C3orf21	chromosome 3 open reading frame 21	chr3q29	226891_at	NM_152531
3.34	3.54	0.21	1.36E-01	4.99E-01	---	---	---	243310_at	---
1.88	2.09	0.21	1.36E-01	4.99E-01	---	---	---	233373_at	---
2.62	2.82	0.21	1.36E-01	4.99E-01	GLYAT	glycine-N-acyltransferase	chr11q12.1	222083_at	NM_005838 /// NM_201648
4.30	4.50	0.19	1.36E-01	4.99E-01	KIAA1920	KIAA1920 protein	chr15q25.2	1561960_at	---
1.95	2.14	0.19	1.36E-01	4.99E-01	---	---	---	239298_at	---
2.22	2.43	0.21	1.36E-01	5.00E-01	---	---	---	234132_at	---
2.08	2.34	0.26	1.36E-01	5.00E-01	C1orf114	chromosome 1 open reading frame 114	chr1q24	1555112_a_at	NM_021179
2.05	2.23	0.18	1.36E-01	5.00E-01	MYOZ2	myozenin 2	chr4q26-q27	207148_x_at	NM_016599
3.75	3.99	0.24	1.36E-01	5.00E-01	KIF2A	kinesin heavy chain member 2A	chr5q12-q13	203086_at	NM_001098511 /// NM_004520
4.29	4.78	0.49	1.36E-01	5.00E-01	ST7L	suppression of tumorigenicity 7 like	chr1p13.2	1552739_s_at	NM_017744 /// NM_138727 /// NM_138728 /// NM_138729
3.98	4.40	0.42	1.36E-01	5.00E-01	ASTN2	astrotactin 2	chr9q33.1	215407_s_at	NM_014010 /// NM_198186 /// NM_198187 /// NM_198188
2.34	2.67	0.34	1.36E-01	5.00E-01	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	chr5p15.2	229427_at	NM_003966
3.25	3.54	0.29	1.36E-01	5.00E-01	RAB23	RAB23, member RAS oncogene family	chr6p11	220955_x_at	NM_016277 /// NM_183227
2.76	3.04	0.28	1.36E-01	5.00E-01	A1BG	alpha-1-B glycoprotein	chr19q13.4	229819_at	NM_130786
3.15	3.35	0.20	1.36E-01	5.00E-01	ACHE	acetylcholinesterase (Yt blood group)	chr7q22	205378_s_at	NM_000665 /// NM_015831
3.03	3.21	0.18	1.36E-01	5.00E-01	---	---	---	222356_at	---
7.03	7.62	0.60	1.36E-01	5.00E-01	---	---	---	AFFX-HUMRGE/M10098_5_at	---
7.07	7.41	0.34	1.36E-01	5.00E-01	ATP6 /// LOC440552	ATP synthase 6; ATPase subunit 6 /// OK/SW-cl.16	chr1p36.33	242131_at	---
2.48	2.79	0.31	1.36E-01	5.00E-01	MCTP2	multiple C2 domains, transmembrane 2	chr15q26.2	243109_at	NM_018349
2.41	2.65	0.24	1.37E-01	5.00E-01	C4orf37	chromosome 4 open reading frame 37	chr4q22.3-q23	1555096_at	NM_174952
5.33	5.59	0.26	1.37E-01	5.00E-01	GTPBP5	GTP binding protein 5 (putative)	chr20q13.33	236890_at	NM_015666
2.74	2.98	0.24	1.37E-01	5.00E-01	---	---	---	225801_at	---
1.96	2.14	0.18	1.37E-01	5.00E-01	---	---	---	236627_at	---
7.75	8.27	0.52	1.37E-01	5.00E-01	RARS2	arginyl-tRNA synthetase 2, mitochondrial	chr6q16.1	225264_at	NM_020320
2.72	3.00	0.28	1.37E-01	5.00E-01	FAM66C /// LOC100132923	family with sequence similarity 66, member C /// similar to hCG1993470	chr12p13.31 /// chr8p23.1	1559950_at	XM_001716286 /// XR_040642 /// XR_040643
2.54	2.81	0.27	1.37E-01	5.00E-01	IL5RA	interleukin 5 receptor, alpha	chr3p26-p24	210744_s_at	NM_000564 /// NM_175724 /// NM_175725 /// NM_175726 /// NM_175727 /// NM_175728

3.73	4.12	0.39	1.37E-01	5.00E-01	GRB10	growth factor receptor-bound protein 10	chr7p12-p11.2	215248_at	NM_001001549 /// NM_001001550 /// NM_001001555 /// NM_005311
4.88	5.24	0.36	1.37E-01	5.00E-01	USP6NL	USP6 N-terminal like	chr10p13	204761_at	NM_001080491
4.73	5.01	0.29	1.37E-01	5.00E-01	TMEM92	transmembrane protein 92	chr17q21.33	235245_at	NM_153229
2.78	2.98	0.20	1.37E-01	5.00E-01	---	---	---	239110_s_at	---
4.00	4.22	0.22	1.37E-01	5.00E-01	---	---	---	242896_at	---
3.49	3.69	0.19	1.37E-01	5.00E-01	KIF20B	kinesin family member 20B	chr10q23.31	205235_s_at	NM_016195
2.04	2.23	0.18	1.37E-01	5.00E-01	SNPH	syntaphilin	chr20p13	215917_at	NM_014723
4.10	4.69	0.59	1.37E-01	5.01E-01	---	---	---	238988_at	---
2.55	2.84	0.29	1.37E-01	5.01E-01	THSD4	Thrombospondin, type I, domain containing 4	chr15q23	234323_at	NM_024817
2.20	2.43	0.22	1.37E-01	5.01E-01	CLASP2	Cytoplasmic linker associated protein 2	chr3p22.3	238048_at	NM_015097
8.12	8.43	0.31	1.37E-01	5.01E-01	---	---	---	214989_x_at	---
6.07	6.84	0.77	1.37E-01	5.01E-01	EPB41L3	erythrocyte membrane protein band 4.1-like 3	chr18p11.32	206710_s_at	NM_012307
4.35	4.68	0.32	1.37E-01	5.01E-01	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	chr9q32	214698_at	NM_005156
5.44	6.06	0.62	1.37E-01	5.01E-01	LACTB2	lactamase, beta 2	chr8p22-q22.3	222714_s_at	NM_016027
3.95	4.35	0.40	1.37E-01	5.01E-01	SPATS2	spermatogenesis associated, serine-rich 2	chr12q13.12	222593_s_at	NM_023071
3.11	3.33	0.21	1.37E-01	5.01E-01	HTR6	5-hydroxytryptamine (serotonin) receptor 6	chr1p36-p35	1552857_a_at	NM_000871
3.98	4.30	0.31	1.37E-01	5.01E-01	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	chr16q12.2	215715_at	NM_001043
5.33	5.60	0.27	1.37E-01	5.01E-01	LRRC16B	leucine rich repeat containing 16B	chr14q11.2-q12	229561_at	NM_138360
5.08	5.34	0.26	1.37E-01	5.01E-01	---	---	---	234327_at	---
2.04	2.28	0.25	1.37E-01	5.01E-01	UBASH3B	ubiquitin associated and SH3 domain containing, B	chr11q24.1	228353_x_at	NM_032873
2.57	2.80	0.23	1.37E-01	5.01E-01	---	---	---	232335_at	---
2.86	3.06	0.20	1.37E-01	5.01E-01	SDK2	sidekick homolog 2 (chicken)	chr17q25.1	232061_at	NM_019064
6.40	7.30	0.90	1.37E-01	5.01E-01	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	chr2p14	200729_s_at	NM_001005386 /// NM_005722
4.35	4.72	0.37	1.37E-01	5.01E-01	MMP15	matrix metallopeptidase 15 (membrane-inserted)	chr16q13-q21	203365_s_at	NM_002428
3.54	3.83	0.29	1.37E-01	5.01E-01	KIF19	kinesin family member 19	chr17q25.1	236426_at	NM_153209
2.75	2.93	0.18	1.37E-01	5.01E-01	---	---	---	1562390_at	---
2.45	2.77	0.32	1.37E-01	5.01E-01	ARHGAP24	Rho GTPase activating protein 24	chr4q21.23-q21.3	230803_s_at	NM_001025616 /// NM_001042669 /// NM_031305
2.55	2.76	0.21	1.37E-01	5.02E-01	VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	chr10q25.2	236849_at	NM_145206
1.90	2.08	0.18	1.37E-01	5.02E-01	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	chr7p15.1-p14.3	239218_at	NM_005020
2.30	2.80	0.50	1.38E-01	5.02E-01	NUMA1	nuclear mitotic apparatus protein 1	chr11q13	1554663_a_at	NM_006185
4.58	4.80	0.22	1.38E-01	5.02E-01	FAM80A	family with sequence similarity 80, member A	chr1p34.2	235948_at	NM_173642
3.48	3.71	0.23	1.38E-01	5.02E-01	PIP5KL1	phosphatidylinositol-4-phosphate 5-kinase-like 1	chr9q34.11	243116_at	NM_173492
2.13	2.36	0.23	1.38E-01	5.02E-01	SEMA6A	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	chr5q23.1	1558338_at	NM_020796
3.28	4.18	0.90	1.38E-01	5.02E-01	PDK4	pyruvate dehydrogenase kinase, isozyme 4	chr7q21.3	1562321_at	NM_002612
3.13	3.41	0.28	1.38E-01	5.02E-01	---	---	---	235772_at	---
3.36	3.63	0.27	1.38E-01	5.02E-01	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	chr2p24.1	234376_at	NM_005378
2.48	2.73	0.25	1.38E-01	5.02E-01	---	---	---	230301_at	---
4.21	4.45	0.23	1.38E-01	5.02E-01	PRELID2	PRELI domain containing 2	chr5q32	235828_at	NM_138492 /// NM_182960 /// NM_205846
2.18	2.42	0.23	1.38E-01	5.02E-01	FLJ32742	hypothetical locus FLJ32742	chrXp21.3	1553467_at	---
2.72	2.91	0.19	1.38E-01	5.02E-01	---	---	---	1559521_at	---
5.90	6.73	0.83	1.38E-01	5.02E-01	GPR34	G protein-coupled receptor 34	chrXp11.4-p11.3	223620_at	NM_001097579 /// NM_005300
4.34	4.64	0.30	1.38E-01	5.02E-01	---	---	---	241448_at	---
3.87	4.37	0.51	1.38E-01	5.02E-01	OLFML1	olfactomedin-like 1	chr11p15.4	217525_at	NM_198474
4.68	5.01	0.32	1.38E-01	5.02E-01	---	---	---	230041_at	---
1.99	2.23	0.24	1.38E-01	5.02E-01	CD1E	CD1e molecule	chr1q22-q23	215784_at	NM_001042583 /// NM_001042584 /// NM_001042585 /// NM_001042586 /// NM_001042587 /// NM_030893
2.55	2.89	0.34	1.38E-01	5.02E-01	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	chr17q11.1-q11.2	227884_at	NM_003487 /// NM_139215

5.94	6.60	0.66	1.38E-01	5.02E-01	RTCD1	RNA terminal phosphate cyclase domain 1	chr1p21.2	203594_at	NM_001130841 /// NM_003729
5.38	5.83	0.45	1.38E-01	5.02E-01	CUL5	cullin 5	chr11q22-q23	203533_s_at	NM_003478
2.37	2.65	0.28	1.38E-01	5.02E-01	---	---	---	242532_at	---
2.96	3.20	0.25	1.38E-01	5.02E-01	LOC100134123	hypothetical protein LOC100134123	---	229737_at	XM_001719358
2.97	3.17	0.21	1.38E-01	5.02E-01	---	---	---	224011_at	---
2.65	2.86	0.22	1.38E-01	5.02E-01	---	---	---	238556_at	---
1.82	2.01	0.20	1.38E-01	5.02E-01	---	---	---	232257_s_at	---
5.22	5.83	0.61	1.38E-01	5.03E-01	GPRC5B	G protein-coupled receptor, family C, group 5, member B	chr16p12	203632_s_at	NM_016235
7.16	7.70	0.54	1.38E-01	5.03E-01	SEC62	SEC62 homolog (S. cerevisiae)	chr3q26.2	225352_at	NM_003262
2.13	2.38	0.25	1.38E-01	5.03E-01	LOC727924 /// OR4N4	hypothetical LOC727924 /// olfactory receptor, family 4, subfamily N, member 4	chr15q11.2	1564856_s_at	NM_001005241 /// XR_039952
5.27	5.94	0.67	1.38E-01	5.03E-01	---	---	---	244579_at	---
7.18	7.40	0.21	1.38E-01	5.03E-01	---	---	---	208246_x_at	---
1.93	2.08	0.15	1.38E-01	5.03E-01	ZNF642	zinc finger protein 642	chr1p34.2	1569107_s_at	NM_198494
6.31	7.23	0.92	1.38E-01	5.03E-01	EPB41L3	erythrocyte membrane protein band 4.1-like 3	chr18p11.32	211776_s_at	NM_012307
4.95	5.47	0.52	1.38E-01	5.03E-01	FAM115A /// FAM115B	family with sequence similarity 115, member A /// family with sequence similarity 115, member B (pseudogene)	chr7q35	210529_s_at	NM_014719 /// XM_001714706 /// XM_001719004 /// XM_001732820
2.31	2.52	0.20	1.38E-01	5.03E-01	ARG1	Arginase, liver	chr6q23	231662_at	NM_000045
4.91	5.14	0.23	1.38E-01	5.03E-01	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	chr16p13.3	204267_x_at	NM_004203 /// NM_182687
2.96	3.15	0.20	1.38E-01	5.03E-01	---	---	---	232225_at	---
1.89	2.04	0.15	1.38E-01	5.03E-01	CYLC1	cylicin, basic protein of sperm head cytoskeleton 1	chrXq21.1	216778_s_at	NM_021118
2.41	2.60	0.18	1.39E-01	5.03E-01	---	---	---	239103_at	---
2.18	2.45	0.28	1.39E-01	5.03E-01	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	chr4q21.23	222063_s_at	NM_001263
4.28	5.45	1.16	1.39E-01	5.03E-01	NIPBL	Nipped-B homolog (Drosophila)	chr5p13.2	207108_s_at	NM_015384 /// NM_133433
2.52	2.92	0.40	1.39E-01	5.03E-01	---	---	---	1559394_a_at	---
6.57	6.98	0.40	1.39E-01	5.03E-01	TBC1D5	TBC1 domain family, member 5	chr3p24.3	201813_s_at	NM_001134380 /// NM_001134381 /// NM_014744 /// XM_001716616 /// XM_001718151
4.83	5.11	0.28	1.39E-01	5.03E-01	MMP25	matrix metallopeptidase 25	chr16p13.3	207289_at	NM_022468
3.57	3.77	0.20	1.39E-01	5.03E-01	---	---	---	216329_at	---
2.46	2.68	0.23	1.39E-01	5.03E-01	ITGA8	integrin, alpha 8	chr10p13	239092_at	NM_003638
3.03	3.27	0.25	1.39E-01	5.04E-01	LOC388553	Similar to hCG1645909	chr19q13.32	244123_at	XM_001717914 /// XM_373809 /// XM_944980
2.55	2.76	0.22	1.39E-01	5.04E-01	---	---	---	244816_at	---
7.62	8.33	0.71	1.39E-01	5.04E-01	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	chr1p36.1	208727_s_at	NM_001039802 /// NM_001791 /// NM_044472
2.48	2.83	0.35	1.39E-01	5.04E-01	---	---	---	233058_at	---
6.49	6.97	0.48	1.39E-01	5.04E-01	RSBN1	round spermatid basic protein 1	chr1p13.2	222790_s_at	NM_018364
2.09	2.29	0.20	1.39E-01	5.04E-01	---	---	---	1558764_at	---
6.44	6.90	0.46	1.39E-01	5.04E-01	ARV1	ARV1 homolog (S. cerevisiae)	chr1q42.2	223223_at	NM_022786
4.64	5.48	0.84	1.39E-01	5.04E-01	---	---	---	230791_at	---
5.33	6.14	0.81	1.39E-01	5.04E-01	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	chr4q26	224994_at	NM_001221 /// NM_172115 /// NM_172127 /// NM_172128
5.79	6.25	0.46	1.39E-01	5.04E-01	RPE	ribulose-5-phosphate-3-epimerase	chr2q32-q33.3	221770_at	NM_006916 /// NM_199229
5.82	6.22	0.40	1.39E-01	5.04E-01	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	chr14q23.3	226092_at	NM_022474
2.02	2.42	0.40	1.39E-01	5.04E-01	---	---	---	221205_at	---
4.99	5.37	0.39	1.39E-01	5.04E-01	---	---	---	226594_at	---
3.17	3.47	0.29	1.39E-01	5.04E-01	CACNG5	calcium channel, voltage-dependent, gamma subunit 5	chr17q24	1552602_at	NM_014404 /// NM_145811

4.81	5.07	0.27	1.39E-01	5.04E-01	TBC1D5	TBC1 domain family, member 5	chr3p24.3	201815_s_at	NM_001134380 /// NM_001134381 /// NM_014744 /// XM_001716616 /// XM_001718151
2.95	3.22	0.27	1.39E-01	5.04E-01	RSPO4	R-spondin family, member 4	chr20p13	237423_at	NM_001029871 /// NM_001040007
4.08	4.34	0.26	1.39E-01	5.04E-01	TMEM106A	Transmembrane protein 106A	chr17q21.31	234580_at	NM_145041
2.24	2.50	0.26	1.39E-01	5.04E-01	---	---	---	1563245_at	---
2.08	2.33	0.26	1.39E-01	5.04E-01	---	---	---	1557029_at	---
2.26	2.50	0.25	1.39E-01	5.04E-01	HYDIN /// HYDIN2	hydrocephalus inducing homolog (mouse) /// hydrocephalus inducing homolog 2 (mouse)	chr16q22.1-q22.3 /// chr1q21.1	243354_at	NM_017558 /// NM_032821 /// XM_001717859
2.44	2.67	0.22	1.39E-01	5.04E-01	TFPI	Tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	chr2q32	215447_at	NM_001032281 /// NM_006287
5.11	5.32	0.20	1.39E-01	5.04E-01	LPCAT4	lysophosphatidylcholine acyltransferase 4	chr15q14	239608_at	NM_153613
2.90	3.28	0.38	1.39E-01	5.04E-01	NMUR2	neuromedin U receptor 2	chr5q33.1	224088_at	NM_020167
2.02	2.25	0.23	1.39E-01	5.04E-01	NEGR1	neuronal growth regulator 1	chr1p31.1	229461_x_at	NM_173808
4.39	4.73	0.34	1.39E-01	5.04E-01	LRRC68	leucine rich repeat containing 68	chr19q13.32	229262_at	XM_001722969 /// XM_001723010 /// XM_001724714
3.85	4.99	1.14	1.39E-01	5.04E-01	TPSAB1	tryptase alpha/beta 1	chr16p13.3	210084_x_at	NM_003294 /// XM_001720738 /// XM_001720740
2.46	2.64	0.18	1.39E-01	5.04E-01	PDCD1LG2	programmed cell death 1 ligand 2	chr9p24.2	220049_s_at	NM_025239
2.22	2.43	0.21	1.39E-01	5.04E-01	---	---	---	1570116_at	---
2.05	2.24	0.19	1.39E-01	5.04E-01	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	chr7q21-q22	207870_at	NM_005751 /// NM_147166 /// NM_147171 /// NM_147185
4.59	5.08	0.49	1.39E-01	5.04E-01	FAM114A2	family with sequence similarity 114, member A2	chr5q31-q33	218588_s_at	NM_018691
2.64	2.85	0.21	1.39E-01	5.04E-01	WNT9B	wingless-type MMTV integration site family, member 9B	chr17q21	1552973_at	NM_003396
3.07	3.32	0.25	1.40E-01	5.05E-01	RPS6KL1	ribosomal protein S6 kinase-like 1	chr14q24.3	223534_s_at	NM_031464
2.70	2.93	0.23	1.40E-01	5.05E-01	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	chr11q13	204717_s_at	NM_001532
2.15	2.31	0.17	1.40E-01	5.05E-01	---	---	---	1564389_at	---
5.31	5.67	0.36	1.40E-01	5.05E-01	SFRS12IP1	SFRS12-interacting protein 1	chr5q12.3	227288_at	NM_173829
3.16	3.42	0.26	1.40E-01	5.05E-01	FLJ44606	hypothetical gene supported by AK126569	chr5q23.2	239623_at	XM_001722994 /// XM_932789 /// XM_943643
2.15	2.37	0.22	1.40E-01	5.05E-01	ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	chr3p25.3	239357_at	NM_001001331 /// NM_001683
3.15	3.44	0.30	1.40E-01	5.05E-01	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	chr19q13.43	235773_at	NM_001010879
4.77	5.06	0.29	1.40E-01	5.05E-01	BCL2	B-cell CLL/lymphoma 2	chr18q21.33|18q21.3	207005_s_at	NM_000633 /// NM_000657
2.56	2.78	0.22	1.40E-01	5.05E-01	---	---	---	244384_at	---
2.47	2.67	0.20	1.40E-01	5.05E-01	GPR17	G protein-coupled receptor 17	chr2q21	215225_s_at	NM_005291
6.90	7.44	0.54	1.40E-01	5.05E-01	TRAK2	trafficking protein, kinesin binding 2	chr2q33	202125_s_at	NM_015049
4.35	4.62	0.27	1.40E-01	5.05E-01	LOC729683	hypothetical protein LOC729683	chr17q23.3	236497_at	XR_040516 /// XR_040517 /// XR_040518
3.74	3.97	0.23	1.40E-01	5.05E-01	---	---	---	240087_at	---
2.30	2.53	0.23	1.40E-01	5.05E-01	UPK1A	uroplakin 1A	chr19q13.13	214624_at	NM_007000
2.76	2.98	0.22	1.40E-01	5.05E-01	FLJ12616	hypothetical LOC196707	chr10q26.13	220902_at	XR_040606 /// XR_040607 /// XR_040608
2.32	2.53	0.21	1.40E-01	5.05E-01	LYST	lysosomal trafficking regulator	chr1q42.1-q42.2	1562511_at	NM_000081
2.80	3.00	0.20	1.40E-01	5.05E-01	FMNL2	formin-like 2	chr2q23.3	242665_at	NM_052905
2.26	2.46	0.20	1.40E-01	5.05E-01	CADPS	Ca++-dependent secretion activator	chr3p14.2	233950_at	NM_003716 /// NM_183393 /// NM_183394
1.94	2.10	0.16	1.40E-01	5.05E-01	---	---	---	216828_at	---

4.25	4.56	0.31	1.40E-01	5.05E-01	IQSEC3 /// LOC100134209 /// LOC731035	IQ motif and Sec7 domain 3 /// similar to IQ motif and Sec7 domain-containing protein 3 /// similar to IQ motif and Sec7 domain 3	chr12p13.33	1556872_s_at	NM_015232 /// XM_001126365 /// XM_001720539
2.66	2.96	0.30	1.40E-01	5.05E-01	---	---	---	234574_at	---
5.14	5.96	0.82	1.40E-01	5.05E-01	RBBP6	retinoblastoma binding protein 6	chr16p12.2	212783_at	NM_006910 /// NM_018703 /// NM_032626
6.36	6.69	0.33	1.40E-01	5.05E-01	TNRC6B	trinucleotide repeat containing 6B	chr22q13.1	213254_at	NM_001024843 /// NM_015088
2.79	3.10	0.31	1.40E-01	5.05E-01	DMRTB1	DMRT-like family B with proline-rich C-terminal, 1	chr1p32.3	240313_at	NM_033067
2.48	2.71	0.23	1.40E-01	5.05E-01	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	chr1q32.1	227819_at	NM_001017403 /// NM_001017404 /// NM_021636
2.07	2.26	0.19	1.40E-01	5.05E-01	---	---	---	242031_at	---
2.38	2.65	0.27	1.40E-01	5.05E-01	RD3	retinal degeneration 3	chr1q32.3	236563_at	NM_183059
7.27	8.18	0.91	1.40E-01	5.05E-01	TROVE2	TROVE domain family, member 2	chr1q31	210438_x_at	NM_001042369 /// NM_001042370 /// NM_004600
2.41	2.67	0.26	1.40E-01	5.05E-01	---	---	---	1560352_at	---
2.40	2.61	0.20	1.40E-01	5.05E-01	NCSTN	nicastrin	chr1q22-q23	237076_at	NM_015331
2.03	2.19	0.17	1.40E-01	5.05E-01	PROX2	prospero homeobox 2	chr14q24.3	234804_at	NM_001080408
4.58	5.22	0.64	1.40E-01	5.05E-01	ATMIN	ATM interactor	chr16q23.2	201855_s_at	NM_015251
4.18	4.78	0.60	1.40E-01	5.05E-01	HCFC2	host cell factor C2	chr12q23.3	219484_at	NM_013320
4.72	5.24	0.53	1.40E-01	5.05E-01	NEXN	nexilin (F actin binding protein)	chr1p31.1	226103_at	NM_144573
5.54	6.01	0.47	1.40E-01	5.05E-01	ATXN10	ataxin 10	chr22q13.31	208832_at	NM_013236
5.61	5.91	0.29	1.40E-01	5.05E-01	PURA	purine-rich element binding protein A	chr5q31	204021_s_at	NM_005859
4.62	4.88	0.26	1.40E-01	5.05E-01	FUT2	fucosyltransferase 2 (secretor status included)	chr19q13.3	208505_s_at	NM_000511 /// NM_001097638
4.01	4.26	0.25	1.40E-01	5.05E-01	PCDHGA9	protocadherin gamma subfamily A, 9	chr5q31	211873_s_at	NM_018921 /// NM_032089
2.82	3.05	0.22	1.40E-01	5.05E-01	RIOK2	RIO kinase 2 (yeast)	chr5q15	222663_at	NM_018343
2.43	2.65	0.22	1.40E-01	5.05E-01	---	---	---	234659_at	---
3.82	4.03	0.22	1.40E-01	5.05E-01	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	chr11q13	1560149_at	NM_001532
1.98	2.14	0.16	1.40E-01	5.05E-01	---	---	---	234396_at	---
2.51	2.76	0.25	1.40E-01	5.05E-01	---	---	---	231409_at	---
2.03	2.27	0.24	1.40E-01	5.05E-01	---	---	---	243739_at	---
3.49	3.71	0.22	1.40E-01	5.05E-01	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	221281_at	NM_005417 /// NM_198291
2.61	2.90	0.29	1.40E-01	5.05E-01	TTTY7	testis-specific transcript, Y-linked 7	chrYp11.2	1561185_at	NR_001534
3.59	3.91	0.32	1.40E-01	5.06E-01	CACHD1	Cache domain containing 1	chr1p31.3	234888_at	NM_020925
6.14	7.92	1.78	1.41E-01	5.06E-01	NAMPT	Nicotinamide phosphoribosyltransferase	chr7q22.2	243296_at	NM_005746
6.82	7.42	0.60	1.41E-01	5.06E-01	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	chr17p13.3	200816_s_at	NM_000430
2.99	3.36	0.37	1.41E-01	5.06E-01	---	---	---	1556671_s_at	---
3.03	3.28	0.24	1.41E-01	5.06E-01	---	---	---	236949_at	---
2.42	2.60	0.19	1.41E-01	5.06E-01	HABP4	hyaluronan binding protein 4	chr9q22.3-q31	209819_at	NM_014282
5.12	5.39	0.26	1.41E-01	5.06E-01	---	---	---	204390_at	---
3.75	4.17	0.42	1.41E-01	5.06E-01	YTHDC2	YTH domain containing 2	chr5q22.2	1568680_s_at	NM_022828
4.54	4.93	0.39	1.41E-01	5.06E-01	ZSCAN29	zinc finger and SCAN domain containing 29	chr15q15.3	226562_at	NM_152455
3.03	3.26	0.23	1.41E-01	5.06E-01	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	chr8p23	1554213_at	NM_014629
2.10	2.31	0.21	1.41E-01	5.06E-01	KIAA1244	KIAA1244	chr6q23.3	231856_at	NM_020340
2.07	2.28	0.21	1.41E-01	5.06E-01	SLITRK1	SLIT and NTRK-like family, member 1	chr13q31.1	236734_at	NM_052910
6.69	7.21	0.52	1.41E-01	5.06E-01	MGLL	monoglyceride lipase	chr3q21.3	211026_s_at	NM_001003794 /// NM_007283
3.51	4.13	0.62	1.41E-01	5.06E-01	CPXM2	carboxypeptidase X (M14 family), member 2	chr10q26.13	236144_at	NM_198148
3.13	3.73	0.60	1.41E-01	5.06E-01	ANGPT1	angiopoietin 1	chr8q22.3-q23	205609_at	NM_001146
3.27	3.61	0.35	1.41E-01	5.06E-01	---	---	---	242858_at	---
2.43	2.76	0.33	1.41E-01	5.06E-01	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	chr14q24.1	217042_at	NM_016026
4.39	4.62	0.24	1.41E-01	5.06E-01	---	---	---	244311_at	---
2.36	2.58	0.22	1.41E-01	5.06E-01	---	---	---	1561064_a_at	---
2.00	2.17	0.17	1.41E-01	5.06E-01	---	---	---	239967_at	---
4.96	5.79	0.83	1.41E-01	5.07E-01	HSDL2	hydroxysteroid dehydrogenase like 2	chr9q32	209512_at	NM_032303
3.74	3.99	0.24	1.41E-01	5.07E-01	---	---	---	237607_at	---
4.87	5.06	0.19	1.41E-01	5.07E-01	---	---	---	233424_at	---
3.05	3.46	0.41	1.41E-01	5.07E-01	CFHR2	complement factor H-related 2	chr1q31-q32.1	206910_x_at	NM_005666

5.71	6.61	0.89	1.41E-01	5.07E-01	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	chr7q22.1	223189_x_at	NM_018682 /// NM_182931
8.05	8.35	0.30	1.41E-01	5.07E-01	DBT	dihydrolipoamide branched chain transacylase E2	chr1p31	205370_x_at	NM_001918
2.32	2.57	0.25	1.41E-01	5.07E-01	LOC728987	Hypothetical LOC728987	chr1q42.2	1566464_at	XM_001132417 /// XM_001132664 /// XM_001722952
3.02	3.30	0.28	1.41E-01	5.07E-01	CDCP1	CUB domain containing protein 1	chr3p21.31	234932_s_at	NM_022842 /// NM_178181
7.55	8.05	0.50	1.41E-01	5.07E-01	LRRC37A2	Leucine rich repeat containing 37, member A2	chr17q21.32	224686_x_at	NM_001006607
3.40	3.67	0.28	1.41E-01	5.07E-01	CMKLR1	chemokine-like receptor 1	chr12q24.1	207652_s_at	NM_004072
3.03	3.27	0.24	1.41E-01	5.07E-01	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	chr6p21	242757_at	NM_153487
3.17	3.39	0.23	1.41E-01	5.07E-01	---	---	---	241563_at	---
2.09	2.31	0.22	1.41E-01	5.07E-01	---	---	---	237912_at	---
4.44	5.21	0.77	1.41E-01	5.07E-01	ACTG2	actin, gamma 2, smooth muscle, enteric	chr2p13.1	202274_at	NM_001615
2.15	2.32	0.18	1.41E-01	5.07E-01	---	---	---	237578_at	---
2.22	2.53	0.31	1.41E-01	5.07E-01	---	---	---	1556865_at	---
7.66	8.63	0.97	1.42E-01	5.07E-01	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	chr2p14	200728_at	NM_001005386 /// NM_005722
5.50	5.95	0.45	1.42E-01	5.07E-01	LOC728866 /// MAGT1	hypothetical LOC728866 /// magnesium transporter 1	chrXq21.1	221553_at	NM_032121 /// XM_001717240
2.79	3.08	0.29	1.42E-01	5.07E-01	---	---	---	1561967_at	---
1.85	2.13	0.28	1.42E-01	5.07E-01	BIC	BIC transcript	---	229437_at	NR_001458
2.28	2.53	0.25	1.42E-01	5.07E-01	---	---	---	244098_at	---
1.85	2.01	0.16	1.42E-01	5.07E-01	---	---	---	1563660_at	---
1.86	2.02	0.15	1.42E-01	5.07E-01	DYDC1	DPY30 domain containing 1	chr10q23.1	1552993_at	NM_138812
1.75	1.90	0.15	1.42E-01	5.07E-01	---	---	---	1563881_at	---
5.89	6.49	0.60	1.42E-01	5.07E-01	ING3	inhibitor of growth family, member 3	chr7q31	205070_at	NM_019071 /// NM_198267
2.72	3.00	0.29	1.42E-01	5.07E-01	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	chr1q32	206244_at	NM_000573 /// NM_000651
4.32	4.56	0.24	1.42E-01	5.07E-01	UBR4	ubiquitin protein ligase E3 component n-recognin 4	chr1p36.13	232907_at	NM_020765
1.95	2.18	0.23	1.42E-01	5.07E-01	---	---	---	216378_at	---
2.44	2.61	0.17	1.42E-01	5.07E-01	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	chr11q13	204941_s_at	NM_000695 /// NM_001031615
12.10	12.35	0.25	1.42E-01	5.07E-01	FTL	ferritin, light polypeptide	chr19q13.3-q13.4|19q13.3	212788_x_at	NM_000146
2.04	2.22	0.17	1.42E-01	5.07E-01	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	chr2q24.1	207142_at	NM_002239
4.42	4.96	0.53	1.42E-01	5.07E-01	WSCD1	WSC domain containing 1	chr17p13.2	213157_s_at	NM_015253
5.67	5.89	0.22	1.42E-01	5.07E-01	RMND5B	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	chr5q35.3	213297_at	NM_022762
2.30	2.54	0.24	1.42E-01	5.07E-01	NLGN4X	neuroligin 4, X-linked	chrXp22.32-p22.31	221933_at	NM_020742 /// NM_181332
2.59	2.78	0.19	1.42E-01	5.07E-01	SOX5	SRY (sex determining region Y)-box 5	chr12p12.1	238285_at	NM_006940 /// NM_152989 /// NM_178010
5.96	6.57	0.62	1.42E-01	5.08E-01	ERGIC2	ERGIC and golgi 2	chr12p11.22	218135_at	NM_016570
1.95	2.21	0.26	1.42E-01	5.08E-01	C6orf65	chromosome 6 open reading frame 65	chr6p12.1	231175_at	NM_152731
3.49	3.73	0.24	1.42E-01	5.08E-01	PVRL4	poliovirus receptor-related 4	chr1q22-q23.2	223540_at	NM_030916
2.26	2.53	0.28	1.42E-01	5.08E-01	---	---	---	242275_at	---
6.27	6.79	0.52	1.42E-01	5.08E-01	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	chr17q25.1	201349_at	NM_004252
5.20	6.34	1.14	1.42E-01	5.08E-01	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	chr8q24.1	209392_at	NM_001040092 /// NM_001130863 /// NM_006209
5.93	6.99	1.06	1.42E-01	5.08E-01	SEC63	SEC63 homolog (S. cerevisiae)	chr6q21	201914_s_at	NM_007214
4.31	4.61	0.30	1.42E-01	5.08E-01	TSEN15	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	chr1q25	225400_at	NM_001127394 /// NM_052965 /// NR_023349
2.12	2.43	0.31	1.42E-01	5.08E-01	ARID5B	AT rich interactive domain 5B (MRF1-like)	chr10q21.2	241969_at	NM_032199
2.59	2.88	0.29	1.42E-01	5.08E-01	---	---	---	1554963_at	---
2.03	2.25	0.22	1.42E-01	5.08E-01	---	---	---	233784_at	---
4.55	4.77	0.21	1.42E-01	5.08E-01	LOC126520	hypothetical protein LOC126520	chr19p13.3	1558897_at	XR_015464 /// XR_015543 /// XR_041162
1.88	2.07	0.20	1.42E-01	5.08E-01	---	---	---	240965_at	---
5.08	5.52	0.45	1.42E-01	5.08E-01	ZFAND6	Zinc finger, AN1-type domain 6	chr15q25.1	239757_at	NM_019006

2.11	2.29	0.18	1.42E-01	5.08E-01	LARP2	La ribonucleoprotein domain family, member 2	chr4q28.2	231824_at	NM_018078 /// NM_032239 /// NM_178043																				
2.15	2.35	0.20	1.42E-01	5.08E-01	---	---	---	1567078_x_at	---																				
3.99	4.22	0.23	1.42E-01	5.08E-01	APC2	adenomatosis polyposis coli 2	chr19p13.3	217174_s_at	NM_005883																				
2.57	2.81	0.24	1.42E-01	5.08E-01	---	---	---	1560643_x_at	---																				
4.49	4.72	0.23	1.42E-01	5.08E-01	DST	dystonin	chr6p12.1	216918_s_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380																				
2.21	2.40	0.19	1.42E-01	5.08E-01	MYRIP	myosin VIIA and Rab interacting protein	chr3p22.1	242730_at	NM_015460																				
2.84	3.15	0.30	1.42E-01	5.08E-01	LOC100129346	similar to FLJ42875 protein	chr1p36.32	231275_at	XM_001713947 /// XM_001719060 /// XM_001724234																				
3.38	3.67	0.29	1.42E-01	5.08E-01	---	---	---	1559991_s_at	---																				
2.15	2.37	0.22	1.42E-01	5.08E-01	---	---	---	1556828_at	---																				
7.35	7.93	0.58	1.42E-01	5.08E-01	IQWD1	IQ motif and WD repeats 1	chr1q24.2	217908_s_at	NM_001017977 /// NM_018442																				
7.25	7.81	0.56	1.42E-01	5.08E-01	CCDC53	coiled-coil domain containing 53	chr12q23.2	218628_at	NM_016053																				
2.74	3.07	0.34	1.42E-01	5.08E-01	ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	chr7p14	207151_at	NM_001118																				
5.12	6.04	0.92	1.42E-01	5.08E-01	NBEA	neurobeachin	chr13q13	226439_s_at	NM_015678																				
4.79	5.61	0.82	1.42E-01	5.08E-01	LPHN3	latrophilin 3	chr4q13.1	236264_at	NM_015236																				
3.47	3.72	0.25	1.42E-01	5.08E-01	LOC652346 /// PML	similar to promyelocytic leukemia protein isoform 1 /// promyelocytic leukemia	chr15q22	211588_s_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250 /// XM_001716106																				
3.56	3.99	0.43	1.42E-01	5.08E-01	AHI1	Abelson helper integration site 1	chr6q23.3	220841_s_at	NM_017651																				
2.83	3.02	0.20	1.42E-01	5.08E-01	ZNF101	zinc finger protein 101	chr19p13.11	1552633_at	NM_033204																				
3.76	4.09	0.34	1.43E-01	5.09E-01	DAAM1	Dishevelled associated activator of morphogenesis 1	chr14q23.1	232552_at	NM_014992																				
2.35	2.54	0.19	1.43E-01	5.09E-01	---	---	---	1562752_at	---																				
3.52	3.99	0.48	1.43E-01	5.09E-01	---	---	---	230651_at	---																				
4.56	5.65	1.10	1.43E-01	5.09E-01	CALD1	caldesmon 1	chr7q33	201617_x_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157																				
2.77	3.04	0.27	1.43E-01	5.09E-01	SRR	serine racemase	chr17p13	222844_s_at	NM_021947																				
2.44	2.68	0.24	1.43E-01	5.09E-01	---	---	---	1561293_at	---																				
2.49	2.76	0.27	1.43E-01	5.09E-01	CXCL3	chemokine (C-X-C motif) ligand 3	chr4q21	207850_at	NM_002090																				
4.38	4.91	0.53	1.43E-01	5.09E-01	---	---	---	242059_at	---																				
2.14	2.51	0.38	1.43E-01	5.09E-01	CLIC3	chloride intracellular channel 3	chr9q34.3	219529_at	NM_004669																				
5.30	5.83	0.53	1.43E-01	5.09E-01	MIB1	mindbomb homolog 1 (Drosophila)	chr18q11.2	224726_at	NM_020774																				
4.85	5.09	0.24	1.43E-01	5.09E-01	CRB3	crumbs homolog 3 (Drosophila)	chr19p13.3	232609_at	NM_139161 /// NM_174881																				
2.31	2.54	0.23	1.43E-01	5.09E-01	RNF133	ring finger protein 133	chr7q31.32	231373_at	NM_139175																				
5.55	6.50	0.95	1.43E-01	5.09E-01	ZNF12	zinc finger protein 12	chr7p22.1	219571_s_at	NM_006956 /// NM_016265																				
7.86	8.09	0.24	1.43E-01	5.09E-01	---	---	---	216187_x_at	---																				
3.84	4.06	0.22	1.43E-01	5.09E-01	FBXO21	F-box protein 21	chr12q24.22	214891_at	NM_015002 /// NM_033624																				
3.11	3.39	0.28	1.43E-01	5.09E-01	ACTA1	actin, alpha 1, skeletal muscle	chr1q42.13|1q42.13-q42.2	203872_at	NM_001100																				
4.92	5.34	0.42	1.43E-01	5.09E-01	CD84	CD84 molecule	chr1q24	205988_at	NM_003874																				
3.58	3.85	0.28	1.43E-01	5.09E-01	ASXL3	additional sex combs like 3 (Drosophila)	chr18q11	233686_at	NM_030632																				
2.13	2.36	0.23	1.43E-01	5.09E-01	---	---	---	237705_at	---																				
5.26	5.48	0.23	1.43E-01	5.09E-01	HMX1	H6 family homeobox 1	chr4p16.1	214386_at	NM_018942																				
2.57	2.78	0.21	1.43E-01	5.09E-01	---	---	---	230931_at	---																				
2.57	2.86	0.29	1.43E-01	5.10E-01	OR51B2	olfactory receptor, family 51, subfamily B, member 2	chr11p15	234486_at	NM_033180																				

2.27	2.49	0.22	1.43E-01	5.10E-01	MIPOL1	mirror-image polydactyly 1	chr14q13.3-q21.1	1570052_at	NM_138731
7.15	7.38	0.23	1.43E-01	5.10E-01	ARMC10	armadillo repeat containing 10	chr7q22.1	223328_at	NM_031905
3.77	4.02	0.25	1.43E-01	5.10E-01	POLA2	Polymerase (DNA directed), alpha 2 (70kD subunit)	chr11q13.1	244575_at	NM_002689
3.36	3.64	0.28	1.43E-01	5.10E-01	LOC374890	hypothetical gene supported by BC030765	chr19p12	1556405_s_at	---
3.66	4.39	0.73	1.43E-01	5.10E-01	ARFIP1	ADP-ribosylation factor interacting protein 1	chr4q31.3	214483_s_at	NM_001025593 /// NM_001025595 /// NM_014447
4.90	5.17	0.28	1.43E-01	5.10E-01	IL27RA	interleukin 27 receptor, alpha	chr19p13.11	217702_at	NM_004843
3.78	4.39	0.61	1.43E-01	5.10E-01	MALL	mal, T-cell differentiation protein-like	chr2q13	209373_at	NM_005434
4.17	4.63	0.46	1.43E-01	5.10E-01	C14orf132	chromosome 14 open reading frame 132	chr14q32.2	218820_at	NR_023938 /// XR_040536 /// XR_040537 /// XR_040538
8.72	9.16	0.44	1.43E-01	5.10E-01	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	chr2p23	208631_s_at	NM_000182
5.53	5.91	0.38	1.43E-01	5.10E-01	TGFB3	transforming growth factor, beta 3	chr14q24	209747_at	NM_003239
12.34	12.68	0.34	1.43E-01	5.10E-01	RPS27A /// UBA52 /// UBB /// UBC	ribosomal protein S27a /// ubiquitin A-52 residue ribosomal protein fusion product 1 /// ubiquitin B /// ubiquitin C	chr12q24.3 /// chr17p12-p11.2 /// chr19p13.1-p12 /// chr2p16	211296_x_at	NM_001033930 /// NM_002954 /// NM_003333 /// NM_018955 /// NM_021009
3.14	3.37	0.23	1.43E-01	5.10E-01	---	---	---	217581_at	---
3.09	3.30	0.20	1.43E-01	5.10E-01	---	---	---	233871_at	---
7.82	8.65	0.83	1.43E-01	5.10E-01	CREBL2	cAMP responsive element binding protein-like 2	chr12p13	201988_s_at	NM_001310
2.08	2.30	0.22	1.44E-01	5.10E-01	CCDC88A	Coiled-coil domain containing 88A	chr2p16.1	1562648_at	NM_018084
1.97	2.14	0.17	1.44E-01	5.10E-01	STATH	statherin	chr4q11-q13	206835_at	NM_001009181 /// NM_003154
3.09	3.37	0.28	1.44E-01	5.10E-01	ASMT	acetylserotonin O-methyltransferase	chrXp22.3 or Yp11.3	210551_s_at	NM_004043
2.23	2.40	0.18	1.44E-01	5.10E-01	DLGAP3	Discs, large (Drosophila) homolog-associated protein 3	chr1p35.3-p34.1	1559630_at	NM_001080418
5.01	5.35	0.33	1.44E-01	5.10E-01	NAPSA	napsin A aspartic peptidase	chr19q13.33	223806_s_at	NM_004851
4.02	4.43	0.41	1.44E-01	5.10E-01	PLXNA4	plexin A4	chr7q32.3	228104_at	NM_001105543 /// NM_020911 /// NM_181775
3.93	4.24	0.31	1.44E-01	5.10E-01	HRASLS3	HRAS-like suppressor 3	chr11q12.3-q13.1	235110_at	NM_001128203 /// NM_007069
2.01	2.18	0.17	1.44E-01	5.11E-01	CLASP2	cytoplasmic linker associated protein 2	chr3p22.3	238224_at	NM_015097
6.25	6.60	0.35	1.44E-01	5.11E-01	NUP37	nucleoporin 37kDa	chr12q23.2	218622_at	NM_024057
6.39	7.34	0.95	1.44E-01	5.11E-01	ANXA1	annexin A1	chr9q12-q21.2|9q12-q21.2	201012_at	NM_000700
3.39	4.01	0.62	1.44E-01	5.11E-01	---	---	---	215574_at	---
5.06	5.58	0.53	1.44E-01	5.11E-01	CD93	CD93 molecule	chr20p11.21	202877_s_at	NM_012072
6.42	6.68	0.26	1.44E-01	5.11E-01	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	chr7q22	220371_s_at	NM_020246
2.67	2.91	0.24	1.44E-01	5.11E-01	ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	chr6p24.2	213712_at	NM_017770
2.09	2.31	0.22	1.44E-01	5.11E-01	RBL1	retinoblastoma-like 1 (p107)	chr20q11.2	1559307_s_at	NM_002895 /// NM_183404
2.11	2.30	0.18	1.44E-01	5.11E-01	---	---	---	217372_at	---
2.26	2.42	0.16	1.44E-01	5.11E-01	---	---	---	233876_at	---
4.13	4.86	0.73	1.44E-01	5.11E-01	LOC100132218 /// LOC728555	hypothetical protein LOC100132218 /// hypothetical LOC728555	chr5q13.2	230653_at	XM_001127758 /// XM_001715393
4.06	4.64	0.58	1.44E-01	5.11E-01	OMA1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	chr1p32.1	226019_at	NM_145243
5.16	5.64	0.48	1.44E-01	5.11E-01	WDR41	WD repeat domain 41	chr5q14.1	218055_s_at	NM_018268
3.26	3.54	0.29	1.44E-01	5.11E-01	FCN1	ficolin (collagen/fibrinogen domain containing) 1	chr9q34	205237_at	NM_002003
5.19	5.45	0.26	1.44E-01	5.11E-01	---	---	---	238150_at	---
4.13	4.37	0.24	1.44E-01	5.11E-01	---	---	---	216160_at	---
2.60	2.82	0.22	1.44E-01	5.11E-01	---	---	---	238826_x_at	---
2.28	2.48	0.20	1.44E-01	5.11E-01	---	---	---	1570093_at	---
2.11	2.30	0.19	1.44E-01	5.11E-01	LOC387895	hypothetical gene supported by BC040060	chr12q24.32	243905_at	XM_373553 /// XM_945559
1.84	2.03	0.19	1.44E-01	5.11E-01	GYPE	glycophorin E	chr4q31.1	1561136_at	NM_002102 /// NM_198682
2.06	2.23	0.17	1.44E-01	5.11E-01	SCN7A	sodium channel, voltage-gated, type VII, alpha	chr2q21-q23	207864_at	NM_002976
4.82	5.21	0.38	1.44E-01	5.11E-01	ZNF134	zinc finger protein 134	chr19q13.4	206182_at	NM_003435
3.38	3.71	0.33	1.44E-01	5.11E-01	NPAS1	neuronal PAS domain protein 1	chr19q13.2-q13.3	206699_x_at	NM_002517

1.87	2.12	0.25	1.44E-01	5.11E-01	---	---	---	237508_at	---
2.26	2.50	0.25	1.44E-01	5.11E-01	---	---	---	1556171_a_at	---
4.13	4.37	0.24	1.44E-01	5.11E-01	---	---	---	230605_at	---
2.70	2.94	0.24	1.44E-01	5.11E-01	RNF7	Ring finger protein 7	chr3q22-q24	239820_at	NM_014245 /// NM_183237
2.38	2.61	0.22	1.44E-01	5.11E-01	---	---	---	1567697_at	---
3.01	3.21	0.20	1.44E-01	5.11E-01	CDC42BPG	CDC42 binding protein kinase gamma (DMPK-like)	chr11q13.1	1564823_at	NM_017525
2.07	2.26	0.19	1.44E-01	5.11E-01	FRAS1	Fraser syndrome 1	chr4q21.21	243935_at	NM_025074
3.63	3.84	0.21	1.44E-01	5.11E-01	OSBPL7	oxysterol binding protein-like 7	chr17q21	210344_at	NM_145798
5.62	6.59	0.97	1.45E-01	5.11E-01	SCARB2	scavenger receptor class B, member 2	chr4q21.1	201646_at	NM_005506
4.73	5.66	0.93	1.45E-01	5.11E-01	MTUS1	mitochondrial tumor suppressor 1	chr8p22	212095_s_at	NM_001001924 /// NM_001001925 /// NM_001001931 /// NM_020749
4.56	5.07	0.51	1.45E-01	5.11E-01	---	---	---	233228_at	---
5.68	6.06	0.39	1.45E-01	5.11E-01	---	---	---	241617_x_at	---
3.00	3.33	0.34	1.45E-01	5.11E-01	---	---	---	216890_at	---
2.15	2.36	0.21	1.44E-01	5.11E-01	---	---	---	239631_at	---
2.13	2.33	0.21	1.45E-01	5.11E-01	---	---	---	234067_at	---
2.29	2.50	0.21	1.45E-01	5.11E-01	STRN	striatin, calmodulin binding protein	chr2p22-p21	1569815_x_at	NM_003162
6.10	6.37	0.27	1.45E-01	5.11E-01	OTUB1	OTU domain, ubiquitin aldehyde binding 1	chr11q13.1	201246_s_at	NM_017670 /// NR_003089
2.99	3.17	0.18	1.45E-01	5.11E-01	NAGLU	N-acetylglucosaminidase, alpha-	chr17q21	215880_at	NM_000263
3.17	3.63	0.46	1.45E-01	5.11E-01	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	chr5qter	214454_at	NM_014244 /// NM_021599
5.37	6.23	0.86	1.45E-01	5.11E-01	PAPD5	PAP associated domain containing 5	chr16q12.1	226843_s_at	NM_001040284 /// NM_001040285
2.76	3.05	0.29	1.45E-01	5.11E-01	---	---	---	1562712_at	---
2.94	3.18	0.25	1.45E-01	5.11E-01	GLT8D3	glycosyltransferase 8 domain containing 3	chr12q12	232021_at	NM_001099650 /// NM_173601
4.66	4.91	0.25	1.45E-01	5.11E-01	---	---	---	240617_at	---
2.47	2.73	0.26	1.45E-01	5.11E-01	---	---	---	234246_at	---
2.47	2.75	0.28	1.45E-01	5.11E-01	---	---	---	1566098_at	---
3.40	3.64	0.25	1.45E-01	5.11E-01	---	---	---	234120_at	---
2.03	2.26	0.23	1.45E-01	5.11E-01	---	---	---	237328_at	---
3.99	4.43	0.44	1.45E-01	5.11E-01	ODZ4	odz, odd Oz/ten-m homolog 4 (Drosophila)	chr11q14.1	213273_at	NM_001098816
4.87	5.24	0.38	1.45E-01	5.11E-01	---	---	---	227965_at	---
3.45	3.71	0.27	1.45E-01	5.11E-01	---	---	---	243279_at	---
2.02	2.22	0.21	1.45E-01	5.11E-01	---	---	---	243177_at	---
8.84	9.51	0.67	1.45E-01	5.12E-01	ACTA2	actin, alpha 2, smooth muscle, aorta	chr10q23.3	200974_at	NM_001613
5.83	6.15	0.32	1.45E-01	5.12E-01	IPO11	importin 11	chr5q12.1	222659_at	NM_016338
2.27	2.44	0.17	1.45E-01	5.12E-01	SSX3	synovial sarcoma, X breakpoint 3	chrXp11.23	207666_x_at	NM_021014 /// NM_175711
4.63	5.16	0.53	1.45E-01	5.12E-01	---	---	---	242110_at	---
2.79	3.01	0.22	1.45E-01	5.12E-01	C20orf43	chromosome 20 open reading frame 43	chr20q13.31	224128_at	NM_016407
7.70	8.23	0.54	1.45E-01	5.12E-01	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	chr11p15.5	204487_s_at	NM_000218 /// NM_181798
2.32	2.54	0.22	1.45E-01	5.12E-01	FOXD3	forkhead box D3	chr1p32-p31	208500_x_at	NM_012183
1.97	2.15	0.18	1.45E-01	5.12E-01	---	---	---	1557832_at	---
2.14	2.96	0.82	1.45E-01	5.12E-01	PLN	phospholamban	chr6q22.1	204940_at	NM_002667
3.13	3.67	0.54	1.45E-01	5.12E-01	---	---	---	216756_at	---
2.36	2.54	0.18	1.45E-01	5.12E-01	---	---	---	1563297_s_at	---
3.50	4.17	0.66	1.45E-01	5.12E-01	STARD4	StAR-related lipid transfer (START) domain containing 4	chr5q22.1	226390_at	NM_139164
2.02	2.22	0.20	1.45E-01	5.12E-01	DKFZP434L187	Hypothetical LOC26082	chr15q13.2	230861_at	XM_496054
2.05	2.24	0.19	1.45E-01	5.12E-01	---	---	---	239321_at	---
2.54	2.81	0.27	1.45E-01	5.12E-01	---	---	---	234837_at	---
2.11	2.36	0.24	1.45E-01	5.12E-01	AMPD1	adenosine monophosphate deaminase 1 (isoform M)	chr1p13	206121_at	NM_000036
1.96	2.18	0.23	1.45E-01	5.12E-01	---	---	---	237057_at	---
5.78	6.32	0.54	1.45E-01	5.12E-01	CRIM1	Cysteine rich transmembrane BMP regulator 1 (chordin-like)	chr2p21	228496_s_at	NM_016441
5.23	5.58	0.35	1.45E-01	5.12E-01	LOC100131062 /// PTP4A3	similar to protein tyrosine phosphatase type IVA, member 3 /// protein tyrosine phosphatase type IVA, member 3	chr8q24.3	209695_at	NM_007079 /// NM_032611 /// XM_001717048
2.54	2.74	0.20	1.45E-01	5.12E-01	IL23R	interleukin 23 receptor	chr1p31.3	1561853_a_at	NM_144701
2.08	2.27	0.20	1.45E-01	5.12E-01	CDC25A	cell division cycle 25 homolog A (S. pombe)	chr3p21	1555772_a_at	NM_001789 /// NM_201567
2.36	2.54	0.18	1.45E-01	5.12E-01	C12orf51	chromosome 12 open reading frame 51	chr12q24.13	1553821_at	NM_001109662
2.30	2.46	0.17	1.45E-01	5.12E-01	PITPNM3	PITPNM family member 3	chr17p13	221254_s_at	NM_031220

2.11	2.40	0.29	1.45E-01	5.12E-01	FAM65B	family with sequence similarity 65, member B	chr6p22.3-p21.32	209829_at	NM_014722 /// NM_015864
2.14	2.42	0.28	1.45E-01	5.12E-01	TAAR3	trace amine associated receptor 3 (gene/pseudogene)	chr6q23-q24	221393_at	---
2.57	2.78	0.21	1.45E-01	5.12E-01	NUP205	nucleoporin 205kDa	chr7q33	222382_x_at	NM_015135
2.40	2.59	0.19	1.45E-01	5.12E-01	---	---	---	233482_at	---
4.64	4.83	0.19	1.45E-01	5.12E-01	hCG_1732469	HCG1732469	chr2q13	220823_at	XR_041019 /// XR_041020 /// XR_041021
2.34	2.55	0.21	1.45E-01	5.12E-01	MGC16121	Hypothetical protein MGC16121	chrXq26.3	232822_x_at	XM_001128419 /// XM_001715787 /// XM_001715872
5.32	5.65	0.33	1.46E-01	5.12E-01	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	chr19q13.2-q13.4	207105_s_at	NM_005027
2.71	3.00	0.30	1.46E-01	5.12E-01	---	---	---	1569153_at	---
2.99	3.24	0.25	1.46E-01	5.12E-01	ASB14	Ankyrin repeat and SOCS box-containing 14	chr3p21.1	237785_at	NM_130387
3.17	3.47	0.30	1.46E-01	5.12E-01	RPH3A	rabphilin 3A homolog (mouse)	chr12q24.13	205230_at	NM_014954
2.71	2.96	0.25	1.46E-01	5.12E-01	---	---	---	208145_at	---
3.40	3.73	0.33	1.46E-01	5.12E-01	ALG14	Asparagine-linked glycosylation 14 homolog (S. cerevisiae)	chr1p21.3	228871_at	NM_144988
7.35	8.09	0.74	1.46E-01	5.12E-01	YIPF6	Yip1 domain family, member 6	chrXq12	212341_at	NM_173834
2.19	2.43	0.25	1.46E-01	5.12E-01	---	---	---	215262_at	---
2.71	2.94	0.23	1.46E-01	5.12E-01	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	chr13q34	1563405_at	NM_000705
5.28	5.58	0.29	1.46E-01	5.12E-01	LRPPRC	leucine-rich PPR-motif containing	chr2p21	230194_at	NM_133259
2.39	2.61	0.22	1.46E-01	5.12E-01	---	---	---	241107_at	---
1.86	2.01	0.16	1.46E-01	5.13E-01	---	---	---	1567000_at	---
2.41	2.60	0.19	1.46E-01	5.13E-01	---	---	---	1566504_at	---
3.12	3.38	0.26	1.46E-01	5.13E-01	C10orf137	chromosome 10 open reading frame 137	chr10q26.13-q26.2	208115_x_at	NM_015608
2.79	3.02	0.23	1.46E-01	5.13E-01	---	---	---	235842_at	---
2.87	3.41	0.54	1.46E-01	5.13E-01	FAM38B	family with sequence similarity 38, member B	chr18p11.22	219602_s_at	NM_022068
6.70	7.43	0.73	1.46E-01	5.13E-01	CKAP5	cytoskeleton associated protein 5	chr11p11.2	1555278_a_at	NM_001008938 /// NM_014756
3.21	3.61	0.40	1.46E-01	5.13E-01	CXCL9	chemokine (C-X-C motif) ligand 9	chr4q21	203915_at	NM_002416
3.99	4.28	0.29	1.46E-01	5.13E-01	DKFZp451A211	DKFZp451A211 protein	chr13q34	1556113_at	XR_041296 /// XR_041297
4.38	4.64	0.25	1.46E-01	5.13E-01	APBA1	amyloid beta (A4) precursor protein-binding, family A, member 1	chr9q13-q21.1	206679_at	NM_001163
4.34	4.59	0.25	1.46E-01	5.13E-01	ADO	2-aminoethanethiol (cysteamine) dioxygenase	chr10q21.2	229409_s_at	NM_032804
2.12	2.34	0.22	1.46E-01	5.13E-01	CSN3	casein kappa	chr4q21.1	207803_s_at	NM_005212
2.18	2.39	0.21	1.46E-01	5.13E-01	---	---	---	1560891_a_at	---
2.09	2.30	0.21	1.46E-01	5.13E-01	ZKSCAN3	zinc finger with KRAB and SCAN domains 3	chr6p22.1	1562303_at	NM_024493
2.25	2.46	0.21	1.46E-01	5.13E-01	---	---	---	237550_at	---
3.11	3.30	0.20	1.46E-01	5.13E-01	KIAA1804	mixed lineage kinase 4	chr1q42	228565_at	NM_032435
2.39	2.68	0.29	1.46E-01	5.13E-01	---	---	---	215163_at	---
2.02	2.18	0.16	1.46E-01	5.13E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	209700_x_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359
4.58	5.32	0.74	1.46E-01	5.13E-01	KIAA1267	KIAA1267	chr17q21.31	243589_at	NM_015443
6.34	6.59	0.25	1.46E-01	5.13E-01	CTNNBL1	catenin, beta like 1	chr20q11.23-q12	221021_s_at	NM_030877
2.54	2.73	0.18	1.46E-01	5.13E-01	SHB	Src homology 2 domain containing adaptor protein B	chr9p13.2-p13.1	230459_s_at	NM_003028
4.09	4.45	0.36	1.46E-01	5.13E-01	---	---	---	228589_at	---
2.63	2.86	0.23	1.46E-01	5.13E-01	FLJ36032 /// LOC100132502	hypothetical protein FLJ36032 /// hypothetical protein LOC100132502	chr1q21.3	237131_at	XM_001721352 /// XM_001721355 /// XM_001724330 /// XM_001724358 /// XM_371311 /// XM_937062

2.24	2.45	0.21	1.46E-01	5.13E-01	GSN	Gelsolin (amyloidosis, Finnish type)	chr9q33	227958_s_at	NM_000177 /// NM_001127662 /// NM_001127663 /// NM_001127664 /// NM_001127665 /// NM_001127666 /// NM_001127667 /// NM_198252
1.94	2.14	0.20	1.46E-01	5.13E-01	CDY1	chromodomain protein, Y-linked, 1	chrYq11.23	207647_at	NM_004680 /// NM_170723
4.99	5.22	0.24	1.46E-01	5.13E-01	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	chr14q32.3-qter|14q32	241084_x_at	NM_001376
1.99	2.21	0.22	1.46E-01	5.13E-01	---	---	---	244021_at	---
5.62	6.02	0.40	1.46E-01	5.13E-01	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF3 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.12 /// chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	1562062_at	NM_001037675 /// NM_001039703 /// NM_001101663 /// NM_001102663 /// NM_015383 /// NM_017940 /// NM_032264 /// NM_173638 /// NM_183372 /// XM_001717398 /// XM_001717802 /// XM_001721345 /// XM_001721349 /// XM_001722184 /// XM_001723523 /// XM_001726946
6.22	6.74	0.53	1.46E-01	5.13E-01	G6PD	glucose-6-phosphate dehydrogenase	chrXq28	202275_at	NM_000402 /// NM_001042351
2.17	2.41	0.24	1.46E-01	5.13E-01	MOBP	myelin-associated oligodendrocyte basic protein	chr3p22.1	235794_at	NM_182935 /// NR_003090
1.96	2.12	0.16	1.46E-01	5.13E-01	---	---	---	243339_at	---
3.62	3.87	0.25	1.46E-01	5.13E-01	DLX1	distal-less homeobox 1	chr2q32	1560100_at	NM_001038493 /// NM_178120
2.86	3.13	0.26	1.46E-01	5.13E-01	ACSM3	acyl-CoA synthetase medium-chain family member 3	chr16p13.11	210377_at	NM_005622 /// NM_202000
6.36	6.66	0.30	1.46E-01	5.13E-01	MTFR1	mitochondrial fission regulator 1	chr8q13.1	203208_s_at	NM_014637
2.56	2.84	0.28	1.46E-01	5.13E-01	L1CAM	L1 cell adhesion molecule	chrXq28	204584_at	NM_000425 /// NM_024003
4.02	4.18	0.16	1.46E-01	5.13E-01	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	chr17p13	1555063_at	NM_004505
3.35	3.75	0.40	1.47E-01	5.13E-01	KLHL28	kelch-like 28 (Drosophila)	chr14q21.3	228328_at	NM_017658
2.46	2.70	0.24	1.47E-01	5.13E-01	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	chr7p15-p14	204702_s_at	NM_004289
4.59	5.19	0.60	1.47E-01	5.13E-01	CYGB	cytoglobin	chr17q25.3	226632_at	NM_134268
2.48	2.83	0.34	1.47E-01	5.14E-01	---	---	---	1566229_a_at	---
1.85	2.08	0.23	1.47E-01	5.14E-01	---	---	---	243548_x_at	---
3.62	3.89	0.27	1.47E-01	5.14E-01	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	chr4p15.2	227982_at	NM_016955 /// NM_153825
6.76	7.45	0.70	1.47E-01	5.14E-01	EZR	ezrin	chr6q25.2-q26	208621_s_at	NM_001111077 /// NM_003379
5.10	5.59	0.49	1.47E-01	5.14E-01	---	---	---	1562144_at	---
3.12	3.56	0.44	1.47E-01	5.14E-01	---	---	---	1556314_a_at	---
4.54	4.87	0.33	1.47E-01	5.14E-01	CD22	CD22 molecule	chr19q13.1	204581_at	NM_001771

4.49	4.82	0.33	1.47E-01	5.14E-01	CYLD	cylindromatosis (turban tumor syndrome)	chr16q12.1	214272_at	NM_001042355 /// NM_001042412 /// NM_015247																				
2.99	3.19	0.21	1.47E-01	5.14E-01	---	---	---	239055_at	---																				
5.91	6.96	1.05	1.47E-01	5.14E-01	RAD21	RAD21 homolog (S. pombe)	chr8q24	200607_s_at	NM_006265																				
5.27	6.17	0.90	1.47E-01	5.14E-01	RRM1	ribonucleotide reductase M1	chr11p15.5	201476_s_at	NM_001033																				
4.50	4.80	0.29	1.47E-01	5.14E-01	---	---	---	233771_at	---																				
1.89	2.08	0.20	1.47E-01	5.14E-01	RP9P	retinitis pigmentosa 9 pseudogene	chr7p14.3	1560340_s_at	NR_003500																				
3.78	4.18	0.40	1.47E-01	5.14E-01	CLIP4	CAP-GLY domain containing linker protein family, member 4	chr2p23.2	219944_at	NM_024692																				
2.13	2.32	0.19	1.47E-01	5.14E-01	---	---	---	221138_s_at	---																				
5.28	5.83	0.55	1.47E-01	5.14E-01	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	chr3q22.1	212467_at	NM_015268																				
4.98	5.70	0.72	1.47E-01	5.14E-01	STK17A	serine/threonine kinase 17a	chr7p12-p14	202693_s_at	NM_004760																				
3.97	4.37	0.40	1.47E-01	5.14E-01	USP2	ubiquitin specific peptidase 2	chr11q23.3	230965_at	NM_004205 /// NM_171997																				
2.72	2.94	0.22	1.47E-01	5.14E-01	APOH	Apolipoprotein H (beta-2-glycoprotein I)	chr17q23-qter	231359_at	NM_000042																				
3.50	3.83	0.34	1.47E-01	5.14E-01	---	---	---	241227_at	---																				
5.36	5.54	0.18	1.47E-01	5.14E-01	ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1	chr19q13.13	1560445_x_at	NM_004706 /// NM_198977 /// NM_199002																				
4.66	5.53	0.87	1.47E-01	5.14E-01	PDE1A	phosphodiesterase 1A, calmodulin-dependent	chr2q32.1	208396_s_at	NM_001003683 /// NM_005019																				
2.04	2.25	0.21	1.47E-01	5.14E-01	CLCN5	chloride channel 5	chrXp11.23-p11.22|Xp11.23	232127_at	NM_000084 /// NM_001127898 /// NM_001127899																				
3.49	3.86	0.37	1.47E-01	5.14E-01	KIAA1161	KIAA1161	chr9p13.3	231185_at	NM_020702																				
2.41	2.69	0.28	1.47E-01	5.15E-01	---	---	---	216467_s_at	---																				
1.94	2.13	0.19	1.47E-01	5.15E-01	PANK2	Pantothenate kinase 2	chr20p13	228735_s_at	NM_024960 /// NM_153638 /// NM_153640																				
3.74	4.11	0.37	1.47E-01	5.15E-01	---	---	---	242052_at	---																				
2.33	2.61	0.28	1.47E-01	5.15E-01	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	chr16q13	241739_at	NM_018233																				
2.38	2.66	0.28	1.47E-01	5.15E-01	---	---	---	1556796_at	---																				
2.09	2.26	0.18	1.47E-01	5.15E-01	HMGA2	high mobility group AT-hook 2	chr12q15	1567223_at	NM_003483 /// NM_003484																				
2.57	2.91	0.33	1.47E-01	5.15E-01	USP6NL	USP6 N-terminal like	chr10p13	238164_at	NM_001080491																				
5.23	5.56	0.33	1.47E-01	5.15E-01	ACVR2B	activin A receptor, type IIB	chr3p22	236126_at	NM_001106																				
2.49	2.76	0.27	1.47E-01	5.15E-01	LOC730057	Hypothetical LOC730057	chr3p14.1	1559296_at	XM_001132251 /// XM_001132871 /// XM_001716450																				
5.56	6.20	0.63	1.48E-01	5.15E-01	DCBLD2	discoidin, CUB and LCCL domain containing 2	chr3q12.1|3	224911_s_at	NM_080927																				
2.58	3.20	0.62	1.48E-01	5.15E-01	SYNE1	spectrin repeat containing, nuclear envelope 1	chr6q25	215350_at	NM_015293 /// NM_033071 /// NM_133650 /// NM_182961																				
5.52	5.94	0.42	1.48E-01	5.15E-01	B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	chr6p21.3	210205_at	NM_003782																				

2.05	2.39	0.34	1.48E-01	5.15E-01	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	chr14q32.1	211428_at	NM_000295 /// NM_001002235 /// NM_001002236 /// NM_001127700 /// NM_001127701 /// NM_001127702 /// NM_001127703 /// NM_001127704 /// NM_001127705 /// NM_001127706 /// NM_001127707																				
3.63	3.95	0.32	1.48E-01	5.15E-01	C14orf132 /// LOC100132684	chromosome 14 open reading frame 132 /// hypothetical protein LOC100132684	chr14q32.2	231859_at	NR_023938 /// XM_001724179 /// XM_001724602 /// XM_001726369 /// XR_040536 /// XR_040537 /// XR_040538																				
2.04	2.31	0.27	1.48E-01	5.15E-01	KIAA2022	KIAA2022	chrXq13.3	244076_at	NM_001008537																				
3.84	4.09	0.25	1.48E-01	5.15E-01	PRKAG2	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	chr7q36.1	231224_x_at	NM_001040633 /// NM_016203 /// NM_024429																				
3.40	3.62	0.22	1.48E-01	5.15E-01	TNNT2	troponin T type 2 (cardiac)	chr1q32	215389_s_at	NM_000364 /// NM_001001430 /// NM_001001431 /// NM_001001432																				
2.70	2.91	0.21	1.48E-01	5.15E-01	---	---	---	243182_at	---																				
2.15	2.35	0.21	1.48E-01	5.15E-01	IGH@ /// IGHA1 /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM /// LOC100126583 /// LOC100133739 /// LOC652494	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// hypothetical LOC100126583 /// similar to hCG2038920 /// similar to Ig heavy chain V-III region VH26 precursor	chr14q32.33	211646_at	XM_001717586 /// XM_001718220 /// XM_001719484																				
2.03	2.22	0.19	1.48E-01	5.15E-01	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	chr10q23.33	219903_s_at	NM_000770																				
2.56	2.74	0.18	1.48E-01	5.15E-01	---	---	---	1559691_at	---																				
2.25	2.42	0.17	1.48E-01	5.15E-01	---	---	---	1557241_a_at	---																				
2.02	2.18	0.16	1.48E-01	5.15E-01	ASNS	Asparagine synthetase	chr7q21.3	241082_at	NM_001673 /// NM_133436 /// NM_183356																				
2.71	2.86	0.16	1.48E-01	5.15E-01	STK35	Serine/threonine kinase 35	chr20p13	232006_at	NM_080836																				
1.95	2.12	0.17	1.48E-01	5.15E-01	---	---	---	236603_at	---																				
6.06	6.84	0.78	1.48E-01	5.15E-01	HBS1L	HBS1-like (S. cerevisiae)	chr6q23-q24	209316_s_at	NM_006620																				
5.48	6.18	0.70	1.48E-01	5.15E-01	---	---	---	228349_at	---																				
3.66	4.23	0.57	1.48E-01	5.15E-01	COL1A2	collagen, type I, alpha 2	chr7q22.1	229218_at	NM_000089																				
3.89	4.46	0.56	1.48E-01	5.15E-01	CUL5	cullin 5	chr11q22-q23	203532_x_at	NM_003478																				
6.71	7.26	0.55	1.48E-01	5.15E-01	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	chr1p36.1	202741_at	NM_002731 /// NM_182948 /// NM_207578																				
5.26	5.75	0.49	1.48E-01	5.15E-01	---	---	---	228573_at	---																				
3.81	4.28	0.47	1.48E-01	5.15E-01	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	chr4q32.3	218986_s_at	NM_017631																				
4.92	5.37	0.45	1.48E-01	5.15E-01	---	---	---	226832_at	---																				
2.05	2.49	0.45	1.48E-01	5.15E-01	C12orf35	chromosome 12 open reading frame 35	chr12p11.21	227152_at	NM_018169																				
3.33	3.72	0.39	1.48E-01	5.15E-01	WASL	Wiskott-Aldrich syndrome-like	chr7q31.3	205809_s_at	NM_003941																				
2.99	3.38	0.39	1.48E-01	5.15E-01	---	---	---	230003_at	---																				
8.90	9.27	0.37	1.48E-01	5.15E-01	C20orf108	chromosome 20 open reading frame 108	chr20q13.2	224690_at	NM_080821																				

6.32	6.66	0.34	1.48E-01	5.15E-01	NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	chr6q22.2	225071_at	NM_138459
5.11	5.42	0.31	1.48E-01	5.15E-01	FAM120B	Family with sequence similarity 120B	chr6q27	226774_at	NM_032448
6.39	6.70	0.31	1.48E-01	5.15E-01	C5orf4	chromosome 5 open reading frame 4	chr5q31-q32	220751_s_at	NM_016348 /// NM_032385
4.49	4.77	0.28	1.48E-01	5.15E-01	HSPG2	heparan sulfate proteoglycan 2	chr1p36.1-p34	201654_s_at	NM_005529
4.72	4.97	0.25	1.48E-01	5.15E-01	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	chr9q34	212772_s_at	NM_001606 /// NM_212533
3.83	4.07	0.25	1.48E-01	5.15E-01	PRDM10	PR domain containing 10	chr11q25	214158_s_at	NM_020228 /// NM_199437 /// NM_199438 /// NM_199439
5.62	5.84	0.22	1.48E-01	5.15E-01	LOC388210	Similar to LD15094p	chr16p13.13	244889_at	XM_001716361 /// XM_370934 /// XM_940577
1.91	2.13	0.22	1.48E-01	5.15E-01	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	chr17q24-q25|17q25.1	209601_at	NM_004035 /// NM_007292
2.20	2.42	0.21	1.48E-01	5.15E-01	---	---	---	236822_at	---
2.34	2.56	0.21	1.48E-01	5.15E-01	---	---	---	241231_at	---
4.46	4.66	0.19	1.48E-01	5.15E-01	MPPED1	metallophosphoesterase domain containing 1	chr22q13.31	206436_at	NM_001044370 /// XM_001713873 /// XM_001725743
1.90	2.08	0.19	1.48E-01	5.15E-01	---	---	---	242772_x_at	---
1.73	1.92	0.18	1.48E-01	5.15E-01	EEA1	early endosome antigen 1	chr12q22	204840_s_at	NM_003566
1.99	2.17	0.18	1.48E-01	5.15E-01	LOC730272	similar to protein immuno-reactive with anti-PTH polyclonal antibodies	chr2p11.2	216686_at	XR_041839 /// XR_041840 /// XR_041841
3.93	4.20	0.28	1.48E-01	5.15E-01	ORAOV1	oral cancer overexpressed 1	chr11q13.2	228676_at	NM_153451
7.36	7.63	0.27	1.48E-01	5.15E-01	ECE1	endothelin converting enzyme 1	chr1p36.1	201750_s_at	NM_001113347 /// NM_001113348 /// NM_001113349 /// NM_001397
3.22	3.40	0.19	1.48E-01	5.15E-01	FOXH1	forkhead box H1	chr8q24.3	231407_s_at	NM_003923
1.91	2.15	0.24	1.48E-01	5.15E-01	LVRN	laeverin	chr5q23.1	235382_at	NM_173800
7.98	8.73	0.75	1.48E-01	5.15E-01	C9orf5	chromosome 9 open reading frame 5	chr9q31	223008_s_at	NM_001099734 /// NM_032012
4.30	4.62	0.32	1.48E-01	5.15E-01	---	---	---	232096_x_at	---
2.21	2.49	0.28	1.48E-01	5.15E-01	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	chr6q14-q15	236146_at	NM_006372
2.72	2.92	0.20	1.48E-01	5.15E-01	---	---	---	239940_at	---
2.45	2.64	0.19	1.48E-01	5.15E-01	LRRCC1	leucine rich repeat and coiled-coil domain containing 1	chr8q21.2	231872_at	NM_001077501 /// NM_033402
2.08	2.26	0.18	1.48E-01	5.15E-01	---	---	---	1557641_at	---
3.12	3.73	0.61	1.48E-01	5.15E-01	FLJ13197	hypothetical FLJ13197	chr4p14	219871_at	XR_040784 /// XR_040785 /// XR_040786
2.30	2.52	0.22	1.48E-01	5.15E-01	SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	chr8p21.3	207074_s_at	NM_003053
5.97	6.32	0.35	1.48E-01	5.15E-01	SP110	SP110 nuclear body protein	chr2q37.1	208012_x_at	NM_004509 /// NM_004510 /// NM_080424
3.89	4.18	0.29	1.48E-01	5.15E-01	HAPLN2	hyaluronan and proteoglycan link protein 2	chr1q23.1	220142_at	NM_021817
2.05	2.26	0.21	1.49E-01	5.15E-01	---	---	---	1568938_at	---
4.46	5.25	0.79	1.49E-01	5.15E-01	USP10	ubiquitin specific peptidase 10	chr16q24.1	209136_s_at	NM_005153
2.96	3.27	0.31	1.49E-01	5.15E-01	---	---	---	232435_at	---
4.96	5.23	0.27	1.49E-01	5.15E-01	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	chr19p13.1	207187_at	NM_000215
1.96	2.20	0.24	1.49E-01	5.15E-01	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	chr15q11.2-q12	215531_s_at	NM_000810
3.74	3.96	0.23	1.49E-01	5.15E-01	TNRC6C	Trinucleotide repeat containing 6C	chr17q25.3	242314_at	NM_018996
5.75	6.26	0.51	1.49E-01	5.15E-01	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	chr9q32	213247_at	NM_153366
2.91	3.11	0.20	1.49E-01	5.15E-01	---	---	---	242278_at	---
6.89	7.65	0.75	1.49E-01	5.15E-01	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	chr2p23	208629_s_at	NM_000182
3.44	3.93	0.50	1.49E-01	5.15E-01	---	---	---	242144_at	---
3.65	3.99	0.34	1.49E-01	5.15E-01	HS3ST1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	chr4p16	213991_s_at	NM_005114
1.92	2.13	0.21	1.49E-01	5.15E-01	AQP4	aquaporin 4	chr18q11.2-q12.1	210067_at	NM_001650 /// NM_004028

2.66	3.03	0.38	1.49E-01	5.15E-01	CGREF1	cell growth regulator with EF-hand domain 1	chr2p23.3	205937_at	NM_006569
3.21	3.64	0.43	1.49E-01	5.16E-01	UNQ6228	Hypothetical LOC100131541	chr11q21	1558569_at	XM_001725293 /// XM_001725359 /// XM_001726164
3.12	3.43	0.32	1.49E-01	5.16E-01	ANGPTL2	angiopoietin-like 2	chr9q34	219514_at	NM_012098
3.90	4.21	0.31	1.49E-01	5.16E-01	PPIA	Peptidylprolyl isomerase A (cyclophilin A)	chr7p13	235741_at	NM_021130
2.07	2.28	0.20	1.49E-01	5.16E-01	---	---	---	234482_at	---
1.76	1.94	0.18	1.49E-01	5.16E-01	---	---	---	1555373_at	---
7.80	8.72	0.92	1.49E-01	5.16E-01	GDI2	GDP dissociation inhibitor 2	chr10p15	200008_s_at	NM_001115156 /// NM_001494
5.05	5.74	0.69	1.49E-01	5.16E-01	FIBIN	fin bud initiation factor	chr11p14.2	226769_at	NM_203371
2.92	3.53	0.61	1.49E-01	5.16E-01	TM4SF18	Transmembrane 4 L six family member 18	chr3q25.1	230061_at	NM_138786
4.67	5.27	0.60	1.49E-01	5.16E-01	---	---	---	237881_at	---
6.10	6.64	0.55	1.49E-01	5.16E-01	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	chr10p11.22-p11.21	221526_x_at	NM_019619
3.86	4.40	0.53	1.49E-01	5.16E-01	---	---	---	1557240_a_at	---
2.31	2.83	0.52	1.49E-01	5.16E-01	XKR4	XK, Kell blood group complex subunit-related family, member 4	chr8q12.1	237802_at	NM_052898
4.44	4.85	0.41	1.49E-01	5.16E-01	DBT	dihydrolipoamide branched chain transacylase E2	chr1p31	205369_x_at	NM_001918
3.76	4.13	0.38	1.49E-01	5.16E-01	FOXP1	forkhead box P1	chr3p14.1	223936_s_at	NM_001012505 /// NM_032682
6.42	6.79	0.36	1.49E-01	5.16E-01	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	chr12p13	217264_s_at	NM_001038
7.40	7.74	0.34	1.49E-01	5.16E-01	ZFYVE1	zinc finger, FYVE domain containing 1	chr14q22-q24	223387_at	NM_021260 /// NM_178441
6.80	7.12	0.33	1.49E-01	5.16E-01	RAB1A	RAB1A, member RAS oncogene family	chr2p14	213440_at	NM_004161
3.90	4.21	0.30	1.49E-01	5.16E-01	FAM83F	family with sequence similarity 83, member F	chr22q13.1	235269_at	NM_138435
2.86	3.16	0.30	1.49E-01	5.16E-01	C21orf125	chromosome 21 open reading frame 125	chr21q22.3	236631_at	XR_041147 /// XR_041148 /// XR_041149
4.38	4.65	0.27	1.49E-01	5.16E-01	CCDC13	coiled-coil domain containing 13	chr3p22.1	1554023_s_at	NM_144719
2.13	2.40	0.27	1.49E-01	5.16E-01	TUBAL3	tubulin, alpha-like 3	chr10p15.1	220310_at	NM_024803
3.46	3.73	0.26	1.49E-01	5.16E-01	TYSND1	Trypsin domain containing 1	chr10q22.1	225873_at	NM_001040273 /// NM_173555
2.32	2.57	0.25	1.49E-01	5.16E-01	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	chrXp11.23	208586_s_at	NM_001034832 /// NM_001040612 /// NM_005636 /// NM_175729 /// XM_001725018
2.85	3.10	0.25	1.49E-01	5.16E-01	FGF5	fibroblast growth factor 5	chr4q21	208378_x_at	NM_004464 /// NM_033143
4.15	4.40	0.25	1.49E-01	5.16E-01	BMP7	bone morphogenetic protein 7	chr20q13	211260_at	NM_001719
2.14	2.38	0.25	1.49E-01	5.16E-01	---	---	---	236180_at	---
3.01	3.24	0.24	1.50E-01	5.16E-01	---	---	---	242863_at	---
2.50	2.73	0.23	1.49E-01	5.16E-01	---	---	---	244059_at	---
2.58	2.81	0.23	1.50E-01	5.16E-01	---	---	---	216771_at	---
2.08	2.30	0.22	1.49E-01	5.16E-01	WDR72	WD repeat domain 72	chr15q21.3	1563874_at	NM_182758
3.33	3.55	0.22	1.49E-01	5.16E-01	IDI2	isopentenyl-diphosphate delta isomerase 2	chr10p15.3	1552491_at	NM_033261
1.91	2.12	0.22	1.49E-01	5.16E-01	---	---	---	1569375_at	---
2.58	2.80	0.21	1.49E-01	5.16E-01	ABCG8	ATP-binding cassette, sub-family G (WHITE), member 8	chr2p21	231751_at	NM_022437
2.16	2.37	0.21	1.49E-01	5.16E-01	---	---	---	243831_at	---
4.75	4.95	0.20	1.49E-01	5.16E-01	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	chr9p21	211156_at	NM_000077 /// NM_058195 /// NM_058197
1.97	2.17	0.20	1.49E-01	5.16E-01	---	---	---	1560066_at	---
2.43	2.62	0.20	1.49E-01	5.16E-01	OR2K2	olfactory receptor, family 2, subfamily K, member 2	chr9q31.3	1567273_at	NM_205859
2.51	2.70	0.19	1.50E-01	5.16E-01	CLDN10	claudin 10	chr13q31-q34	205328_at	NM_006984 /// NM_182848
2.30	2.46	0.16	1.50E-01	5.16E-01	IPO9	importin 9	chr1q32.1	244703_x_at	NM_018085
1.78	1.94	0.16	1.49E-01	5.16E-01	RTTN	rotatin	chr18q22.2	1553277_at	NM_173630
1.91	2.06	0.15	1.49E-01	5.16E-01	CLTC	clathrin, heavy chain (Hc)	chr17q11-qter	210498_at	NM_004859
2.10	2.25	0.15	1.49E-01	5.16E-01	---	---	---	1566203_at	---
5.82	6.98	1.16	1.50E-01	5.16E-01	COL6A3	collagen, type VI, alpha 3	chr2q37	201438_at	NM_004369 /// NM_057164 /// NM_057165 /// NM_057166 /// NM_057167
6.11	6.70	0.58	1.50E-01	5.16E-01	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	chr6q24-q25	208857_s_at	NM_005389

4.42	4.92	0.49	1.50E-01	5.16E-01	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	chr4q26	228555_at	NM_001221 /// NM_172115 /// NM_172127 /// NM_172128
3.19	3.48	0.29	1.50E-01	5.16E-01	COL8A2	collagen, type VIII, alpha 2	chr1p34.2	52651_at	NM_005202
2.39	2.67	0.28	1.50E-01	5.16E-01	C21orf62	chromosome 21 open reading frame 62	chr21q22.11	220543_at	NM_019596
2.61	2.86	0.26	1.50E-01	5.16E-01	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	chr17q23.3	208425_s_at	NM_025185
3.81	4.05	0.24	1.50E-01	5.16E-01	COIL	coilin	chr17q22-q23	203653_s_at	NM_004645
2.34	2.56	0.22	1.50E-01	5.16E-01	---	---	---	230862_at	---
1.89	2.08	0.19	1.50E-01	5.16E-01	---	---	---	237001_at	---
3.26	3.45	0.19	1.50E-01	5.16E-01	---	---	---	237424_at	---
3.12	3.29	0.16	1.50E-01	5.16E-01	---	---	---	1568643_a_at	---
1.83	1.99	0.16	1.50E-01	5.16E-01	---	---	---	215962_at	---
8.55	9.33	0.77	1.50E-01	5.16E-01	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	chr7p15	200976_s_at	NM_001079864 /// NM_006024
3.69	4.23	0.54	1.50E-01	5.16E-01	ESRRG	estrogen-related receptor gamma	chr1q41	209966_x_at	NM_001134285 /// NM_001438 /// NM_206594 /// NM_206595 /// NR_024099
4.71	5.09	0.38	1.50E-01	5.16E-01	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	chr10q22.2	211874_s_at	NM_012330
3.52	3.82	0.31	1.50E-01	5.16E-01	LOC284296	hypothetical LOC284296	chr19q13.42	238136_at	XR_041409 /// XR_041410 /// XR_041411
4.79	5.08	0.29	1.50E-01	5.16E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	220464_at	NM_001112732 /// NM_024979
2.66	2.94	0.28	1.50E-01	5.16E-01	GSG2	germ cell associated 2 (haspin)	chr17p13	223759_s_at	NM_031965
2.96	3.20	0.24	1.50E-01	5.16E-01	RGPD1 /// RGPD2	RANBP2-like and GRIP domain containing 1 /// RANBP2-like and GRIP domain containing 2	chr2p11.2	235597_s_at	NM_001024457 /// NM_001078170
3.33	3.57	0.24	1.50E-01	5.16E-01	KLHL35	kelch-like 35 (Drosophila)	chr11q13.4	1553611_s_at	NM_001039548
4.78	5.18	0.40	1.50E-01	5.16E-01	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	chr8q22.1	218640_s_at	NM_024613
2.08	2.31	0.23	1.50E-01	5.16E-01	---	---	---	244657_at	---
2.17	2.39	0.22	1.50E-01	5.16E-01	---	---	---	1570597_at	---
1.93	2.12	0.19	1.50E-01	5.16E-01	CXCL5	chemokine (C-X-C motif) ligand 5	chr4q12-q13	207852_at	NM_002994
2.24	2.43	0.19	1.50E-01	5.16E-01	LOC152578	hypothetical protein LOC152578	chr4q12	1564881_at	XM_931829 /// XM_942803
4.67	5.07	0.39	1.50E-01	5.16E-01	NUDT18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	chr8p21.3	219665_at	NM_024815
3.05	3.33	0.28	1.50E-01	5.16E-01	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	chr3q26.1	210078_s_at	NM_003471 /// NM_172159 /// NM_172160
2.61	2.89	0.28	1.50E-01	5.16E-01	KIAA1919	KIAA1919	chr6q22	232139_s_at	NM_153369
2.37	2.63	0.26	1.50E-01	5.16E-01	RAD51L1	RAD51-like 1 (S. cerevisiae)	chr14q23-q24.2	210255_at	NM_002877 /// NM_133509 /// NM_133510
2.14	2.38	0.23	1.50E-01	5.16E-01	---	---	---	1564940_at	---
3.23	3.50	0.27	1.50E-01	5.16E-01	ADCY1	adenylate cyclase 1 (brain)	chr7p13-p12	235049_at	NM_021116
2.55	2.80	0.26	1.50E-01	5.16E-01	---	---	---	1566786_at	---
2.34	2.53	0.19	1.50E-01	5.16E-01	LRRC17	leucine rich repeat containing 17	chr7q22.1	232924_at	NM_001031692 /// NM_005824
5.73	6.59	0.86	1.50E-01	5.16E-01	C5orf41	chromosome 5 open reading frame 41	chr5q35.2	225956_at	NM_153607
2.95	3.26	0.31	1.50E-01	5.16E-01	FANCM	Fanconi anemia, complementation group M	chr14q21.3	234733_s_at	NM_020937
2.47	2.72	0.25	1.50E-01	5.16E-01	CORO2A	Coronin, actin binding protein, 2A	chr9q22.3	227177_at	NM_003389 /// NM_052820
1.86	2.04	0.18	1.50E-01	5.16E-01	PIK3C3	phosphoinositide-3-kinase, class 3	chr18q12.3	241304_at	NM_002647
2.15	2.32	0.17	1.50E-01	5.16E-01	LOC283547	hypothetical protein LOC283547	chr14q21.1	1557821_at	XR_041511 /// XR_041512 /// XR_041513 /// XR_041514 /// XR_041515 /// XR_041516
2.19	2.34	0.15	1.50E-01	5.16E-01	KCMF1	potassium channel modulatory factor 1	chr2p11.2	242887_at	NM_020122
3.05	3.30	0.25	1.50E-01	5.16E-01	KLF9	Kruppel-like factor 9	chr9q13	203541_s_at	NM_001206
3.17	3.39	0.22	1.50E-01	5.17E-01	THSD3	thrombospondin, type I, domain containing 3	chr14q24.3	228212_at	NM_182509 /// NM_199265 /// NM_199296
2.57	2.76	0.19	1.50E-01	5.17E-01	---	---	---	243215_at	---

3.98	4.22	0.24	1.50E-01	5.17E-01	CEP78	centrosomal protein 78kDa	chr9q21.2	1557985_s_at	NM_001098802 /// NM_032171																					
5.98	6.42	0.44	1.51E-01	5.17E-01	KTN1	kinectin 1 (kinesin receptor)	chr14q22.1	200914_x_at	NM_001079521 /// NM_001079522 /// NM_004986 /// NM_182926																					
5.47	6.44	0.98	1.51E-01	5.17E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	224568_x_at	NR_002819																					
3.31	3.92	0.61	1.51E-01	5.17E-01	JAG1	jagged 1 (Alagille syndrome)	chr20p12.1-p11.23	209098_s_at	NM_000214																					
4.05	4.50	0.45	1.51E-01	5.17E-01	---	---	---	222375_at	---																					
3.31	3.70	0.39	1.51E-01	5.17E-01	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	chr8q22	216831_s_at	NM_004349 /// NM_175634 /// NM_175635 /// NM_175636																					
1.75	1.89	0.14	1.51E-01	5.17E-01	MARK1	MAP/microtubule affinity-regulating kinase 1	chr1q41	231613_at	NM_018650																					
2.52	2.77	0.25	1.51E-01	5.17E-01	---	---	---	236127_at	---																					
5.10	6.08	0.98	1.51E-01	5.17E-01	PTER	phosphotriesterase related	chr10p12	222798_at	NM_001001484 /// NM_030664																					
2.26	2.55	0.29	1.51E-01	5.17E-01	GPR171	G protein-coupled receptor 171	chr3q25.1	207651_at	NM_013308																					
1.87	2.03	0.16	1.51E-01	5.17E-01	FLJ30672	hypothetical protein FLJ30672	chrXq26.3	1553357_at	---																					
3.54	4.08	0.53	1.51E-01	5.17E-01	---	---	---	242598_at	---																					
3.30	3.60	0.30	1.51E-01	5.17E-01	FYB	FYN binding protein (FYB-120/130)	chr5p13.1	205285_s_at	NM_001465 /// NM_199335																					
1.80	2.06	0.27	1.51E-01	5.17E-01	CXCL13	chemokine (C-X-C motif) ligand 13	chr4q21	205242_at	NM_006419																					
2.20	2.58	0.38	1.51E-01	5.17E-01	NBLA00301	Nbla00301	chr4q34.1	219791_s_at	NR_003679																					
6.87	7.52	0.65	1.51E-01	5.17E-01	MYLK	myosin light chain kinase	chr3q21	224823_at	NM_053025 /// NM_053026 /// NM_053027 /// NM_053028 /// NM_053031 /// NM_053032																					
4.68	4.96	0.28	1.51E-01	5.17E-01	EML2	echinoderm microtubule associated protein like 2	chr19q13.32	204399_s_at	NM_012155																					
3.11	3.52	0.41	1.51E-01	5.17E-01	SLC43A3	solute carrier family 43, member 3	chr11q11	210692_s_at	NM_014096 /// NM_017611 /// NM_199329																					
2.48	2.68	0.20	1.51E-01	5.17E-01	hCG_17241	flamingo-like	chr22q11.21	1569445_at	XM_001126962																					
1.93	2.12	0.19	1.51E-01	5.17E-01	---	---	---	241651_at	---																					
5.33	5.64	0.31	1.51E-01	5.18E-01	PCYT2	phosphate cytidylyltransferase 2, ethanolamine	chr17q25.3	209577_at	NM_002861 /// XM_001714257																					
2.91	3.13	0.22	1.51E-01	5.18E-01	KIAA0492	KIAA0492 protein	chr1q25.1	215109_at	XR_040636 /// XR_040637 /// XR_040638																					
4.63	4.91	0.28	1.51E-01	5.18E-01	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	chr12q24	207321_s_at	NM_019624 /// NM_019625 /// NM_203444																					
4.00	4.25	0.25	1.51E-01	5.18E-01	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	chr5q35.2	214244_s_at	NM_003945																					
3.36	3.60	0.24	1.51E-01	5.18E-01	COPG2IT1	coatomer protein complex, subunit gamma 2, intronic transcript 1	chr7q32	213486_at	NR_024086																					
2.66	2.92	0.26	1.51E-01	5.18E-01	---	---	---	231215_at	---																					
2.56	2.81	0.25	1.51E-01	5.18E-01	TCL6	T-cell leukemia/lymphoma 6	chr14q32.1	221624_at	NM_012468 /// NM_014418 /// NM_020550 /// NM_020552 /// NM_020553 /// NM_020554																					
2.10	2.31	0.21	1.51E-01	5.18E-01	ZNF160	zinc finger protein 160	chr19q13.41	1567031_at	NM_001102603 /// NM_033288 /// NM_198893																					
2.43	2.65	0.21	1.51E-01	5.18E-01	---	---	---	237638_at	---																					
2.83	3.20	0.37	1.51E-01	5.18E-01	C1orf194	chromosome 1 open reading frame 194	chr1p13.3	231044_at	NM_001122961 /// XM_001722455 /// XM_059104 /// XM_938238																					
3.99	4.43	0.44	1.51E-01	5.18E-01	WDR89	WD repeat domain 89	chr14q23.2	244038_at	NM_001008726 /// NM_080666																					

4.91	5.20	0.29	1.51E-01	5.18E-01	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	chr5q23-q31	224118_at	NM_003337
3.39	3.66	0.27	1.51E-01	5.18E-01	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	chr9q34	228163_at	NM_175039 /// NM_175040
5.09	5.39	0.30	1.51E-01	5.18E-01	PCP2	Purkinje cell protein 2	chr19p13.2	244751_at	NM_174895
4.02	4.34	0.32	1.51E-01	5.18E-01	CLIC5 /// LOC100131610	chloride intracellular channel 5 /// similar to chloride intracellular channel 5	chr6p21.1-p12.1	219866_at	NM_001114086 /// NM_016929 /// XM_001723558
3.08	3.38	0.30	1.51E-01	5.18E-01	FAM167A	family with sequence similarity 167, member A	chr8p23-p22	226614_s_at	NM_053279
4.76	5.13	0.37	1.51E-01	5.18E-01	PEX6	peroxisomal biogenesis factor 6	chr6p21.1	320_at	NM_000287
3.09	3.36	0.27	1.51E-01	5.18E-01	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	chr3p21.3	204811_s_at	NM_001005505 /// NM_006030
2.50	2.75	0.25	1.51E-01	5.18E-01	---	---	---	230610_at	---
3.37	3.58	0.21	1.52E-01	5.18E-01	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	chr1q32.2	210827_s_at	NM_001114309 /// NM_004433
2.43	2.64	0.21	1.52E-01	5.18E-01	---	---	---	237037_at	---
2.78	3.04	0.26	1.52E-01	5.18E-01	ACCN2	amiloride-sensitive cation channel 2, neuronal	chr12q12	205156_s_at	NM_001095 /// NM_020039
4.50	4.83	0.33	1.52E-01	5.18E-01	---	---	---	244095_at	---
2.12	2.36	0.24	1.52E-01	5.18E-01	---	---	---	241124_at	---
7.43	8.14	0.71	1.52E-01	5.18E-01	WAC	WW domain containing adaptor with coiled-coil	---	222389_s_at	NM_016628 /// NM_100264 /// NM_100486
2.47	2.72	0.25	1.52E-01	5.18E-01	LOC100128830	hypothetical protein LOC100128830	chr10q26.3	1564490_at	XM_001715157 /// XM_001716061 /// XM_001719712
6.02	6.77	0.75	1.52E-01	5.19E-01	SLC25A36	solute carrier family 25, member 36	chr3q23	201917_s_at	NM_001104647 /// NM_018155
3.16	3.45	0.29	1.52E-01	5.19E-01	---	---	---	241138_at	---
2.65	2.93	0.28	1.52E-01	5.19E-01	FLJ39632	hypothetical LOC642477	chr14q11.1	242546_at	XR_015133 /// XR_041395
2.75	3.12	0.37	1.52E-01	5.19E-01	C15orf57	chromosome 15 open reading frame 57	chr15q15.1	1560814_a_at	NM_001080791 /// NM_001080792 /// NM_052849
3.68	4.03	0.34	1.52E-01	5.19E-01	PAK3	p21 protein (Cdc42/Rac)-activated kinase 3	chrXq22.3	214607_at	NM_001128166 /// NM_001128167 /// NM_001128168 /// NM_001128172 /// NM_001128173 /// NM_002578 /// XM_001714511 /// XM_001718168
2.14	2.43	0.29	1.52E-01	5.19E-01	COX5A	cytochrome c oxidase subunit Va	chr15q24.1	217451_at	NM_004255
2.54	2.76	0.21	1.52E-01	5.19E-01	LYPD5	LY6/PLAUR domain containing 5	chr19q13.31	236039_at	NM_001031749 /// NM_182573
2.02	2.21	0.19	1.52E-01	5.19E-01	ST20	suppressor of tumorigenicity 20	chr15q25.1	217104_at	NM_001100879 /// NM_001100880
1.81	2.03	0.22	1.52E-01	5.19E-01	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	chr15q13-q15	218469_at	NM_013372
3.18	3.35	0.17	1.52E-01	5.19E-01	AQP8	aquaporin 8	chr16p12	206784_at	NM_001169
2.09	2.35	0.26	1.52E-01	5.19E-01	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	chr13q32	205337_at	NM_001129889 /// NM_001922
2.07	2.28	0.21	1.52E-01	5.19E-01	TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2	chr2q32.3	233910_at	NM_016192
2.43	2.70	0.27	1.52E-01	5.19E-01	BCL2L15	BCL2-like 15	chr1p13.2	236083_at	NM_001010922
2.30	2.58	0.27	1.52E-01	5.19E-01	LOC440570	LOC440570	chr1p36.13	242884_at	XR_041951 /// XR_041952
2.69	2.90	0.22	1.52E-01	5.19E-01	NEGR1	neuronal growth regulator 1	chr1p31.1	1553194_at	NM_173808

1.97	2.14	0.17	1.52E-01	5.19E-01	---	---	---	1564936_at	---
2.43	2.68	0.25	1.52E-01	5.19E-01	---	---	---	231039_at	---
2.28	2.50	0.22	1.52E-01	5.19E-01	DEPDC4	DEP domain containing 4	chr12q23.1	1553365_at	NM_152317
2.20	2.40	0.20	1.52E-01	5.19E-01	LDHAL6A	lactate dehydrogenase A-like 6A	chr11p15.1	1553888_at	NM_144972
2.80	2.98	0.18	1.52E-01	5.19E-01	---	---	---	215862_at	---
6.10	6.99	0.89	1.52E-01	5.19E-01	TCF4	transcription factor 4	chr18q21.1	212385_at	NM_001083962 /// NM_003199
8.28	8.76	0.48	1.52E-01	5.19E-01	PTEN	phosphatase and tensin homolog	chr10q23.3	225363_at	NM_000314
4.48	4.82	0.33	1.52E-01	5.19E-01	RHBDD1	rhomboid domain containing 1	chr2q36.3	226948_at	NM_032276
2.32	2.57	0.25	1.52E-01	5.19E-01	---	---	---	244859_at	---
1.87	2.09	0.22	1.52E-01	5.19E-01	LOC339535	hypothetical LOC339535	chr1q43	235599_at	XM_001132766 /// XM_001132951
2.03	2.24	0.21	1.52E-01	5.19E-01	---	---	---	1562894_at	---
2.44	2.64	0.20	1.52E-01	5.19E-01	---	---	---	234385_at	---
2.73	2.91	0.18	1.52E-01	5.19E-01	---	---	---	240367_at	---
2.38	2.78	0.39	1.52E-01	5.19E-01	DUOX2	dual oxidase 2	chr15q15.3	219727_at	NM_014080
5.25	5.52	0.27	1.52E-01	5.19E-01	CASZ1	castor zinc finger 1	chr1p36.22	235605_at	NM_001079843 /// NM_017766
2.86	3.12	0.26	1.52E-01	5.19E-01	CALCR	calcitonin receptor	chr7q21.3	207887_s_at	NM_001742
2.33	2.52	0.20	1.52E-01	5.19E-01	CPEB3	cytoplasmic polyadenylation element binding protein 3	chr10q23.32	1555250_a_at	NM_014912
2.09	2.27	0.17	1.52E-01	5.19E-01	FAS	Fas (TNF receptor superfamily, member 6)	chr10q24.1	237522_at	NM_000043 /// NM_152871 /// NM_152872 /// NM_152873 /// NM_152874 /// NM_152875 /// NM_152876 /// NM_152877
1.97	2.15	0.18	1.52E-01	5.19E-01	---	---	---	1559990_at	---
3.35	3.79	0.44	1.52E-01	5.19E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	201981_at	NM_002581
3.15	3.53	0.38	1.52E-01	5.19E-01	FLJ33630	hypothetical LOC644873	chr5q23.3	228686_at	NR_015360 /// XM_932475
3.85	4.16	0.31	1.52E-01	5.19E-01	SAPS2	SAPS domain family, member 2	chr22q13.33	238110_at	NM_014678
4.50	4.72	0.22	1.52E-01	5.19E-01	NKX3-1	NK3 homeobox 1	chr8p21	211498_s_at	NM_006167
2.24	2.43	0.19	1.52E-01	5.19E-01	---	---	---	1554766_s_at	---
2.42	2.58	0.16	1.53E-01	5.19E-01	---	---	---	237635_at	---
2.08	2.29	0.21	1.53E-01	5.19E-01	GIMAP5	GTPase, IMAP family member 5	chr7q36.1	215352_at	NM_018384
2.79	2.97	0.18	1.53E-01	5.19E-01	---	---	---	236877_at	---
3.29	3.59	0.30	1.53E-01	5.19E-01	---	---	---	243518_at	---
8.21	8.67	0.45	1.53E-01	5.19E-01	DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2	chr2q31.1	211684_s_at	NM_001378
2.61	2.83	0.22	1.53E-01	5.19E-01	TMEM182	transmembrane protein 182	chr2q12.1	1555090_x_at	NM_144632
2.87	3.12	0.25	1.53E-01	5.20E-01	FOLR1	folate receptor 1 (adult)	chr11q13.3-q14.1	204437_s_at	NM_000802 /// NM_016724 /// NM_016725 /// NM_016729 /// NM_016730 /// NM_016731
3.16	3.37	0.22	1.53E-01	5.20E-01	---	---	---	241261_x_at	---
2.15	2.32	0.18	1.53E-01	5.20E-01	---	---	---	233393_at	---
9.38	9.78	0.40	1.53E-01	5.20E-01	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	chr5p13	201280_s_at	NM_001343
5.86	6.19	0.33	1.53E-01	5.20E-01	KLK15	kallikrein-related peptidase 15	chr19q13.41	234495_at	NM_017509 /// NM_138563 /// NM_138564
2.97	3.20	0.23	1.53E-01	5.20E-01	---	---	---	230548_at	---
2.72	2.93	0.21	1.53E-01	5.20E-01	---	---	---	234253_at	---
4.79	5.08	0.29	1.53E-01	5.20E-01	PYGO2	Pygopus homolog 2 (Drosophila)	chr1q21.3	239666_at	NM_138300
2.51	2.77	0.26	1.53E-01	5.20E-01	RGS6	regulator of G-protein signaling 6	chr14q24.3	236726_at	NM_004296
1.85	2.02	0.17	1.53E-01	5.20E-01	---	---	---	241135_at	---
3.61	4.01	0.40	1.53E-01	5.20E-01	ADAMTSL2	ADAMTS-like 2	chr9q34.2	206629_at	NM_014694
4.27	4.56	0.29	1.53E-01	5.20E-01	ITPRIPL2	Inositol 1,4,5-triphosphate receptor interacting protein-like 2	chr16p12.3	227956_at	NM_001034841
4.48	4.83	0.35	1.53E-01	5.20E-01	---	---	---	1567219_at	---
5.33	6.13	0.80	1.53E-01	5.20E-01	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	chr9p22.3	212257_s_at	NM_003070 /// NM_139045
4.03	4.78	0.76	1.53E-01	5.20E-01	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	chrXq28	216521_s_at	NM_001018055 /// NM_024332
2.53	2.96	0.43	1.53E-01	5.20E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	241752_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097

5.58	6.00	0.42	1.53E-01	5.20E-01	---	---	---	214808_at	---
4.22	4.58	0.36	1.53E-01	5.20E-01	---	---	---	236742_at	---
3.72	4.06	0.34	1.53E-01	5.20E-01	---	---	---	235830_at	---
4.99	5.31	0.32	1.53E-01	5.20E-01	MGAT5B	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	chr17q25.2	238445_x_at	NM_144677 /// NM_198955
5.21	5.51	0.30	1.53E-01	5.20E-01	CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit	chr22q13.1	208299_at	NM_001003406 /// NM_021096
2.17	2.44	0.27	1.53E-01	5.20E-01	---	---	---	233005_at	---
3.82	4.08	0.26	1.53E-01	5.20E-01	---	---	---	241577_at	---
2.28	2.50	0.22	1.53E-01	5.20E-01	---	---	---	1566966_at	---
2.00	2.24	0.24	1.53E-01	5.20E-01	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	chr10q23.33	208147_s_at	NM_000770
1.92	2.12	0.21	1.53E-01	5.20E-01	---	---	---	1563724_at	---
4.15	4.46	0.31	1.53E-01	5.20E-01	---	---	---	233877_at	---
2.07	2.30	0.22	1.53E-01	5.20E-01	---	---	---	233059_at	---
2.08	2.29	0.21	1.53E-01	5.20E-01	---	---	---	1558466_at	---
2.21	2.41	0.20	1.53E-01	5.20E-01	PCDHB8	protocadherin beta 8	chr5q31	221319_at	NM_019120
3.78	4.00	0.22	1.53E-01	5.20E-01	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	chr7p11	214347_s_at	NM_000790 /// NM_001082971
2.20	2.38	0.18	1.53E-01	5.20E-01	---	---	---	215746_at	---
2.21	2.46	0.25	1.53E-01	5.20E-01	---	---	---	224086_at	---
2.06	2.24	0.18	1.53E-01	5.20E-01	---	---	---	240152_at	---
2.92	3.28	0.35	1.54E-01	5.20E-01	CDKN3	cyclin-dependent kinase inhibitor 3	chr14q22	209714_s_at	NM_001130851 /// NM_005192
4.62	4.93	0.31	1.54E-01	5.20E-01	---	---	---	234342_at	---
2.69	2.93	0.24	1.54E-01	5.21E-01	C14orf93	chromosome 14 open reading frame 93	chr14q11.2	219009_at	NM_001130706 /// NM_001130708 /// NM_021944
3.38	3.73	0.35	1.54E-01	5.21E-01	NRP2	neuropilin 2	chr2q33.3	1555468_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279
3.73	4.33	0.61	1.54E-01	5.21E-01	TLK1	tousled-like kinase 1	chr2q31.1	210379_s_at	NM_012290
4.02	4.53	0.51	1.54E-01	5.21E-01	GPHN	gephyrin	chr14q23.3	220773_s_at	NM_001024218 /// NM_020806
5.83	6.30	0.46	1.54E-01	5.21E-01	KIAA0196	KIAA0196	chr8q24.13	201985_at	NM_014846
2.09	2.49	0.41	1.54E-01	5.21E-01	KIAA1211	KIAA1211 protein	chr4q12	227230_s_at	NM_020722
3.98	4.32	0.35	1.54E-01	5.21E-01	---	---	---	244642_at	---
3.52	3.82	0.31	1.54E-01	5.21E-01	LOC729436	Hypothetical LOC729436	chr6q25.2	227866_at	XM_001133246 /// XM_001133721 /// XM_001721774
2.13	2.38	0.26	1.54E-01	5.21E-01	NOL4	nucleolar protein 4	chr18q12	206045_s_at	NM_003787
2.36	2.61	0.25	1.54E-01	5.21E-01	FBXW12	F-box and WD repeat domain containing 12	chr3p21.31	1564138_at	NM_207102
7.07	7.32	0.24	1.54E-01	5.21E-01	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	chr1q21.1	209207_s_at	NM_004892
2.23	2.46	0.23	1.54E-01	5.21E-01	---	---	---	1561113_at	---
2.54	2.77	0.23	1.54E-01	5.21E-01	RABGAP1L	RAB GTPase activating protein 1-like	chr1q24	215342_s_at	NM_001035230 /// NM_014857
2.37	2.57	0.20	1.54E-01	5.21E-01	---	---	---	217424_at	---
2.89	3.38	0.50	1.54E-01	5.21E-01	CPD	carboxypeptidase D	chr17q11.2	201942_s_at	NM_001304
2.43	2.69	0.25	1.54E-01	5.21E-01	CADM3	cell adhesion molecule 3	chr1q21.2-q22	216535_at	NM_001127173 /// NM_021189
1.92	2.10	0.19	1.54E-01	5.21E-01	DCX	doublecortin	chrXq22.3|Xq22.3-q23	204851_s_at	NM_000555 /// NM_178151 /// NM_178152 /// NM_178153
3.43	4.38	0.94	1.54E-01	5.21E-01	KIAA0746 /// SERINC2	KIAA0746 protein /// serine incorporator 2	chr1p35.1 /// chr4p15.2	212314_at	NM_015187 /// NM_178865
2.84	3.14	0.30	1.54E-01	5.21E-01	LOC144817	hypothetical protein LOC144817	chr13q14.11	1564263_at	XR_040343 /// XR_040344 /// XR_040345
2.12	2.35	0.24	1.54E-01	5.21E-01	hCG_25653	hCG25653	chr10p11.21	237339_at	XM_001724231 /// XM_933553 /// XM_944750
3.24	3.47	0.23	1.54E-01	5.21E-01	APCS	amyloid P component, serum	chr1q21-q23	206350_at	NM_001639
1.99	2.22	0.23	1.54E-01	5.21E-01	ZNF501	zinc finger protein 501	chr3p21.31	1562386_s_at	NM_145044

2.70	2.93	0.22	1.54E-01	5.21E-01	---	---	---	1558101_at	---
1.98	2.18	0.20	1.54E-01	5.21E-01	LOC100009676	Putative uncharacterized protein LOC100009676	chr3q12.3	232260_at	---
2.20	2.40	0.20	1.54E-01	5.21E-01	THPO	thrombopoietin	chr3q27	211154_at	NM_000460
6.08	6.83	0.74	1.54E-01	5.21E-01	PECAM1	platelet/endothelial cell adhesion molecule	chr17q23	208982_at	NM_000442
7.47	7.93	0.46	1.54E-01	5.21E-01	RAB18	RAB18, member RAS oncogene family	chr10p12.1	223336_s_at	NM_021252
4.84	5.16	0.32	1.54E-01	5.21E-01	ZRANB3	zinc finger, RAN-binding domain containing 3	chr2q21.3	239538_at	NM_032143
5.47	5.74	0.27	1.54E-01	5.21E-01	GOSR1	golgi SNAP receptor complex member 1	chr17q11	213020_at	NM_001007024 /// NM_001007025 /// NM_004871
3.94	4.20	0.27	1.54E-01	5.21E-01	---	---	---	243237_at	---
3.66	3.93	0.26	1.54E-01	5.21E-01	---	---	---	216405_at	---
3.03	3.28	0.26	1.54E-01	5.21E-01	---	---	---	226873_at	---
2.47	2.72	0.25	1.54E-01	5.21E-01	---	---	---	230523_at	---
2.07	2.25	0.17	1.54E-01	5.21E-01	---	---	---	233579_at	---
4.90	5.53	0.63	1.54E-01	5.21E-01	SWAP70	SWAP-70 protein	chr11p15	209306_s_at	NM_015055
2.53	2.69	0.16	1.54E-01	5.21E-01	---	---	---	221200_at	---
3.12	3.33	0.21	1.54E-01	5.21E-01	NEUROG3	neurogenin 3	chr10q21.3	207965_at	NM_020999
3.03	3.27	0.24	1.54E-01	5.21E-01	C16orf81	chromosome 16 open reading frame 81	chr16q24.3	1553449_at	XM_001126835 /// XM_001134340 /// XM_001719860
2.01	2.19	0.18	1.54E-01	5.21E-01	---	---	---	231690_at	---
2.41	2.64	0.22	1.54E-01	5.21E-01	---	---	---	241492_at	---
6.64	7.19	0.55	1.54E-01	5.21E-01	C2	complement component 2	chr6p21.3	203052_at	NM_000063
2.08	2.48	0.41	1.54E-01	5.21E-01	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	chr1q31	210121_at	NM_003783
2.42	2.71	0.29	1.54E-01	5.21E-01	---	---	---	236797_at	---
4.31	4.56	0.25	1.54E-01	5.21E-01	PPM1J	protein phosphatase 1J (PP2C domain containing)	chr1p13.2	229484_at	NM_005167
3.36	3.55	0.19	1.54E-01	5.21E-01	HDLBP	high density lipoprotein binding protein	chr2q37.3	219674_s_at	NM_005336 /// NM_203346
2.26	2.45	0.20	1.54E-01	5.21E-01	LOC651721	hypothetical protein LOC651721	---	1557027_at	XM_940938
2.84	3.27	0.42	1.55E-01	5.21E-01	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	chr21q22.12	1553313_s_at	NM_006933
2.56	2.81	0.24	1.55E-01	5.21E-01	KRT18P50	keratin 18 pseudogene 50	chr6q16.1	217000_at	XM_001716480 /// XM_001719397 /// XM_001721473
2.85	3.10	0.24	1.55E-01	5.21E-01	SLC2A4RG	SLC2A4 regulator	chr20q13.33	227362_at	NM_020062
3.53	3.75	0.23	1.55E-01	5.21E-01	TRPM6	Transient receptor potential cation channel, subfamily M, member 6	chr9q21.13	240389_at	NM_017662
6.06	6.62	0.56	1.55E-01	5.21E-01	---	---	---	225008_at	---
5.37	5.60	0.23	1.55E-01	5.21E-01	FLJ36031	Hypothetical protein FLJ36031	chr7q22.3	228668_x_at	NM_175884
2.08	2.29	0.20	1.55E-01	5.21E-01	FLJ35934	FLJ35934 protein	chr17p11.2	1564383_s_at	XR_041166
5.57	5.82	0.25	1.55E-01	5.21E-01	ADORA1	adenosine A1 receptor	chr1q32.1	216220_s_at	NM_000674 /// NM_001048230
2.66	2.89	0.23	1.55E-01	5.22E-01	ELP1P	endozepine-like peptide 1 pseudogene	---	224258_at	---
2.13	2.34	0.21	1.55E-01	5.22E-01	---	---	---	217082_at	---
2.77	3.16	0.38	1.55E-01	5.22E-01	---	---	---	243385_at	---
5.38	5.67	0.29	1.55E-01	5.22E-01	LOC100128008	Hypothetical protein LOC100128008	chr17q21.31	222197_s_at	XM_001715548 /// XM_001717318 /// XM_001719113
2.00	2.27	0.26	1.55E-01	5.22E-01	FOXP2	forkhead box P2	chr7q31	1555516_at	NM_014491 /// NM_148898 /// NM_148899
2.82	3.04	0.23	1.55E-01	5.22E-01	MPHOSPH9	M-phase phosphoprotein 9	chr12q24.31	237158_s_at	NM_022782
5.03	5.25	0.22	1.55E-01	5.22E-01	LRRC56	leucine rich repeat containing 56	chr11p15.5	232554_at	NM_198075
2.77	2.97	0.20	1.55E-01	5.22E-01	TCP10	t-complex 10 homolog (mouse)	chr6q27	207503_at	NM_004610
2.34	2.53	0.19	1.55E-01	5.22E-01	---	---	---	230042_at	---
2.26	2.43	0.18	1.55E-01	5.22E-01	SHMT1	serine hydroxymethyltransferase 1 (soluble)	chr17p11.2	217304_at	NM_004169 /// NM_148918
2.57	2.84	0.26	1.55E-01	5.22E-01	---	---	---	1566824_at	---
3.16	3.45	0.29	1.55E-01	5.22E-01	---	---	---	1567320_at	---
2.20	2.36	0.15	1.55E-01	5.22E-01	LOC400794	hypothetical gene supported by BC030596	chr1q23.2	1561693_at	---
6.42	6.65	0.22	1.55E-01	5.22E-01	TSC1	tuberous sclerosis 1	chr9q34	209390_at	NM_000368 /// NM_001008567

2.70	2.93	0.23	1.55E-01	5.22E-01	---	---	---	1560771_at	---
3.17	3.40	0.23	1.55E-01	5.22E-01	RYR1	ryanodine receptor 1 (skeletal)	chr19q13.1	205485_at	NM_000540 /// NM_001042723
3.91	4.06	0.16	1.55E-01	5.22E-01	BAT1	HLA-B associated transcript 1	chr6p21.3	212384_at	NM_004640 /// NM_080598
6.65	7.13	0.48	1.55E-01	5.22E-01	NSDHL	NAD(P) dependent steroid dehydrogenase-like	chrXq28	209279_s_at	NM_001129765 /// NM_015922
2.01	2.16	0.15	1.55E-01	5.22E-01	---	---	---	239985_at	---
2.05	2.28	0.23	1.55E-01	5.22E-01	---	---	---	238369_s_at	---
4.25	4.84	0.59	1.55E-01	5.22E-01	---	---	---	216614_at	---
3.73	3.97	0.25	1.55E-01	5.22E-01	---	---	---	240352_at	---
5.65	5.89	0.24	1.55E-01	5.22E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	237367_x_at	NM_001127183 /// NM_001127184 /// NM_003879
2.18	2.33	0.15	1.55E-01	5.22E-01	YTHDC1	YTH domain containing 1	chr4q13.2	239905_at	NM_001031732 /// NM_133370
2.93	3.14	0.21	1.55E-01	5.22E-01	FANCA	Fanconi anemia, complementation group A	chr16q24.3	203806_s_at	NM_000135 /// NM_001018112
2.81	3.04	0.23	1.55E-01	5.22E-01	DENND5B	DENN/MADD domain containing 5B	chr12p11.21	236415_at	NM_144973
7.75	8.24	0.49	1.55E-01	5.22E-01	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	chr22q13.2	208667_s_at	NM_003932
4.88	5.19	0.30	1.55E-01	5.22E-01	PIB5PA	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	chr22q11.2-q13.2	213651_at	NM_001002837 /// NM_014422
1.88	2.09	0.21	1.55E-01	5.22E-01	---	---	---	237788_at	---
5.22	5.48	0.26	1.55E-01	5.23E-01	APOL6	apolipoprotein L, 6	chr22q12.3	219716_at	NM_030641
6.03	6.19	0.16	1.55E-01	5.23E-01	---	---	---	217703_x_at	---
11.06	11.30	0.23	1.55E-01	5.23E-01	SOD1	superoxide dismutase 1, soluble	chr21q22.1|21q22.11	200642_at	NM_000454
3.91	4.36	0.45	1.55E-01	5.23E-01	ZNF518A	Zinc finger protein 518A	chr10q23.33	244132_x_at	NM_014803
4.12	4.49	0.38	1.55E-01	5.23E-01	JAG2	jagged 2	chr14q32	209784_s_at	NM_002226 /// NM_145159
3.92	4.28	0.36	1.55E-01	5.23E-01	GPHN	gephyrin	chr14q23.3	234941_s_at	NM_001024218 /// NM_020806
2.71	2.93	0.22	1.55E-01	5.23E-01	---	---	---	235697_at	---
1.94	2.14	0.21	1.55E-01	5.23E-01	PIAS2	protein inhibitor of activated STAT, 2	chr18q21.1	1555513_at	NM_004671 /// NM_173206
2.29	2.43	0.15	1.55E-01	5.23E-01	LOC285045	hypothetical LOC285045	chr2p22.3	1564309_at	---
2.21	2.43	0.22	1.56E-01	5.23E-01	S100G	S100 calcium binding protein G	chrXp22.2	207885_at	NM_004057
4.20	4.50	0.30	1.56E-01	5.23E-01	---	---	---	228685_at	---
2.08	2.28	0.20	1.56E-01	5.23E-01	---	---	---	243504_at	---
2.26	2.51	0.26	1.56E-01	5.23E-01	SCN3B	sodium channel, voltage-gated, type III, beta	chr11q23.3	204722_at	NM_001040151 /// NM_018400
5.34	5.94	0.60	1.56E-01	5.23E-01	SLC40A1	Solute carrier family 40 (iron-regulated transporter), member 1	chr2q32	233123_at	NM_014585
2.45	2.70	0.25	1.56E-01	5.23E-01	---	---	---	243693_at	---
5.00	5.30	0.31	1.56E-01	5.23E-01	LOC731656	Hypothetical protein LOC731656	---	241533_at	XM_001716424 /// XM_001716555
2.39	2.63	0.24	1.56E-01	5.23E-01	FBXO10	F-box protein 10	chr9p13.2	236100_at	NM_012166
1.85	2.04	0.19	1.56E-01	5.23E-01	---	---	---	241061_at	---
2.47	2.62	0.15	1.56E-01	5.23E-01	---	---	---	244850_at	---
7.13	7.44	0.32	1.56E-01	5.23E-01	MXRA7	matrix-remodelling associated 7	chr17q25.1-q25.2	227326_at	NM_001008528 /// NM_001008529 /// NM_198530
7.11	7.47	0.36	1.56E-01	5.23E-01	C6orf72	chromosome 6 open reading frame 72	chr6q25.1	225576_at	NM_138785
5.50	6.16	0.66	1.56E-01	5.23E-01	GPC3	glypican 3	chrXq26.1	209220_at	NM_004484
3.53	3.81	0.29	1.56E-01	5.23E-01	NUDCD3	NudC domain containing 3	chr7p13-p12	201269_s_at	NM_015332
2.38	2.65	0.27	1.56E-01	5.23E-01	---	---	---	242950_x_at	---
3.91	4.17	0.26	1.56E-01	5.23E-01	LOC645027	similar to Envoplakin (210 kDa paraneoplastic pemphigus antigen) (p210) (210 kDa cornified envelope precursor protein)	chr17p11.2	236933_at	XR_040221 /// XR_040222 /// XR_040223
2.31	2.48	0.17	1.56E-01	5.23E-01	ISX	intestine-specific homeobox	chr22q12.3	232707_at	NM_001008494
2.50	2.67	0.16	1.56E-01	5.23E-01	ITFG1	integrin alpha FG-GAP repeat containing 1	chr16q12.1	239044_at	NM_030790
2.36	2.56	0.20	1.56E-01	5.24E-01	---	---	---	236480_at	---
4.22	4.66	0.44	1.56E-01	5.24E-01	ZNF615	zinc finger protein 615	chr19q13.33	241827_at	NM_198480
7.52	7.91	0.39	1.56E-01	5.24E-01	WWC3	WWC family member 3	chrXp22.32	225273_at	NM_015691

3.52	3.72	0.20	1.56E-01	5.24E-01	---	---	---	234365_at	---
2.72	3.06	0.34	1.56E-01	5.24E-01	USP2	ubiquitin specific peptidase 2	chr11q23.3	207213_s_at	NM_004205 /// NM_171997
2.70	2.92	0.22	1.56E-01	5.24E-01	LOC129293	Hypothetical protein LOC129293	chr2p11.2	231429_at	NM_001080824
2.17	2.37	0.19	1.56E-01	5.24E-01	FLJ20323	hypothetical protein FLJ20323	chr7p22-p21	209672_s_at	NM_019005
2.72	2.97	0.25	1.56E-01	5.24E-01	---	---	---	242208_at	---
4.31	4.48	0.17	1.56E-01	5.24E-01	hCG_2009921	hypothetical locus LOC441204	chr7p15.2	240194_at	NR_015364 /// XM_001722132 /// XM_001723644 /// XM_001723694 /// XM_499061 /// XM_943507
2.70	3.16	0.46	1.56E-01	5.24E-01	---	---	---	234276_at	---
2.52	2.76	0.24	1.56E-01	5.24E-01	---	---	---	233402_at	---
6.90	7.12	0.22	1.56E-01	5.24E-01	SPDEF	SAM pointed domain containing ets transcription factor	chr6p21.3	214403_x_at	NM_012391
4.09	4.47	0.38	1.56E-01	5.24E-01	FNBP1L	formin binding protein 1-like	chr1p22.1	215017_s_at	NM_001024948 /// NM_017737
3.10	3.34	0.24	1.56E-01	5.24E-01	---	---	---	1565582_at	---
2.45	2.68	0.23	1.56E-01	5.24E-01	LOC341912	similar to developmental pluripotency associated 5; embryonal stem cell specific gene 1	chr14q24.3	234463_at	---
2.36	2.72	0.35	1.56E-01	5.24E-01	---	---	---	235740_at	---
3.07	3.28	0.22	1.56E-01	5.24E-01	KLRG2	killer cell lectin-like receptor subfamily G, member 2	chr7q34	231195_at	NM_198508
5.75	6.88	1.12	1.57E-01	5.24E-01	COL1A2	collagen, type I, alpha 2	chr7q22.1	202404_s_at	NM_000089
6.25	6.71	0.46	1.57E-01	5.24E-01	SCARB1	scavenger receptor class B, member 1	chr12q24.31	215834_x_at	NM_001082959 /// NM_005505
7.56	7.99	0.42	1.57E-01	5.24E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	211984_at	NM_001743 /// NM_005184 /// NM_006888
4.49	4.85	0.36	1.57E-01	5.24E-01	FLJ11151	hypothetical protein FLJ11151	chr16p13.12	239135_at	NM_001099455 /// NM_018340
3.10	3.40	0.31	1.57E-01	5.24E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHG1 /// IGHM /// LOC642131	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu /// similar to hCG1812074	chr14q32.33 /// chr15q11.2	211649_x_at	XM_001716198 /// XM_001716834 /// XM_001717736
3.72	4.02	0.30	1.57E-01	5.24E-01	---	---	---	243290_at	---
5.55	5.84	0.29	1.57E-01	5.24E-01	PPFIBP2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	chr11p15.4	212841_s_at	NM_003621
2.62	2.89	0.27	1.57E-01	5.24E-01	MON2	MON2 homolog (S. cerevisiae)	chr12q14.1	212755_at	NM_015026
3.72	3.99	0.27	1.57E-01	5.24E-01	---	---	---	231214_at	---
2.21	2.47	0.25	1.57E-01	5.24E-01	---	---	---	1562100_at	---
2.21	2.45	0.24	1.57E-01	5.24E-01	---	---	---	232713_at	---
3.21	3.44	0.24	1.57E-01	5.24E-01	ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	chr2p13.1	1554847_at	NM_001692
2.88	3.10	0.23	1.57E-01	5.24E-01	HK2	hexokinase 2	chr2p13	222305_at	NM_000189
2.95	3.17	0.22	1.57E-01	5.24E-01	EDN1	endothelin 1	chr6p24.1	1564630_at	NM_001955
2.69	2.89	0.20	1.57E-01	5.24E-01	---	---	---	222370_x_at	---
1.97	2.15	0.18	1.57E-01	5.24E-01	PTPRD	protein tyrosine phosphatase, receptor type, D	chr9p23-p24.3	242493_at	NM_001040712 /// NM_002839 /// NM_130391 /// NM_130392 /// NM_130393
1.91	2.08	0.18	1.57E-01	5.24E-01	---	---	---	237416_at	---
3.21	3.46	0.24	1.57E-01	5.25E-01	ANXA9	annexin A9	chr1q21	210085_s_at	NM_003568
2.40	2.62	0.22	1.57E-01	5.25E-01	---	---	---	244269_at	---
4.83	5.04	0.21	1.57E-01	5.25E-01	hCG_2033649	hypothetical LOC57244	chr1p36.32	215137_at	---
2.22	2.42	0.20	1.57E-01	5.25E-01	TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	chr10q25.3	236020_s_at	NM_139169
6.58	7.26	0.68	1.57E-01	5.25E-01	CCDC25	coiled-coil domain containing 25	chr8p21.1	222525_s_at	NM_018246
3.22	3.66	0.44	1.57E-01	5.25E-01	---	---	---	238775_at	---
7.89	8.20	0.31	1.57E-01	5.25E-01	C20orf108	chromosome 20 open reading frame 108	chr20q13.2	224693_at	NM_080821
4.00	4.30	0.30	1.57E-01	5.25E-01	DPYSL4	dihydropyrimidinase-like 4	chr10q26	205492_s_at	NM_006426
2.81	3.09	0.28	1.57E-01	5.25E-01	PSG6	pregnancy specific beta-1-glycoprotein 6	chr19q13.2	208106_x_at	NM_001031850 /// NM_002782
5.08	5.33	0.25	1.57E-01	5.25E-01	SLC6A17	solute carrier family 6, member 17	chr1p13.3	229925_at	NM_001010898
2.37	2.61	0.24	1.57E-01	5.25E-01	---	---	---	232855_at	---
2.34	2.54	0.20	1.57E-01	5.25E-01	ZNF114	zinc finger protein 114	chr19q13.32	1552946_at	NM_153608
6.21	7.05	0.85	1.57E-01	5.25E-01	RNF150	ring finger protein 150	chr4q31.21	227657_at	NM_020724

6.16	6.49	0.32	1.57E-01	5.25E-01	---	---	---	229746_x_at	---
3.49	3.73	0.23	1.57E-01	5.25E-01	---	---	---	238971_at	---
4.30	4.52	0.22	1.57E-01	5.25E-01	TRIM25	tripartite motif-containing 25	chr17q23.2	206911_at	NM_005082
3.16	3.35	0.19	1.57E-01	5.25E-01	---	---	---	229380_at	---
2.62	2.89	0.26	1.57E-01	5.25E-01	ANXA2P1	annexin A2 pseudogene 1	chr4q21-q31	210876_at	NR_001562
2.05	2.24	0.19	1.57E-01	5.25E-01	---	---	---	1560258_a_at	---
1.83	1.99	0.15	1.57E-01	5.25E-01	---	---	---	220700_at	---
2.83	3.30	0.47	1.57E-01	5.25E-01	ESR2	estrogen receptor 2 (ER beta)	chr14q23.2	211117_x_at	NM_001040275 /// NM_001040276 /// NM_001437
3.48	3.86	0.38	1.57E-01	5.25E-01	---	---	---	236131_at	---
5.32	5.66	0.34	1.57E-01	5.25E-01	BEST1	bestrophin 1	chr11q13	207671_s_at	NM_004183
5.22	5.55	0.33	1.57E-01	5.25E-01	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	chr10q22.2	212452_x_at	NM_012330
6.77	7.08	0.31	1.57E-01	5.25E-01	LOC400027	hypothetical gene supported by BC047417	chr12q12	238916_at	XM_001718517 /// XM_931434 /// XM_943193
4.13	4.40	0.27	1.57E-01	5.25E-01	XAGE1A /// XAGE1B /// XAGE1C /// XAGE1D /// XAGE1E	X antigen family, member 1A /// X antigen family, member 1B /// X antigen family, member 1C /// X antigen family, member 1D /// X antigen family, member 1E	chrXp11.22	220057_at	NM_001097591 /// NM_001097592 /// NM_001097593 /// NM_001097594 /// NM_001097595 /// NM_001097596 /// NM_001097597 /// NM_001097598 /// NM_001097602 /// NM_001097603 /// NM_001097604 /// NM_001097605 /// NM_020411 /// NM_133430 /// NM_133431 /// XM_927237 /// XM_931959
3.90	4.16	0.27	1.57E-01	5.25E-01	LOC606495	hypothetical protein LOC606495	chr1p32.3	229605_at	NM_001031672
2.03	2.21	0.17	1.57E-01	5.25E-01	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	chr2q14	209642_at	NM_004336
1.77	1.92	0.15	1.57E-01	5.25E-01	---	---	---	241567_at	---
2.16	2.35	0.19	1.57E-01	5.25E-01	FEZF2	FEZ family zinc finger 2	chr3p14.2	233972_s_at	NM_018008
1.86	2.04	0.18	1.57E-01	5.25E-01	---	---	---	1561140_at	---
2.03	2.24	0.21	1.57E-01	5.25E-01	MYO5B	myosin VB	chr18q21	1570141_at	NM_001080467
4.03	4.49	0.46	1.58E-01	5.25E-01	LOC100131039	Hypothetical protein LOC100131039	chr2q31.2	242679_at	XM_001722439 /// XM_001722454 /// XM_001726001
2.11	2.29	0.18	1.58E-01	5.25E-01	---	---	---	237936_at	---
5.27	5.95	0.68	1.58E-01	5.25E-01	ETFDH	electron-transferring-flavoprotein dehydrogenase	chr4q32-q35	33494_at	NM_004453
2.23	2.50	0.27	1.58E-01	5.25E-01	---	---	---	242196_at	---
4.71	5.15	0.43	1.58E-01	5.25E-01	AP3B1	adaptor-related protein complex 3, beta 1 subunit	chr5q14.1	203141_s_at	NM_003664
3.14	3.44	0.30	1.58E-01	5.25E-01	HOMER1	homer homolog 1 (Drosophila)	chr5q14.2	226651_at	NM_004272
7.17	7.39	0.22	1.58E-01	5.25E-01	---	---	---	242235_x_at	---
2.26	2.48	0.22	1.58E-01	5.25E-01	ZNF682	zinc finger protein 682	chr19p12	242915_at	NM_001077349 /// NM_033196
4.01	4.22	0.21	1.58E-01	5.25E-01	CRYBB1	crystallin, beta B1	chr22q11.2|22q12.1	206185_at	NM_001887
2.04	2.22	0.17	1.58E-01	5.25E-01	HUMBINDC	DNA binding protein for surfactant protein B	---	221352_at	---
3.99	5.22	1.23	1.58E-01	5.25E-01	OSTalpha	organic solute transporter alpha	chr3q29	229230_at	NM_152672
7.02	7.57	0.55	1.58E-01	5.25E-01	EPRS	glutamyl-prolyl-tRNA synthetase	chr1q41-q42	200843_s_at	NM_004446
5.90	6.19	0.30	1.58E-01	5.25E-01	IER5L	immediate early response 5-like	chr9q34.11	226559_at	NM_203434

4.70	4.98	0.29	1.58E-01	5.25E-01	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	chr19q13.3	206187_at	NM_000960
4.03	4.31	0.28	1.58E-01	5.25E-01	HCRP1	hepatocellular carcinoma-related HCRP1	---	216174_at	XM_001722898 /// XM_001724271 /// XM_001725456
2.23	2.50	0.27	1.58E-01	5.25E-01	---	---	---	241404_at	---
3.97	4.24	0.27	1.58E-01	5.25E-01	TMEM53	transmembrane protein 53	chr1p34.1	230647_at	NM_024587
3.35	3.59	0.24	1.58E-01	5.25E-01	SNORA71B	small nucleolar RNA, H/ACA box 71B	chr20q11.23	1568248_x_at	NR_002910
4.31	4.54	0.23	1.58E-01	5.25E-01	LOC541471	Hypothetical LOC541471	chr2q13	232918_at	XR_039885 /// XR_039886
2.09	2.32	0.23	1.58E-01	5.25E-01	---	---	---	231064_s_at	---
2.25	2.46	0.21	1.58E-01	5.25E-01	---	---	---	241295_at	---
1.78	1.96	0.19	1.58E-01	5.25E-01	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	chrXq22.1	210800_at	NM_004085
2.66	2.84	0.18	1.58E-01	5.25E-01	HLA-A29.1	major histocompatibility complex class I HLA-A29.1	---	215974_at	NM_001080840 /// XM_001716873
3.18	3.46	0.28	1.58E-01	5.26E-01	---	---	---	240494_at	---
7.96	8.45	0.49	1.58E-01	5.26E-01	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	chr7p15-p13	224880_at	NM_005402
2.22	2.50	0.28	1.58E-01	5.26E-01	---	---	---	237579_at	---
3.01	3.25	0.23	1.58E-01	5.26E-01	CCL23	chemokine (C-C motif) ligand 23	chr17q12	210549_s_at	NM_005064 /// NM_145898
4.91	5.13	0.22	1.58E-01	5.26E-01	---	---	---	239628_at	---
2.30	2.52	0.21	1.58E-01	5.26E-01	THAP2	THAP domain containing, apoptosis associated protein 2	chr12q21.1	223588_at	NM_031435
2.34	2.54	0.19	1.58E-01	5.26E-01	SERPINA7	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7	chrXq22.2	206386_at	NM_000354
7.83	8.27	0.44	1.58E-01	5.26E-01	GNPAT	glyceronephosphate O-acyltransferase	chr1q42	201956_s_at	NM_014236
6.50	7.15	0.64	1.58E-01	5.26E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	211985_s_at	NM_001743 /// NM_005184 /// NM_006888
6.62	7.23	0.61	1.58E-01	5.26E-01	KIAA0368	KIAA0368	chr9q31.3	214356_s_at	NM_001080398
2.17	2.34	0.17	1.58E-01	5.26E-01	NARG1	NMDA receptor regulated 1	chr4q31.1	1556381_at	NM_057175
2.29	2.48	0.19	1.58E-01	5.26E-01	ERAP1	Endoplasmic reticulum aminopeptidase 1	chr5q15	212580_at	NM_001040458 /// NM_016442
2.18	2.69	0.51	1.58E-01	5.26E-01	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	chr11p11.2	205860_x_at	NM_001014986 /// NM_004476
1.99	2.17	0.18	1.58E-01	5.26E-01	APOL6	apolipoprotein L, 6	chr22q12.3	1557236_at	NM_030641
2.90	3.10	0.20	1.58E-01	5.26E-01	hCG_1776047	HCG1776047	chr18q21.2	244296_at	XM_001127598 /// XM_001131423 /// XM_001719393
4.52	4.87	0.34	1.58E-01	5.26E-01	ORAI2	ORAI calcium release-activated calcium modulator 2	chr7q22.1	230347_at	NM_001126340 /// NM_032831
9.93	10.21	0.28	1.58E-01	5.26E-01	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	chr11p15	211730_s_at	NM_021128
5.75	6.22	0.47	1.58E-01	5.26E-01	C9orf125	chromosome 9 open reading frame 125	chr9q31.1	224458_at	NM_032342
2.00	2.17	0.17	1.58E-01	5.26E-01	LOC100128178	similar to hCG2041313	chr1q24.3	232090_at	XM_001715447 /// XM_001718852 /// XM_001718912
4.12	4.42	0.30	1.58E-01	5.26E-01	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)	chr9p21.2	219265_at	NM_024761
5.68	6.29	0.61	1.58E-01	5.26E-01	---	---	---	240651_at	---
5.10	5.37	0.27	1.58E-01	5.26E-01	SELI	selenoprotein I	chr2p23.3	224888_at	NM_033505
3.32	3.74	0.41	1.59E-01	5.27E-01	---	---	---	232925_at	---
3.30	3.51	0.21	1.59E-01	5.27E-01	FAM27E3	family with sequence similarity 27, member E3	chr9q12	227563_at	XM_001720463
2.50	2.71	0.21	1.59E-01	5.27E-01	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	chr2q31	1567015_at	NM_006164
7.34	7.77	0.43	1.59E-01	5.27E-01	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	chrXq13.3	201311_s_at	NM_003022
3.84	4.13	0.30	1.59E-01	5.27E-01	SIT1	signaling threshold regulating transmembrane adaptor 1	chr9p13-p12	205484_at	NM_014450
4.02	4.31	0.29	1.59E-01	5.27E-01	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	chr14q32	202509_s_at	NM_006291
3.90	4.16	0.26	1.59E-01	5.27E-01	---	---	---	1567035_at	---
2.12	2.33	0.20	1.59E-01	5.27E-01	---	---	---	243733_at	---
6.51	6.89	0.38	1.59E-01	5.27E-01	C6orf203	chromosome 6 open reading frame 203	chr6q21	223576_at	NM_016487
3.48	3.68	0.20	1.59E-01	5.27E-01	TTC26	tetratricopeptide repeat domain 26	chr7q34	219758_at	NM_024926
2.50	2.68	0.18	1.59E-01	5.27E-01	C10orf18	chromosome 10 open reading frame 18	chr10p15.1	1556758_at	NM_017782
6.79	7.48	0.69	1.59E-01	5.27E-01	IQGAP1	IQ motif containing GTPase activating protein 1	chr15q26.1	210840_s_at	NM_003870

3.18	3.53	0.35	1.59E-01	5.27E-01	OR2H1	olfactory receptor, family 2, subfamily H, member 1	chr6p21.3	1556986_at	NM_030883
3.94	4.22	0.27	1.59E-01	5.27E-01	PLAC2	Placenta-specific 2 (non-protein coding)	chr19p13.3	235994_s_at	XR_040439 /// XR_040440 /// XR_040441
2.72	2.96	0.24	1.59E-01	5.27E-01	ALOX12B	arachidonate 12-lipoxygenase, 12R type	chr17p13.1	207381_at	NM_001139
2.91	3.15	0.24	1.59E-01	5.27E-01	---	---	---	215959_at	---
2.11	2.32	0.21	1.59E-01	5.27E-01	---	---	---	210699_at	---
5.18	5.39	0.21	1.59E-01	5.27E-01	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	chr21q22.1|21q22.11	212379_at	NM_000819 /// NM_175085
1.90	2.09	0.20	1.59E-01	5.27E-01	---	---	---	224546_at	---
5.99	6.41	0.42	1.59E-01	5.27E-01	PPM1B	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	chr2p21	209296_at	NM_001033556 /// NM_001033557 /// NM_002706 /// NM_177968 /// NM_177969
3.08	3.43	0.35	1.59E-01	5.27E-01	SIRPB2	signal-regulatory protein beta 2	chr20p13	1559034_at	NM_001122962 /// NR_021484 /// XM_001724775 /// XM_209363 /// XM_939897
3.18	3.49	0.31	1.59E-01	5.27E-01	TANC1	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	chr2q24.1-q24.2	234039_at	NM_033394
6.45	6.75	0.30	1.59E-01	5.27E-01	MLL	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	212080_at	NM_005933
2.28	2.49	0.22	1.59E-01	5.27E-01	---	---	---	240609_at	---
4.81	5.37	0.56	1.59E-01	5.27E-01	---	---	---	227107_at	---
2.16	2.34	0.18	1.59E-01	5.27E-01	---	---	---	1567076_at	---
5.18	5.80	0.62	1.59E-01	5.27E-01	---	---	---	226250_at	---
4.35	5.11	0.76	1.59E-01	5.27E-01	TTC3	tetratricopeptide repeat domain 3	chr21q22.2	208664_s_at	NM_001001894 /// NM_003316
6.09	6.73	0.64	1.59E-01	5.27E-01	PRKG1	protein kinase, cGMP-dependent, type I	chr10q11.2	228396_at	NM_001098512 /// NM_006258
3.86	4.24	0.38	1.59E-01	5.27E-01	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	chr15q21.2	205768_s_at	NM_003645
4.01	4.39	0.38	1.59E-01	5.27E-01	---	---	---	215577_at	---
4.10	4.84	0.74	1.59E-01	5.27E-01	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	chr3p26-p25	216944_s_at	NM_001099952 /// NM_002222
8.44	8.91	0.47	1.59E-01	5.27E-01	UQCRC2	ubiquinol-cytochrome c reductase core protein II	chr16p12	212600_s_at	NM_003366
3.45	3.81	0.36	1.59E-01	5.27E-01	C1orf59	chromosome 1 open reading frame 59	chr1p13.3	225841_at	NM_001102592 /// NM_144584
4.38	4.71	0.32	1.59E-01	5.27E-01	KIR2DL1 /// KIR2DL2 /// KIR2DL3 /// KIR2DL5A /// KIR2DL5B /// KIR2DS1 /// KIR2DS2 /// KIR2DS3 /// KIR2DS4 /// KIR2DS5 /// KIR3DL1 /// KIR3DL2 /// KIR3DL3 /// KIR3DP1 /// KIR3DP1 /// LOC652001 /// LOC652779 /// LOC727787	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5B /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 3 /// killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5 /// killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3 /// killer cell immunoglobulin	chr19p13.3 /// chr19q13.4 /// chr19q13.42	217318_x_at	NM_001015070 /// NM_001018081 /// NM_006737 /// NM_012312 /// NM_012313 /// NM_012314 /// NM_013289 /// NM_014218 /// NM_014219 /// NM_014511 /// NM_014512 /// NM_014513 /// NM_015868 /// NM_020535 /// NM_153443 /// XM_001713705 /// XM_001718625 /// XM_001719864 /// XM_941297

2.95	3.19	0.24	1.59E-01	5.27E-01	PRB2 /// PRB4 /// PRH1 /// PRH2	proline-rich protein BstNI subfamily 2 /// proline-rich protein BstNI subfamily 4 /// proline-rich protein HaeIII subfamily 1 /// proline-rich protein HaeIII subfamily 2	chr12p13.2	216881_x_at	NM_001110213 /// NM_002723 /// NM_005042 /// NM_006248 /// NM_006250
3.04	3.27	0.23	1.59E-01	5.27E-01	MKI67	antigen identified by monoclonal antibody Ki-67	chr10q25-qter	212022_s_at	NM_002417
2.72	2.95	0.23	1.59E-01	5.27E-01	LOC554203	hypothetical LOC554203	chrXq13.2	1554448_at	XR_017716 /// XR_017797
2.47	2.66	0.19	1.59E-01	5.28E-01	---	---	---	240504_at	---
2.27	2.42	0.15	1.59E-01	5.28E-01	LOC284926	hypothetical protein LOC284926	chr22q13.31	1556064_at	---
2.32	2.52	0.20	1.59E-01	5.28E-01	ISYNA1	Myo-inositol 1-phosphate synthase A1	chr19p13.11	228417_at	NM_016368
2.06	2.22	0.16	1.59E-01	5.28E-01	---	---	---	244302_at	---
3.42	3.68	0.26	1.59E-01	5.28E-01	A2BP1	ataxin 2-binding protein 1	chr16p13.3	221217_s_at	NM_018723 /// NM_145891 /// NM_145892 /// NM_145893
5.03	5.22	0.18	1.60E-01	5.28E-01	GOSR2	golgi SNAP receptor complex member 2	chr17q21	213207_s_at	NM_001012511 /// NM_004287 /// NM_054022
3.79	4.08	0.29	1.60E-01	5.28E-01	ABHD1	abhydrolase domain containing 1	chr2p23.3	232550_at	NM_032604
3.17	3.46	0.29	1.60E-01	5.28E-01	---	---	---	242658_at	---
10.73	11.00	0.27	1.60E-01	5.28E-01	FTHP1	ferritin, heavy polypeptide pseudogene 1	chr6p21.3-p12	211628_x_at	---
2.10	2.31	0.22	1.60E-01	5.28E-01	L2HGDH	L-2-hydroxyglutarate dehydrogenase	chr14q22.1	224459_at	NM_024884
2.32	2.53	0.22	1.60E-01	5.28E-01	NPAL1	NIPA-like domain containing 1	chr4p12	1562792_at	NM_207330
4.96	5.16	0.21	1.60E-01	5.28E-01	CLCN7	chloride channel 7	chr16p13	221961_at	NM_001114331 /// NM_001287
2.25	2.44	0.19	1.60E-01	5.28E-01	LOC285740	hypothetical protein LOC285740	chr6q24.2	237614_at	---
2.74	2.93	0.19	1.60E-01	5.28E-01	LOC440894	hypothetical protein LOC440894	chr2q13	242222_at	---
1.97	2.16	0.20	1.60E-01	5.28E-01	---	---	---	237384_x_at	---
2.71	2.90	0.19	1.60E-01	5.28E-01	---	---	---	242511_at	---
2.06	2.26	0.20	1.60E-01	5.28E-01	VGLL1	vestigial like 1 (Drosophila)	chrXq26.3	215729_s_at	NM_016267
3.12	3.36	0.24	1.60E-01	5.28E-01	TNXB	tenascin XB	chr6p21.3	216654_at	NM_019105 /// NM_032470
2.99	3.71	0.72	1.60E-01	5.28E-01	CCDC80	coiled-coil domain containing 80	chr3q13.2	243864_at	NM_199511 /// NM_199512
3.39	3.70	0.31	1.60E-01	5.28E-01	KLK4	kallikrein-related peptidase 4	chr19q13.41	224062_x_at	NM_004917
4.60	4.89	0.29	1.60E-01	5.28E-01	MGC16121	hypothetical protein MGC16121	chrXq26.3	237986_at	XM_001128419 /// XM_001715787 /// XM_001715872
2.08	2.35	0.27	1.60E-01	5.28E-01	---	---	---	234030_at	---
1.94	2.13	0.18	1.60E-01	5.28E-01	SLCO1A2	solute carrier organic anion transporter family, member 1A2	chr12p12	211481_at	NM_005075 /// NM_021094 /// NM_134431
2.20	2.37	0.17	1.60E-01	5.28E-01	PCDHA2	protocadherin alpha 2	chr5q31	211365_s_at	NM_018905 /// NM_031495 /// NM_031496
3.12	3.43	0.30	1.60E-01	5.28E-01	CTTN	cortactin	chr11q13	1567277_at	NM_005231 /// NM_138565
2.65	2.88	0.22	1.60E-01	5.28E-01	TRAF3IP3	TRAF3 interacting protein 3	chr1q32.3-q41	231932_at	NM_025228
1.88	2.10	0.22	1.60E-01	5.28E-01	GNGT1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	chr7q21.3	207166_at	NM_021955
4.83	5.17	0.34	1.60E-01	5.29E-01	ATOH8	atonal homolog 8 (Drosophila)	chr2p11.2	228890_at	NM_032827
2.16	2.34	0.17	1.60E-01	5.29E-01	SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	chr11p14.3	220551_at	NM_020346
2.65	2.87	0.23	1.60E-01	5.29E-01	BRWD1	Bromodomain and WD repeat domain containing 1	chr21q22.2	244622_at	NM_001007246 /// NM_018963 /// NM_033656
4.15	4.53	0.38	1.60E-01	5.29E-01	LOC100130097	Hypothetical protein LOC100130097	chr1q44	241376_at	XM_001717074 /// XM_001717121 /// XM_001717268
2.63	2.97	0.33	1.60E-01	5.29E-01	SALL3	sal-like 3 (Drosophila)	chr18q23	232847_at	NM_171999
2.13	2.30	0.17	1.60E-01	5.29E-01	---	---	---	235738_at	---
2.02	2.24	0.22	1.60E-01	5.29E-01	---	---	---	AFFX-LysX-5_at	---

3.18	3.39	0.21	1.60E-01	5.29E-01	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	chr17q21-q22	205592_at	NM_000342
4.84	5.26	0.42	1.60E-01	5.29E-01	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	chr1q42.11	215296_at	NM_003607 /// NM_014826
7.75	8.53	0.78	1.60E-01	5.29E-01	FNDC3B	fibronectin type III domain containing 3B	chr3q26.31	218618_s_at	NM_022763
6.80	7.44	0.64	1.60E-01	5.29E-01	DHCR7	7-dehydrocholesterol reductase	chr11q13.2-q13.5	201791_s_at	NM_001360
1.84	1.99	0.16	1.60E-01	5.29E-01	LOC161635	similar to casein kinase I alpha	chr15q13.3	1559651_at	---
3.75	4.29	0.54	1.61E-01	5.29E-01	RHCG	Rh family, C glycoprotein	chr15q25	219554_at	NM_016321
3.46	3.89	0.43	1.61E-01	5.29E-01	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	chr3p14.3-p14.2	226814_at	NM_182920
2.96	3.22	0.26	1.60E-01	5.29E-01	LOC283688	Hypothetical protein LOC283688	chr15q25.1	1559579_at	XM_001127453 /// XM_001132532 /// XM_001714631
3.71	3.95	0.25	1.61E-01	5.29E-01	AHDC1	AT hook, DNA binding motif, containing 1	chr1p36.13	229379_at	NM_001029882
2.79	3.01	0.22	1.60E-01	5.29E-01	RP3-398D13.1	hypothetical protein FLJ33708	chr6p25.1	1556365_at	NM_173675
1.89	2.10	0.22	1.61E-01	5.29E-01	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	chr13q32.1	233945_at	NM_020121
2.21	2.39	0.17	1.61E-01	5.29E-01	TULP2	tubby like protein 2	chr19q13.1	206733_at	NM_003323
8.40	9.08	0.68	1.61E-01	5.29E-01	RP1-21O18.1	kazrin	chr1p36.21	213478_at	NM_001017999 /// NM_001018000 /// NM_001018001 /// NM_015209 /// NM_201628
2.70	2.90	0.21	1.61E-01	5.29E-01	---	---	---	239690_at	---
3.26	3.57	0.31	1.61E-01	5.29E-01	IGLV4-60	immunoglobulin lambda variable 4-60	chr22q11.2	215777_at	---
2.47	2.67	0.21	1.61E-01	5.29E-01	---	---	---	239184_at	---
2.11	2.30	0.20	1.61E-01	5.29E-01	PLCB4	phospholipase C, beta 4	chr20p12	203895_at	NM_000933 /// NM_182797
2.75	2.94	0.19	1.61E-01	5.29E-01	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	chr12q13.13	234990_at	NM_001127321 /// NM_001127322 /// NM_012117
2.34	2.52	0.18	1.61E-01	5.29E-01	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	chr2q23.3-q24.1	236536_at	NM_052917
2.17	2.46	0.29	1.61E-01	5.29E-01	C5orf29	chromosome 5 open reading frame 29	chr5q11.2	1552386_at	NM_152687
2.26	2.48	0.22	1.61E-01	5.29E-01	---	---	---	1567334_at	---
4.08	4.43	0.35	1.61E-01	5.29E-01	IKZF5	IKAROS family zinc finger 5 (Pegasus)	chr10q26	226680_at	NM_022466
3.06	3.34	0.28	1.61E-01	5.29E-01	FAM80B	family with sequence similarity 80, member B	chr12p13.31	225999_at	NM_020734
8.72	9.12	0.40	1.61E-01	5.29E-01	SEC31A	SEC31 homolog A (S. cerevisiae)	chr4q21.22	200945_s_at	NM_001077206 /// NM_001077207 /// NM_001077208 /// NM_014933 /// NM_016211
2.12	2.31	0.18	1.61E-01	5.29E-01	---	---	---	237000_at	---
3.55	3.84	0.29	1.61E-01	5.29E-01	SRCAP	Snf2-related CREBBP activator protein	chr16p11.2	213667_at	NM_006662
2.01	2.25	0.24	1.61E-01	5.29E-01	---	---	---	238484_s_at	---
2.40	2.62	0.23	1.61E-01	5.29E-01	---	---	---	1557542_at	---
5.72	6.56	0.84	1.61E-01	5.29E-01	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	chr1p22.2	202269_x_at	NM_002053
5.62	6.57	0.95	1.61E-01	5.29E-01	PDCD6IP	programmed cell death 6 interacting protein	chr3p22.3	222394_at	NM_013374
5.53	6.19	0.67	1.61E-01	5.29E-01	TTF1	transcription termination factor, RNA polymerase I	chr9q34.13	204771_s_at	NM_007344
7.26	7.90	0.64	1.61E-01	5.29E-01	MORF4 /// MORF4L1	mortality factor 4 /// mortality factor 4 like 1	chr15q24 /// chr4q33-q34.1	221381_s_at	NM_006791 /// NM_006792 /// NM_206839
1.91	2.08	0.16	1.61E-01	5.29E-01	LOC202451	hypothetical protein LOC202451	chr6q23.3	236037_at	XM_928403 /// XM_941101
4.13	4.38	0.25	1.61E-01	5.29E-01	ZDHHC24	zinc finger, DHHC-type containing 24	chr11q13.1	232091_s_at	NM_207340
3.25	4.08	0.83	1.61E-01	5.29E-01	DOK5	docking protein 5	chr20q13.2	214844_s_at	NM_018431
5.69	6.19	0.51	1.61E-01	5.29E-01	SAMHD1	SAM domain and HD domain 1	chr20pter-q12	204502_at	NM_015474
6.62	6.92	0.30	1.61E-01	5.29E-01	SUFU	suppressor of fused homolog (Drosophila)	chr10q24.32	222749_at	NM_016169
7.55	7.98	0.43	1.61E-01	5.29E-01	---	---	---	212608_s_at	---
2.13	2.46	0.33	1.61E-01	5.29E-01	---	---	---	242756_at	---
2.86	3.15	0.29	1.61E-01	5.29E-01	CRLF2	cytokine receptor-like factor 2	chrXp22.3; Yp11.3	208303_s_at	NM_001012288 /// NM_022148
2.27	2.53	0.26	1.61E-01	5.29E-01	---	---	---	241279_at	---
3.39	3.60	0.21	1.61E-01	5.30E-01	---	---	---	231643_s_at	---

2.34	2.58	0.24	1.61E-01	5.30E-01	TMOD3	tropomodulin 3 (ubiquitous)	chr15q21.1-q21.2	220800_s_at	NM_014547
2.56	2.80	0.24	1.61E-01	5.30E-01	ZNF350	zinc finger protein 350	chr19q13.33	233169_at	NM_021632
3.17	3.43	0.26	1.61E-01	5.30E-01	---	---	---	1564438_at	---
2.87	3.13	0.27	1.61E-01	5.30E-01	---	---	---	241531_at	---
5.97	6.51	0.53	1.61E-01	5.30E-01	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	chr6q14-q15	209025_s_at	NM_006372
4.37	4.84	0.46	1.61E-01	5.30E-01	MCAM	melanoma cell adhesion molecule	chr11q23.3	210869_s_at	NM_006500
6.34	6.63	0.29	1.61E-01	5.30E-01	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	chr15q25.1-q25.2	202070_s_at	NM_005530
2.63	2.84	0.21	1.61E-01	5.30E-01	---	---	---	244357_at	---
2.97	3.18	0.21	1.61E-01	5.30E-01	LOC643837	hypothetical LOC643837	chr1p36.33	227201_at	NR_015368 /// XM_927114
4.68	5.16	0.48	1.62E-01	5.30E-01	CHPT1	choline phosphotransferase 1	chr12q	230364_at	NM_020244
6.23	6.70	0.47	1.62E-01	5.30E-01	WDR7	WD repeat domain 7	chr18q21.1-q22	212880_at	NM_015285 /// NM_052834
4.93	5.26	0.33	1.62E-01	5.30E-01	LOC727901 /// VWA1	hypothetical LOC727901 /// von Willebrand factor A domain containing 1	chr1p36.33	218731_s_at	NM_022834 /// NM_199121 /// XR_042309 /// XR_042470
2.37	2.68	0.31	1.62E-01	5.30E-01	COBLL1	COBL-like 1	chr2q24.3	229598_at	NM_014900
2.78	3.07	0.28	1.62E-01	5.30E-01	PRPH2	peripherin 2 (retinal degeneration, slow)	chr6p21.2-p12.3	206625_at	NM_000322
2.17	2.41	0.23	1.62E-01	5.30E-01	---	---	---	236774_at	---
2.02	2.24	0.22	1.62E-01	5.30E-01	---	---	---	1567706_at	---
1.85	2.06	0.22	1.62E-01	5.30E-01	---	---	---	1569551_at	---
1.95	2.15	0.21	1.62E-01	5.30E-01	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	chr2q34	215465_at	NM_015657 /// NM_173076
2.81	3.01	0.20	1.62E-01	5.30E-01	C8orf17	chromosome 8 open reading frame 17	chr8q24.3	208266_at	NM_020237
2.74	2.91	0.18	1.62E-01	5.30E-01	---	---	---	235105_at	---
2.03	2.20	0.17	1.62E-01	5.30E-01	LOC100128977	Similar to hCG1654542	chr17q21.31	1563367_at	XM_001715841 /// XM_001717446 /// XM_001719146
1.92	2.08	0.16	1.62E-01	5.30E-01	C1orf83	chromosome 1 open reading frame 83	chr1p32.3	1562470_at	NM_153035
7.73	8.56	0.83	1.62E-01	5.30E-01	HSPA9	heat shock 70kDa protein 9 (mortalin)	chr5q31.1	200692_s_at	NM_004134
3.88	4.23	0.35	1.62E-01	5.30E-01	USP48	ubiquitin specific peptidase 48	chr1p36.12	220078_at	NM_001032730 /// NM_032236
2.70	3.00	0.30	1.62E-01	5.30E-01	---	---	---	1569477_at	---
4.76	4.96	0.20	1.62E-01	5.30E-01	IL18BP	interleukin 18 binding protein	chr11q13	219323_s_at	NM_001039659 /// NM_001039660 /// NM_173042
1.82	2.02	0.21	1.62E-01	5.30E-01	GLOD5	Glyoxalase domain containing 5	chrXp11.23	241564_at	NM_001080489
3.29	3.75	0.46	1.62E-01	5.30E-01	---	---	---	237006_at	---
2.58	2.86	0.28	1.62E-01	5.30E-01	---	---	---	240224_at	---
3.80	4.08	0.28	1.62E-01	5.30E-01	---	---	---	242479_s_at	---
6.54	6.83	0.29	1.62E-01	5.30E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	211316_x_at	NM_001127183 /// NM_001127184 /// NM_003879
4.35	4.68	0.33	1.62E-01	5.30E-01	CORO7	coronin 7	chr16p13.3	219040_at	NM_024535
1.94	2.11	0.17	1.62E-01	5.30E-01	---	---	---	237859_at	---
6.32	6.79	0.47	1.62E-01	5.30E-01	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	chr2p16.1	226230_at	NM_001122964 /// NM_020463
4.55	4.93	0.38	1.62E-01	5.30E-01	CPT1C	carnitine palmitoyltransferase 1C	chr19q13.33	227468_at	NM_152359
6.35	6.64	0.30	1.62E-01	5.30E-01	ST6GALNAC6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	chr9q34.11	222571_at	NM_013443
4.52	4.82	0.29	1.62E-01	5.30E-01	C19orf34	chromosome 19 open reading frame 34	chr19p13.3	1553871_at	NM_152771
2.57	2.86	0.28	1.62E-01	5.30E-01	DNAL1	dynein, axonemal, light chain 1	chr14q24.3	223959_at	NM_031427
3.54	3.80	0.26	1.62E-01	5.30E-01	SLC46A1	Solute carrier family 46 (folate transporter), member 1	chr17q11.2	233531_at	NM_080669
6.24	6.50	0.26	1.62E-01	5.30E-01	LEF1	lymphoid enhancer-binding factor 1	chr4q23-q25	221557_s_at	NM_001130713 /// NM_001130714 /// NM_016269
2.28	2.53	0.25	1.62E-01	5.30E-01	---	---	---	240743_at	---
3.87	4.12	0.25	1.62E-01	5.30E-01	---	---	---	229921_at	---
2.89	3.11	0.22	1.62E-01	5.30E-01	AKAP4	A kinase (PRKA) anchor protein 4	chrXp11.2	207019_s_at	NM_003886 /// NM_139289
2.27	2.48	0.21	1.62E-01	5.30E-01	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	chr6p12	214451_at	NM_003221

3.46	3.66	0.21	1.62E-01	5.30E-01	LOC100134053 /// POLR2J /// POLR2J2 /// POLR2J3 /// POLR2J4	similar to POLR2J4 protein /// polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa /// polymerase (RNA) II (DNA directed) polypeptide J2 /// polymerase (RNA) II (DNA directed) polypeptide J3 /// polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13 /// chr7q22.1	214740_at	NM_001097615 /// NM_006234 /// NM_032959 /// NR_003655 /// XM_001717094 /// XR_042143 /// XR_042182
2.67	2.87	0.20	1.62E-01	5.30E-01	---	---	---	241090_at	---
1.86	2.03	0.16	1.62E-01	5.30E-01	ZNF674	zinc finger family member 674	---	215309_at	NM_001039891
1.99	2.14	0.15	1.62E-01	5.30E-01	TBR1	T-box, brain, 1	chr2q24	220025_at	NM_006593
5.03	5.44	0.40	1.62E-01	5.31E-01	DZIP3	DAZ interacting protein 3, zinc finger	chr3q13.13	207232_s_at	NM_014648
3.99	4.51	0.52	1.62E-01	5.31E-01	NAV1	neuron navigator 1	chr1q32.3	224771_at	NM_020443
2.84	3.18	0.34	1.62E-01	5.31E-01	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	chr21q22.13	211541_s_at	NM_001396 /// NM_101395 /// NM_130436 /// NM_130437 /// NM_130438
2.63	2.88	0.25	1.62E-01	5.31E-01	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	chr19p13.2	235572_at	NM_182513
5.69	5.92	0.22	1.63E-01	5.31E-01	TPPP	tubulin polymerization promoting protein	chr5p15.3	206179_s_at	NM_007030
4.11	4.30	0.19	1.63E-01	5.31E-01	---	---	---	243111_at	---
3.79	4.47	0.69	1.63E-01	5.31E-01	ZCCHC6	zinc finger, CCHC domain containing 6	chr9q21	242776_at	NM_024617
4.34	4.98	0.64	1.63E-01	5.31E-01	FYN	FYN oncogene related to SRC, FGR, YES	chr6q21	216033_s_at	NM_002037 /// NM_153047 /// NM_153048
4.78	5.25	0.46	1.63E-01	5.31E-01	---	---	---	230987_at	---
2.20	2.43	0.23	1.63E-01	5.31E-01	---	---	---	232451_at	---
3.34	3.53	0.20	1.63E-01	5.31E-01	FBXO31	F-box protein 31	chr16q24.2	223745_at	NM_024735
2.35	2.52	0.18	1.63E-01	5.31E-01	---	---	---	231482_at	---
2.04	2.22	0.17	1.63E-01	5.31E-01	SPAG17	sperm associated antigen 17	chr1p12	233516_s_at	NM_206996
3.81	4.77	0.96	1.63E-01	5.31E-01	TPSAB1	tryptase alpha/beta 1	chr16p13.3	215382_x_at	NM_003294 /// XM_001720738 /// XM_001720740
3.21	3.47	0.26	1.63E-01	5.31E-01	---	---	---	244809_at	---
3.33	3.57	0.24	1.63E-01	5.31E-01	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	chr22q12.3-q13.1|22q13.1	216055_at	NM_002608 /// NM_033016
2.32	2.53	0.21	1.63E-01	5.31E-01	AKAP5	A kinase (PRKA) anchor protein 5	chr14q21-q24	230846_at	NM_004857
2.44	2.60	0.16	1.63E-01	5.31E-01	---	---	---	229339_at	---
2.82	3.08	0.26	1.63E-01	5.31E-01	C20orf112 /// LOC284804	chromosome 20 open reading frame 112 /// hypothetical protein LOC284804	chr20q11.1-q11.23 /// chr20q11.21	1558679_at	NM_080616
2.72	2.98	0.26	1.63E-01	5.31E-01	---	---	---	238023_at	---
4.78	5.01	0.23	1.63E-01	5.31E-01	STRBP	spermatid perinuclear RNA binding protein	chr9q33.3	223246_s_at	NM_018387
3.39	4.15	0.76	1.63E-01	5.31E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	224342_x_at	---
6.21	6.89	0.67	1.63E-01	5.31E-01	AGTR1	angiotensin II receptor, type 1	chr3q21-q25	208016_s_at	NM_000685 /// NM_004835 /// NM_009585 /// NM_031850 /// NM_032049
6.25	6.59	0.34	1.63E-01	5.31E-01	---	---	---	242824_at	---
2.10	2.27	0.17	1.63E-01	5.31E-01	PRO2214	hypothetical protein PRO2214	chr5q12.2	222965_at	---
2.30	2.46	0.17	1.63E-01	5.31E-01	OR2W3	olfactory receptor, family 2, subfamily W, member 3	chr1q44	241881_at	NM_001001957
1.98	2.18	0.20	1.63E-01	5.31E-01	---	---	---	233485_at	---
2.29	2.45	0.16	1.63E-01	5.31E-01	---	---	---	238282_at	---
3.70	3.98	0.28	1.63E-01	5.31E-01	PFKP	phosphofructokinase, platelet	chr10p15.3-p15.2	240202_x_at	NM_002627
4.90	5.18	0.27	1.63E-01	5.31E-01	TMEM120B	transmembrane protein 120B	chr12q24.31	236667_at	NM_001080825
2.50	2.75	0.26	1.63E-01	5.31E-01	TPD52	tumor protein D52	chr8q21	201688_s_at	NM_001025252 /// NM_001025253 /// NM_005079
2.68	3.09	0.41	1.63E-01	5.31E-01	PRICKLE1	prickle homolog 1 (Drosophila)	chr12q12	226069_at	NM_153026
3.27	3.55	0.28	1.63E-01	5.31E-01	SLC18A3	solute carrier family 18 (vesicular acetylcholine), member 3	chr10q11.2	207150_at	NM_003055
3.53	3.91	0.37	1.63E-01	5.31E-01	DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1	chr7q21.3-q22.1	205348_s_at	NM_004411
2.58	2.85	0.27	1.63E-01	5.31E-01	---	---	---	234287_at	---

4.25	5.02	0.77	1.63E-01	5.31E-01	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	chr9q22.1-q22.3	217077_s_at	NM_005458
3.07	3.64	0.56	1.63E-01	5.31E-01	---	---	---	237616_at	---
1.95	2.13	0.19	1.63E-01	5.31E-01	---	---	---	240601_at	---
2.44	2.66	0.22	1.63E-01	5.31E-01	GPR176	G protein-coupled receptor 176	chr15q14-q15.1	206673_at	NM_007223
3.53	3.73	0.20	1.63E-01	5.31E-01	---	---	---	241074_at	---
3.12	3.47	0.35	1.63E-01	5.31E-01	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	chr3q26.1	205352_at	NM_001122752 /// NM_005025
4.77	5.10	0.32	1.63E-01	5.31E-01	CABC1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	chr1q42.13	222542_x_at	NM_020247
3.09	3.42	0.32	1.63E-01	5.31E-01	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	chr1q42.13	232499_at	NM_002221
4.05	4.32	0.27	1.63E-01	5.31E-01	FER1L3	fer-1-like 3, myoferlin (C. elegans)	chr10q24	217518_at	NM_013451 /// NM_133337
2.78	3.01	0.23	1.63E-01	5.31E-01	GOLM1	golgi membrane protein 1	chr9q21.33	1558248_at	NM_016548 /// NM_177937
3.10	3.29	0.20	1.63E-01	5.31E-01	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	chr22q13.1|22q12.3	242773_at	NM_000343
5.77	6.16	0.39	1.63E-01	5.31E-01	FPR3	formyl peptide receptor 3	chr19q13.3-q13.4	230422_at	NM_002030
9.44	9.79	0.35	1.63E-01	5.31E-01	CCND2	cyclin D2	chr12p13	200953_s_at	NM_001759
2.01	2.17	0.15	1.63E-01	5.32E-01	EPOR	erythropoietin receptor	chr19p13.3-p13.2	216999_at	NM_000121
4.44	5.38	0.94	1.63E-01	5.32E-01	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	chr6q21	210639_s_at	NM_004849
2.57	2.75	0.19	1.64E-01	5.32E-01	OR8G1	olfactory receptor, family 8, subfamily G, member 1	chr11q24.2	1567060_at	NM_001002905
2.16	2.33	0.17	1.64E-01	5.32E-01	---	---	---	1564699_at	---
5.01	5.97	0.96	1.64E-01	5.32E-01	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	chrXq13.1-q21.1	228483_s_at	NM_015975
9.77	10.39	0.63	1.64E-01	5.32E-01	S100A10	S100 calcium binding protein A10	chr1q21	200872_at	NM_002966
5.89	6.46	0.57	1.64E-01	5.32E-01	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	chr4q21-q25	208848_at	NM_000671
2.07	2.40	0.33	1.64E-01	5.32E-01	CD24	CD24 molecule	chr6q21	266_s_at	NM_013230 /// XM_001725629
3.83	4.16	0.33	1.64E-01	5.32E-01	---	---	---	240446_at	---
3.09	3.30	0.21	1.64E-01	5.32E-01	SETDB2	SET domain, bifurcated 2	chr13q14	1564972_x_at	NM_031915
2.97	3.19	0.21	1.64E-01	5.32E-01	FRMD7	FERM domain containing 7	chrXq26-q27	233047_at	NM_194277
2.62	2.83	0.21	1.64E-01	5.32E-01	KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	chr17p11.2	207110_at	NM_021012
2.47	2.68	0.21	1.64E-01	5.32E-01	LOC100128868	testin-related protein TRG	chr7q31.2	1555392_at	XM_001720810 /// XM_001722096 /// XM_001726148
2.25	2.47	0.22	1.64E-01	5.32E-01	TINAG	tubulointerstitial nephritis antigen	chr6p11.2-p12	223782_s_at	NM_014464
5.96	6.75	0.79	1.64E-01	5.32E-01	ZFR	zinc finger RNA binding protein	chr5p13.3	201856_s_at	NM_016107
6.32	6.53	0.21	1.64E-01	5.32E-01	TTC38	Tetratricopeptide repeat domain 38	chr22q13	216768_x_at	NM_017931
1.79	1.96	0.17	1.64E-01	5.32E-01	IL22	interleukin 22	chr12q15	222974_at	NM_020525
4.97	5.29	0.32	1.64E-01	5.32E-01	---	---	---	217054_at	---
3.19	3.41	0.22	1.64E-01	5.32E-01	---	---	---	237726_at	---
1.98	2.15	0.17	1.64E-01	5.32E-01	RSHL3	radial spokehead-like 3	chr6q22.1	233071_at	NM_001010892
3.95	4.34	0.39	1.64E-01	5.32E-01	TAC3	tachykinin 3	chr12q13-q21	219992_at	NM_001006667 /// NM_013251
2.43	2.65	0.23	1.64E-01	5.32E-01	SLC22A16	solute carrier family 22 (organic cation/carnitine transporter), member 16	chr6q22.1|6q21-q22.1	232232_s_at	NM_033125
2.03	2.22	0.19	1.64E-01	5.32E-01	---	---	---	207731_at	---
2.87	3.13	0.26	1.64E-01	5.32E-01	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	chr11q21	242456_at	NM_005590 /// NM_005591
3.38	3.70	0.32	1.64E-01	5.32E-01	---	---	---	236857_at	---
8.47	9.47	1.00	1.64E-01	5.32E-01	ABCB1 /// ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 1 /// ATP-binding cassette, sub-family B (MDR/TAP), member 4	chr7q21.1	209994_s_at	NM_000443 /// NM_000927 /// NM_018849 /// NM_018850
8.82	9.75	0.93	1.64E-01	5.32E-01	---	---	---	228222_at	---
6.07	6.62	0.55	1.64E-01	5.32E-01	TPST2	tyrosylprotein sulfotransferase 2	chr22q12.1	204079_at	NM_001008566 /// NM_003595
8.44	8.73	0.30	1.64E-01	5.32E-01	TMEM111	transmembrane protein 111	chr3p25.3	217882_at	NM_018447
2.34	2.64	0.29	1.64E-01	5.32E-01	ZDHHC23	zinc finger, DHHC-type containing 23	chr3q13.31	226912_at	NM_173570
3.39	3.68	0.29	1.64E-01	5.32E-01	OMD	osteomodulin	chr9q22.31	205907_s_at	NM_005014
3.89	4.17	0.28	1.64E-01	5.32E-01	---	---	---	216446_at	---
4.32	4.59	0.27	1.64E-01	5.32E-01	CNOT6	CCR4-NOT transcription complex, subunit 6	chr5q35.3	217970_s_at	NM_015455

2.55	2.76	0.21	1.64E-01	5.32E-01	LOC100130232	LP2209	chr8q22.3	239860_at	XM_001724024 /// XM_001724069 /// XM_001724127																				
2.48	2.69	0.21	1.64E-01	5.32E-01	CRYGB	crystallin, gamma B	chr2q33-q35	207715_at	NM_005210																				
1.79	1.99	0.20	1.64E-01	5.32E-01	---	---	---	1570233_at	---																				
4.60	4.80	0.20	1.64E-01	5.32E-01	CYBA	cytochrome b-245, alpha polypeptide	chr16q24	229445_at	NM_000101																				
4.82	5.28	0.45	1.64E-01	5.32E-01	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	chr2q11.2-q12	206571_s_at	NM_004834 /// NM_145686 /// NM_145687																				
5.76	6.07	0.31	1.64E-01	5.32E-01	NOTCH1	Notch homolog 1, translocation-associated (Drosophila)	chr9q34.3	218902_at	NM_017617																				
2.35	2.59	0.24	1.64E-01	5.32E-01	MYOCD	myocardin	chr17p11.2	237206_at	NM_153604																				
1.87	2.03	0.15	1.64E-01	5.32E-01	LOC340107	hypothetical protein LOC340107	chr5p14.1	1557009_a_at	---																				
4.89	5.58	0.69	1.64E-01	5.33E-01	MUT	methylmalonyl Coenzyme A mutase	chr6p12.3	202959_at	NM_000255																				
2.19	2.57	0.38	1.64E-01	5.33E-01	ECT2	epithelial cell transforming sequence 2 oncogene	chr3q26.1-q26.2	234992_x_at	NM_018098																				
2.66	2.88	0.22	1.64E-01	5.33E-01	C8orf44 /// SGK3	chromosome 8 open reading frame 44 /// serum/glucocorticoid regulated kinase family, member 3	chr8q12.3-q13.1 /// chr8q13.1	243264_s_at	NM_001033578 /// NM_013257 /// NM_019607 /// NM_170709																				
2.31	2.48	0.17	1.64E-01	5.33E-01	LINGO2	leucine rich repeat and Ig domain containing 2	chr9p21.2-p21.1	232720_at	NM_152570																				
2.67	2.92	0.25	1.65E-01	5.33E-01	LOC643749	hypothetical LOC643749	chr6q21	240577_at	XR_041901 /// XR_041902 /// XR_041903																				
4.79	5.04	0.25	1.65E-01	5.33E-01	FAM83A	family with sequence similarity 83, member A	chr8q24.13	238741_at	NM_032899 /// NM_207006																				
3.60	4.33	0.73	1.65E-01	5.33E-01	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	chr9q22.1-q22.3	209991_x_at	NM_005458																				
7.72	8.14	0.41	1.65E-01	5.33E-01	CBWD1 /// CBWD2 /// CBWD3 /// CBWD5 /// CBWD6	COBW domain containing 1 /// COBW domain containing 2 /// COBW domain containing 3 /// COBW domain containing 5 /// COBW domain containing 6	chr2q14.1 /// chr9p24.3 /// chr9q12 /// chr9q13	226193_x_at	NM_001024916 /// NM_001085457 /// NM_018491 /// NM_172003 /// NM_201453 /// XM_001716392																				
5.54	5.81	0.27	1.65E-01	5.33E-01	TCF3	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	213731_s_at	NM_003200																				
2.88	3.12	0.25	1.65E-01	5.33E-01	LOC100130502	hypothetical LOC100130502	chr2p21	244744_at	XM_001724222 /// XM_001725289 /// XM_001726912																				
4.64	5.32	0.68	1.65E-01	5.33E-01	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	chr5q11	211000_s_at	NM_002184 /// NM_175767																				
2.95	3.14	0.19	1.65E-01	5.33E-01	POMGNT1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	chr1p34.1	233639_at	NM_017739																				
4.15	4.70	0.56	1.65E-01	5.33E-01	---	---	---	235299_at	---																				
6.46	6.79	0.32	1.65E-01	5.33E-01	BAT5	HLA-B associated transcript 5	chr6p21.3	230221_at	NM_021160																				
3.77	3.98	0.20	1.65E-01	5.33E-01	GUCA1B	guanylate cyclase activator 1B (retina)	chr6p21.1	215841_at	NM_002098																				
3.72	4.19	0.47	1.65E-01	5.33E-01	---	---	---	228304_at	---																				
10.10	10.32	0.21	1.65E-01	5.33E-01	---	---	---	213655_at	---																				
2.11	3.26	1.15	1.65E-01	5.33E-01	CPA3	carboxypeptidase A3 (mast cell)	chr3q21-q25	205624_at	NM_001870																				
3.35	3.79	0.44	1.65E-01	5.33E-01	---	---	---	239892_at	---																				
3.15	3.53	0.39	1.65E-01	5.33E-01	HSDL2	Hydroxysteroid dehydrogenase like 2	chr9q32	215436_at	NM_032303																				
3.00	3.24	0.24	1.65E-01	5.33E-01	---	---	---	234677_at	---																				
2.62	2.85	0.24	1.65E-01	5.33E-01	MAGEC2	melanoma antigen family C, 2	chrXq27	220062_s_at	NM_016249																				
2.08	2.30	0.22	1.65E-01	5.33E-01	---	---	---	234821_at	---																				
2.22	2.44	0.21	1.65E-01	5.33E-01	---	---	---	214139_at	---																				
2.77	2.97	0.20	1.65E-01	5.33E-01	---	---	---	238260_at	---																				
1.90	2.05	0.15	1.65E-01	5.33E-01	---	---	---	234501_x_at	---																				
3.56	3.82	0.25	1.65E-01	5.33E-01	---	---	---	230889_at	---																				
2.39	2.54	0.15	1.65E-01	5.33E-01	---	---	---	239488_at	---																				
1.80	2.02	0.22	1.65E-01	5.33E-01	---	---	---	240000_at	---																				
2.13	2.36	0.23	1.65E-01	5.33E-01	DMRTC2	DMRT-like family C2	chr19q13.2	236811_at	NM_001040283																				
2.50	2.71	0.21	1.65E-01	5.33E-01	KRT72	keratin 72	chr12q13.13	1564435_a_at	NM_080747																				
2.68	2.95	0.27	1.65E-01	5.33E-01	RECQL5	RecQ protein-like 5	chr17q25.2-q25.3	210309_at	NM_001003715 /// NM_001003716 /// NM_004259																				

1.90	2.07	0.17	1.65E-01	5.33E-01	---	---	---	1570316_at	---
2.92	3.20	0.28	1.65E-01	5.33E-01	RNASET2	ribonuclease T2	chr6q27	1556201_at	NM_003730
4.76	5.00	0.24	1.65E-01	5.33E-01	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	chr13q12-q14	215979_s_at	NM_003045
3.71	3.94	0.23	1.65E-01	5.33E-01	CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6	chr19q13.2	214320_x_at	NM_000762
5.55	5.76	0.21	1.65E-01	5.33E-01	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	chr9q21	211426_x_at	NM_002072
5.04	5.45	0.40	1.65E-01	5.34E-01	LOC285949	hypothetical protein LOC285949	chr7p15.1	1563781_at	---
2.73	2.96	0.23	1.65E-01	5.34E-01	PTRH1	Peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	chr9q34.11	1569430_at	NM_001002913
2.35	2.55	0.19	1.65E-01	5.34E-01	---	---	---	1556256_a_at	---
6.42	6.99	0.56	1.65E-01	5.34E-01	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	chr11q12	1555728_a_at	NM_024021 /// NM_148975
3.14	3.38	0.24	1.65E-01	5.34E-01	JPH3	junctophilin 3	chr16q24.3	234736_at	NM_020655
1.92	2.14	0.22	1.65E-01	5.34E-01	---	---	---	237911_at	---
2.65	2.84	0.19	1.65E-01	5.34E-01	C9orf85	chromosome 9 open reading frame 85	chr9q21.13	238579_at	NM_182505
2.02	2.20	0.18	1.65E-01	5.34E-01	---	---	---	243725_at	---
2.17	2.38	0.20	1.65E-01	5.34E-01	OK/SW-CL.36	OK/SW-CL.36	chr4q21.23	1555000_at	XM_001721868 /// XM_001721925 /// XM_001723322
2.70	2.92	0.22	1.65E-01	5.34E-01	---	---	---	234499_at	---
10.38	10.96	0.58	1.65E-01	5.34E-01	LDHB	lactate dehydrogenase B	chr12p12.2-p12.1	213564_x_at	NM_002300
4.86	5.16	0.30	1.65E-01	5.34E-01	---	---	---	242978_x_at	---
2.97	3.28	0.32	1.66E-01	5.34E-01	TACSTD2	Tumor-associated calcium signal transducer 2	chr1p32-p31	227128_s_at	NM_002353
3.98	4.21	0.23	1.66E-01	5.34E-01	---	---	---	234446_at	---
3.15	3.43	0.28	1.66E-01	5.34E-01	---	---	---	215401_at	---
4.42	5.09	0.68	1.66E-01	5.34E-01	DENND4C	DENN/MADD domain containing 4C	chr9p22.1	205684_s_at	NM_017925
2.43	2.65	0.22	1.66E-01	5.34E-01	---	---	---	237203_at	---
2.71	3.14	0.43	1.66E-01	5.34E-01	STS	steroid sulfatase (microsomal), isozyme S	chrXp22.32	203767_s_at	NM_000351
2.65	2.89	0.24	1.66E-01	5.34E-01	---	---	---	1561446_at	---
6.29	7.05	0.76	1.66E-01	5.34E-01	NFIB	Nuclear factor I/B	chr9p24.1	230291_s_at	NM_005596
4.66	4.96	0.30	1.66E-01	5.34E-01	EIF1	Eukaryotic translation initiation factor 1	chr17q21.2	228967_at	NM_005801
2.54	2.73	0.19	1.66E-01	5.34E-01	HELB	helicase (DNA) B	chr12q14.3	1552788_a_at	NM_033647
3.29	3.92	0.63	1.66E-01	5.34E-01	SMAD4	SMAD family member 4	chr18q21.1	1565703_at	NM_005359
5.41	5.74	0.32	1.66E-01	5.34E-01	TYRO3	TYRO3 protein tyrosine kinase	chr15q15.1-q21.1	211432_s_at	NM_006293
6.22	6.56	0.34	1.66E-01	5.34E-01	---	---	---	244533_at	---
2.47	2.66	0.19	1.66E-01	5.34E-01	FNTA	farnesyltransferase, CAAX box, alpha	chr8p11	230808_at	NM_001018676 /// NM_001018677 /// NM_002027
4.24	4.50	0.26	1.66E-01	5.34E-01	C9orf169	chromosome 9 open reading frame 169	chr9q34.3	1569144_a_at	NM_199001 /// XM_926890
1.85	2.07	0.23	1.66E-01	5.34E-01	---	---	---	233133_at	---
3.98	4.46	0.48	1.66E-01	5.34E-01	---	---	---	243808_at	---
1.78	1.96	0.18	1.66E-01	5.35E-01	ICA1	islet cell autoantigen 1, 69kDa	chr7p22	211740_at	NM_004968 /// NM_022307
4.81	5.06	0.25	1.66E-01	5.35E-01	PARG	poly (ADP-ribose) glycohydrolase	chr10q11.23	205060_at	NM_003631
3.74	4.01	0.26	1.66E-01	5.35E-01	---	---	---	227483_s_at	---
1.89	2.07	0.18	1.66E-01	5.35E-01	---	---	---	1562860_at	---
1.86	2.02	0.16	1.66E-01	5.35E-01	---	---	---	1569664_at	---
4.86	5.99	1.13	1.66E-01	5.35E-01	LOC284801	hypothetical protein LOC284801	chr20p11.1	225767_at	XM_001714287 /// XM_378973 /// XM_944897
4.92	5.17	0.25	1.66E-01	5.35E-01	PTBP1	Polypyrimidine tract binding protein 1	chr19p13.3	231158_x_at	NM_002819 /// NM_031990 /// NM_031991 /// NM_175847
3.12	3.64	0.52	1.66E-01	5.35E-01	---	---	---	220702_at	---
7.79	8.21	0.43	1.66E-01	5.35E-01	NPC1	Niemann-Pick disease, type C1	chr18q11-q12	202679_at	NM_000271
3.44	3.79	0.35	1.66E-01	5.35E-01	FRMD3	FERM domain containing 3	chr9q21.32	242600_at	NM_174938
2.67	2.95	0.28	1.66E-01	5.35E-01	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	chr8q11.2	1557585_at	NM_015941 /// NM_213619 /// NM_213620
2.89	3.05	0.17	1.66E-01	5.35E-01	RHO	rhodopsin	chr3q21-q24	206454_s_at	NM_000539
2.77	3.01	0.24	1.66E-01	5.35E-01	SYTL4	synaptotagmin-like 4	chrXq21.33	227703_s_at	NM_001129896 /// NM_080737
2.98	3.22	0.24	1.66E-01	5.35E-01	HS6ST1	Heparan sulfate 6-O-sulfotransferase 1	chr2q21	214165_s_at	NM_004807

2.43	2.65	0.22	1.66E-01	5.35E-01	ATXN2L	ataxin 2-like	chr16p11	207798_s_at	NM_007245 /// NM_145714 /// NM_148414 /// NM_148415 /// NM_148416																				
2.32	2.52	0.20	1.66E-01	5.35E-01	CASP5	caspase 5, apoptosis-related cysteine peptidase	chr11q22.2-q22.3	207500_at	NM_004347																				
2.15	2.33	0.18	1.66E-01	5.35E-01	KIAA2022	KIAA2022	chrXq13.3	244370_at	NM_001008537																				
2.69	2.87	0.18	1.66E-01	5.35E-01	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	chr17q24	1565778_at	NM_007168																				
2.82	3.07	0.25	1.67E-01	5.35E-01	C3orf34	chromosome 3 open reading frame 34	chr3q29	1553158_at	NM_032898																				
5.93	6.80	0.87	1.67E-01	5.35E-01	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	chr15q22.2	217777_s_at	NM_016395																				
2.25	2.43	0.18	1.67E-01	5.35E-01	PADI1	peptidyl arginine deiminase, type I	chr1p36.13	223739_at	NM_013358																				
3.85	4.09	0.24	1.67E-01	5.35E-01	LOC284930	Hypothetical protein LOC284930	chr22q13.32	1563009_at	---																				
3.36	3.56	0.20	1.67E-01	5.35E-01	LOC100130648 /// SSX1 /// SSX10 /// SSX2 /// SSX2B /// SSX3 /// SSX5 /// SSX7 /// SSX9	similar to Protein SSX2 (Synovial sarcoma, X breakpoint 2) (Cancer/testis antigen 5.2) (CT5.2) (SSX) (HOM-MEL-40) /// synovial sarcoma, X breakpoint 1 /// synovial sarcoma, X breakpoint 10 /// synovial sarcoma, X breakpoint 2 /// synovial sarcoma, X breakpoint 2B /// synovial sarcoma, X breakpoint 3 /// synovial sarcoma, X breakpoint 5 /// synovial sarcoma, X breakpoint 7 /// synovial sarcoma, X breakpoint 9	chrXp11.22 /// chrXp11.23 /// chrXp11.23-p11.22	215881_x_at	NM_003147 /// NM_005635 /// NM_021014 /// NM_021015 /// NM_173358 /// NM_174962 /// NM_175698 /// NM_175711 /// NM_175723 /// XM_001714824 /// XM_001719568 /// XM_001720499																				
3.17	3.39	0.23	1.67E-01	5.35E-01	RAB40AL	RAB40A, member RAS oncogene family-like	chrXq22.2	215782_at	NM_001031834																				
2.40	2.63	0.23	1.67E-01	5.35E-01	ZNF229	zinc finger protein 229	chr19q13.31	1562789_at	NM_014518																				
3.61	3.83	0.21	1.67E-01	5.35E-01	SLC35D2	solute carrier family 35, member D2	chr9q22.32	233325_at	NM_007001																				
2.29	2.60	0.31	1.67E-01	5.36E-01	GLE1	GLE1 RNA export mediator homolog (yeast)	chr9q34.11	206921_at	NM_001003722 /// NM_001499																				
2.14	2.36	0.22	1.67E-01	5.36E-01	GLRB	glycine receptor, beta	chr4q31.3	205280_at	NM_000824																				
2.44	2.65	0.21	1.67E-01	5.36E-01	ITGA6	Integrin, alpha 6	chr2q31.1	229643_at	NM_000210 /// NM_001079818																				
2.62	2.85	0.23	1.67E-01	5.36E-01	DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	chr17q21.31	231184_at	NM_004941																				
2.20	2.42	0.21	1.67E-01	5.36E-01	---	---	---	241665_x_at	---																				
3.15	3.59	0.44	1.67E-01	5.36E-01	---	---	---	240608_at	---																				
2.03	2.24	0.21	1.67E-01	5.36E-01	PRKG1	protein kinase, cGMP-dependent, type I	chr10q11.2	207119_at	NM_001098512 /// NM_006258																				
5.09	5.49	0.40	1.67E-01	5.36E-01	CITED4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	chr1p34.2|1p35-p34	228625_at	NM_133467																				
3.78	4.02	0.25	1.67E-01	5.36E-01	---	---	---	239689_at	---																				
2.82	3.02	0.20	1.67E-01	5.36E-01	TRPV5	transient receptor potential cation channel, subfamily V, member 5	chr7q35	1555042_at	NM_019841																				
2.92	3.11	0.19	1.67E-01	5.36E-01	GPR20	G protein-coupled receptor 20	chr8q24.2-q24.3	214510_at	NM_005293																				
3.44	3.64	0.20	1.67E-01	5.36E-01	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	chr16q13	208354_s_at	NM_000339 /// NM_001126107 /// NM_001126108																				
2.26	2.47	0.21	1.67E-01	5.36E-01	C11orf88	chromosome 11 open reading frame 88	chr11q23.1	1568606_at	NM_001100388 /// NM_207430																				
8.23	8.74	0.52	1.67E-01	5.37E-01	PSMD6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	chr3p14.1	202753_at	NM_014814																				
3.04	3.48	0.44	1.67E-01	5.37E-01	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	chr12q13	205700_at	NM_003725																				
6.59	6.81	0.23	1.67E-01	5.37E-01	TMEM63A	transmembrane protein 63A	chr1q42.12	202700_s_at	NM_014698																				
2.37	2.60	0.23	1.67E-01	5.37E-01	---	---	---	1563507_at	---																				
2.05	2.24	0.19	1.67E-01	5.37E-01	C14orf48	chromosome 14 open reading frame 48	chr14q32.13	1570111_at	NM_152777																				
2.06	2.22	0.16	1.67E-01	5.37E-01	EIF2C4	Eukaryotic translation initiation factor 2C, 4	chr1p34.3	1569408_at	NM_017629																				
5.59	5.92	0.33	1.67E-01	5.37E-01	RBM17	RNA binding motif protein 17	chr10p15.1	225751_at	NM_032905																				
2.91	3.14	0.23	1.67E-01	5.37E-01	KCND1	potassium voltage-gated channel, Shal-related subfamily, member 1	chrXp11.23	206842_at	NM_004979																				
3.39	4.00	0.60	1.67E-01	5.37E-01	---	---	---	232297_at	---																				
6.37	6.67	0.30	1.67E-01	5.37E-01	---	---	---	240241_at	---																				
4.07	4.30	0.23	1.67E-01	5.37E-01	GZMM	granzyme M (lymphocyte met-ase 1)	chr19p13.3	207460_at	NM_005317																				
2.71	2.89	0.18	1.68E-01	5.37E-01	OLIG2	oligodendrocyte lineage transcription factor 2	chr21q22.11	213824_at	NM_005806																				
2.24	2.41	0.17	1.68E-01	5.37E-01	C14orf145	chromosome 14 open reading frame 145	chr14q31.1	232635_at	NM_152446																				

3.27	3.43	0.16	1.68E-01	5.37E-01	GFI1	growth factor independent 1 transcription repressor	chr1p22	206589_at	NM_001127215 /// NM_001127216 /// NM_005263																				
2.86	3.08	0.23	1.68E-01	5.37E-01	IL29	interleukin 29 (interferon, lambda 1)	chr19q13.13	1552917_at	NM_172140																				
5.90	6.26	0.36	1.68E-01	5.37E-01	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	chr3p22.2	220610_s_at	NM_001134369 /// NM_006309 /// NM_017724																				
5.35	5.94	0.59	1.68E-01	5.37E-01	CALD1	caldesmon 1	chr7q33	201615_x_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157																				
2.73	3.02	0.29	1.68E-01	5.37E-01	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	chr14q23	232648_at	NM_002788 /// NM_152132																				
3.46	3.75	0.29	1.68E-01	5.37E-01	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	chr14q32.2	222840_at	NM_018036																				
4.92	5.19	0.27	1.68E-01	5.37E-01	WDR61	WD repeat domain 61	chr15q25.1	215156_at	NM_025234																				
2.41	2.59	0.18	1.68E-01	5.37E-01	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D	chr7q22.1	242635_s_at	NM_001122838 /// NM_198990																				
3.48	3.68	0.21	1.68E-01	5.37E-01	BTNL9	butyrophilin-like 9	chr5q35.3	230992_at	NM_152547																				
2.77	3.01	0.23	1.68E-01	5.37E-01	KLK15	kallikrein-related peptidase 15	chr19q13.41	233477_at	NM_017509 /// NM_138563 /// NM_138564																				
2.16	2.53	0.37	1.68E-01	5.38E-01	TPR	translocated promoter region (to activated MET oncogene)	chr1q25	1557227_s_at	NM_003292																				
3.19	3.46	0.27	1.68E-01	5.38E-01	KIAA1654	KIAA1654 protein	---	215680_at	---																				
4.61	4.80	0.19	1.68E-01	5.38E-01	UNC13A	unc-13 homolog A (C. elegans)	chr19p13.11	214817_at	NM_001080421																				
2.04	2.22	0.18	1.68E-01	5.38E-01	---	---	---	1566441_at	---																				
3.04	3.69	0.65	1.68E-01	5.38E-01	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	chr5p15.2	213169_at	NM_003966																				
2.90	3.16	0.26	1.68E-01	5.38E-01	RAD51L1	RAD51-like 1 (S. cerevisiae)	chr14q23-q24.2	1554496_at	NM_002877 /// NM_133509 /// NM_133510																				
2.35	2.58	0.23	1.68E-01	5.38E-01	JPH1	junctophilin 1	chr8q21	229139_at	NM_020647																				
2.70	2.92	0.22	1.68E-01	5.38E-01	---	---	---	217439_at	---																				
2.47	2.67	0.20	1.68E-01	5.38E-01	PCDH7	protocadherin 7	chr4p15	205534_at	NM_002589 /// NM_032456 /// NM_032457																				
2.05	2.23	0.17	1.68E-01	5.38E-01	---	---	---	240462_at	---																				
4.45	4.77	0.32	1.68E-01	5.38E-01	ANKRD53	ankyrin repeat domain 53	chr2p13.3	244453_at	NM_001115116 /// NM_024933																				
2.46	2.64	0.19	1.68E-01	5.38E-01	SFT2D3	SFT2 domain containing 3	chr2q14.3	229472_at	NM_032740																				
3.20	3.45	0.25	1.68E-01	5.38E-01	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	chr2q33.3	1553917_at	NM_015040 /// NM_152671																				
3.06	3.37	0.31	1.68E-01	5.38E-01	RREB1	ras responsive element binding protein 1	chr6p25	216649_at	NM_001003698 /// NM_001003699 /// NM_002955																				
1.94	2.09	0.15	1.68E-01	5.38E-01	PTCHD1	patched domain containing 1	chrXp22.11	240041_at	NM_173495																				
2.23	2.39	0.17	1.68E-01	5.38E-01	---	---	---	1563136_at	---																				
4.82	5.27	0.45	1.68E-01	5.38E-01	---	---	---	230309_at	---																				
4.72	5.09	0.37	1.68E-01	5.38E-01	RGMB	RGM domain family, member B	chr5q21.1	226989_at	NM_001012761 /// NM_173670																				
3.83	4.17	0.33	1.68E-01	5.38E-01	ERCC8 /// FLJ12595	excision repair cross-complementing rodent repair deficiency, complementation group 8 /// guanine nucleotide binding protein-like 3 (nucleolar)-like pseudogene	chr5q12.1	205162_at	NM_000082 /// NM_001007233 /// NM_001007234																				
2.08	2.26	0.18	1.68E-01	5.38E-01	LOC100128434	Hypothetical protein LOC100128434	chr15q14	1561292_at	XM_001714798 /// XM_001717705 /// XM_001718958																				

2.03	2.20	0.17	1.68E-01	5.38E-01	LOC100128594	similar to hCG1791139	chrXq22.2	1564691_at	XM_001714144 /// XM_001716268 /// XM_001723420
3.47	3.76	0.30	1.68E-01	5.38E-01	DTWD1	DTW domain containing 1	chr15q21.2	219291_at	NM_020234
2.46	2.73	0.27	1.68E-01	5.38E-01	ZNF132	zinc finger protein 132	chr19q13.4	207402_at	NM_003433
3.23	3.48	0.25	1.68E-01	5.38E-01	ACPL2	acid phosphatase-like 2	chr3q23	239475_at	NM_001037172 /// NM_152282
2.32	2.53	0.21	1.68E-01	5.38E-01	---	---	---	241688_at	---
2.37	2.57	0.20	1.68E-01	5.38E-01	LOC400541	hypothetical gene supported by AK096066	chr16q22.1	1562568_at	---
2.27	2.53	0.26	1.69E-01	5.38E-01	TRPC6	transient receptor potential cation channel, subfamily C, member 6	chr11q21-q22	217287_s_at	NM_004621
2.95	3.27	0.32	1.69E-01	5.38E-01	---	---	---	229537_at	---
3.24	3.47	0.23	1.69E-01	5.38E-01	PRY /// PRY2	PTPN13-like, Y-linked /// PTPN13-like, Y-linked 2	chrYq11.223	208332_at	NM_001002758 /// NM_004676
5.31	5.94	0.63	1.69E-01	5.38E-01	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	chr8q22.3	226463_at	NM_001695
2.29	2.53	0.24	1.69E-01	5.38E-01	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	chr5q12	211840_s_at	NM_001104631 /// NM_006203
3.05	3.25	0.21	1.69E-01	5.38E-01	C11orf21	chromosome 11 open reading frame 21	chr11p15.5	220560_at	XR_042066 /// XR_042067 /// XR_042068
3.16	3.44	0.28	1.69E-01	5.38E-01	KIAA1652	KIAA1652 protein	---	1560671_at	---
1.84	2.01	0.17	1.69E-01	5.38E-01	CSMD1	CUB and Sushi multiple domains 1	chr8p23.2	231223_at	NM_033225
3.07	3.28	0.21	1.69E-01	5.38E-01	TSPYL3	TSPY-like 3 (pseudogene)	chr20q11.21	233617_at	NR_002781
2.16	2.35	0.19	1.69E-01	5.38E-01	---	---	---	1559403_at	---
5.86	6.37	0.51	1.69E-01	5.39E-01	MTIF3	mitochondrial translational initiation factor 3	chr13q12.2	223356_s_at	NM_152912
4.57	5.01	0.44	1.69E-01	5.39E-01	GIN1	gypsy retrotransposon integrase 1	chr5q21.1	219467_at	NM_017676
2.70	2.99	0.30	1.69E-01	5.39E-01	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	chr21q21.3	235368_at	NM_007038
3.96	4.21	0.25	1.69E-01	5.39E-01	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	chr16p11.2	238130_at	NM_032815
3.74	3.98	0.25	1.69E-01	5.39E-01	RASAL2	RAS protein activator like 2	chr1q24	234343_s_at	NM_004841 /// NM_170692
2.37	2.60	0.23	1.69E-01	5.39E-01	ZNF81	zinc finger protein 81	chrXp11.23	242083_at	NM_007137
1.89	2.05	0.15	1.69E-01	5.39E-01	C14orf166B	chromosome 14 open reading frame 166B	chr14q24.3	234453_s_at	NM_001081002 /// NM_194287
2.14	2.32	0.18	1.69E-01	5.39E-01	---	---	---	1557427_at	---
7.02	7.61	0.60	1.69E-01	5.39E-01	---	---	---	239066_at	---
2.97	3.24	0.26	1.69E-01	5.39E-01	KIAA1257	KIAA1257	chr3q21.3	1554852_a_at	NM_020741
8.41	9.52	1.11	1.69E-01	5.39E-01	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	chr5q31-q34	205097_at	NM_000112
7.76	8.49	0.73	1.69E-01	5.39E-01	REEP5	receptor accessory protein 5	chr5q22-q23	208873_s_at	NM_005669
5.85	6.49	0.64	1.69E-01	5.39E-01	PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	chr2p23	201408_at	NM_002709 /// NM_206876
4.59	5.04	0.45	1.69E-01	5.39E-01	ZNF398	zinc finger protein 398	chr7q36.1	226202_at	NM_020781 /// NM_170686
2.81	3.08	0.27	1.69E-01	5.39E-01	---	---	---	231596_at	---
3.02	3.27	0.25	1.69E-01	5.39E-01	RPL3L	ribosomal protein L3-like	chr16p13.3	206768_at	NM_005061
2.18	2.38	0.20	1.69E-01	5.39E-01	---	---	---	1566243_at	---
2.24	2.55	0.31	1.69E-01	5.39E-01	NOS1	Nitric oxide synthase 1 (neuronal)	chr12q24.2-q24.31	239132_at	NM_000620
2.79	3.07	0.28	1.69E-01	5.39E-01	---	---	---	231047_at	---
2.31	2.49	0.17	1.69E-01	5.39E-01	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	chr22q13.1	207264_at	NM_006855 /// NM_016657
4.61	5.31	0.70	1.69E-01	5.39E-01	DENND1B	DENN/MADD domain containing 1B	chr1q31.3	219696_at	NM_019049 /// NM_144977
3.26	3.54	0.28	1.70E-01	5.39E-01	C16orf82	chromosome 16 open reading frame 82	chr16p12.1	231076_at	NM_182831
3.48	3.72	0.24	1.70E-01	5.39E-01	---	---	---	244018_at	---
2.71	2.91	0.19	1.70E-01	5.39E-01	LOC100049716	hypothetical protein LOC100049716	chr12p13.33	236886_at	XR_041967 /// XR_041968 /// XR_041969
2.00	2.18	0.17	1.69E-01	5.39E-01	---	---	---	1560769_at	---
3.47	4.46	0.98	1.70E-01	5.39E-01	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	chr18p11.2	217434_at	NM_000529
6.26	6.79	0.52	1.70E-01	5.39E-01	ALDOC	aldolase C, fructose-bisphosphate	chr17cen-q12	202022_at	NM_005165
4.85	5.38	0.52	1.70E-01	5.39E-01	PTCD2	pentatricopeptide repeat domain 2	chr5q13.2	219658_at	NM_024754
2.33	2.83	0.51	1.70E-01	5.39E-01	---	---	---	1570120_at	---
3.17	3.56	0.39	1.70E-01	5.39E-01	CD1C	CD1c molecule	chr1q22-q23	205987_at	NM_001765

2.52	2.86	0.34	1.70E-01	5.39E-01	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	chr1p34.1	1555703_at	NM_006279 /// NM_174963 /// NM_174964 /// NM_174965 /// NM_174966 /// NM_174967 /// NM_174968 /// NM_174969 /// NM_174970 /// NM_174971
2.70	2.95	0.25	1.70E-01	5.39E-01	---	---	---	237060_at	---
5.37	5.60	0.23	1.70E-01	5.39E-01	C1orf163	chromosome 1 open reading frame 163	chr1p32.3	222883_at	NM_023077
2.67	2.89	0.22	1.70E-01	5.39E-01	CROCC	ciliary rootlet coiled-coil, rootletin	chr1pter-p36.11	216419_at	NM_014675
2.37	2.55	0.18	1.70E-01	5.39E-01	WDR16	WD repeat domain 16	chr17p13.1	237755_s_at	NM_001080556 /// NM_145054
3.09	3.30	0.21	1.70E-01	5.40E-01	---	---	---	243397_at	---
6.76	7.25	0.49	1.70E-01	5.40E-01	FOXO3	forkhead box O3	chr6q21	204131_s_at	NM_001455 /// NM_201559
2.38	2.54	0.16	1.70E-01	5.40E-01	SYTL3	Synaptotagmin-like 3	chr6q25.3	242109_at	NM_001009991
3.82	4.06	0.24	1.70E-01	5.40E-01	CCND3	Cyclin D3	chr6p21	1562028_at	NM_001760
3.96	4.38	0.41	1.70E-01	5.40E-01	SSBP3	single stranded DNA binding protein 3	chr1p32.3	217991_x_at	NM_001009955 /// NM_018070 /// NM_145716
7.61	7.99	0.38	1.70E-01	5.40E-01	RRAGC	Ras-related GTP binding C	chr1p34	218088_s_at	NM_022157
3.24	3.47	0.23	1.70E-01	5.40E-01	CREB3L1	cAMP responsive element binding protein 3-like 1	chr11p11.2	213498_at	NM_052854
2.14	2.33	0.19	1.70E-01	5.40E-01	LOC100132999	hypothetical protein LOC100132999	chr1q21.1	231247_s_at	XM_001722799
5.98	6.45	0.48	1.70E-01	5.40E-01	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	chr6q12	204058_at	NM_002395
2.65	2.93	0.28	1.70E-01	5.40E-01	ZNF214	zinc finger protein 214	chr11p15.4	243457_s_at	NM_013249
1.95	2.16	0.21	1.70E-01	5.40E-01	SOST	sclerosteosis	chr17q11.2	223869_at	NM_025237
2.22	2.40	0.18	1.70E-01	5.40E-01	NLRP3	NLR family, pyrin domain containing 3	chr1q44	216015_s_at	NM_001079821 /// NM_001127461 /// NM_001127462 /// NM_004895 /// NM_183395
3.35	3.66	0.30	1.70E-01	5.40E-01	---	---	---	240176_at	---
2.57	3.71	1.14	1.70E-01	5.40E-01	CD24	CD24 molecule	chr6q21	209771_x_at	NM_013230 /// XM_001725629
3.34	3.60	0.26	1.70E-01	5.40E-01	TMEM165	Transmembrane protein 165	chr4q12	230512_x_at	NM_018475
2.35	2.59	0.24	1.70E-01	5.40E-01	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	chr1p13.3-p13.1	206060_s_at	NM_012411 /// NM_015967
2.00	2.20	0.20	1.70E-01	5.40E-01	LOC374443	CLR pseudogene	chr12p13.31	238790_at	NR_002814
1.85	2.04	0.19	1.70E-01	5.40E-01	DPY19L1	dpy-19-like 1 (C. elegans)	chr7p14.3	1560915_at	NM_015283
2.47	2.68	0.21	1.70E-01	5.40E-01	ZC3H7B	zinc finger CCCH-type containing 7B	chr22q13.2	216844_at	NM_017590
2.16	2.37	0.21	1.70E-01	5.40E-01	SBNO1	Strawberry notch homolog 1 (Drosophila)	chr12q24.31	216161_at	NM_018183
5.32	5.54	0.23	1.70E-01	5.40E-01	BRAP	BRCA1 associated protein	chr12q24	209923_s_at	NM_006768
2.80	2.98	0.18	1.70E-01	5.40E-01	---	---	---	239923_at	---
2.21	2.49	0.28	1.70E-01	5.40E-01	---	---	---	1566867_at	---
6.60	6.93	0.33	1.70E-01	5.41E-01	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	222424_s_at	NM_022731
5.51	5.81	0.30	1.70E-01	5.41E-01	PICK1	protein interacting with PRKCA 1	chr22q13.1	204746_s_at	NM_001039583 /// NM_001039584 /// NM_012407
2.44	2.69	0.25	1.70E-01	5.41E-01	C1orf210	chromosome 1 open reading frame 210	chr1p34.2	1554246_at	NM_182517
3.51	3.72	0.21	1.71E-01	5.41E-01	GPR44	G protein-coupled receptor 44	chr11q12-q13.3	206361_at	NM_004778
2.99	3.24	0.25	1.71E-01	5.41E-01	---	---	---	1569933_at	---
6.25	6.79	0.54	1.71E-01	5.41E-01	ANKIB1	ankyrin repeat and IBR domain containing 1	chr7q21.2	224682_at	NM_019004
2.29	2.80	0.51	1.71E-01	5.41E-01	FST	follistatin	chr5q11.2	226847_at	NM_006350 /// NM_013409
4.45	4.78	0.33	1.71E-01	5.41E-01	---	---	---	1570198_x_at	---
2.87	3.17	0.30	1.71E-01	5.41E-01	PELO	pelota homolog (Drosophila)	chr5q11.2	1553140_at	NM_015946
2.76	3.02	0.27	1.71E-01	5.41E-01	USP54	Ubiquitin specific peptidase 54	chr10q22.2	238522_at	NM_152586
5.62	5.88	0.26	1.71E-01	5.41E-01	THAP3	THAP domain containing, apoptosis associated protein 3	chr1p36.31	217658_at	NM_138350
2.64	2.89	0.24	1.71E-01	5.41E-01	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	chr6p21.3	227053_at	NM_020804
2.55	2.77	0.23	1.71E-01	5.41E-01	---	---	---	226812_at	---
2.57	2.79	0.21	1.71E-01	5.41E-01	PLCL2	phospholipase C-like 2	chr3p24.3	216217_at	NM_015184

1.87	2.05	0.18	1.71E-01	5.41E-01	FAM63B	family with sequence similarity 63, member B	chr15q22.1	37802_r_at	NM_001040450 /// NM_001040453
3.62	3.82	0.20	1.71E-01	5.41E-01	---	---	---	215615_x_at	---
7.52	8.05	0.53	1.71E-01	5.41E-01	REEP6	receptor accessory protein 6	chr19p13.3	226597_at	NM_138393
3.33	3.75	0.43	1.71E-01	5.41E-01	SETBP1	SET binding protein 1	chr18q21.1	227478_at	NM_001130110 /// NM_015559
2.60	2.81	0.21	1.71E-01	5.41E-01	---	---	---	216110_x_at	---
4.23	4.49	0.26	1.71E-01	5.41E-01	NFAM1	NFAT activating protein with ITAM motif 1	chr22q13.2	243099_at	NM_145912
2.51	2.70	0.19	1.71E-01	5.41E-01	ASB14	ankyrin repeat and SOCS box-containing 14	chr3p21.1	1553453_at	NM_130387
6.35	6.84	0.49	1.71E-01	5.41E-01	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	chrXq12-q13	209620_s_at	NM_004299
2.99	3.25	0.27	1.71E-01	5.41E-01	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	chr2p13.3	234721_s_at	NM_019885
2.55	2.76	0.22	1.71E-01	5.41E-01	---	---	---	230944_at	---
2.46	2.66	0.20	1.71E-01	5.41E-01	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	chr8q23-q24	215431_at	NM_021021
5.53	6.20	0.67	1.71E-01	5.41E-01	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	chr1p13	201179_s_at	NM_006496
2.90	3.17	0.27	1.71E-01	5.41E-01	---	---	---	1559321_at	---
4.37	4.66	0.28	1.71E-01	5.41E-01	FYB	FYN binding protein (FYB-120/130)	chr5p13.1	211794_at	NM_001465 /// NM_199335
3.16	3.42	0.26	1.71E-01	5.41E-01	---	---	---	237220_at	---
5.23	6.37	1.14	1.71E-01	5.41E-01	KLHL4	kelch-like 4 (Drosophila)	chrXq21.3	1553027_a_at	NM_019117 /// NM_057162
3.60	3.92	0.32	1.71E-01	5.41E-01	C15orf38	chromosome 15 open reading frame 38	chr15q26.1	228666_at	NM_182616
2.70	2.90	0.20	1.71E-01	5.41E-01	MGAT5	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	chr2q21	206720_at	NM_002410
2.01	2.16	0.15	1.71E-01	5.41E-01	SORCS3	sortilin-related VPS10 domain containing receptor 3	chr10q23-q25	215522_at	NM_014978
5.22	5.54	0.32	1.71E-01	5.41E-01	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	chr16q13	231951_at	NM_020988 /// NM_138736
2.26	2.46	0.20	1.71E-01	5.41E-01	---	---	---	240676_at	---
4.90	5.23	0.32	1.71E-01	5.41E-01	---	---	---	1555848_at	---
1.81	1.99	0.18	1.71E-01	5.41E-01	---	---	---	1564672_at	---
2.67	2.86	0.18	1.71E-01	5.41E-01	FLJ36144	hypothetical protein FLJ36144	chr15q11.2	1560790_at	XR_040632 /// XR_040633 /// XR_040634
2.27	2.49	0.22	1.71E-01	5.41E-01	GIPC3	GIPC PDZ domain containing family, member 3	chr19p13.3	1553058_at	NM_133261
2.00	2.17	0.17	1.71E-01	5.41E-01	MYO3B	myosin IIIB	chr2q31.1-q31.2	1555257_a_at	NM_001083615 /// NM_138995
6.56	7.10	0.55	1.71E-01	5.41E-01	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	chr18q12.1	201722_s_at	NM_020474
3.65	4.13	0.48	1.71E-01	5.41E-01	---	---	---	236660_at	---
2.77	3.03	0.26	1.71E-01	5.41E-01	---	---	---	216145_at	---
5.89	6.14	0.25	1.71E-01	5.41E-01	LOC439985	hypothetical gene supported by AK125693	chr10q22.2	227225_at	XR_041625 /// XR_041626
3.05	3.29	0.24	1.71E-01	5.41E-01	ADRB3	adrenergic, beta-3-, receptor	chr8p12-p11.2	206812_at	NM_000025
2.19	2.35	0.16	1.71E-01	5.41E-01	TMEM106A	Transmembrane protein 106A	chr17q21.31	234589_at	NM_145041
4.53	4.88	0.35	1.71E-01	5.41E-01	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	chr17q23.1	204171_at	NM_003161
3.05	3.36	0.30	1.71E-01	5.41E-01	NARG1	NMDA receptor regulated 1	chr4q31.1	222836_at	NM_057175
2.42	2.75	0.33	1.71E-01	5.41E-01	TTYH1	tweety homolog 1 (Drosophila)	chr19q13.4	219415_at	NM_001005367 /// NM_020659
3.19	3.51	0.32	1.71E-01	5.41E-01	BMP2K	BMP2 inducible kinase	chr4q21.21	37170_at	NM_017593 /// NM_198892
2.98	3.25	0.27	1.71E-01	5.41E-01	BLM	Bloom syndrome	chr15q26.1	205733_at	NM_000057
2.39	2.66	0.27	1.71E-01	5.41E-01	DHRS9	dehydrogenase/reductase (SDR family) member 9	chr2q31.1	223952_x_at	NM_005771 /// NM_199204
2.66	2.86	0.20	1.71E-01	5.41E-01	PCDHGA12 /// PCDHGC4	protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily C, 4	chr5q31	231753_s_at	NM_003735 /// NM_018928 /// NM_032094 /// NM_032406
2.18	2.37	0.19	1.71E-01	5.41E-01	---	---	---	1563064_at	---
2.55	2.73	0.19	1.71E-01	5.41E-01	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	chr3q27-q28	235770_at	NM_001031849 /// NM_001879 /// NM_139125
3.21	3.61	0.40	1.72E-01	5.41E-01	KCNK5	potassium channel, subfamily K, member 5	chr6p21	219615_s_at	NM_003740
2.33	2.57	0.23	1.71E-01	5.41E-01	---	---	---	1566597_at	---
2.71	2.89	0.18	1.72E-01	5.41E-01	ARHGAP26	Rho GTPase activating protein 26	chr5q31	205069_s_at	NM_015071
3.11	3.36	0.25	1.72E-01	5.41E-01	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	chr5q33.1	213108_at	NM_015981 /// NM_171825
4.81	5.28	0.47	1.72E-01	5.41E-01	TRIM2	tripartite motif-containing 2	chr4q31.3	202342_s_at	NM_001130067 /// NM_015271

4.03	4.25	0.21	1.72E-01	5.41E-01	---	---	---	236801_at	---
2.26	2.42	0.16	1.72E-01	5.42E-01	---	---	---	1554957_at	---
6.20	7.07	0.86	1.72E-01	5.42E-01	PLDN	pallidin homolog (mouse)	chr15q21.1	222826_at	NM_012388
4.38	4.70	0.32	1.72E-01	5.42E-01	---	---	---	227036_at	---
2.76	3.02	0.26	1.72E-01	5.42E-01	SH3GL3	SH3-domain GRB2-like 3	chr15q24	205637_s_at	NM_003027
2.73	2.98	0.25	1.72E-01	5.42E-01	MED12	Mediator complex subunit 12	chrXq13	214275_at	NM_005120
2.60	2.83	0.22	1.72E-01	5.42E-01	HFE	hemochromatosis	chr6p21.3	1553402_a_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
2.15	2.32	0.17	1.72E-01	5.42E-01	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	chr12q21.3	206376_at	NM_018057 /// NM_182767
5.53	6.35	0.82	1.72E-01	5.42E-01	USP34	ubiquitin specific peptidase 34	chr2p15	233595_at	NM_014709
3.25	3.46	0.20	1.72E-01	5.42E-01	---	---	---	239613_at	---
2.36	2.56	0.19	1.72E-01	5.42E-01	ZNF346	zinc finger protein 346	chr5q35.2	232753_at	NM_012279
3.46	3.75	0.29	1.72E-01	5.42E-01	NRGN	neurogranin (protein kinase C substrate, RC3)	chr11q24	204081_at	NM_001126181 /// NM_006176
1.98	2.17	0.19	1.72E-01	5.42E-01	---	---	---	233262_at	---
7.39	8.05	0.66	1.72E-01	5.42E-01	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	chr2q33-q34	203039_s_at	NM_005006
3.54	3.99	0.45	1.72E-01	5.42E-01	---	---	---	241891_at	---
2.75	3.08	0.33	1.72E-01	5.42E-01	---	---	---	220514_at	---
2.70	2.99	0.29	1.72E-01	5.42E-01	---	---	---	234033_at	---
2.26	2.48	0.22	1.72E-01	5.42E-01	MCFD2	multiple coagulation factor deficiency 2	chr2p21	1559309_at	NM_139279
2.01	2.22	0.20	1.72E-01	5.42E-01	---	---	---	216703_at	---
2.47	2.66	0.20	1.72E-01	5.42E-01	---	---	---	238876_at	---
1.78	1.97	0.19	1.72E-01	5.42E-01	---	---	---	240254_at	---
2.35	2.53	0.19	1.72E-01	5.42E-01	---	---	---	239863_at	---
2.18	2.35	0.18	1.72E-01	5.42E-01	---	---	---	232729_at	---
2.34	2.51	0.17	1.72E-01	5.42E-01	---	---	---	236873_at	---
1.87	2.03	0.16	1.72E-01	5.42E-01	C3orf65	Chromosome 3 open reading frame 65	chr3q27.2	1563207_at	NM_001039788
3.43	3.76	0.33	1.72E-01	5.42E-01	---	---	---	240069_at	---
2.72	2.95	0.23	1.72E-01	5.42E-01	---	---	---	239850_at	---
2.35	2.57	0.21	1.72E-01	5.42E-01	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	chrXq13	220594_at	NM_181672 /// NM_181673
4.67	4.91	0.24	1.72E-01	5.42E-01	FLJ90757	hypothetical protein LOC440465	chr17q25.3	1566558_x_at	XR_017883 /// XR_017982 /// XR_040055
3.43	3.67	0.24	1.72E-01	5.42E-01	FAM93B /// LOC389634 /// OR7E140P	family with sequence similarity 93, member B /// hypothetical LOC389634 /// olfactory receptor, family 7, subfamily E, member 140 pseudogene	chr12p13.31 /// chr8p23.1	240002_at	XR_041469 /// XR_041470 /// XR_041471
2.23	2.41	0.18	1.72E-01	5.42E-01	---	---	---	217540_at	---
6.70	7.19	0.49	1.72E-01	5.42E-01	CRBN	cereblon	chr3p26.3	218142_s_at	NM_016302
2.94	3.30	0.36	1.72E-01	5.42E-01	OGN	osteoglycin	chr9q22	218730_s_at	NM_014057 /// NM_024416 /// NM_033014
3.92	4.17	0.26	1.72E-01	5.42E-01	SARDH	sarcosine dehydrogenase	chr9q33-q34	210063_at	NM_001134707 /// NM_007101
5.60	5.80	0.21	1.72E-01	5.42E-01	---	---	---	241268_x_at	---
1.93	2.13	0.20	1.72E-01	5.42E-01	---	---	---	1570043_at	---
4.71	5.40	0.69	1.72E-01	5.43E-01	FAM114A2	family with sequence similarity 114, member A2	chr5q31-q33	222682_s_at	NM_018691
5.08	5.42	0.34	1.73E-01	5.43E-01	RPL23AP13	ribosomal protein L23a pseudogene 13	chr2p16.2	207283_at	NR_002229
7.54	7.82	0.29	1.72E-01	5.43E-01	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	chr18p11.32	201672_s_at	NM_001037334 /// NM_005151
4.54	4.83	0.28	1.73E-01	5.43E-01	FLJ90757	hypothetical protein LOC440465	chr17q25.3	1558148_x_at	XR_017883 /// XR_017982 /// XR_040055
3.18	3.44	0.26	1.72E-01	5.43E-01	---	---	---	235227_at	---
2.27	2.52	0.25	1.73E-01	5.43E-01	DKFZp564H213	hypothetical gene supported by AL049275	chr17q12	234787_at	---
4.45	4.69	0.24	1.72E-01	5.43E-01	---	---	---	237171_at	---
2.23	2.47	0.24	1.73E-01	5.43E-01	---	---	---	233283_at	---
2.15	2.36	0.21	1.73E-01	5.43E-01	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	chr5q12	1570351_at	NM_197941
2.21	2.41	0.20	1.73E-01	5.43E-01	LOC221814	Hypothetical protein LOC221814	chr7p21.3	233043_at	---
2.13	2.31	0.19	1.73E-01	5.43E-01	RP11-145E5.4	antisense noncoding RNA in the INK4 locus	chr9p21.3	1559884_at	NR_003529
2.20	2.38	0.18	1.73E-01	5.43E-01	SLC25A30	Solute carrier family 25, member 30	chr13q14.12	216721_at	NM_001010875
3.59	3.75	0.16	1.72E-01	5.43E-01	EPHA8	EPH receptor A8	chr1p36.12	1554069_at	NM_001006943 /// NM_020526

2.08	2.30	0.22	1.73E-01	5.43E-01	---	---	---	220854_at	---
3.91	4.30	0.38	1.73E-01	5.43E-01	---	---	---	243158_at	---
2.32	2.60	0.28	1.73E-01	5.43E-01	---	---	---	243063_at	---
4.12	4.33	0.21	1.73E-01	5.43E-01	FBXO24	F-box protein 24	chr7q22	223941_at	NM_012172 /// NM_033506
4.24	4.45	0.21	1.73E-01	5.43E-01	ARSK	Arylsulfatase family, member K	chr5q15	1569132_s_at	NM_198150
2.67	2.86	0.19	1.73E-01	5.43E-01	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	chr3q25.2	227197_at	NM_015595
4.77	5.28	0.51	1.73E-01	5.43E-01	CCPG1	cell cycle progression 1	chr15q21.1	214152_at	NM_004748 /// NM_020739
2.39	2.62	0.23	1.73E-01	5.43E-01	---	---	---	231648_at	---
2.88	3.06	0.18	1.73E-01	5.43E-01	---	---	---	233263_at	---
2.23	2.39	0.16	1.73E-01	5.43E-01	---	---	---	242085_at	---
2.26	2.58	0.31	1.73E-01	5.43E-01	SYT13	synaptotagmin XIII	chr11p12-p11	226086_at	NM_020826
4.69	5.41	0.72	1.73E-01	5.43E-01	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	chr2p24	202762_at	NM_004850
3.16	3.39	0.23	1.73E-01	5.43E-01	---	---	---	216123_x_at	---
2.55	2.74	0.19	1.73E-01	5.43E-01	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	chr5p15.1-p14	210601_at	NM_004932
4.30	4.53	0.22	1.73E-01	5.43E-01	---	---	---	237110_at	---
5.90	6.32	0.42	1.73E-01	5.43E-01	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	chr12q13.13	209715_at	NM_001127321 /// NM_001127322 /// NM_012117
3.22	3.48	0.26	1.73E-01	5.43E-01	RGMA	RGM domain family, member A	chr15q26.1	234406_at	NM_020211
1.95	2.11	0.16	1.73E-01	5.43E-01	---	---	---	240226_at	---
5.67	6.25	0.58	1.73E-01	5.43E-01	DICER1	dicer 1, ribonuclease type III	chr14q32.13	206061_s_at	NM_030621 /// NM_177438
2.12	2.37	0.24	1.73E-01	5.43E-01	NIN	ninein (GSK3B interacting protein)	chr14q22.1	219285_s_at	NM_016350 /// NM_020921 /// NM_182944 /// NM_182946
2.49	2.71	0.22	1.73E-01	5.43E-01	---	---	---	232582_at	---
2.15	2.34	0.19	1.73E-01	5.43E-01	---	---	---	1561250_at	---
4.02	4.19	0.18	1.73E-01	5.43E-01	GJD3	gap junction protein, delta 3, 31.9kDa	chr17q21.2	1553511_at	NM_152219
2.26	2.44	0.18	1.73E-01	5.43E-01	ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13	chr21q11.2	233371_at	NR_003087 /// NR_003088
2.21	2.37	0.16	1.73E-01	5.43E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	1556487_a_at	NM_033364
6.49	7.08	0.59	1.73E-01	5.44E-01	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	chr6q21	202511_s_at	NM_004849
2.87	3.06	0.18	1.73E-01	5.44E-01	WFDC2	WAP four-disulfide core domain 2	chr20q12-q13.2	1553089_a_at	NM_006103
2.23	2.47	0.23	1.73E-01	5.44E-01	---	---	---	1570158_at	---
3.26	3.69	0.43	1.74E-01	5.44E-01	EFCAB7	EF-hand calcium binding domain 7	chr1p31.3	226800_at	NM_032437
3.55	3.93	0.39	1.74E-01	5.44E-01	SYT11	synaptotagmin XI	chr1q21.2	209197_at	NM_152280
5.61	5.94	0.33	1.74E-01	5.44E-01	FYCO1	FYVE and coiled-coil domain containing 1	chr3p21.31	218204_s_at	NM_024513
2.49	2.81	0.32	1.74E-01	5.44E-01	---	---	---	1562655_at	---
3.52	3.72	0.20	1.74E-01	5.44E-01	RNF130	Ring finger protein 130	chr5q35.3	1563975_at	NM_018434
1.93	2.09	0.16	1.74E-01	5.44E-01	---	---	---	243789_at	---
2.75	3.16	0.40	1.74E-01	5.44E-01	---	---	---	244300_at	---
7.16	7.52	0.36	1.74E-01	5.44E-01	41526	septin 9	chr17q25	208657_s_at	NM_001113491 /// NM_001113492 /// NM_001113493 /// NM_001113494 /// NM_001113495 /// NM_001113496 /// NM_006640
1.93	2.16	0.24	1.74E-01	5.44E-01	---	---	---	207273_at	---
2.97	3.19	0.22	1.74E-01	5.44E-01	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	chr1q21-q22	1554783_s_at	NM_004723
3.59	3.85	0.27	1.74E-01	5.44E-01	FLJ39632	hypothetical LOC642477	chr14q11.1	1558139_at	XR_015133 /// XR_041395
2.96	3.18	0.22	1.74E-01	5.44E-01	---	---	---	244836_at	---
5.18	6.18	1.00	1.74E-01	5.44E-01	FYTTD1	forty-two-three domain containing 1	chr3q29	224642_at	NM_001011537 /// NM_032288
2.59	2.83	0.24	1.74E-01	5.44E-01	---	---	---	234401_at	---
3.86	4.13	0.27	1.74E-01	5.44E-01	HNRNPR	heterogeneous nuclear ribonucleoprotein R	chr1p36.12	232004_at	NM_001102397 /// NM_001102398 /// NM_001102399 /// NM_005826

7.35	8.04	0.69	1.74E-01	5.44E-01	CYBB	cytochrome b-245, beta polypeptide	chrXp21.1	203923_s_at	NM_000397
3.69	4.03	0.34	1.74E-01	5.44E-01	---	---	---	229291_at	---
2.94	3.17	0.23	1.74E-01	5.44E-01	CPLX2	complexin 2	chr5q35.2	206368_at	NM_001008220 /// NM_006650
2.12	2.29	0.17	1.74E-01	5.44E-01	---	---	---	240816_at	---
1.86	2.03	0.17	1.74E-01	5.44E-01	MGC13053	hypothetical MGC13053	chr11q23.3	211775_x_at	---
2.20	2.34	0.14	1.74E-01	5.44E-01	CTNNA2	catenin (cadherin-associated protein), alpha 2	chr2p12-p11.1	205373_at	NM_004389
4.90	5.26	0.36	1.74E-01	5.44E-01	PDPK1	3-phosphoinositide dependent protein kinase-1	chr16p13.3	204524_at	NM_002613 /// NM_031268
2.75	3.06	0.31	1.74E-01	5.44E-01	---	---	---	1566284_at	---
6.47	6.76	0.29	1.74E-01	5.44E-01	---	---	---	241921_x_at	---
7.58	7.87	0.28	1.74E-01	5.44E-01	MRAS	muscle RAS oncogene homolog	chr3q22.3	225185_at	NM_001085049 /// NM_012219
4.98	5.23	0.26	1.74E-01	5.44E-01	GOPC	golgi associated PDZ and coiled-coil motif containing	chr6q21	227215_at	NM_001017408 /// NM_020399
2.81	2.98	0.17	1.74E-01	5.44E-01	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	chr1p36.1	1570627_at	NM_003198
4.85	5.09	0.24	1.74E-01	5.44E-01	EHMT2	euchromatic histone-lysine N-methyltransferase 2	chr6p21.31	207484_s_at	NM_006709 /// NM_025256
5.40	5.69	0.29	1.74E-01	5.44E-01	---	---	---	228231_at	---
3.51	3.83	0.32	1.74E-01	5.44E-01	SLC35D2	solute carrier family 35, member D2	chr9q22.32	231437_at	NM_007001
6.71	7.02	0.30	1.74E-01	5.44E-01	GP1BB	glycoprotein Ib (platelet), beta polypeptide	chr22q11.21-q11.23|22q11.21	209769_s_at	NM_000407
2.71	2.88	0.18	1.74E-01	5.44E-01	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	1565436_s_at	NM_005933
7.14	8.08	0.93	1.74E-01	5.44E-01	CANX	calnexin	chr5q35	208853_s_at	NM_001024649 /// NM_001746
7.60	8.04	0.44	1.74E-01	5.44E-01	TMEM167B	transmembrane protein 167B	chr1p13.3	222495_at	NM_020141
3.06	3.26	0.19	1.74E-01	5.44E-01	C15orf40	chromosome 15 open reading frame 40	chr15q25.2	235840_at	NM_144597
4.59	4.93	0.33	1.74E-01	5.44E-01	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	chr19q13.11	225527_at	NM_001806
6.91	7.23	0.32	1.74E-01	5.44E-01	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	chr11q13	205640_at	NM_000694 /// NM_001030010
2.28	2.55	0.26	1.74E-01	5.44E-01	SNX20	sorting nexin 20	chr16q12.1	229045_at	NM_182854
3.48	3.79	0.31	1.74E-01	5.45E-01	GCGR	glucagon receptor	chr17q25	210565_at	NM_000160
2.49	3.07	0.58	1.74E-01	5.45E-01	---	---	---	242500_at	---
4.22	4.69	0.47	1.74E-01	5.45E-01	TOP1	topoisomerase (DNA) I	chr20q12-q13.1	208900_s_at	NM_003286
3.83	4.29	0.46	1.74E-01	5.45E-01	ZFP3	zinc finger protein 3 homolog (mouse)	chr17p13.2	235728_at	NM_153018
3.92	4.37	0.45	1.74E-01	5.45E-01	KIAA1333	KIAA1333	chr14q12	223256_at	NM_017769
6.37	6.76	0.39	1.74E-01	5.45E-01	CHST11	Carbohydrate (chondroitin 4) sulfotransferase 11	chr12q	226372_at	NM_018413
4.30	4.58	0.28	1.74E-01	5.45E-01	KCTD5	Potassium channel tetramerisation domain containing 5	chr16p13.3	229837_s_at	NM_018992
2.51	2.78	0.27	1.74E-01	5.45E-01	BIRC3	baculoviral IAP repeat-containing 3	chr11q22	210538_s_at	NM_001165 /// NM_182962
6.44	6.69	0.25	1.74E-01	5.45E-01	ZNF444	zinc finger protein 444	chr19q13.42	218707_at	NM_018337
2.50	2.73	0.23	1.74E-01	5.45E-01	LOC283854	hypothetical protein LOC283854	chr16q12.1	1556954_at	---
1.99	2.20	0.21	1.74E-01	5.45E-01	ACSL6	Acyl-CoA synthetase long-chain family member 6	chr5q31	229725_at	NM_001009185 /// NM_015256
2.19	2.40	0.21	1.74E-01	5.45E-01	ROR1	receptor tyrosine kinase-like orphan receptor 1	chr1p32-p31	232060_at	NM_001083592 /// NM_005012
2.06	2.26	0.20	1.74E-01	5.45E-01	LOC100128590	hypothetical protein LOC100128590	chr2p22.1	1558920_at	XM_001723678 /// XM_001726900
3.20	3.55	0.36	1.75E-01	5.45E-01	RSF1	remodeling and spacing factor 1	chr11q14.1	223818_s_at	NM_016578
4.41	4.71	0.30	1.75E-01	5.45E-01	PDCD2	programmed cell death 2	chr6q27	228420_at	NM_002598 /// NM_144781
1.91	2.07	0.17	1.74E-01	5.45E-01	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	chr19p13.12	1554593_s_at	NM_005071
5.36	5.60	0.24	1.75E-01	5.45E-01	TPMT	thiopurine S-methyltransferase	chr6p22.3	203671_at	NM_000367
2.85	3.16	0.31	1.75E-01	5.45E-01	---	---	---	234958_at	---
1.80	2.00	0.20	1.75E-01	5.45E-01	---	---	---	1555646_at	---
5.46	5.69	0.23	1.75E-01	5.45E-01	AUTS2	autism susceptibility candidate 2	chr7q11.22	212599_at	NM_001127231 /// NM_001127232 /// NM_015570
5.75	6.52	0.77	1.75E-01	5.45E-01	ENDOD1	endonuclease domain containing 1	chr11q21	212573_at	NM_015036
2.40	2.56	0.16	1.75E-01	5.45E-01	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	chr9p13-p12	1558116_x_at	NM_021111
6.75	6.95	0.20	1.75E-01	5.45E-01	---	---	---	217363_x_at	---

2.37	2.56	0.19	1.75E-01	5.45E-01	LOC100129069	hypothetical protein LOC100129069	chr11q24.2	234121_at	XM_001717421 /// XM_001726472 /// XM_001726502																				
5.72	6.07	0.35	1.75E-01	5.45E-01	MITF	microphthalmia-associated transcription factor	chr3p14.2-p14.1	207233_s_at	NM_000248 /// NM_006722 /// NM_198158 /// NM_198159 /// NM_198177 /// NM_198178																				
2.74	3.04	0.30	1.75E-01	5.45E-01	DSCAML1	Down syndrome cell adhesion molecule like 1	chr11q23	234908_s_at	NM_020693																				
2.16	2.33	0.17	1.75E-01	5.45E-01	UBE3C	ubiquitin protein ligase E3C	chr7q36.3	1555405_at	NM_014671																				
1.91	2.11	0.20	1.75E-01	5.45E-01	---	---	---	1560182_at	---																				
4.22	4.46	0.25	1.75E-01	5.45E-01	OR1I1	olfactory receptor, family 1, subfamily I, member 1	chr19p13.12	234403_at	NM_001004713																				
2.27	2.44	0.17	1.75E-01	5.45E-01	HIPK3	homeodomain interacting protein kinase 3	chr11p13	213697_at	NM_001048200 /// NM_005734																				
2.98	3.27	0.29	1.75E-01	5.45E-01	---	---	---	237704_at	---																				
2.04	2.25	0.22	1.75E-01	5.45E-01	FN1	fibronectin 1	chr2q34	214702_at	NM_002026 /// NM_054034 /// NM_212474 /// NM_212475 /// NM_212476 /// NM_212478 /// NM_212482																				
3.87	4.18	0.31	1.75E-01	5.45E-01	TK1	thymidine kinase 1, soluble	chr17q23.2-q25.3	202338_at	NM_003258																				
3.86	4.29	0.43	1.75E-01	5.45E-01	VIPR1	vasoactive intestinal peptide receptor 1	chr3p22	205019_s_at	NM_004624																				
2.26	2.43	0.17	1.75E-01	5.45E-01	IAPP	islet amyloid polypeptide	chr12p12.3-p12.1	207062_at	NM_000415																				
2.57	2.82	0.24	1.75E-01	5.45E-01	SPANXA1 /// SPANXA2 /// SPANXC	sperm protein associated with the nucleus, X-linked, family member A1 /// SPANX family, member A2 /// SPANX family, member C	chrXq27.1	224032_x_at	NM_013453 /// NM_022661 /// NM_145662 /// XM_001713760																				
2.49	2.75	0.26	1.75E-01	5.46E-01	DTL	denticleless homolog (Drosophila)	chr1q32.1-q32.2	218585_s_at	NM_016448																				
2.08	2.24	0.15	1.75E-01	5.46E-01	---	---	---	215539_at	---																				
5.97	6.28	0.31	1.75E-01	5.46E-01	GPC2	glypican 2	chr7q22.1	239422_at	NM_152742																				
5.93	6.22	0.30	1.75E-01	5.46E-01	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	212076_at	NM_005933																				
2.95	3.16	0.22	1.75E-01	5.46E-01	---	---	---	1565846_at	---																				
2.33	2.52	0.19	1.75E-01	5.46E-01	TMPRSS2	transmembrane protease, serine 2	chr21q22.3	1570433_at	NM_005656 /// XM_001717226 /// XM_001722209 /// XM_001726078																				
1.89	2.04	0.15	1.75E-01	5.46E-01	---	---	---	234185_at	---																				
3.47	3.81	0.34	1.75E-01	5.46E-01	ICOSLG	inducible T-cell co-stimulator ligand	chr21q22.3	228976_at	NM_015259																				
6.65	6.98	0.33	1.75E-01	5.46E-01	C16orf72	chromosome 16 open reading frame 72	chr16p13.2	225183_at	NM_014117																				
3.62	3.85	0.23	1.75E-01	5.46E-01	PAPPA2	pappalysin 2	chr1q23-q25	214689_at	NM_020318 /// NM_021936																				
3.31	3.54	0.23	1.75E-01	5.46E-01	CRYGD	crystallin, gamma D	chr2q33-q35	207532_at	NM_006891																				
3.97	4.19	0.22	1.75E-01	5.46E-01	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	chr7q31.1-q31.33	222560_at	NM_018697																				
2.30	2.51	0.21	1.76E-01	5.46E-01	PTPRJ	Protein tyrosine phosphatase, receptor type, J	chr11p11.2	214137_at	NM_001098503 /// NM_002843																				
1.92	2.13	0.21	1.75E-01	5.46E-01	ZMYND8	Zinc finger, MYND-type containing 8	chr20q13.12	1558571_at	NM_012408 /// NM_183047 /// NM_183048																				
1.81	2.00	0.18	1.76E-01	5.46E-01	SGK2	Serum/glucocorticoid regulated kinase 2	chr20q13.2	230573_at	NM_016276 /// NM_170693																				
3.25	3.43	0.17	1.75E-01	5.46E-01	LOC284669	hypothetical protein LOC284669	chr1q32.3	1560935_s_at	---																				
2.92	3.09	0.17	1.75E-01	5.46E-01	CLC	Charcot-Leyden crystal protein	chr19q13.1	206207_at	NM_001828																				
2.26	2.43	0.17	1.75E-01	5.46E-01	UNC13C	unc-13 homolog C (C. elegans)	chr15q21.3	1562074_a_at	NM_001080534																				
2.01	2.17	0.17	1.76E-01	5.46E-01	---	---	---	1562373_at	---																				
3.89	4.55	0.65	1.76E-01	5.46E-01	---	---	---	242134_at	---																				
5.67	5.94	0.27	1.76E-01	5.46E-01	TMEM175	transmembrane protein 175	chr4p16.3	223462_at	NM_032326																				
2.98	3.25	0.27	1.76E-01	5.46E-01	KIF1C	kinesin family member 1C	chr17p13.2	209245_s_at	NM_006612																				

2.69	2.91	0.22	1.76E-01	5.46E-01	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	chr1p34	243209_at	NM_004700 /// NM_172163																				
4.30	4.55	0.25	1.76E-01	5.46E-01	L1CAM	L1 cell adhesion molecule	chrXq28	204585_s_at	NM_000425 /// NM_024003																				
6.05	6.61	0.56	1.76E-01	5.46E-01	AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	chr10p15-p14	211653_x_at	NM_001354 /// NM_205845																				
3.19	3.42	0.24	1.76E-01	5.46E-01	TXNDC2	thioredoxin domain-containing 2 (spermatozoa)	---	1552657_a_at	NM_001098529 /// NM_001098530 /// NM_032243 /// XM_001721366 /// XM_001721367																				
1.77	1.92	0.15	1.76E-01	5.46E-01	FAM98B	family with sequence similarity 98, member B	chr15q14	1553625_at	NM_001042429 /// NM_173611																				
5.73	6.34	0.61	1.76E-01	5.46E-01	AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	chr10p15-p14	209699_x_at	NM_001354 /// NM_205845																				
5.26	5.85	0.58	1.76E-01	5.46E-01	---	---	---	244433_at	---																				
3.15	3.43	0.28	1.76E-01	5.46E-01	FBXW10	F-box and WD repeat domain containing 10	chr17p12	223870_at	NM_031456																				
3.37	3.62	0.25	1.76E-01	5.46E-01	SCLY	selenocysteine lyase	chr2q37.3	219808_at	NM_016510																				
6.43	6.67	0.24	1.76E-01	5.46E-01	RTEL1	regulator of telomere elongation helicase 1	chr20q13.3	213829_x_at	NM_016434 /// NM_032957																				
2.40	2.63	0.23	1.76E-01	5.46E-01	CLCN5	chloride channel 5	chrXp11.23-p11.22|Xp11.23	206704_at	NM_000084 /// NM_001127898 /// NM_001127899																				
2.12	2.27	0.15	1.76E-01	5.46E-01	---	---	---	1565873_at	---																				
6.55	6.81	0.26	1.76E-01	5.46E-01	RTEL1	regulator of telomere elongation helicase 1	chr20q13.3	206092_x_at	NM_016434 /// NM_032957																				
2.37	2.60	0.22	1.76E-01	5.46E-01	LEKR1	leucine, glutamate and lysine rich 1	chr3q25.31-q25.32	1559105_at	NM_001004316 /// XM_001724269 /// XM_001725663 /// XM_001725985																				
6.81	7.83	1.01	1.76E-01	5.46E-01	ADD3	adducin 3 (gamma)	chr10q24.2-q24.3	201752_s_at	NM_001121 /// NM_016824 /// NM_019903																				
3.87	4.61	0.74	1.76E-01	5.46E-01	FRYL	FRY-like	chr4p12	212546_s_at	NM_015030																				
6.52	6.80	0.28	1.76E-01	5.46E-01	LILRA6 /// LILRB3	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	chr19q13.4	211133_x_at	NM_001081450 /// NM_006864 /// NM_024318																				
6.65	6.92	0.27	1.76E-01	5.46E-01	TSC22D4	TSC22 domain family, member 4	chr7p21-p15	208104_s_at	NM_030935																				
3.11	3.37	0.26	1.76E-01	5.46E-01	SLC45A1	solute carrier family 45, member 1	chr1p36.1-p36.2	230458_at	NM_001080397																				
2.59	2.82	0.23	1.76E-01	5.46E-01	---	---	---	1562801_at	---																				
2.64	2.85	0.20	1.76E-01	5.46E-01	LRFN2	leucine rich repeat and fibronectin type III domain containing 2	chr6p21.2-p21.1	232697_at	NM_020737																				
2.64	2.88	0.24	1.76E-01	5.46E-01	ZNF688	Zinc finger protein 688	chr16p11.2	228631_s_at	NM_001024683 /// NM_145271																				
8.26	8.90	0.64	1.76E-01	5.46E-01	SPARCL1	SPARC-like 1 (hevin)	chr4q22.1	200795_at	NM_001128310 /// NM_004684																				
3.62	3.81	0.19	1.76E-01	5.46E-01	TLK2	tousled-like kinase 2	chr17q23	228627_at	NM_001112707 /// NM_006852																				
3.97	4.29	0.32	1.76E-01	5.46E-01	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	chr2q24.1	229555_at	NM_014568																				
5.02	5.29	0.27	1.76E-01	5.46E-01	KIAA1683	KIAA1683	chr19p13.1	232433_at	NM_025249																				
3.93	5.01	1.09	1.76E-01	5.46E-01	LOC652493	similar to Ig kappa chain V-I region HK102 precursor	---	216401_x_at	XM_001724425																				
6.52	7.15	0.63	1.76E-01	5.46E-01	CHD9	chromodomain helicase DNA binding protein 9	chr16q12.2	212616_at	NM_025134																				

2.50	3.05	0.55	1.76E-01	5.46E-01	PCSK6	Proprotein convertase subtilisin/kexin type 6	chr15q26.3	242662_at	NM_002570 /// NM_138319 /// NM_138320 /// NM_138321 /// NM_138322 /// NM_138323 /// NM_138324 /// NM_138325																			
4.01	4.49	0.48	1.76E-01	5.46E-01	TDRD3	tudor domain containing 3	chr13q21.2	1569069_s_at	NM_030794																			
8.94	9.26	0.32	1.76E-01	5.46E-01	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	chr14q24.3	212352_s_at	NM_006827																			
2.74	2.99	0.24	1.76E-01	5.46E-01	C1orf68	chromosome 1 open reading frame 68	chr1q21.3	217087_at	NM_001024679 /// XM_001721554 /// XM_001724444 /// XM_001724465																			
2.73	2.97	0.24	1.76E-01	5.46E-01	SYVN1	Synovial apoptosis inhibitor 1, synoviolin	chr11q13	244522_at	NM_032431 /// NM_172230																			
2.52	2.74	0.22	1.76E-01	5.46E-01	ANKRD18A /// ANKRD18B /// ANKRD19 /// LOC645626 /// LOC728897 /// RP11-195B21.3	ankyrin repeat domain 18A /// ankyrin repeat domain 18B /// ankyrin repeat domain 19 /// similar to coiled-coil domain containing 29 /// hypothetical protein LOC728897 /// hypothetical LOC644249	chr13q11 /// chr9p13.1 /// chr9p13.3 /// chr9q12 /// chr9q22.31	233592_at	XM_001713927 /// XM_001713970 /// XM_001714242 /// XM_001716325 /// XM_001717197 /// XM_001717620 /// XM_001718334 /// XM_001726105 /// XM_927429 /// XM_928641 /// XR_040005 /// XR_040006 /// XR_040007																			
2.63	2.84	0.22	1.76E-01	5.46E-01	---	---	---	231519_at	---																			
2.17	2.39	0.21	1.76E-01	5.46E-01	C2orf21	chromosome 2 open reading frame 21	chr2q35	243836_at	NM_032504 /// NM_182587 /// XM_001715588 /// XM_001717212 /// XM_001717654																			
2.56	2.76	0.20	1.76E-01	5.46E-01	SYT6	synaptotagmin VI	chr1p13.2	244227_at	NM_205848																			
2.17	2.34	0.17	1.76E-01	5.46E-01	---	---	---	1560086_at	---																			
2.31	2.48	0.17	1.76E-01	5.46E-01	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	chr11q25	220676_at	NM_007037																			
2.10	2.25	0.16	1.76E-01	5.46E-01	---	---	---	233671_at	---																			
4.63	5.16	0.53	1.76E-01	5.47E-01	PHKB	phosphorylase kinase, beta	chr16q12-q13	238601_at	NM_000293 /// NM_001031835																			
2.94	3.19	0.26	1.76E-01	5.47E-01	---	---	---	237611_at	---																			
7.03	7.33	0.29	1.77E-01	5.47E-01	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	chr1q21.1	209206_at	NM_004892																			
3.95	4.25	0.30	1.77E-01	5.47E-01	RSPH3	radial spoke 3 homolog (Chlamydomonas)	chr6q25.3	223713_at	NM_031924																			
2.65	2.93	0.28	1.77E-01	5.47E-01	LOC253039	hypothetical LOC253039	chr9q33.2	241249_at	XM_001715306 /// XM_001719409 /// XM_001725827																			
2.04	2.25	0.20	1.77E-01	5.47E-01	---	---	---	1568647_at	---																			
4.28	4.53	0.25	1.77E-01	5.47E-01	DOCK9	dedicator of cytokinesis 9	chr13q32.3	215238_s_at	NM_001130048 /// NM_001130049 /// NM_001130050 /// NM_015296																			

5.84	6.29	0.45	1.77E-01	5.47E-01	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	chr3q26.32	222633_at	NM_024665
2.18	2.35	0.18	1.77E-01	5.47E-01	PROSC	proline synthetase co-transcribed homolog (bacterial)	chr8p11.2	216519_s_at	NM_007198
4.65	5.65	1.00	1.77E-01	5.47E-01	LOC339562	similar to hCG1742442	chr2p11.1	217480_x_at	XM_001713985
3.85	4.79	0.95	1.77E-01	5.47E-01	ADRA2A	adrenergic, alpha-2A-, receptor	chr10q24-q26	209869_at	NM_000681
8.58	9.10	0.53	1.77E-01	5.47E-01	CALD1	caldesmon 1	chr7q33	212077_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
4.66	5.12	0.47	1.77E-01	5.47E-01	BMP2K	BMP2 inducible kinase	chr4q21.21	226853_at	NM_017593 /// NM_198892
6.44	6.83	0.39	1.77E-01	5.47E-01	LOC492311	similar to bovine IgA regulatory protein	chr5q31	226977_at	NM_001007189
2.86	3.25	0.39	1.77E-01	5.47E-01	CC2D2A	coiled-coil and C2 domain containing 2A	chr4p15.33	236473_at	NM_001080522 /// NM_020785 /// NR_024098
3.42	3.66	0.25	1.77E-01	5.47E-01	ZNF467	Zinc finger protein 467	chr7q36.1	213559_s_at	NM_207336
1.91	2.15	0.24	1.77E-01	5.47E-01	---	---	---	237865_x_at	---
3.53	3.77	0.24	1.77E-01	5.47E-01	DMWD	dystrophia myotonica, WD repeat containing	chr19q13.3	213231_at	NM_004943
2.65	2.88	0.22	1.77E-01	5.47E-01	FAM24B	family with sequence similarity 24, member B	chr10q26.13	231146_at	NM_152644
5.33	5.55	0.22	1.77E-01	5.47E-01	ARSD	arylsulfatase D	chrXp22.3	207784_at	NM_001669 /// NM_009589
6.37	6.58	0.21	1.77E-01	5.47E-01	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	chr1q32.1	223662_x_at	NM_001031725 /// NM_031306
2.04	2.25	0.21	1.77E-01	5.47E-01	---	---	---	1561813_at	---
2.79	3.00	0.21	1.77E-01	5.47E-01	PTPN5	Protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	chr11p15.1	233470_at	NM_001039970 /// NM_006906 /// NM_032781
2.57	2.77	0.20	1.77E-01	5.47E-01	PTPRD	protein tyrosine phosphatase, receptor type, D	chr9p23-p24.3	214043_at	NM_001040712 /// NM_002839 /// NM_130391 /// NM_130392 /// NM_130393
2.76	2.95	0.19	1.77E-01	5.47E-01	EPHA3	EPH receptor A3	chr3p11.2	206071_s_at	NM_005233 /// NM_182644
1.95	2.12	0.17	1.77E-01	5.47E-01	---	---	---	1560517_s_at	---
2.73	2.90	0.16	1.77E-01	5.47E-01	C12orf54	chromosome 12 open reading frame 54	chr12q13.11	237701_at	NM_152319
2.52	2.68	0.16	1.77E-01	5.47E-01	C1orf116	chromosome 1 open reading frame 116	chr1q32.1	219476_at	NM_001083924 /// NM_023938
2.21	2.37	0.16	1.77E-01	5.47E-01	C13orf15	Chromosome 13 open reading frame 15	chr13q14.11	239827_at	NM_014059
3.23	3.41	0.18	1.77E-01	5.47E-01	HAVCR2	hepatitis A virus cellular receptor 2	chr5q33.3	1555629_at	NM_032782
4.22	4.48	0.26	1.77E-01	5.47E-01	---	---	---	243266_at	---
3.48	3.71	0.23	1.77E-01	5.47E-01	---	---	---	224006_at	---
2.08	2.30	0.22	1.77E-01	5.47E-01	TFRC	transferrin receptor (p90, CD71)	chr3q29	237214_at	NM_001128148 /// NM_003234
3.40	3.61	0.21	1.77E-01	5.47E-01	ARR3	arrestin 3, retinal (X-arrestin)	chrXcen-q21	207136_at	NM_004312
3.98	4.19	0.21	1.77E-01	5.47E-01	LOC100130054	Hypothetical protein LOC100130054	chr9q21.11	243344_at	XM_001716125 /// XM_001721751
2.77	3.03	0.26	1.77E-01	5.47E-01	BNIPL	BCL2/adenovirus E1B 19kD interacting protein like	chr1q21.2	1553072_at	NM_138278
2.96	3.40	0.44	1.77E-01	5.48E-01	CYSLTR1	cysteinyl leukotriene receptor 1	chrXq13.2-q21.1	231747_at	NM_006639
3.18	3.50	0.33	1.78E-01	5.48E-01	---	---	---	234986_at	---
5.46	5.70	0.25	1.77E-01	5.48E-01	VPRBP	Vpr (HIV-1) binding protein	chr3p21.2	226476_s_at	NM_014703
2.08	2.32	0.24	1.77E-01	5.48E-01	EYA4	eyes absent homolog 4 (Drosophila)	chr6q23	1561088_at	NM_004100 /// NM_172103 /// NM_172105
2.85	3.32	0.47	1.78E-01	5.48E-01	HINT3	histidine triad nucleotide binding protein 3	chr6q22.32	228697_at	NM_138571
1.86	2.06	0.20	1.78E-01	5.48E-01	FYB	FYN binding protein (FYB-120/130)	chr5p13.1	224148_at	NM_001465 /// NM_199335
5.63	5.94	0.32	1.78E-01	5.48E-01	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	chr9q34.11-q34.12	225214_at	NM_002799
4.63	4.90	0.27	1.78E-01	5.48E-01	FOXK1	Forkhead box K1	chr7p22.1	235519_at	NM_001037165
4.58	4.85	0.27	1.78E-01	5.48E-01	IL3RA	interleukin 3 receptor, alpha (low affinity)	chrXp22.3 or Yp11.3	206148_at	NM_002183
2.77	3.01	0.23	1.78E-01	5.48E-01	---	---	---	216337_at	---
2.39	2.58	0.19	1.78E-01	5.48E-01	SLC7A14	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	chr3q26.2	232904_at	NM_020949 /// XM_001723366 /// XM_930209 /// XM_941578
3.54	3.78	0.23	1.78E-01	5.48E-01	PIGR	Polymeric immunoglobulin receptor	chr1q31-q41	229659_s_at	NM_002644

3.15	3.37	0.22	1.78E-01	5.48E-01	SPEG	SPEG complex locus	chr2q35	1559474_at	NM_005876
2.70	2.91	0.21	1.78E-01	5.48E-01	RP5-886K2.1	neuronal thread protein AD7c-NTP	chr1p36	208014_x_at	---
2.27	2.45	0.18	1.78E-01	5.48E-01	LILRA1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	chr19q13.4	210660_at	NM_006863
2.70	2.97	0.26	1.78E-01	5.48E-01	---	---	---	238498_at	---
2.44	2.62	0.18	1.78E-01	5.48E-01	---	---	---	238928_at	---
5.69	6.22	0.52	1.78E-01	5.48E-01	---	---	---	225553_at	---
5.71	5.91	0.20	1.78E-01	5.48E-01	---	---	---	215587_x_at	---
2.59	2.83	0.24	1.78E-01	5.48E-01	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	chr14q23.3	217044_s_at	NM_015549
1.98	2.11	0.14	1.78E-01	5.48E-01	---	---	---	233012_at	---
2.82	3.06	0.25	1.78E-01	5.48E-01	LOC197350	hypothetical protein LOC197350	chr16p13.3	234231_at	XM_001715723 /// XM_001717642 /// XM_113871
3.54	3.74	0.20	1.78E-01	5.48E-01	GABRR2	gamma-aminobutyric acid (GABA) receptor, rho 2	chr6q14-q21|6q13-q16.3	208217_at	NM_002043
2.00	2.18	0.18	1.78E-01	5.48E-01	---	---	---	241318_at	---
6.14	7.00	0.86	1.78E-01	5.48E-01	---	---	---	242471_at	---
5.01	5.71	0.70	1.78E-01	5.48E-01	ITM2A	integral membrane protein 2A	chrXq13.3-Xq21.2	202747_s_at	NM_004867
2.46	2.76	0.30	1.78E-01	5.48E-01	---	---	---	1556172_at	---
3.44	3.70	0.26	1.78E-01	5.48E-01	HRASLS2	HRAS-like suppressor 2	chr11q12.3	216760_at	NM_017878
2.45	2.71	0.26	1.78E-01	5.48E-01	DLC1	deleted in liver cancer 1	chr8p22	220511_s_at	NM_006094 /// NM_024767 /// NM_182643
2.18	2.43	0.25	1.78E-01	5.48E-01	VGLL3	vestigial like 3 (Drosophila)	chr3p12.1	227399_at	NM_016206
2.37	2.62	0.25	1.78E-01	5.48E-01	---	---	---	243018_at	---
2.44	2.68	0.24	1.78E-01	5.48E-01	L1TD1	LINE-1 type transposase domain containing 1	chr1p31.3	236894_at	NM_019079
2.46	2.67	0.22	1.78E-01	5.48E-01	---	---	---	237055_at	---
2.76	2.97	0.21	1.78E-01	5.48E-01	GNA14	guanine nucleotide binding protein (G protein), alpha 14	chr9q21	243580_at	NM_004297
2.38	2.58	0.20	1.78E-01	5.48E-01	EHD3	EH-domain containing 3	chr2p21	241267_at	NM_014600
2.25	2.45	0.19	1.78E-01	5.48E-01	---	---	---	1560960_at	---
1.94	2.12	0.19	1.78E-01	5.48E-01	---	---	---	1559288_at	---
3.28	3.47	0.19	1.78E-01	5.48E-01	---	---	---	228838_at	---
2.72	2.89	0.17	1.78E-01	5.48E-01	---	---	---	242659_at	---
2.02	2.19	0.17	1.78E-01	5.48E-01	GOT1L1	glutamic-oxaloacetic transaminase 1-like 1	chr8p12	1553878_at	NM_152413
2.18	2.32	0.14	1.78E-01	5.48E-01	---	---	---	243732_at	---
6.03	6.36	0.33	1.78E-01	5.48E-01	SOS1	son of sevenless homolog 1 (Drosophila)	chr2p22-p21	227426_at	NM_005633
4.27	4.57	0.30	1.78E-01	5.48E-01	CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	chr19p13.11	227721_at	NM_015692
4.12	4.38	0.26	1.78E-01	5.48E-01	PYY	peptide YY	chr17q21.1	211253_x_at	NM_004160
3.88	4.08	0.20	1.78E-01	5.48E-01	AHDC1	AT hook, DNA binding motif, containing 1	chr1p36.13	243793_at	NM_001029882
2.16	2.34	0.19	1.78E-01	5.48E-01	---	---	---	241043_at	---
2.19	2.38	0.19	1.78E-01	5.48E-01	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	chr4q11-q13	1554828_at	NM_006206
2.01	2.19	0.18	1.78E-01	5.48E-01	C11orf55	Chromosome 11 open reading frame 55	chr11p13	244557_at	NM_207428
2.11	2.26	0.15	1.78E-01	5.48E-01	GNRHR	gonadotropin-releasing hormone receptor	chr4q21.2	211523_at	NM_000406 /// NM_001012763
2.01	2.25	0.24	1.78E-01	5.48E-01	ZNF407	zinc finger protein 407	chr18q23	234844_at	NM_017757
5.09	6.08	0.99	1.78E-01	5.48E-01	NMD3	NMD3 homolog (S. cerevisiae)	chr3q26.1	218036_x_at	NM_015938
4.24	4.52	0.29	1.79E-01	5.48E-01	CCDC85A	coiled-coil domain containing 85A	chr2p16.1	233846_at	NM_001080433
2.51	2.71	0.20	1.79E-01	5.48E-01	---	---	---	239177_at	---
2.84	3.02	0.18	1.79E-01	5.48E-01	CASP9	caspase 9, apoptosis-related cysteine peptidase	chr1p36.3-p36.1	240437_at	NM_001229 /// NM_032996
2.62	2.86	0.24	1.79E-01	5.48E-01	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	chr1q22	218554_s_at	NM_018489
4.09	4.36	0.27	1.79E-01	5.48E-01	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	chr1q41	1554575_a_at	NM_006085
3.47	3.84	0.37	1.79E-01	5.48E-01	---	---	---	241489_at	---
2.19	2.37	0.18	1.79E-01	5.48E-01	TTK	TTK protein kinase	chr6q13-q21	204822_at	NM_003318
5.89	6.39	0.50	1.79E-01	5.48E-01	ECHDC1	enoyl Coenzyme A hydratase domain containing 1	chr6q22.33	233124_s_at	NM_001002030 /// NM_001105544 /// NM_001105545 /// NM_018479
5.82	6.16	0.34	1.79E-01	5.48E-01	FAF2	Fas associated factor family member 2	chr5q35.2	212106_at	NM_014613
3.43	3.67	0.24	1.79E-01	5.48E-01	CA13	carbonic anhydrase XIII	chr8q21.2	231270_at	NM_198584
2.30	2.75	0.45	1.79E-01	5.49E-01	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	chr1q32.1	209396_s_at	NM_001276
2.95	3.13	0.19	1.79E-01	5.49E-01	LOC147791	hypothetical protein LOC147791	chr19p13.3	240298_at	---
2.11	2.31	0.21	1.79E-01	5.49E-01	---	---	---	240805_at	---
3.99	4.60	0.61	1.79E-01	5.49E-01	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	chr2q32	210664_s_at	NM_001032281 /// NM_006287
4.09	4.37	0.28	1.79E-01	5.49E-01	---	---	---	216741_at	---

1.97	2.19	0.22	1.79E-01	5.49E-01	WDR89	WD repeat domain 89	chr14q23.2	235025_at	NM_001008726 /// NM_080666
2.05	2.22	0.17	1.79E-01	5.49E-01	PARP15	poly (ADP-ribose) polymerase family, member 15	chr3q21.1	1564310_a_at	NM_001113523 /// NM_152615
4.72	5.32	0.59	1.79E-01	5.49E-01	---	---	---	215385_at	---
3.48	3.86	0.38	1.79E-01	5.49E-01	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	chr3q23	203589_s_at	NM_006286
4.57	4.89	0.32	1.79E-01	5.49E-01	DNASE1	deoxyribonuclease I	chr16p13.3	228929_at	NM_005223
2.19	2.45	0.26	1.79E-01	5.49E-01	PTCHD1	patched domain containing 1	chrXp22.11	1552848_a_at	NM_173495
5.26	5.51	0.25	1.79E-01	5.49E-01	GRK6	G protein-coupled receptor kinase 6	chr5q35	202848_s_at	NM_001004105 /// NM_001004106 /// NM_002082
2.61	2.83	0.22	1.79E-01	5.49E-01	FAM159A	family with sequence similarity 159, member A	chr1p32.3	1555379_at	NM_001042693
2.61	2.82	0.20	1.79E-01	5.49E-01	C14orf167	chromosome 14 open reading frame 167	chr14q11.2-q21.3	224153_s_at	NR_023921 /// NR_023922 /// NR_023923 /// NR_023924
5.22	6.23	1.02	1.79E-01	5.49E-01	WAC	WW domain containing adaptor with coiled-coil	---	219679_s_at	NM_016628 /// NM_100264 /// NM_100486
1.98	2.14	0.16	1.79E-01	5.49E-01	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	chr6q24-q25.1	1570231_at	NM_004690
5.84	6.49	0.65	1.79E-01	5.49E-01	C7orf10	chromosome 7 open reading frame 10	chr7p14.1	219655_at	NM_024728
1.90	2.05	0.15	1.79E-01	5.49E-01	PDE11A	phosphodiesterase 11A	chr2q31.2	224224_s_at	NM_001077196 /// NM_001077197 /// NM_001077358 /// NM_016953
2.26	2.44	0.18	1.79E-01	5.49E-01	---	---	---	1569665_at	---
3.21	3.43	0.22	1.79E-01	5.49E-01	---	---	---	237487_at	---
2.08	2.27	0.19	1.79E-01	5.49E-01	C1orf114	chromosome 1 open reading frame 114	chr1q24	206721_at	NM_021179
8.04	8.79	0.75	1.79E-01	5.49E-01	CANX	calnexin	chr5q35	208852_s_at	NM_001024649 /// NM_001746
6.15	6.89	0.74	1.79E-01	5.49E-01	LPHN3	latrophilin 3	chr4q13.1	209867_s_at	NM_015236
5.38	6.04	0.67	1.79E-01	5.49E-01	---	---	---	216028_at	---
4.63	5.17	0.54	1.79E-01	5.49E-01	MAMDC2	MAM domain containing 2	chr9q21.11	228885_at	NM_153267
4.23	4.73	0.50	1.79E-01	5.49E-01	PIAS2	protein inhibitor of activated STAT, 2	chr18q21.1	1555514_a_at	NM_004671 /// NM_173206
8.63	9.11	0.48	1.79E-01	5.49E-01	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	chr3p22	208944_at	NM_001024847 /// NM_003242
3.47	3.79	0.32	1.79E-01	5.49E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	1563808_at	NM_001112732 /// NM_024979
6.88	7.14	0.27	1.79E-01	5.49E-01	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	chr17p13.3	218155_x_at	NM_018128
2.61	2.82	0.21	1.79E-01	5.49E-01	---	---	---	234490_at	---
2.06	2.24	0.18	1.79E-01	5.49E-01	ACTA2	Actin, alpha 2, smooth muscle, aorta	chr10q23.3	215787_at	NM_001613
2.64	2.84	0.20	1.79E-01	5.49E-01	UCP1	uncoupling protein 1 (mitochondrial, proton carrier)	chr4q28-q31	221384_at	NM_021833
1.96	2.16	0.19	1.79E-01	5.49E-01	---	---	---	238958_at	---
2.46	2.70	0.25	1.80E-01	5.50E-01	ATAD4	ATPase family, AAA domain containing 4	chr17q21.32	219127_at	NM_024320
3.56	3.87	0.30	1.80E-01	5.50E-01	---	---	---	240630_at	---
1.99	2.13	0.14	1.80E-01	5.50E-01	MBTPS2	membrane-bound transcription factor peptidase, site 2	chrXp22.13	1554604_at	NM_015884
3.08	3.37	0.29	1.80E-01	5.50E-01	WDR67	WD repeat domain 67	chr8q24.13	214061_at	NM_145647
2.33	2.48	0.15	1.80E-01	5.50E-01	---	---	---	243072_at	---
3.54	3.77	0.23	1.80E-01	5.50E-01	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	chr9q34	210099_at	NM_001606 /// NM_212533
3.10	3.44	0.35	1.80E-01	5.50E-01	---	---	---	237459_at	---
2.02	2.22	0.19	1.80E-01	5.50E-01	PCDHB10	protocadherin beta 10	chr5q31	223854_at	NM_018930
2.09	2.25	0.15	1.80E-01	5.50E-01	PDLIM3	PDZ and LIM domain 3	chr4q35	210170_at	NM_001114107 /// NM_014476
3.22	3.43	0.21	1.80E-01	5.50E-01	---	---	---	238950_at	---
1.89	2.04	0.15	1.80E-01	5.50E-01	---	---	---	241136_at	---
2.07	2.23	0.16	1.80E-01	5.50E-01	---	---	---	237999_at	---
3.28	3.51	0.23	1.80E-01	5.50E-01	C15orf62	chromosome 15 open reading frame 62	chr15q15.1	1569065_s_at	NM_001130448 /// XR_041736 /// XR_041737 /// XR_041738
2.73	3.00	0.27	1.80E-01	5.50E-01	---	---	---	1565696_at	---
4.06	4.30	0.24	1.80E-01	5.50E-01	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	chr19p13.12	212962_at	NM_033025
2.55	2.78	0.24	1.80E-01	5.50E-01	EPHB1	EPH receptor B1	chr3q21-q23	210753_s_at	NM_004441

5.99	6.74	0.76	1.80E-01	5.50E-01	GPR116	G protein-coupled receptor 116	chr6p12.3	212951_at	NM_001098518 /// NM_015234
2.40	2.58	0.18	1.80E-01	5.50E-01	LOC285593	hypothetical protein LOC285593	chr5q35.2	1562739_at	---
3.44	3.61	0.17	1.80E-01	5.50E-01	---	---	---	1555631_at	---
2.07	2.24	0.17	1.80E-01	5.50E-01	---	---	---	221228_s_at	---
3.56	3.92	0.36	1.80E-01	5.50E-01	ZCCHC6	Zinc finger, CCHC domain containing 6	chr9q21	236155_at	NM_024617
2.67	2.92	0.25	1.80E-01	5.50E-01	GRAMD1A	GRAM domain containing 1A	chr19q13.11	244808_at	NM_020895
2.51	2.76	0.25	1.80E-01	5.50E-01	CLSTN2	calsyntenin 2	chr3q23-q24	219414_at	NM_022131
1.92	2.08	0.16	1.80E-01	5.50E-01	RPE65	retinal pigment epithelium-specific protein 65kDa	chr1p31	207107_at	NM_000329
3.28	3.63	0.35	1.80E-01	5.50E-01	---	---	---	236229_at	---
3.72	3.91	0.19	1.80E-01	5.50E-01	ACTL6B	actin-like 6B	chr7q22	206014_at	NM_016188
2.31	2.49	0.18	1.80E-01	5.50E-01	---	---	---	232934_at	---
1.78	1.93	0.15	1.80E-01	5.50E-01	ATPBD4	ATP binding domain 4	chr15q14	1560404_a_at	NM_080650
2.21	2.50	0.29	1.80E-01	5.50E-01	---	---	---	1559450_at	---
2.04	2.18	0.14	1.80E-01	5.51E-01	LMO3	LIM domain only 3 (rhombotin-like 2)	chr12p12.3	231348_s_at	NM_001001395 /// NM_018640
7.60	8.44	0.84	1.80E-01	5.51E-01	ZBTB38	zinc finger and BTB domain containing 38	chr3q23	219221_at	NM_001080412
2.77	3.10	0.34	1.80E-01	5.51E-01	MKLN1	Muskelin 1, intracellular mediator containing kelch motifs	chr7q32	1560145_at	NM_013255
3.69	3.97	0.28	1.80E-01	5.51E-01	HNT	Neurotrimin	chr11q25	241934_at	NM_001048209 /// NM_016522
2.90	3.18	0.28	1.80E-01	5.51E-01	---	---	---	237190_at	---
2.53	2.78	0.25	1.80E-01	5.51E-01	CDKN3	cyclin-dependent kinase inhibitor 3	chr14q22	1555758_a_at	NM_001130851 /// NM_005192
2.11	2.36	0.25	1.80E-01	5.51E-01	LOC440934	Hypothetical gene supported by BC008048	chr2q36.1	244159_at	XR_015854 /// XR_016028 /// XR_041304
2.49	2.73	0.24	1.80E-01	5.51E-01	MYO10	myosin X	chr5p15.1-p14.3	236718_at	NM_012334
2.51	2.75	0.23	1.80E-01	5.51E-01	---	---	---	233658_at	---
3.82	4.05	0.22	1.80E-01	5.51E-01	SPTBN4	spectrin, beta, non-erythrocytic 4	chr19q13.13	224144_at	NM_020971 /// NM_025213
2.62	2.81	0.19	1.80E-01	5.51E-01	---	---	---	1556161_a_at	---
2.23	2.41	0.18	1.80E-01	5.51E-01	KCNIP3	Kv channel interacting protein 3, calsenilin	chr2q21.1	233688_at	NM_001034914 /// NM_013434
2.58	2.74	0.15	1.80E-01	5.51E-01	---	---	---	243532_at	---
2.09	2.23	0.15	1.80E-01	5.51E-01	---	---	---	234595_at	---
6.30	6.99	0.69	1.81E-01	5.51E-01	---	---	---	242403_at	---
8.56	8.85	0.29	1.81E-01	5.51E-01	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	211452_x_at	NM_004735
7.46	7.98	0.52	1.81E-01	5.51E-01	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	chr4q21-q24	202425_x_at	NM_000944 /// NM_001130691 /// NM_001130692
1.96	2.18	0.22	1.81E-01	5.51E-01	GSC2	goosecoid homeobox 2	chr22q11.21	221441_at	NM_005315
2.62	2.83	0.21	1.81E-01	5.51E-01	GUCA2B	guanylate cyclase activator 2B (uroguanylin)	chr1p34-p33	207502_at	NM_007102
2.64	2.84	0.20	1.81E-01	5.51E-01	HNRNPM	heterogeneous nuclear ribonucleoprotein M	chr19p13.3-p13.2	214918_at	NM_005968 /// NM_031203
2.46	2.64	0.18	1.81E-01	5.51E-01	---	---	---	242643_x_at	---
9.57	9.93	0.36	1.81E-01	5.51E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	211945_s_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376
3.57	3.77	0.20	1.81E-01	5.51E-01	LOC285535	hypothetical protein LOC285535	chr4p16.1	235386_at	---
3.48	3.72	0.23	1.81E-01	5.51E-01	OR2H2	olfactory receptor, family 2, subfamily H, member 2	chr6p21.3	217081_at	NM_007160
2.70	2.87	0.17	1.81E-01	5.51E-01	LOC91316	similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific)	chr22q11.23	215816_at	XR_038140 /// XR_040205 /// XR_040206
2.15	2.32	0.17	1.81E-01	5.51E-01	RBM25	RNA binding motif protein 25	chr14q24.3	236613_at	NM_021239
2.99	3.24	0.25	1.81E-01	5.51E-01	INA	internexin neuronal intermediate filament protein, alpha	chr10q24.33	204465_s_at	NM_032727
2.25	2.42	0.17	1.81E-01	5.51E-01	MAP3K3	Mitogen-activated protein kinase kinase kinase 3	chr17q23.3	243505_at	NM_002401 /// NM_203351
4.43	5.01	0.58	1.81E-01	5.51E-01	---	---	---	244633_at	---
6.61	6.83	0.22	1.81E-01	5.51E-01	---	---	---	233041_x_at	---
6.16	7.01	0.85	1.81E-01	5.51E-01	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	chr5q11.2	212896_at	NM_015360
4.17	4.68	0.51	1.81E-01	5.51E-01	RSL1D1	ribosomal L1 domain containing 1	chr16p13.13	212019_at	NM_015659
4.07	4.51	0.44	1.81E-01	5.51E-01	---	---	---	239476_at	---
3.28	3.56	0.29	1.81E-01	5.51E-01	CD84	CD84 molecule	chr1q24	211191_at	NM_003874

6.42	6.69	0.28	1.81E-01	5.51E-01	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	chr1p34-p33	209413_at	NM_001005417 /// NM_003780
2.10	2.30	0.20	1.81E-01	5.51E-01	---	---	---	1561389_at	---
2.53	2.72	0.19	1.81E-01	5.51E-01	PLXNA4	plexin A4	chr7q32.3	234859_at	NM_001105543 /// NM_020911 /// NM_181775
1.83	1.99	0.16	1.81E-01	5.51E-01	---	---	---	237528_at	---
3.45	3.74	0.29	1.81E-01	5.51E-01	KIAA1833	hypothetical protein KIAA1833	chr8q24.3	232498_at	NM_001099280 /// NM_001099281 /// NM_032450
4.00	4.30	0.30	1.81E-01	5.51E-01	---	---	---	237103_at	---
2.14	2.41	0.27	1.81E-01	5.51E-01	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	chr1q21-q23	203296_s_at	NM_000702
3.23	3.53	0.30	1.81E-01	5.51E-01	MED26	Mediator complex subunit 26	chr19p13.11	1559593_a_at	NM_004831
3.68	3.86	0.18	1.81E-01	5.51E-01	---	---	---	237835_at	---
7.69	8.03	0.34	1.81E-01	5.51E-01	GLG1	golgi apparatus protein 1	chr16q22-q23	207966_s_at	NM_012201
1.82	1.98	0.16	1.81E-01	5.51E-01	---	---	---	1566762_at	---
6.29	6.84	0.56	1.81E-01	5.51E-01	PCGF5	polycomb group ring finger 5	chr10q23.32	226326_at	NM_032373
2.48	2.64	0.17	1.81E-01	5.51E-01	LOC400960	Hypothetical gene supported by BC040598	chr2p14	240017_at	XM_934552 /// XM_945536
6.08	6.41	0.33	1.81E-01	5.51E-01	---	---	---	228006_at	---
3.24	3.47	0.23	1.81E-01	5.51E-01	ANKRD42	Ankyrin repeat domain 42	chr11q14.1	243151_at	NM_182603
2.21	2.38	0.18	1.81E-01	5.51E-01	PCGEM1	prostate-specific transcript 1 (non-protein coding)	chr2q32	234529_at	NR_002769
3.37	3.64	0.27	1.81E-01	5.51E-01	LRRC29	leucine rich repeat containing 29	chr16q22.1	232545_at	NM_001004055 /// NM_012163
3.37	3.60	0.23	1.81E-01	5.51E-01	RBM35B	RNA binding motif protein 35B	chr16q22.1	219395_at	NM_024939
1.99	2.18	0.19	1.81E-01	5.51E-01	SPAG6	sperm associated antigen 6	chr10p12.2	210033_s_at	NM_012443 /// NM_172242
2.18	3.28	1.10	1.81E-01	5.52E-01	MAB21L2	mab-21-like 2 (C. elegans)	chr4q31	210302_s_at	NM_006439
3.57	3.80	0.23	1.81E-01	5.52E-01	---	---	---	233453_at	---
2.41	2.63	0.21	1.81E-01	5.52E-01	LOC100131825	Hypothetical protein LOC100131825	chr1q23.2	217442_at	XM_001722692 /// XM_001725593 /// XM_001725598
2.13	2.27	0.14	1.81E-01	5.52E-01	ODF4	outer dense fiber of sperm tails 4	chr17p13.1	1552408_at	NM_153007
6.52	6.93	0.41	1.82E-01	5.52E-01	ARMC1	armadillo repeat containing 1	chr8q13.1	222550_at	NM_018120
3.86	4.09	0.22	1.82E-01	5.52E-01	VANGL1	vang-like 1 (van gogh, Drosophila)	chr1p11-p13.1	229134_at	NM_138959
4.24	5.26	1.03	1.82E-01	5.52E-01	IGK@ /// IGKC /// IGKV3-20 /// IGKV3D-11 /// IGKV3D-15	immunoglobulin kappa locus /// immunoglobulin kappa constant /// immunoglobulin kappa variable 3-20 /// immunoglobulin kappa variable 3D-11 /// immunoglobulin kappa variable 3D-15	chr2p12	211644_x_at	---
8.22	8.61	0.40	1.82E-01	5.52E-01	POR	P450 (cytochrome) oxidoreductase	chr7q11.2	208928_at	NM_000941
3.69	4.07	0.37	1.82E-01	5.52E-01	ACVR2B	activin A receptor, type IIB	chr3p22	220028_at	NM_001106
3.88	4.23	0.34	1.82E-01	5.52E-01	TTYH2	tweety homolog 2 (Drosophila)	chr17q25.1	232042_at	NM_032646 /// NM_052869
5.88	6.21	0.33	1.82E-01	5.52E-01	CSNK2A2	casein kinase 2, alpha prime polypeptide	chr16q21	224922_at	NM_001896
2.21	2.51	0.30	1.82E-01	5.52E-01	TAPT1	transmembrane anterior posterior transformation 1	chr4p15.32	216373_at	NM_153365
2.54	2.83	0.30	1.82E-01	5.52E-01	---	---	---	211146_at	---
4.16	4.43	0.28	1.82E-01	5.52E-01	SPATA3	spermatogenesis associated 3	chr2q37.1	240340_at	XR_015911 /// XR_017695 /// XR_040698
2.10	2.36	0.27	1.82E-01	5.52E-01	THSD7B	thrombospondin, type I, domain containing 7B	chr2q21-q22	232327_at	NM_001080427
3.47	3.71	0.24	1.82E-01	5.52E-01	BMP6	bone morphogenetic protein 6	chr6p24-p23	206176_at	NM_001718
5.24	5.47	0.23	1.82E-01	5.52E-01	---	---	---	244875_at	---
2.14	2.37	0.23	1.82E-01	5.52E-01	LOC728196	hypothetical protein LOC728196	chr11q23.1	1568906_at	XR_040780 /// XR_040781
2.34	2.56	0.23	1.82E-01	5.52E-01	---	---	---	238307_at	---
2.11	2.33	0.23	1.82E-01	5.52E-01	SLC13A4	solute carrier family 13 (sodium/sulfate symporters), member 4	chr7q33	1558578_a_at	NM_012450
7.40	7.63	0.23	1.82E-01	5.52E-01	---	---	---	214316_x_at	---
2.04	2.26	0.22	1.82E-01	5.52E-01	GABRA6	gamma-aminobutyric acid (GABA) A receptor, alpha 6	chr5q34	207182_at	NM_000811
2.59	2.79	0.20	1.82E-01	5.52E-01	---	---	---	237125_at	---
2.37	2.57	0.20	1.82E-01	5.52E-01	RBBP9	retinoblastoma binding protein 9	chr20p11.2	221439_at	NM_006606
3.07	3.27	0.20	1.82E-01	5.52E-01	MYOZ1	myozenin 1	chr10q22.1	219509_at	NM_021245
2.62	2.82	0.20	1.82E-01	5.52E-01	---	---	---	1559540_at	---
4.22	4.41	0.19	1.82E-01	5.52E-01	---	---	---	236708_at	---
2.04	2.22	0.18	1.82E-01	5.52E-01	RFTN2	raftlin family member 2	chr2q33.1	241698_at	NM_144629
1.96	2.13	0.18	1.82E-01	5.52E-01	MPZL3	myelin protein zero-like 3	chr11q23.3	1570585_at	NM_198275
2.14	2.32	0.18	1.82E-01	5.52E-01	MMP20	matrix metallopeptidase 20	chr11q22.3	207599_at	NM_004771
5.50	5.67	0.17	1.82E-01	5.52E-01	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	chr12p13	243400_x_at	NM_002342

2.24	2.43	0.20	1.82E-01	5.52E-01	FAM98A	family with sequence similarity 98, member A	chr2p22.3	241832_at	NM_015475
5.46	5.96	0.50	1.82E-01	5.52E-01	MRPS10	mitochondrial ribosomal protein S10	chr6p21.1	224247_s_at	NM_018141
2.78	3.03	0.26	1.82E-01	5.52E-01	DIRC2	disrupted in renal carcinoma 2	chr3q21.1	229213_at	NM_032839
3.19	3.45	0.25	1.82E-01	5.52E-01	ASCC3	activating signal cointegrator 1 complex subunit 3	chr6q16.1-q16.3	231269_at	NM_006828 /// NM_022091
2.08	2.25	0.17	1.82E-01	5.52E-01	POU4F2	POU class 4 homeobox 2	chr4q31.2	207725_at	NM_004575
2.21	2.36	0.15	1.82E-01	5.52E-01	PBOV1	prostate and breast cancer overexpressed 1	chr6q23-q24	208329_at	NM_021635
2.87	3.13	0.26	1.82E-01	5.52E-01	---	---	---	206863_x_at	---
2.16	2.42	0.26	1.82E-01	5.52E-01	HAL	histidine ammonia-lyase	chr12q22-q24.1	206643_at	NM_002108
2.07	2.31	0.24	1.82E-01	5.52E-01	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	chr20q11.22-q11.23	235057_at	NM_031483
2.96	3.18	0.22	1.82E-01	5.52E-01	IGHA1 /// LOC100131845	immunoglobulin heavy constant alpha 1 /// similar to hCG1742309	chr14q32.33	234792_x_at	XM_001720439
1.92	2.08	0.16	1.82E-01	5.52E-01	ASB17	ankyrin repeat and SOCS box-containing 17	chr1p31.1	231622_at	NM_080868
1.98	2.12	0.15	1.82E-01	5.52E-01	MYT1L	myelin transcription factor 1-like	chr2p25.3	241485_at	NM_015025
3.84	4.52	0.68	1.82E-01	5.52E-01	FST	follistatin	chr5q11.2	204948_s_at	NM_006350 /// NM_013409
2.90	3.10	0.20	1.82E-01	5.52E-01	FLJ90680	FLJ90680 protein	chr22q12.3	244237_at	XR_041668 /// XR_041669 /// XR_041670
5.61	5.81	0.20	1.82E-01	5.52E-01	HRH3	histamine receptor H3	chr20q13.33	221663_x_at	NM_007232
2.90	3.08	0.17	1.82E-01	5.52E-01	---	---	---	240909_at	---
6.64	7.13	0.49	1.82E-01	5.52E-01	---	---	---	224778_s_at	---
2.81	3.03	0.22	1.82E-01	5.52E-01	LOC100130429	hypothetical LOC100130429	chr2p21	241851_x_at	XM_001724412 /// XM_001725414 /// XM_001726917
1.88	2.04	0.17	1.82E-01	5.52E-01	AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	chr7q32-q33	207102_at	NM_005989
3.27	3.52	0.24	1.82E-01	5.53E-01	AHNAK2	AHNAK nucleoprotein 2	chr14q32.33	1558378_a_at	NM_138420
3.59	3.79	0.19	1.82E-01	5.53E-01	---	---	---	242337_at	---
2.22	2.38	0.16	1.83E-01	5.53E-01	---	---	---	234357_at	---
3.70	3.98	0.27	1.83E-01	5.53E-01	UPK3B	uroplakin 3B	chr7q11.2	206658_at	NM_001130866 /// NM_030570 /// NM_182684
2.02	2.18	0.16	1.83E-01	5.53E-01	AICDA	activation-induced cytidine deaminase	chr12p13	224499_s_at	NM_020661
3.67	4.06	0.39	1.83E-01	5.53E-01	CDC27	cell division cycle 27 homolog (S. cerevisiae)	chr17q12-q23.2	217878_s_at	NM_001114091 /// NM_001256
3.88	4.17	0.28	1.83E-01	5.53E-01	ZNF30	zinc finger protein 30	chr19q13.11	232014_at	NM_001099437 /// NM_001099438 /// NM_194325 /// NR_024018
3.14	3.38	0.24	1.83E-01	5.53E-01	---	---	---	229972_at	---
3.14	3.35	0.22	1.83E-01	5.53E-01	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)	chr17q25.3	215989_at	NM_005189 /// NM_032647
2.53	2.71	0.17	1.83E-01	5.53E-01	---	---	---	221184_at	---
2.24	2.41	0.18	1.83E-01	5.53E-01	IQCH	IQ motif containing H	chr15q23	239813_at	NM_001031715 /// NM_022784
5.23	5.71	0.48	1.83E-01	5.53E-01	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	chr5p13.2	238337_s_at	NM_001012339 /// NM_194283
1.96	2.12	0.15	1.83E-01	5.53E-01	---	---	---	1568711_a_at	---
2.70	2.94	0.24	1.83E-01	5.53E-01	---	---	---	235373_at	---
2.41	2.60	0.19	1.83E-01	5.53E-01	ADAM7	ADAM metallopeptidase domain 7	chr8p21.2	211238_at	NM_003817
3.70	4.13	0.42	1.83E-01	5.53E-01	SAMD9L	sterile alpha motif domain containing 9-like	chr7q21.2-q21.3	226603_at	NM_152703
2.90	3.14	0.24	1.83E-01	5.53E-01	CCNG2	cyclin G2	chr4q21.1	1555056_at	NM_004354
2.37	2.60	0.23	1.83E-01	5.53E-01	ISL2	ISL LIM homeobox 2	chr15q23	232352_at	NM_145805
2.55	2.82	0.27	1.83E-01	5.53E-01	---	---	---	233448_s_at	---
2.39	2.66	0.28	1.83E-01	5.54E-01	IL20	interleukin 20	chr1q32	224071_at	NM_018724
5.07	5.51	0.44	1.83E-01	5.54E-01	AIFM2	apoptosis-inducing factor, mitochondrion-associated, 2	chr10q22.1	224461_s_at	NM_032797
1.97	2.15	0.18	1.83E-01	5.54E-01	---	---	---	239138_at	---
2.77	2.96	0.19	1.83E-01	5.54E-01	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D	chr7q22.1	238722_x_at	NM_001122838 /// NM_198990
2.72	2.95	0.23	1.83E-01	5.54E-01	---	---	---	237427_at	---
2.53	2.76	0.24	1.83E-01	5.54E-01	FASLG	Fas ligand (TNF superfamily, member 6)	chr1q23	210865_at	NM_000639
2.31	2.56	0.25	1.83E-01	5.54E-01	GRAMD1C	GRAM domain containing 1C	chr3q13.31	219313_at	NM_017577
2.21	2.41	0.20	1.83E-01	5.54E-01	FBXO3	F-box protein 3	chr11p13	232815_at	NM_012175 /// NM_033406
1.98	2.17	0.19	1.83E-01	5.54E-01	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	chr18p11.22	239750_x_at	NM_003574 /// NM_194434
6.11	6.41	0.30	1.84E-01	5.54E-01	ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	chr12q24.12	219986_s_at	NM_025247

7.74	8.29	0.55	1.84E-01	5.54E-01	CD59	CD59 molecule, complement regulatory protein	chr11p13	200984_s_at	NM_000611 /// NM_001127223 /// NM_001127225 /// NM_001127226 /// NM_001127227 /// NM_203329 /// NM_203330 /// NM_203331
6.34	6.77	0.42	1.84E-01	5.54E-01	CHURC1	churchill domain containing 1	chr14q23.3	223210_at	NM_145165
2.49	2.91	0.42	1.84E-01	5.54E-01	CAPS2	calcyphosine 2	chr12q21.1	224370_s_at	NM_032606
2.51	2.72	0.22	1.84E-01	5.54E-01	---	---	---	1570089_at	---
10.37	10.96	0.58	1.84E-01	5.54E-01	LDHB	lactate dehydrogenase B	chr12p12.2-p12.1	201030_x_at	NM_002300
3.32	3.65	0.33	1.84E-01	5.54E-01	---	---	---	239845_at	---
2.14	2.36	0.22	1.84E-01	5.54E-01	---	---	---	237983_at	---
5.62	6.17	0.55	1.84E-01	5.54E-01	MAP3K7	mitogen-activated protein kinase kinase kinase 7	chr6q16.1-q16.3	211536_x_at	NM_003188 /// NM_145331 /// NM_145332 /// NM_145333
4.65	4.86	0.21	1.84E-01	5.54E-01	SLC19A1	solute carrier family 19 (folate transporter), member 1	chr21q22.3	209775_x_at	NM_194255
4.94	5.33	0.39	1.84E-01	5.54E-01	LOC729446	hypothetical LOC729446	---	238043_at	XM_001133842
2.06	2.20	0.14	1.84E-01	5.54E-01	---	---	---	244480_at	---
4.70	5.38	0.68	1.84E-01	5.54E-01	THUMPD3	THUMP domain containing 3	chr3p25.3	225730_s_at	NM_001114092 /// NM_015453
3.19	3.41	0.22	1.84E-01	5.54E-01	MED13L	mediator complex subunit 13-like	chr12q24.21	242911_at	NM_015335
6.54	7.21	0.67	1.84E-01	5.55E-01	PSMC6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	chr14q22.1	201699_at	NM_002806
5.30	5.55	0.25	1.84E-01	5.55E-01	EMID2	EMI domain containing 2	chr7q22.1	233894_x_at	NM_133457
7.53	8.29	0.76	1.84E-01	5.55E-01	FXR1	fragile X mental retardation, autosomal homolog 1	chr3q28	201637_s_at	NM_001013438 /// NM_001013439 /// NM_005087
2.79	3.00	0.21	1.84E-01	5.55E-01	RPA4	replication protein A4, 34kDa	chrXq21.33	221143_at	NM_013347
5.44	6.18	0.74	1.84E-01	5.55E-01	NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	chr6q22.2	225070_at	NM_138459
4.42	5.10	0.68	1.84E-01	5.55E-01	ACBD3	acyl-Coenzyme A binding domain containing 3	chr1q42.12	202323_s_at	NM_022735
5.57	6.23	0.67	1.84E-01	5.55E-01	---	---	---	214807_at	---
6.24	6.77	0.52	1.84E-01	5.55E-01	MXRA8	matrix-remodelling associated 8	chr1p36.33	213422_s_at	NM_032348
9.70	10.21	0.51	1.84E-01	5.55E-01	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	chr1p13.2	211755_s_at	NM_001688
5.05	5.42	0.36	1.84E-01	5.55E-01	RCN3	reticulocalbin 3, EF-hand calcium binding domain	chr19q13.33	61734_at	NM_020650
3.37	3.66	0.28	1.84E-01	5.55E-01	---	---	---	216568_x_at	---
2.46	2.65	0.20	1.84E-01	5.55E-01	DICER1	dicer 1, ribonuclease type III	chr14q32.13	216281_at	NM_030621 /// NM_177438
2.10	2.28	0.18	1.84E-01	5.55E-01	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	chr10q23.31	206029_at	NM_014391
2.44	2.72	0.28	1.84E-01	5.55E-01	LOC100132678	similar to hCG1993567	chr9p11.2	236453_at	XM_001719500
2.38	2.56	0.18	1.84E-01	5.55E-01	---	---	---	1556465_at	---
7.05	7.26	0.21	1.84E-01	5.55E-01	GPR107	G protein-coupled receptor 107	chr9q34.11	211979_at	NM_020960
4.13	4.42	0.29	1.84E-01	5.55E-01	CRMP1	collapsin response mediator protein 1	chr4p16.1-p15	202517_at	NM_001014809 /// NM_001313
7.45	8.10	0.65	1.84E-01	5.55E-01	LRPPRC	leucine-rich PPR-motif containing	chr2p21	211971_s_at	NM_133259
7.91	8.44	0.53	1.84E-01	5.55E-01	SAR1A	SAR1 gene homolog A (S. cerevisiae)	chr10q22.1	201542_at	NM_020150
5.27	5.60	0.34	1.84E-01	5.55E-01	---	---	---	230599_at	---
6.14	6.41	0.26	1.84E-01	5.55E-01	AKAP8L	A kinase (PRKA) anchor protein 8-like	chr19p13.12	215741_x_at	NM_014371
2.60	2.86	0.25	1.84E-01	5.55E-01	TNS3	Tensin 3	chr7p12.3	234257_at	NM_022748
3.43	3.66	0.22	1.84E-01	5.55E-01	CASKIN1	CASK interacting protein 1	chr16p13.3	1569737_a_at	NM_020764
3.45	3.63	0.19	1.84E-01	5.55E-01	PHF7	PHD finger protein 7	chr3p21.1	215622_x_at	NM_016483 /// NM_173341
2.43	2.62	0.19	1.84E-01	5.55E-01	---	---	---	239701_at	---
2.50	2.67	0.17	1.84E-01	5.55E-01	LOC100131017	Similar to zinc finger protein 316	chr7p22.1	235910_x_at	XM_001721918 /// XM_001721974
2.11	2.26	0.15	1.84E-01	5.55E-01	---	---	---	1556760_a_at	---
2.48	2.70	0.22	1.84E-01	5.55E-01	HR44	Hr44 antigen	---	216879_at	---
2.08	2.23	0.16	1.85E-01	5.55E-01	---	---	---	242721_at	---
3.23	3.45	0.22	1.85E-01	5.55E-01	LOC400620	hypothetical LOC400620	chr17q25.1	1557731_at	---
5.96	6.44	0.47	1.85E-01	5.55E-01	LOC100132235 /// PNRC2	hypothetical protein LOC100132235 /// proline-rich nuclear receptor coactivator 2	chr1p36.11	222406_s_at	NM_017761 /// XM_001713881
1.84	2.00	0.16	1.85E-01	5.55E-01	SLC17A1	Solute carrier family 17 (sodium phosphate), member 1	chr6p23-p21.3	1560885_x_at	NM_005074

3.69	3.99	0.31	1.85E-01	5.55E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	211181_x_at	NM_001001890 /// NM_001122607 /// NM_001754
4.63	4.85	0.22	1.85E-01	5.55E-01	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	chr2p24.1	211377_x_at	NM_005378
2.04	2.20	0.15	1.85E-01	5.55E-01	ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	chr1q32	205994_at	NM_001973 /// NM_021795
9.85	10.42	0.57	1.85E-01	5.55E-01	GDI2	GDP dissociation inhibitor 2	chr10p15	200009_at	NM_001115156 /// NM_001494
1.78	1.94	0.16	1.85E-01	5.55E-01	---	---	---	1568867_x_at	---
4.46	5.28	0.83	1.85E-01	5.55E-01	---	---	---	230135_at	---
3.39	3.57	0.18	1.85E-01	5.55E-01	---	---	---	230790_x_at	---
3.56	3.82	0.27	1.85E-01	5.55E-01	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	chrXq13	204572_s_at	NM_006223
2.63	2.91	0.28	1.85E-01	5.55E-01	ADCY5	adenylate cyclase 5	chr3q13.2-q21	228182_at	NM_183357
2.47	2.66	0.19	1.85E-01	5.56E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	239636_at	NM_001112732 /// NM_024979
2.34	2.51	0.17	1.85E-01	5.56E-01	BHMT	Betaine-homocysteine methyltransferase	chr5q13.1-q15	231591_at	NM_001713
3.84	4.03	0.20	1.85E-01	5.56E-01	FYN	FYN oncogene related to SRC, FGR, YES	chr6q21	1559101_at	NM_002037 /// NM_153047 /// NM_153048
7.20	8.08	0.88	1.85E-01	5.56E-01	IDI1	isopentenyl-diphosphate delta isomerase 1	chr10p15.3	204615_x_at	NM_004508
3.35	3.51	0.17	1.85E-01	5.56E-01	SLC5A11	solute carrier family 5 (sodium/glucose cotransporter), member 11	chr16pter-p11	237254_at	NM_052944
8.37	8.58	0.21	1.85E-01	5.56E-01	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	chr1q21.1	214257_s_at	NM_004892
7.33	7.77	0.44	1.85E-01	5.56E-01	CADM1	cell adhesion molecule 1	chr11q23.2	209031_at	NM_001098517 /// NM_014333
2.65	2.93	0.28	1.85E-01	5.56E-01	---	---	---	216067_at	---
4.65	5.00	0.35	1.85E-01	5.56E-01	---	---	---	237377_at	---
2.61	2.90	0.29	1.85E-01	5.56E-01	SORD	sorbitol dehydrogenase	chr15q15.3	230782_at	NM_003104
4.15	4.50	0.35	1.85E-01	5.56E-01	TRPM4	transient receptor potential cation channel, subfamily M, member 4	chr19q13.33	219360_s_at	NM_017636
3.80	4.11	0.31	1.85E-01	5.56E-01	---	---	---	233004_x_at	---
1.89	2.07	0.18	1.85E-01	5.56E-01	ZBTB1	Zinc finger and BTB domain containing 1	chr14q23.3	1557036_at	NM_001123329 /// NM_014950
3.69	3.95	0.26	1.85E-01	5.56E-01	---	---	---	241067_at	---
3.32	3.66	0.34	1.85E-01	5.56E-01	FAR2	fatty acyl CoA reductase 2	chr12p11.22	220615_s_at	NM_018099
1.86	2.09	0.23	1.85E-01	5.56E-01	---	---	---	234548_at	---
7.28	8.06	0.78	1.85E-01	5.56E-01	CSE1L	CSE1 chromosome segregation 1-like (yeast)	chr20q13	201112_s_at	NM_001316
3.31	3.81	0.50	1.85E-01	5.56E-01	HNMT	histamine N-methyltransferase	chr2q22.1	228772_at	NM_001024074 /// NM_001024075 /// NM_006895
3.46	3.68	0.22	1.85E-01	5.56E-01	TEX13A	testis expressed 13A	chrXq22.3	236848_s_at	NM_031274
9.76	9.95	0.19	1.85E-01	5.56E-01	TPM3	tropomyosin 3	chr1q21.2	222976_s_at	NM_001043351 /// NM_001043352 /// NM_001043353 /// NM_152263 /// NM_153649
6.25	6.71	0.47	1.85E-01	5.56E-01	AP3B1	adaptor-related protein complex 3, beta 1 subunit	chr5q14.1	203142_s_at	NM_003664
2.93	3.18	0.25	1.86E-01	5.57E-01	PYDC1	PYD (pyrin domain) containing 1	chr16p11.2	243722_at	NM_152901
2.05	2.22	0.18	1.86E-01	5.57E-01	---	---	---	239887_at	---
3.27	3.58	0.30	1.86E-01	5.57E-01	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	chr3q29	1559490_at	NM_032773
4.46	4.75	0.29	1.86E-01	5.57E-01	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	chr15q23	218161_s_at	NM_017882
2.41	2.58	0.18	1.86E-01	5.57E-01	UPB1	ureidopropionase, beta	chr22q11.2	224043_s_at	NM_016327
2.22	2.39	0.17	1.86E-01	5.57E-01	CEP63	centrosomal protein 63kDa	chr3q22.1-q22.2	233650_at	NM_001042383 /// NM_001042384 /// NM_001042400 /// NM_025180
2.18	2.39	0.21	1.86E-01	5.57E-01	---	---	---	1561489_at	---
8.64	9.30	0.66	1.86E-01	5.57E-01	TUG1	taurine upregulated gene 1	chr22q12.2	222244_s_at	NR_002323
4.90	5.09	0.19	1.86E-01	5.57E-01	C20orf201	chromosome 20 open reading frame 201	chr20q13.33	1554977_at	NM_001007125
2.18	2.36	0.18	1.86E-01	5.57E-01	---	---	---	1558672_at	---
3.51	3.78	0.27	1.86E-01	5.57E-01	---	---	---	1561273_at	---

2.21	2.38	0.17	1.86E-01	5.57E-01	PKN2	protein kinase N2	chr1p22.2	230400_s_at	NM_006256
2.39	3.31	0.93	1.86E-01	5.57E-01	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	chr17q24.2	230748_at	NM_004694
2.51	2.68	0.16	1.86E-01	5.57E-01	CEP68	Centrosomal protein 68kDa	chr2p14	239570_at	NM_015147
2.92	3.17	0.25	1.86E-01	5.57E-01	CCDC153	coiled-coil domain containing 153	chr11q23.3	240293_at	NM_001033658
2.45	2.68	0.22	1.86E-01	5.57E-01	GPR63	G protein-coupled receptor 63	chr6q16.1-q16.3	220993_s_at	NM_030784
4.73	5.70	0.96	1.86E-01	5.57E-01	HP /// HPR	haptoglobin /// haptoglobin-related protein	chr16q22.1	206697_s_at	NM_001126102 /// NM_005143 /// NM_020995
3.92	4.14	0.23	1.86E-01	5.57E-01	CHDH	choline dehydrogenase	chr3p21.1	1559591_s_at	NM_018397
6.35	6.83	0.48	1.86E-01	5.57E-01	IFIT5	interferon-induced protein with tetratricopeptide repeats 5	chr10q23.31	203595_s_at	NM_012420
8.84	9.18	0.34	1.86E-01	5.57E-01	41524	septin 7	chr7p14.3-p14.1	213151_s_at	NM_001011553 /// NM_001788
5.79	6.12	0.32	1.86E-01	5.57E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	219028_at	NM_001113239 /// NM_022740
3.31	3.51	0.20	1.86E-01	5.57E-01	KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	chr17p13.1	221413_at	NM_004732
2.51	2.68	0.17	1.86E-01	5.57E-01	PBX4	pre-B-cell leukemia homeobox 4	chr19p12	230536_at	NM_025245
2.00	2.17	0.17	1.86E-01	5.57E-01	---	---	---	1556388_a_at	---
6.05	6.39	0.34	1.86E-01	5.57E-01	TFRC	Transferrin receptor (p90, CD71)	chr3q29	240686_x_at	NM_001128148 /// NM_003234
3.36	3.58	0.22	1.86E-01	5.57E-01	BCL7A	B-cell CLL/lymphoma 7A	chr12q24.13	203796_s_at	NM_001024808 /// NM_020993
2.04	2.19	0.15	1.86E-01	5.57E-01	HMGA2	high mobility group AT-hook 2	chr12q15	1558682_at	NM_003483 /// NM_003484
9.68	10.13	0.45	1.86E-01	5.57E-01	CREBL2	cAMP responsive element binding protein-like 2	chr12p13	201989_s_at	NM_001310
2.22	2.44	0.22	1.86E-01	5.57E-01	FLJ32810	hypothetical protein FLJ32810	chr11q22.1	230047_at	XM_001127597 /// XM_001725431 /// XM_001726122
2.19	2.40	0.21	1.86E-01	5.57E-01	LRRC59	leucine rich repeat containing 59	chr17q21.33	1569371_at	NM_018509
3.26	3.53	0.27	1.86E-01	5.57E-01	FOXA2	forkhead box A2	chr20p11	214312_at	NM_021784 /// NM_153675
3.68	3.92	0.25	1.86E-01	5.57E-01	DNASE1L2	deoxyribonuclease I-like 2	chr16p13.3	207192_at	NM_001374
5.87	6.07	0.20	1.86E-01	5.57E-01	HIP1R	huntingtin interacting protein 1 related	chr12q24	209559_at	NM_003959
3.42	3.65	0.23	1.86E-01	5.57E-01	---	---	---	1563089_at	---
2.92	3.20	0.28	1.87E-01	5.58E-01	MAPK11	mitogen-activated protein kinase 11	chr22q13.33	211499_s_at	NM_002751
3.77	3.99	0.22	1.87E-01	5.58E-01	---	---	---	215869_at	---
2.77	2.99	0.23	1.87E-01	5.58E-01	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	chr6p21.2-p12	206214_at	NM_005084
5.70	6.23	0.53	1.87E-01	5.58E-01	RAB11FIP2	RAB11 family interacting protein 2 (class I)	chr10q26.11	203883_s_at	NM_014904
2.63	2.84	0.21	1.87E-01	5.58E-01	---	---	---	237153_at	---
3.03	3.43	0.40	1.87E-01	5.58E-01	SPA17	sperm autoantigenic protein 17	chr11q24.2	205406_s_at	NM_017425
6.41	6.79	0.38	1.87E-01	5.58E-01	CCDC59	coiled-coil domain containing 59	chr12q21.31	222792_s_at	NM_014167
4.76	5.56	0.80	1.87E-01	5.58E-01	KRIT1	KRIT1, ankyrin repeat containing	chr7q21-q22	34031_i_at	NM_001013406 /// NM_004912 /// NM_194454 /// NM_194455 /// NM_194456
3.48	3.78	0.30	1.87E-01	5.58E-01	PLCXD1	phosphatidylinositol-specific phospholipase C, X domain containing 1	chrXp22.33; Yp11.32	222795_s_at	NM_018390
2.42	2.58	0.16	1.87E-01	5.58E-01	---	---	---	233185_at	---
5.93	6.80	0.88	1.87E-01	5.58E-01	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	chr2q23.3	233080_s_at	NM_017892
3.21	3.70	0.49	1.87E-01	5.58E-01	PLXNC1	plexin C1	chr12q23.3	206470_at	NM_005761
5.41	5.80	0.38	1.87E-01	5.58E-01	DENND5B	DENN/MADD domain containing 5B	chr12p11.21	228551_at	NM_144973
4.74	4.94	0.21	1.87E-01	5.58E-01	KIAA0586	KIAA0586	chr14q23.1	37232_at	NM_014749
2.52	2.73	0.20	1.87E-01	5.58E-01	---	---	---	239109_at	---
2.51	2.79	0.28	1.87E-01	5.58E-01	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	chr9p21	228260_at	NM_004432
2.11	2.36	0.24	1.87E-01	5.58E-01	---	---	---	216723_at	---
2.98	3.40	0.42	1.87E-01	5.58E-01	---	---	---	229004_at	---
3.05	3.45	0.40	1.87E-01	5.58E-01	---	---	---	1562684_at	---
2.78	2.98	0.20	1.87E-01	5.58E-01	ATP13A5	ATPase type 13A5	chr3q29	1561332_at	NM_198505
2.80	2.99	0.18	1.87E-01	5.58E-01	FLJ20712	hypothetical protein FLJ20712	chr7p14.3	220678_at	XR_041417 /// XR_041418 /// XR_041419 /// XR_041420

4.11	4.42	0.32	1.87E-01	5.58E-01	GGT1	gamma-glutamyltransferase 1	chr22q11.23	207131_x_at	NM_001032364 /// NM_001032365 /// NM_005265 /// NM_013430
2.66	2.90	0.24	1.87E-01	5.58E-01	PKNOX2	PBX/knotted 1 homeobox 2	---	222171_s_at	NM_022062
6.57	7.21	0.64	1.87E-01	5.58E-01	SPPL2A	signal peptide peptidase-like 2A	chr15q21.2	226353_at	NM_032802
4.69	5.27	0.57	1.87E-01	5.58E-01	ANKRD28	ankyrin repeat domain 28	chr3p24.3	229307_at	NM_015199
2.25	2.39	0.14	1.87E-01	5.58E-01	---	---	---	1562067_at	---
1.94	2.17	0.23	1.87E-01	5.58E-01	HAPLN1	Hyaluronan and proteoglycan link protein 1	chr5q14.3	230895_at	NM_001884
3.69	3.99	0.30	1.87E-01	5.58E-01	FLJ37453	hypothetical protein LOC729614	chr1p36.21	227664_at	XR_042511 /// XR_042512 /// XR_042513
2.89	3.16	0.27	1.87E-01	5.59E-01	---	---	---	238963_at	---
1.81	1.98	0.17	1.87E-01	5.59E-01	---	---	---	237374_at	---
4.97	5.54	0.58	1.87E-01	5.59E-01	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	chr2q24.2	222757_s_at	NM_016653 /// NM_133646
2.40	2.59	0.19	1.87E-01	5.59E-01	---	---	---	1565861_at	---
2.78	3.71	0.94	1.87E-01	5.59E-01	SAMD12	Sterile alpha motif domain containing 12	chr8q24.12	238673_at	NM_001101676 /// NM_207506
2.96	3.17	0.20	1.87E-01	5.59E-01	DHFR	dihydrofolate reductase	chr5q11.2-q13.2	202532_s_at	NM_000791
2.80	3.05	0.25	1.87E-01	5.59E-01	PTPN5	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	chr11p15.1	236456_at	NM_001039970 /// NM_006906 /// NM_032781
3.71	3.91	0.20	1.87E-01	5.59E-01	---	---	---	216394_x_at	---
2.28	2.45	0.18	1.87E-01	5.59E-01	---	---	---	1566869_at	---
2.99	3.19	0.20	1.88E-01	5.59E-01	NPPB	natriuretic peptide precursor B	chr1p36.2	206801_at	NM_002521
2.19	2.40	0.20	1.88E-01	5.59E-01	C6orf201	chromosome 6 open reading frame 201	chr6p25.2	231642_at	NM_001085401
2.32	2.67	0.35	1.88E-01	5.59E-01	TDRD9	tudor domain containing 9	chr14q32.33	228285_at	NM_153046
3.06	3.30	0.24	1.88E-01	5.59E-01	FLJ33046	hypothetical gene supported by AK057608	chr12p13.32	1560874_at	---
4.79	5.02	0.23	1.88E-01	5.59E-01	CCT4	Chaperonin containing TCP1, subunit 4 (delta)	chr2p15	227171_at	NM_006430
1.96	2.17	0.22	1.88E-01	5.59E-01	---	---	---	242375_x_at	---
2.24	2.44	0.20	1.88E-01	5.59E-01	---	---	---	236815_at	---
2.76	2.94	0.19	1.88E-01	5.59E-01	PLAUR	plasminogen activator, urokinase receptor	chr19q13	214866_at	NM_001005376 /// NM_001005377 /// NM_002659
2.88	3.14	0.26	1.88E-01	5.59E-01	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	chr9q31.1	208958_at	NM_015051
7.26	7.79	0.53	1.88E-01	5.59E-01	FBXL5	F-box and leucine-rich repeat protein 5	chr4p15.33	209004_s_at	NM_012161 /// NM_033535
3.40	3.80	0.40	1.88E-01	5.59E-01	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	chr3p24.3	228501_at	NM_054110
2.64	2.86	0.22	1.88E-01	5.59E-01	---	---	---	1561041_at	---
3.03	3.30	0.27	1.88E-01	5.59E-01	TNNT2	troponin T type 2 (cardiac)	chr1q32	1563655_at	NM_000364 /// NM_001001430 /// NM_001001431 /// NM_001001432
2.43	2.61	0.18	1.88E-01	5.59E-01	PDYN	prodynorphin	chr20pter-p12	206803_at	NM_024411
2.14	2.34	0.21	1.88E-01	5.59E-01	C15orf50	chromosome 15 open reading frame 50	---	1554715_at	---
2.71	2.86	0.15	1.88E-01	5.59E-01	OR10A4	olfactory receptor, family 10, subfamily A, member 4	chr11p15.4	1555655_at	NM_207186
4.76	5.20	0.43	1.88E-01	5.59E-01	ZNF443	zinc finger protein 443	chr19p13.2	205928_at	NM_005815
5.92	6.17	0.24	1.88E-01	5.59E-01	PDCD1	programmed cell death 1	chr2q37.3	207634_at	NM_005018
3.27	3.51	0.23	1.88E-01	5.59E-01	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	chr1q23	1562537_at	NM_002001
4.11	4.28	0.18	1.88E-01	5.60E-01	GPR161	G protein-coupled receptor 161	chr1q24.2	235961_at	NM_007369 /// NM_153832
3.38	3.71	0.33	1.88E-01	5.60E-01	NAT8 /// NAT8B	N-acetyltransferase 8 /// N-acetyltransferase 8B (gene/pseudogene)	chr2p13.1-p12 /// chr2p13.2	206963_s_at	NM_003960 /// NM_016347
2.34	2.54	0.20	1.88E-01	5.60E-01	---	---	---	1558262_at	---
2.42	2.62	0.20	1.88E-01	5.60E-01	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	chr1p34.1	1555171_at	NM_006279 /// NM_174963 /// NM_174964 /// NM_174965 /// NM_174966 /// NM_174967 /// NM_174968 /// NM_174969 /// NM_174970 /// NM_174971

2.23	2.38	0.15	1.88E-01	5.60E-01	---	---	---	241159_x_at	---
2.58	2.80	0.22	1.88E-01	5.60E-01	---	---	---	227963_at	---
2.70	2.94	0.25	1.88E-01	5.60E-01	TTC3	tetratricopeptide repeat domain 3	chr21q22.2	1569472_s_at	NM_001001894 /// NM_003316
2.71	3.02	0.31	1.88E-01	5.60E-01	LOC100130557	hypothetical protein LOC100130557	chr1p34.2	1558782_a_at	XM_001722991 /// XM_001725530 /// XM_001725684
6.89	7.33	0.44	1.88E-01	5.60E-01	BLOC1S2	biogenesis of lysosomal organelles complex-1, subunit 2	chr10q24.31	225049_at	NM_001001342 /// NM_173809
2.67	2.94	0.28	1.88E-01	5.60E-01	---	---	---	240399_at	---
2.11	2.27	0.16	1.88E-01	5.60E-01	---	---	---	1570476_at	---
1.85	2.02	0.18	1.88E-01	5.60E-01	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	chr12p12.2-p11.2	1563101_at	NM_020183
8.86	9.65	0.79	1.88E-01	5.60E-01	PHACTR2	phosphatase and actin regulator 2	chr6q24.2	204048_s_at	NM_001100164 /// NM_001100165 /// NM_001100166 /// NM_014721
3.48	3.66	0.18	1.88E-01	5.60E-01	---	---	---	237318_at	---
4.60	4.87	0.28	1.89E-01	5.60E-01	AAK1	AP2 associated kinase 1	chr2p14	205435_s_at	NM_014911
2.69	2.90	0.21	1.89E-01	5.60E-01	PURB	Purine-rich element binding protein B	chr7p13	228467_at	NM_033224
5.38	6.12	0.74	1.89E-01	5.60E-01	---	---	---	228315_at	---
4.48	4.76	0.28	1.89E-01	5.60E-01	LOC390595	similar to ubiquitin-associated protein 1 (predicted)	chr15q22.31	232557_at	XM_001718742 /// XM_372574 /// XM_940509
4.93	5.19	0.25	1.89E-01	5.60E-01	LOC100127887 /// SYT2	hypothetical protein LOC100127887 /// synaptotagmin II	chr1q32.1	214903_at	NM_177402 /// XM_001723461 /// XM_001725208 /// XM_001726797
3.78	4.01	0.23	1.89E-01	5.60E-01	TMC8	transmembrane channel-like 8	chr17q25.3	242644_at	NM_152468
2.74	2.96	0.22	1.89E-01	5.60E-01	FOXA2	forkhead box A2	chr20p11	210103_s_at	NM_021784 /// NM_153675
2.39	2.60	0.21	1.89E-01	5.60E-01	---	---	---	1569474_at	---
2.49	2.66	0.18	1.89E-01	5.60E-01	GRIK2	glutamate receptor, ionotropic, kainate 2	chr6q16.3-q21	213845_at	NM_021956 /// NM_175768
2.52	2.80	0.28	1.89E-01	5.60E-01	TRA@ /// TRD@	T cell receptor alpha locus /// T cell receptor delta locus	chr14q11.2	217143_s_at	---
2.24	2.46	0.22	1.89E-01	5.60E-01	---	---	---	229300_at	---
3.31	3.63	0.32	1.89E-01	5.60E-01	---	---	---	238041_at	---
2.17	2.41	0.23	1.89E-01	5.60E-01	---	---	---	243168_at	---
2.11	2.28	0.17	1.89E-01	5.60E-01	COL6A6	collagen type VI alpha 6	chr3q22.1	230867_at	NM_001102608
2.18	2.73	0.55	1.89E-01	5.61E-01	OIT3	oncoprotein induced transcript 3	chr10q22.1	230478_at	NM_152635
4.32	4.61	0.29	1.89E-01	5.61E-01	---	---	---	242875_at	---
8.57	8.83	0.25	1.89E-01	5.61E-01	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	chr2q36.1	207988_s_at	NM_005731 /// NM_152862
2.44	2.66	0.22	1.89E-01	5.61E-01	---	---	---	237727_at	---
2.00	2.19	0.20	1.89E-01	5.61E-01	---	---	---	1557506_a_at	---
2.09	2.25	0.16	1.89E-01	5.61E-01	ZNF621	zinc finger protein 621	chr3p22.1	241499_at	NM_001098414 /// NM_198484
2.94	3.10	0.16	1.89E-01	5.61E-01	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	chr10p12.1	220865_s_at	NM_014317
2.70	2.85	0.15	1.89E-01	5.61E-01	AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	chr12p11.21 /// chr1p31.3	230630_at	NM_001002921 /// NM_001005353 /// NM_013410 /// NM_203464 /// XM_001132080 /// XM_001725174 /// XM_928632
5.19	5.44	0.25	1.89E-01	5.61E-01	---	---	---	49111_at	---
3.22	3.45	0.23	1.89E-01	5.61E-01	LOC728613	Programmed cell death 6 pseudogene	chr5p15.33	240931_s_at	NR_003713
2.49	2.72	0.22	1.89E-01	5.61E-01	---	---	---	243451_at	---

2.76	2.97	0.21	1.89E-01	5.61E-01	IGHA1 /// IGHG1 /// LOC100133862	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// similar to hCG1773549	chr14q32.33	216541_x_at	XM_001720441
2.45	2.65	0.20	1.89E-01	5.61E-01	SOCS1	suppressor of cytokine signaling 1	chr16p13.13	210000_s_at	NM_003745
5.90	6.14	0.24	1.89E-01	5.61E-01	SIN3A	SIN3 homolog A, transcription regulator (yeast)	chr15q24.2	238006_at	NM_015477
5.03	5.80	0.77	1.89E-01	5.61E-01	MPHOSPH8	M-phase phosphoprotein 8	chr13q12.11	225041_at	NM_017520
7.43	7.65	0.22	1.89E-01	5.61E-01	LOC152719	hypothetical protein LOC152719	chr4p16.3	215978_x_at	---
4.58	4.78	0.20	1.89E-01	5.61E-01	GRLF1	glucocorticoid receptor DNA binding factor 1	chr19q13.3	202044_at	NM_004491
2.00	2.18	0.17	1.89E-01	5.61E-01	---	---	---	244885_at	---
2.84	3.06	0.22	1.89E-01	5.61E-01	OVOL1	ovo-like 1(Drosophila)	chr11q13	206604_at	NM_004561
2.01	2.15	0.14	1.89E-01	5.61E-01	SCML4	sex comb on midleg-like 4 (Drosophila)	chr6q21	1555356_a_at	NM_198081
4.28	4.62	0.33	1.89E-01	5.61E-01	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	chr13q33	205422_s_at	NM_004791
3.77	4.03	0.26	1.89E-01	5.61E-01	---	---	---	239171_at	---
2.19	2.47	0.28	1.89E-01	5.61E-01	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	chr1q42.11	240735_at	NM_003607 /// NM_014826
1.97	2.13	0.16	1.89E-01	5.61E-01	FOXR2	forkhead box R2	chrXp11.21	1569669_at	NM_198451
3.80	4.03	0.23	1.90E-01	5.61E-01	TRAF7	TNF receptor-associated factor 7	chr16p13.3	223030_at	NM_032271
4.11	4.27	0.16	1.90E-01	5.61E-01	LOC100131096	hypothetical protein LOC100131096	chr17q25.3	242364_x_at	XM_001720907 /// XM_001726205 /// XM_001726705
3.51	3.99	0.47	1.90E-01	5.61E-01	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	chr5q13-q14	205071_x_at	NM_001131022 /// NM_003401 /// NM_022406 /// NM_022550
4.10	4.36	0.26	1.90E-01	5.61E-01	PIGR	polymeric immunoglobulin receptor	chr1q31-q41	204213_at	NM_002644
2.92	3.14	0.22	1.90E-01	5.61E-01	TRIM16L	tripartite motif-containing 16-like	chr17p11.2	1559681_a_at	NM_001037330
2.19	2.40	0.22	1.90E-01	5.61E-01	---	---	---	234571_at	---
2.31	2.53	0.21	1.90E-01	5.61E-01	---	---	---	240178_at	---
2.95	3.15	0.20	1.90E-01	5.61E-01	TTLL5	tubulin tyrosine ligase-like family, member 5	chr14q24.3	210539_at	NM_015072
3.56	3.76	0.20	1.90E-01	5.61E-01	---	---	---	231246_at	---
2.27	2.46	0.20	1.90E-01	5.61E-01	HCRTR1	hypocretin (orexin) receptor 1	chr1p33	207619_at	NM_001525
2.15	2.32	0.17	1.90E-01	5.61E-01	---	---	---	243206_at	---
3.46	3.71	0.25	1.90E-01	5.61E-01	COL20A1	collagen, type XX, alpha 1	chr20q13.33	232733_s_at	NM_020882
2.42	2.67	0.25	1.90E-01	5.61E-01	ZFP36L1	zinc finger protein 36, C3H type-like 1	chr14q22-q24	213277_at	NM_004926
3.70	3.90	0.19	1.90E-01	5.61E-01	HNRNPC /// HNRNPCL1 /// LOC440563 /// LOC649330	heterogeneous nuclear ribonucleoprotein C (C1/C2) /// heterogeneous nuclear ribonucleoprotein C-like 1 /// similar to heterogeneous nuclear ribonucleoprotein C-like 1 /// similar to Heterogeneous nuclear ribonucleoprotein C-like dJ845O24.4 (hnRNP core protein C-like)	chr14q11.2 /// chr1p36.21	216302_at	NM_001013631 /// NM_001077442 /// NM_001077443 /// NM_004500 /// NM_031314 /// XM_001714578 /// XM_001720694 /// XM_001721509 /// XM_001723218 /// XM_001726972
6.88	7.18	0.31	1.90E-01	5.61E-01	CISD1	CDGSH iron sulfur domain 1	chr10q21.1	218597_s_at	NM_018464
2.19	2.34	0.15	1.90E-01	5.61E-01	---	---	---	237554_at	---
3.61	4.30	0.69	1.90E-01	5.61E-01	41527	septin 10	chr2q13	214720_x_at	NM_144710 /// NM_178584
3.52	3.82	0.30	1.90E-01	5.61E-01	OPRD1	opioid receptor, delta 1	chr1p36.1-p34.3	207792_at	NM_000911
10.04	10.30	0.26	1.90E-01	5.61E-01	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	chr6q27	214288_s_at	NM_002793
2.83	3.00	0.18	1.90E-01	5.61E-01	ESPN	espin	chr1p36.31|1p36.31-p36.11	233979_s_at	NM_031475
5.77	6.54	0.77	1.90E-01	5.62E-01	COMMD10	COMM domain containing 10	chr5q23.1	218439_s_at	NM_016144
2.19	2.36	0.16	1.90E-01	5.62E-01	---	---	---	237468_at	---
2.14	2.31	0.18	1.90E-01	5.62E-01	LOC100129198	PRO2866	chr3p26.3	223848_at	XM_001719139 /// XM_001720650 /// XM_001721003
2.50	2.67	0.17	1.90E-01	5.62E-01	---	---	---	244035_at	---

6.00	6.28	0.28	1.90E-01	5.62E-01	C17orf51	chromosome 17 open reading frame 51	chr17p11.2	238167_at	NM_001113434 /// XM_001725854 /// XM_378661 /// XM_944416
4.66	4.89	0.22	1.90E-01	5.62E-01	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	chr11p15.5	214303_x_at	NM_017511 /// XM_001134429 /// XM_001714104 /// XM_001714774
3.06	3.29	0.24	1.90E-01	5.62E-01	ZMIZ1	zinc finger, MIZ-type containing 1	chr10q22.3	233060_at	NM_020338
5.08	5.33	0.25	1.90E-01	5.62E-01	IFNAR1	interferon (alpha, beta and omega) receptor 1	chr21q22.1|21q22.11	225669_at	NM_000629
4.82	5.09	0.27	1.90E-01	5.62E-01	BAIAP3	BAI1-associated protein 3	chr16p13.3	216356_x_at	NM_003933
2.20	2.38	0.18	1.90E-01	5.62E-01	WFDC10B	WAP four-disulfide core domain 10B	chr20q13.12	1552999_a_at	NM_172006 /// NM_172131
2.33	2.50	0.17	1.90E-01	5.62E-01	---	---	---	1562905_at	---
1.98	2.17	0.19	1.90E-01	5.62E-01	AOF1	amine oxidase (flavin containing) domain 1	chr6p22.3	1553150_at	NM_153042
3.85	4.10	0.25	1.90E-01	5.62E-01	HIC2	hypermethylated in cancer 2	chr22q11.21	212965_at	NM_015094
4.40	5.04	0.64	1.90E-01	5.62E-01	FGD4	FYVE, RhoGEF and PH domain containing 4	chr12p11.21	227948_at	NM_139241
3.11	3.41	0.30	1.90E-01	5.62E-01	SLC44A1	solute carrier family 44, member 1	chr9q31.2	222364_at	NM_080546
2.43	2.66	0.22	1.90E-01	5.62E-01	---	---	---	1556823_s_at	---
2.71	2.94	0.23	1.90E-01	5.62E-01	ZNRF1	Zinc and ring finger 1	chr16q23.1	231092_s_at	NM_032268
2.20	2.37	0.17	1.91E-01	5.63E-01	LOC145783	hypothetical LOC145783	chr15q21.3	1558570_at	XM_934388
2.40	2.57	0.17	1.91E-01	5.63E-01	ANKRD53	ankyrin repeat domain 53	chr2p13.3	215759_at	NM_001115116 /// NM_024933
2.69	2.85	0.16	1.91E-01	5.63E-01	---	---	---	1559771_at	---
8.44	9.06	0.62	1.91E-01	5.63E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	224559_at	NR_002819
3.40	3.60	0.20	1.91E-01	5.63E-01	MAP6D1	MAP6 domain containing 1	chr3q27.1	221713_s_at	NM_024871
6.79	7.91	1.12	1.91E-01	5.63E-01	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	chr12q24.2-q24.3	200598_s_at	NM_003299
2.29	2.49	0.19	1.91E-01	5.63E-01	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	chr9q33.3	1554745_at	NM_014636
2.55	2.82	0.26	1.91E-01	5.63E-01	---	---	---	1559578_at	---
6.22	6.54	0.32	1.91E-01	5.63E-01	C19orf28	chromosome 19 open reading frame 28	chr19p13.3	226516_at	NM_001042680 /// NM_021731 /// NM_174983
2.18	2.46	0.28	1.91E-01	5.63E-01	ZNF718	zinc finger protein 718	chr4p16.3	1553269_at	NM_001039127
2.60	2.82	0.22	1.91E-01	5.63E-01	OSBPL7	oxysterol binding protein-like 7	chr17q21	208163_s_at	NM_145798
2.07	2.26	0.20	1.91E-01	5.63E-01	LOC100129488	hypothetical protein LOC100129488	chr16p12.3	244723_at	XM_001724110 /// XM_001724617
3.11	3.26	0.16	1.91E-01	5.63E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	217397_at	---
5.16	5.46	0.30	1.91E-01	5.63E-01	C9orf116	chromosome 9 open reading frame 116	chr9q34.3	59437_at	NM_001048265 /// NM_144654
1.95	2.11	0.17	1.91E-01	5.63E-01	---	---	---	233405_at	---
3.60	3.96	0.36	1.91E-01	5.63E-01	SMC5	structural maintenance of chromosomes 5	chr9q21.11	212926_at	NM_015110
3.42	3.73	0.31	1.91E-01	5.63E-01	PHF21A	PHD finger protein 21A	chr11p11.2	1558965_at	NM_001101802 /// NM_016621
3.93	4.13	0.20	1.91E-01	5.63E-01	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	chr19p13.12	206882_at	NM_005071
2.19	2.37	0.18	1.91E-01	5.63E-01	FLJ11292	hypothetical protein FLJ11292	chr5q14.3	220828_s_at	NM_018382
2.23	2.40	0.17	1.91E-01	5.63E-01	PON1	paraoxonase 1	chr7q21.3	206344_at	NM_000446
3.36	3.53	0.17	1.91E-01	5.63E-01	PPM1K	protein phosphatase 1K (PP2C domain containing)	chr4q22.1	244011_at	NM_152542
4.33	4.73	0.40	1.91E-01	5.63E-01	ARID4B	AT rich interactive domain 4B (RBP1-like)	chr1q42.1-q43	223111_x_at	NM_016374 /// NM_031371
2.28	2.46	0.19	1.91E-01	5.63E-01	---	---	---	234174_at	---
2.18	2.35	0.17	1.91E-01	5.63E-01	C10orf79	chromosome 10 open reading frame 79	chr10q25.1	231084_at	NM_025145
3.26	3.44	0.18	1.91E-01	5.63E-01	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	chr17q21.32	223689_at	NM_006546
4.44	5.16	0.72	1.91E-01	5.63E-01	---	---	---	236355_s_at	---
6.53	7.05	0.53	1.91E-01	5.63E-01	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	chr8q11.21	209096_at	NM_003350
6.11	6.62	0.51	1.91E-01	5.63E-01	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	chr10p15-p14	216594_x_at	NM_001353 /// XM_001724839
2.14	2.39	0.25	1.91E-01	5.63E-01	PDZD2	PDZ domain containing 2	chr5p13.3	233025_at	NM_178140
2.10	2.30	0.20	1.91E-01	5.63E-01	HIST1H2AK	histone cluster 1, H2ak	chr6p22-p21.3	239041_at	NM_003510
2.47	2.66	0.19	1.91E-01	5.63E-01	DNAH2	dynein, axonemal, heavy chain 2	chr17p13.1	215840_at	NM_020877
2.31	2.48	0.16	1.91E-01	5.63E-01	TMTC3	transmembrane and tetratricopeptide repeat containing 3	chr12q21.32	1560017_at	NM_181783
2.61	2.77	0.16	1.91E-01	5.63E-01	LOC642311 /// LOC96610	similar to Ribosome beiogenesis protein BMS1 homolog /// hypothetical gene LOC96610	chr15q11.2 /// chr22q11.22	1569013_s_at	XR_017705 /// XR_040596 /// XR_041109

5.97	6.75	0.78	1.91E-01	5.63E-01	FXR1	fragile X mental retardation, autosomal homolog 1	chr3q28	201635_s_at	NM_001013438 /// NM_001013439 /// NM_005087																				
3.76	4.00	0.24	1.91E-01	5.63E-01	MMP14	matrix metallopeptidase 14 (membrane-inserted)	chr14q11-q12	217279_x_at	NM_004995																				
7.39	8.15	0.76	1.91E-01	5.63E-01	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	---	223139_s_at	NM_001114397 /// NM_020865																				
2.67	3.15	0.48	1.91E-01	5.63E-01	DLC1	deleted in liver cancer 1	chr8p22	220512_at	NM_006094 /// NM_024767 /// NM_182643																				
7.06	7.60	0.53	1.91E-01	5.63E-01	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	chr16q12	233864_s_at	NM_018206																				
3.16	3.67	0.51	1.91E-01	5.63E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31 /// LOC100126583 /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant gamma 4 (G4m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical LOC100126583 /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	211637_x_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001724554 /// XM_941465																				
5.15	5.42	0.26	1.91E-01	5.63E-01	ZNF562	zinc finger protein 562	chr19p13.2	219163_at	NM_001130031 /// NM_001130032 /// NM_017656																				
3.27	3.52	0.25	1.91E-01	5.63E-01	SERPINB12	serpin peptidase inhibitor, clade B (ovalbumin), member 12	---	1553057_at	NM_080474																				
4.42	4.61	0.20	1.91E-01	5.63E-01	---	---	---	237467_at	---																				
3.56	3.74	0.18	1.91E-01	5.63E-01	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	chr4q26	230749_s_at	NM_001221 /// NM_172115 /// NM_172127 /// NM_172128																				
2.46	2.62	0.16	1.91E-01	5.63E-01	KCNH1	potassium voltage-gated channel, subfamily H (eag-related), member 1	chr1q32-q41	207635_s_at	NM_002238 /// NM_172362																				
1.96	2.11	0.14	1.91E-01	5.63E-01	---	---	---	1561316_at	---																				
5.26	5.57	0.31	1.92E-01	5.63E-01	BRF1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	chr14q	215676_at	NM_001519 /// NM_145685																				
3.15	3.63	0.48	1.92E-01	5.63E-01	SHISA3	shisa homolog 3 (Xenopus laevis)	chr4p13	229485_x_at	NM_001080505																				
4.18	4.52	0.34	1.92E-01	5.63E-01	TCF4	transcription factor 4	chr18q21.1	228837_at	NM_001083962 /// NM_003199																				
2.03	2.34	0.31	1.92E-01	5.63E-01	GNAT2	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2	chr1p13.1	210604_at	NM_005272																				
2.02	2.22	0.20	1.92E-01	5.63E-01	---	---	---	233692_at	---																				
4.17	4.45	0.28	1.92E-01	5.64E-01	---	---	---	235288_at	---																				
2.39	2.65	0.27	1.92E-01	5.64E-01	RXFP1	relaxin/insulin-like family peptide receptor 1	chr4q32.1	1552715_a_at	NM_021634																				
2.33	2.68	0.35	1.92E-01	5.64E-01	FAM171B	family with sequence similarity 171, member B	chr2q32.1	242762_s_at	NM_177454																				
1.95	2.14	0.19	1.92E-01	5.64E-01	---	---	---	234038_at	---																				
5.11	5.37	0.26	1.92E-01	5.64E-01	SPACA4	sperm acrosome associated 4	chr19q13.33	231054_at	NM_133498																				
4.79	5.53	0.74	1.92E-01	5.64E-01	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	chr12q21.2	203203_s_at	NM_007043																				
5.21	5.47	0.26	1.92E-01	5.64E-01	LZTS1	leucine zipper, putative tumor suppressor 1	chr8p22	222107_x_at	NM_021020																				
2.66	2.90	0.24	1.92E-01	5.64E-01	CYSLTR2	cysteinyl leukotriene receptor 2	chr13q14.12-q21.1	220813_at	NM_020377																				
6.00	6.22	0.22	1.92E-01	5.64E-01	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	chr17q25.3	224466_s_at	NM_002359 /// NM_032711																				
4.92	5.14	0.21	1.92E-01	5.64E-01	MTMR9	myotubularin related protein 9	chr8p23-p22	213278_at	NM_015458																				
3.77	3.97	0.20	1.92E-01	5.64E-01	---	---	---	234431_at	---																				
2.10	2.28	0.18	1.92E-01	5.64E-01	SLC19A3	solute carrier family 19, member 3	chr2q37	239345_at	NM_025243																				
2.20	2.37	0.16	1.92E-01	5.64E-01	---	---	---	243081_at	---																				
1.84	2.00	0.16	1.92E-01	5.64E-01	---	---	---	244283_x_at	---																				
5.68	5.89	0.21	1.92E-01	5.64E-01	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	chr2p22-p21	204211_x_at	NM_002759																				
4.15	4.39	0.24	1.92E-01	5.64E-01	---	---	---	224475_at	---																				
1.81	1.95	0.14	1.92E-01	5.64E-01	---	---	---	215361_at	---																				
4.49	4.74	0.25	1.92E-01	5.64E-01	MMD2	monocyte to macrophage differentiation-associated 2	chr7p22.1	230826_at	NM_001100600 /// NM_198403																				
2.86	3.08	0.22	1.92E-01	5.64E-01	NUDT4	Nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 2	chr12q21	227683_x_at	NM_019094 /// NM_199040																				
2.02	2.17	0.15	1.92E-01	5.65E-01	---	---	---	242628_at	---																				
3.00	3.28	0.27	1.92E-01	5.65E-01	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	chr12q23	206127_at	NM_005230																				
5.45	5.95	0.49	1.92E-01	5.65E-01	KIAA1826	KIAA1826	chr11q22	227418_at	NM_032424																				
2.54	2.88	0.35	1.92E-01	5.65E-01	C1orf212	chromosome 1 open reading frame 212	chr1p34.3	239510_at	NM_138428																				

2.72	2.89	0.17	1.92E-01	5.65E-01	TMC5	transmembrane channel-like 5	chr16p12.3	236983_at	NM_001105248 /// NM_001105249 /// NM_024780
4.93	5.33	0.40	1.92E-01	5.65E-01	TMEM104	transmembrane protein 104	chr17q25.1	220097_s_at	NM_017728
3.37	3.61	0.24	1.92E-01	5.65E-01	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1	chr3q21	228848_at	NM_032548 /// NM_172027 /// NM_172028
2.60	2.95	0.35	1.93E-01	5.65E-01	CEPT1	choline/ethanolamine phosphotransferase 1	chr1p13.3	1561884_at	NM_001007794 /// NM_006090
6.70	7.03	0.32	1.93E-01	5.65E-01	COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	chr10q24	223281_s_at	NM_004376 /// NM_078470
2.78	2.97	0.19	1.93E-01	5.65E-01	MRO	maestro	chr18q21	224324_at	NM_001127174 /// NM_001127175 /// NM_001127176 /// NM_031939
7.70	8.66	0.97	1.93E-01	5.65E-01	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	chr9q31.1	203504_s_at	NM_005502
4.88	5.33	0.44	1.93E-01	5.65E-01	SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin	chr20p13	44673_at	NM_023068
3.39	3.81	0.42	1.93E-01	5.65E-01	PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	chr5q31.2-q34	206623_at	NM_000440
2.75	3.15	0.41	1.93E-01	5.65E-01	CLCN5	chloride channel 5	chrXp11.23-p11.22|Xp11.23	226273_at	NM_000084 /// NM_001127898 /// NM_001127899
2.41	2.71	0.30	1.93E-01	5.65E-01	---	---	---	1568799_at	---
2.14	2.36	0.22	1.93E-01	5.65E-01	---	---	---	1569736_at	---
1.97	2.19	0.22	1.93E-01	5.65E-01	---	---	---	231329_at	---
2.08	2.28	0.20	1.93E-01	5.65E-01	MGC33556	hypothetical LOC339541	chr1p34.1	238365_s_at	XR_039961 /// XR_039962 /// XR_039963
2.04	2.24	0.20	1.93E-01	5.65E-01	---	---	---	237668_at	---
1.97	2.14	0.17	1.93E-01	5.65E-01	---	---	---	241206_at	---
2.52	2.68	0.16	1.93E-01	5.65E-01	ING5	inhibitor of growth family, member 5	chr2q37.3	228672_at	NM_032329
2.24	2.48	0.24	1.93E-01	5.65E-01	MGC42157	hypothetical locus MGC42157	chr4p14	239104_at	XR_017710 /// XR_017809 /// XR_041588
2.60	2.76	0.16	1.93E-01	5.65E-01	C21orf74	chromosome 21 open reading frame 74	chr21q21.1	1552604_at	XR_001010 /// XR_001423
2.28	2.47	0.19	1.93E-01	5.65E-01	DEPDC6	DEP domain containing 6	chr8q24.12	234071_at	NM_022783
4.53	5.11	0.58	1.93E-01	5.65E-01	---	---	---	228105_at	---
5.41	5.78	0.37	1.93E-01	5.65E-01	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	chr22q12.2	221757_at	NM_052880
2.49	2.70	0.21	1.93E-01	5.65E-01	---	---	---	1563178_at	---
2.32	2.55	0.23	1.93E-01	5.65E-01	KIAA0748	KIAA0748	chr12q13.2	222920_s_at	NM_001098815
4.21	4.56	0.35	1.93E-01	5.65E-01	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	chr9q34	221551_x_at	NM_175039 /// NM_175040
3.13	3.39	0.26	1.93E-01	5.65E-01	KRT15	keratin 15	chr17q21.2	204734_at	NM_002275
5.10	5.34	0.24	1.93E-01	5.65E-01	---	---	---	221109_at	---
2.46	2.69	0.23	1.93E-01	5.65E-01	GHRLOS	ghrelin opposite strand (non-protein coding)	chr3p25.3	244695_at	NR_004431
3.13	3.36	0.22	1.93E-01	5.65E-01	RFESD	Rieske (Fe-S) domain containing	chr5q15	239142_at	NM_001131065 /// NM_001131066 /// NM_173362
3.88	4.06	0.19	1.93E-01	5.65E-01	---	---	---	229924_s_at	---
3.80	4.10	0.30	1.93E-01	5.65E-01	VASH1	vasohibin 1	chr14q24.3	230546_at	NM_014909
3.99	4.22	0.23	1.93E-01	5.65E-01	---	---	---	230386_at	---
1.76	1.91	0.14	1.93E-01	5.65E-01	STXBP4	syntaxin binding protein 4	chr17q22	1554328_at	NM_178509
2.59	2.80	0.21	1.93E-01	5.65E-01	TMEM170B	transmembrane protein 170B	chr6p24.1	235798_at	NM_001100829
2.38	2.60	0.22	1.93E-01	5.65E-01	MFGE8	milk fat globule-EGF factor 8 protein	chr15q25	1567539_at	NM_001114614 /// NM_005928
3.64	3.89	0.24	1.93E-01	5.65E-01	---	---	---	1564525_at	---
2.33	2.55	0.22	1.93E-01	5.65E-01	C20orf62	chromosome 20 open reading frame 62	chr20q13.12	233584_at	NM_178476
2.62	2.90	0.28	1.93E-01	5.65E-01	CXorf56	chromosome X open reading frame 56	chrXq23	235442_at	NM_022101
4.33	4.64	0.30	1.93E-01	5.66E-01	PIAS1	protein inhibitor of activated STAT, 1	chr15q	217863_at	NM_016166
5.97	6.27	0.30	1.93E-01	5.66E-01	PSKH1	protein serine kinase H1	chr16q22.1	213141_at	NM_006742
2.92	3.15	0.23	1.94E-01	5.66E-01	DPP9	dipeptidyl-peptidase 9	chr19p13.3	231957_s_at	NM_139159
2.28	2.50	0.21	1.93E-01	5.66E-01	JMJD1C	Jumonji domain containing 1C	chr10q21.2-q21.3	241659_at	NM_004241 /// NM_032776
2.50	2.69	0.19	1.93E-01	5.66E-01	---	---	---	241108_at	---
2.01	2.19	0.18	1.93E-01	5.66E-01	---	---	---	237760_at	---

2.07	2.23	0.17	1.93E-01	5.66E-01	---	---	---	237972_at	---
2.13	2.28	0.15	1.93E-01	5.66E-01	C10orf12	chromosome 10 open reading frame 12	chr10q24.1	216393_at	NM_015652
4.57	5.17	0.60	1.94E-01	5.66E-01	RAB3IP	RAB3A interacting protein (rabin3)	chr12q14.3	223471_at	NM_001024647 /// NM_022456 /// NM_175623 /// NM_175624 /// NM_175625
3.37	3.66	0.29	1.94E-01	5.66E-01	PIGZ	phosphatidylinositol glycan anchor biosynthesis, class Z	chr3q29	220041_at	NM_025163
3.64	4.26	0.62	1.94E-01	5.66E-01	UFM1	Ubiquitin-fold modifier 1	chr13q13.3	242669_at	NM_016617
3.68	4.05	0.37	1.94E-01	5.66E-01	KPNA4	karyopherin alpha 4 (importin alpha 3)	chr3q25.33	209653_at	NM_002268
3.72	4.00	0.29	1.94E-01	5.66E-01	OR3A3	olfactory receptor, family 3, subfamily A, member 3	chr17p13.3	221426_s_at	NM_012373
13.29	13.46	0.18	1.94E-01	5.66E-01	LOC100133315	similar to hCG1640299	chr11q13.4	1553567_s_at	XM_001717628 /// XM_001723215 /// XM_001723302
3.11	3.30	0.19	1.94E-01	5.66E-01	---	---	---	239322_at	---
5.52	6.15	0.63	1.94E-01	5.66E-01	USP25	ubiquitin specific peptidase 25	chr21q11.2	220419_s_at	NM_013396
3.16	3.37	0.21	1.94E-01	5.66E-01	C12orf53	chromosome 12 open reading frame 53	chr12p13.31	228165_at	NM_153685
3.06	3.24	0.18	1.94E-01	5.66E-01	KIAA1009	KIAA1009	chr6q14.3	206006_s_at	NM_014895
2.08	2.26	0.18	1.94E-01	5.66E-01	LOC283588	hypothetical protein LOC283588	chr14q32.11	1557113_at	XR_041538 /// XR_041539 /// XR_041540
1.70	1.84	0.14	1.94E-01	5.66E-01	---	---	---	1557017_at	---
3.84	4.23	0.39	1.94E-01	5.66E-01	---	---	---	1557121_s_at	---
2.95	3.15	0.20	1.94E-01	5.66E-01	LHX4	LIM homeobox 4	chr1q25.2	1553156_at	NM_033343
4.47	5.18	0.70	1.94E-01	5.66E-01	---	---	---	235123_at	---
3.91	4.17	0.26	1.94E-01	5.66E-01	---	---	---	244090_at	---
6.21	6.53	0.32	1.94E-01	5.66E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	208877_at	NM_002577
2.35	2.53	0.19	1.94E-01	5.66E-01	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	chr5q13-q14	205072_s_at	NM_001131022 /// NM_003401 /// NM_022406 /// NM_022550
3.26	3.48	0.21	1.94E-01	5.66E-01	C20orf59	chromosome 20 open reading frame 59	chr20q13.33	233328_x_at	NM_022082
2.42	2.64	0.22	1.94E-01	5.66E-01	PYY	peptide YY	chr17q21.1	207080_s_at	NM_004160
2.74	3.50	0.76	1.94E-01	5.66E-01	C6orf176	chromosome 6 open reading frame 176	chr6q27	230251_at	XR_017929 /// XR_017998 /// XR_040021
9.57	10.02	0.44	1.94E-01	5.66E-01	PPA1	pyrophosphatase (inorganic) 1	chr10q11.1-q24	217848_s_at	NM_021129
3.18	3.51	0.33	1.94E-01	5.66E-01	CALD1	caldesmon 1	chr7q33	215199_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
4.49	4.77	0.28	1.94E-01	5.66E-01	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	chr17q22	211315_s_at	NM_018896 /// NM_198376 /// NM_198377 /// NM_198378 /// NM_198379 /// NM_198380 /// NM_198382 /// NM_198383 /// NM_198384 /// NM_198385 /// NM_198386 /// NM_198387 /// NM_198388 /// NM_198396 /// NM_198397
3.09	3.35	0.26	1.94E-01	5.66E-01	DUSP13	dual specificity phosphatase 13	chr10q22.2	219963_at	NM_001007271 /// NM_001007272 /// NM_001007273 /// NM_016364
3.26	3.45	0.19	1.94E-01	5.66E-01	RASD2	RASD family, member 2	chr22q13.1	223634_at	NM_014310
1.88	2.05	0.17	1.94E-01	5.66E-01	LOC100130740	similar to hCG2042068	chr17q21.32	236892_s_at	XM_001722876 /// XM_001725076 /// XM_001726544
2.03	2.20	0.17	1.94E-01	5.66E-01	---	---	---	244639_at	---

2.21	2.37	0.16	1.94E-01	5.66E-01	CR1L	complement component (3b/4b) receptor 1-like	chr1q32.1	239206_at	NM_175710
2.66	2.90	0.24	1.94E-01	5.67E-01	---	---	---	243762_at	---
4.29	4.72	0.43	1.94E-01	5.67E-01	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	chr20q11.2-q13.1	203936_s_at	NM_004994
2.02	2.18	0.16	1.95E-01	5.67E-01	---	---	---	242965_at	---
2.73	2.96	0.22	1.95E-01	5.67E-01	---	---	---	1560774_at	---
4.19	4.46	0.27	1.95E-01	5.67E-01	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2	chr9q34	207372_s_at	NM_001246 /// NM_203468
6.91	7.39	0.48	1.95E-01	5.67E-01	NUP50	nucleoporin 50kDa	chr22q13.31	213682_at	NM_007172 /// NM_153645
1.95	2.14	0.19	1.95E-01	5.67E-01	YWHAH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	chr22q12.3	236559_at	NM_003405
1.73	1.91	0.18	1.95E-01	5.67E-01	---	---	---	1568866_at	---
3.81	4.08	0.28	1.95E-01	5.67E-01	TSPAN15	tetraspanin 15	chr10q21.3	218693_at	NM_012339
2.75	2.97	0.22	1.95E-01	5.67E-01	PRKG1	protein kinase, cGMP-dependent, type I	chr10q11.2	211380_s_at	NM_001098512 /// NM_006258
2.07	2.27	0.21	1.95E-01	5.67E-01	---	---	---	1566537_at	---
3.96	4.18	0.22	1.95E-01	5.67E-01	DRD2	dopamine receptor D2	chr11q23	211624_s_at	NM_000795 /// NM_016574
5.36	5.60	0.24	1.95E-01	5.67E-01	---	---	---	234201_x_at	---
1.87	2.03	0.16	1.95E-01	5.67E-01	FAM62C	family with sequence similarity 62 (C2 domain containing), member C	chr3q22.3	1554912_at	NM_031913
4.60	5.32	0.72	1.95E-01	5.67E-01	KIAA0776	KIAA0776	chr6q16.1	212634_at	NM_015323
6.89	7.30	0.41	1.95E-01	5.67E-01	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1	chrXq25-q26	205512_s_at	NM_001130846 /// NM_001130847 /// NM_004208 /// NM_145812 /// NM_145813
3.53	3.85	0.33	1.95E-01	5.67E-01	C20orf43	Chromosome 20 open reading frame 43	chr20q13.31	236702_at	NM_016407
3.24	3.55	0.31	1.95E-01	5.67E-01	---	---	---	243450_at	---
2.91	3.19	0.28	1.95E-01	5.67E-01	PIK3C3	phosphoinositide-3-kinase, class 3	chr18q12.3	215394_at	NM_002647
2.21	2.46	0.25	1.95E-01	5.67E-01	---	---	---	239849_at	---
3.88	4.10	0.22	1.95E-01	5.67E-01	---	---	---	1555900_at	---
2.58	2.78	0.21	1.95E-01	5.67E-01	WNT3	wingless-type MMTV integration site family, member 3	chr17q21	221455_s_at	NM_030753
1.84	2.00	0.16	1.95E-01	5.67E-01	---	---	---	241260_at	---
4.54	4.87	0.33	1.95E-01	5.67E-01	CTSD	cathepsin D	chr11p15.5	227886_at	NM_001909
3.15	3.36	0.21	1.95E-01	5.67E-01	DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	chr12q24.33	214968_at	NM_175066
2.41	2.57	0.16	1.95E-01	5.67E-01	---	---	---	1557501_a_at	---
2.75	3.01	0.25	1.95E-01	5.67E-01	---	---	---	241070_at	---
2.52	2.77	0.25	1.95E-01	5.67E-01	C10orf28	chromosome 10 open reading frame 28	chr10q24.2	210455_at	NM_014472
2.94	3.13	0.19	1.95E-01	5.68E-01	GLI4 /// ZFP41	GLI-Kruppel family member GLI4 /// zinc finger protein 41 homolog (mouse)	chr8q24.3	227023_at	NM_138465 /// NM_173832
5.54	6.04	0.50	1.95E-01	5.68E-01	PXDN	peroxidasin homolog (Drosophila)	chr2p25	212012_at	NM_012293
2.83	3.07	0.24	1.95E-01	5.68E-01	---	---	---	241375_at	---
2.50	2.66	0.16	1.95E-01	5.68E-01	---	---	---	215825_at	---
2.39	2.60	0.21	1.95E-01	5.68E-01	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	chr1p34	1563565_at	NM_005540
2.33	2.92	0.59	1.95E-01	5.68E-01	---	---	---	241470_x_at	---
6.68	7.13	0.45	1.96E-01	5.68E-01	YME1L1	YME1-like 1 (S. cerevisiae)	chr10p14	216304_x_at	NM_014263 /// NM_139312
5.12	5.43	0.30	1.95E-01	5.68E-01	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	chr11q13	214368_at	NM_001098670 /// NM_001098671 /// NM_153819
3.40	3.69	0.29	1.96E-01	5.68E-01	C22orf26	chromosome 22 open reading frame 26	chr22q13.31	220681_at	NM_018280
3.76	4.04	0.29	1.95E-01	5.68E-01	SLC38A5	solute carrier family 38, member 5	chrXp11.23	234973_at	NM_033518
3.01	3.24	0.23	1.96E-01	5.68E-01	SMAD5	SMAD family member 5	chr5q31	205187_at	NM_001001419 /// NM_001001420 /// NM_005903
2.52	2.74	0.23	1.96E-01	5.68E-01	MPHOSPH9	M-phase phosphoprotein 9	chr12q24.31	1558369_at	NM_022782
4.15	4.37	0.22	1.95E-01	5.68E-01	SYT12	Synaptotagmin XII	chr11q13.1	215865_at	NM_177963
2.90	3.11	0.21	1.96E-01	5.68E-01	---	---	---	1562033_at	---
2.18	2.35	0.17	1.95E-01	5.68E-01	EYA4	eyes absent homolog 4 (Drosophila)	chr6q23	207327_at	NM_004100 /// NM_172103 /// NM_172105
2.04	2.20	0.16	1.96E-01	5.68E-01	---	---	---	244432_at	---
2.38	2.54	0.16	1.95E-01	5.68E-01	SDCCAG10	serologically defined colon cancer antigen 10	chr5q12.3	1558841_at	NM_005869
4.00	4.18	0.18	1.96E-01	5.68E-01	TRAF4	TNF receptor-associated factor 4	chr17q11-q12	235688_s_at	NM_004295
2.49	2.68	0.19	1.96E-01	5.68E-01	BCAR4	breast cancer anti-estrogen resistance 4	chr16p13.13	230854_at	NR_024049 /// NR_024050
1.92	2.08	0.16	1.96E-01	5.68E-01	---	---	---	1561196_at	---
1.97	2.16	0.19	1.96E-01	5.68E-01	NPAT	nuclear protein, ataxia-telangiectasia locus	chr11q22-q23	211585_at	NM_002519

3.64	3.84	0.20	1.96E-01	5.68E-01	---	---	---	229965_at	---
3.40	3.59	0.19	1.96E-01	5.68E-01	GREB1	GREB1 protein	chr2p25.1	210855_at	NM_014668 /// NM_033090 /// NM_148903
2.42	2.64	0.22	1.96E-01	5.68E-01	---	---	---	244017_at	---
3.67	3.94	0.27	1.96E-01	5.68E-01	IGLL1	immunoglobulin lambda-like polypeptide 1	chr22q11.23	206660_at	NM_020070 /// NM_152855
2.51	2.69	0.18	1.96E-01	5.68E-01	BRSK2	BR serine/threonine kinase 2	chr11p15.5	215010_s_at	NM_003957
1.83	2.00	0.16	1.96E-01	5.68E-01	C9orf68	chromosome 9 open reading frame 68	chr9p24.2-p24.1	237363_at	NM_001039395
2.17	2.40	0.23	1.96E-01	5.68E-01	---	---	---	238249_at	---
2.25	2.44	0.19	1.96E-01	5.68E-01	---	---	---	216616_at	---
4.28	4.44	0.16	1.96E-01	5.68E-01	---	---	---	233003_at	---
2.86	3.14	0.28	1.96E-01	5.68E-01	LRRC41	leucine rich repeat containing 41	chr1p33	215765_at	NM_006369
6.43	6.70	0.27	1.96E-01	5.68E-01	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	chr8p22-p21.3	210980_s_at	NM_001127505 /// NM_004315 /// NM_177924
2.25	2.42	0.17	1.96E-01	5.69E-01	ARD1B	ARD1 homolog B (S. cerevisiae)	chr4q21.21	210603_at	NM_032693
2.11	2.29	0.18	1.96E-01	5.69E-01	---	---	---	231645_s_at	---
2.71	2.87	0.16	1.96E-01	5.69E-01	SP7	Sp7 transcription factor	chr12q13.13	1552340_at	NM_152860
3.58	3.81	0.23	1.96E-01	5.69E-01	DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	chr12q24.33	229482_at	NM_175066
7.31	7.61	0.29	1.96E-01	5.69E-01	IL34	interleukin 34	chr16q22.1	237046_x_at	NM_152456
2.30	2.49	0.20	1.96E-01	5.69E-01	LPAL2	lipoprotein, Lp(a)-like 2	chr6q26-q27	210909_x_at	NM_024492 /// NM_145727
3.06	3.22	0.15	1.96E-01	5.69E-01	---	---	---	239039_at	---
2.13	2.29	0.16	1.96E-01	5.69E-01	LST-3TM12 /// SLCO1B1 /// SLCO1B3	organic anion transporter LST-3b /// solute carrier organic anion transporter family, member 1B1 /// solute carrier organic anion transporter family, member 1B3	chr12p /// chr12p12 /// chr12p12.2	210366_at	NM_001009562 /// NM_006446 /// NM_019844
2.80	3.00	0.20	1.96E-01	5.69E-01	FBXL16	F-box and leucine-rich repeat protein 16	chr16p13.3	232409_x_at	NM_153350
4.92	5.18	0.26	1.96E-01	5.69E-01	KLHL12	kelch-like 12 (Drosophila)	chr1q32.1	219931_s_at	NM_021633
4.26	4.82	0.57	1.96E-01	5.69E-01	SYNPO2	synaptopodin 2	chr4q26	225720_at	NM_001128933 /// NM_001128934 /// NM_133477
2.60	2.82	0.21	1.96E-01	5.69E-01	TMPRSS6	transmembrane protease, serine 6	chr22q12.3	232941_at	NM_153609
6.22	6.79	0.57	1.97E-01	5.69E-01	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	chr7q21.1	243951_at	NM_000927
2.34	2.58	0.24	1.97E-01	5.69E-01	ZFHX3	zinc finger homeobox 3	chr16q22.3-q23.1	233751_at	NM_006885
4.71	5.49	0.78	1.97E-01	5.69E-01	DAB1 /// OMA1	disabled homolog 1 (Drosophila) /// OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	chr1p32-p31 /// chr1p32.1	226020_s_at	NM_021080 /// NM_145243
5.60	6.22	0.62	1.97E-01	5.69E-01	TTC35	tetratricopeptide repeat domain 35	chr8q23.1	203584_at	NM_014673
6.47	7.06	0.59	1.97E-01	5.69E-01	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	chr6p21	209056_s_at	NM_001253
4.26	4.65	0.38	1.97E-01	5.69E-01	HCP5	HLA complex P5	chr6p21.3	206082_at	NM_006674
2.18	2.41	0.23	1.97E-01	5.69E-01	ANGPTL3	Angiopoietin-like 3	chr1p31.1-p22.3	243799_x_at	NM_014495
3.17	3.40	0.23	1.97E-01	5.69E-01	C8orf79	Chromosome 8 open reading frame 79	chr8p22	238770_at	NM_001099677 /// NM_020844
2.66	2.87	0.21	1.97E-01	5.69E-01	DNAI1	dynein, axonemal, intermediate chain 1	chr9p21-p13	233195_at	NM_012144
2.64	2.82	0.19	1.97E-01	5.69E-01	---	---	---	236895_at	---
6.57	7.58	1.01	1.97E-01	5.69E-01	HMBOX1	homeobox containing 1	chr8p21.1	219269_at	NM_024567
3.03	3.30	0.27	1.97E-01	5.69E-01	hCG_2044152	hCG2044152	chr2q33.1	1556536_at	XM_001128832 /// XM_001133424 /// XM_001724531
2.74	2.99	0.25	1.97E-01	5.69E-01	ATP1A3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	chr19q13.31	214432_at	NM_152296
3.02	3.23	0.21	1.97E-01	5.69E-01	P53AIP1	p53-regulated apoptosis-inducing protein 1	chr11q24	223920_s_at	NM_022112
2.39	2.58	0.19	1.97E-01	5.69E-01	FLJ21511	hypothetical protein FLJ21511	chr4p12-p11	220723_s_at	NM_025087
3.43	3.59	0.16	1.97E-01	5.69E-01	---	---	---	237405_at	---
1.96	2.11	0.15	1.97E-01	5.69E-01	TRIM49	tripartite motif-containing 49	chr11p11.12-q12	221154_at	NM_020358
2.59	2.81	0.22	1.97E-01	5.69E-01	RSU1	Ras suppressor protein 1	chr10p13	1560937_at	NM_012425 /// NM_152724
2.13	2.35	0.22	1.97E-01	5.70E-01	BRUNOL5	bruno-like 5, RNA binding protein (Drosophila)	chr19p13	232416_at	NM_021938
2.17	2.36	0.19	1.97E-01	5.70E-01	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	chr19q13.2	217133_x_at	NM_000767
2.83	3.03	0.20	1.97E-01	5.70E-01	---	---	---	240568_at	---
2.60	2.84	0.24	1.97E-01	5.70E-01	GNG2	guanine nucleotide binding protein (G protein), gamma 2	chr14q21	223943_s_at	NM_053064
2.98	3.18	0.20	1.97E-01	5.70E-01	UPK3A	uroplakin 3A	chr22q13.31	206771_at	NM_006953
3.54	3.77	0.23	1.97E-01	5.70E-01	GATA4	GATA binding protein 4	chr8p23.1-p22	230855_at	NM_002052
2.12	2.33	0.21	1.97E-01	5.70E-01	FAM47C	family with sequence similarity 47, member C	chrXp21.1	239732_x_at	NM_001013736
4.01	4.24	0.23	1.97E-01	5.70E-01	HCFC2	host cell factor C2	chr12q23.3	235264_at	NM_013320
2.29	2.46	0.17	1.97E-01	5.70E-01	STRAP	Serine/threonine kinase receptor associated protein	chr12p12.3	1558002_at	NM_007178
2.81	2.97	0.16	1.97E-01	5.70E-01	---	---	---	1556994_at	---
3.66	3.98	0.32	1.97E-01	5.70E-01	---	---	---	239957_at	---
2.78	3.03	0.25	1.97E-01	5.70E-01	DNAJB8	DnaJ (Hsp40) homolog, subfamily B, member 8	chr3q21.3	237284_at	NM_153330

4.73	5.04	0.31	1.97E-01	5.70E-01	LIMCH1	LIM and calponin homology domains 1	chr4p13	232457_at	NM_001112717 /// NM_001112718 /// NM_001112719 /// NM_001112720 /// NM_014988
4.51	4.80	0.29	1.97E-01	5.71E-01	---	---	---	242203_at	---
2.09	2.27	0.18	1.97E-01	5.71E-01	UTS2	urotensin 2	chr1p36	220785_at	NM_006786 /// NM_021995
4.47	4.97	0.50	1.97E-01	5.71E-01	ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	chr17q25.1	204542_at	NM_006456
2.60	2.93	0.34	1.98E-01	5.71E-01	---	---	---	1557487_at	---
2.23	2.39	0.17	1.98E-01	5.71E-01	---	---	---	233668_at	---
2.34	2.50	0.16	1.98E-01	5.71E-01	---	---	---	1570044_at	---
5.64	6.39	0.75	1.98E-01	5.71E-01	MAP3K7	mitogen-activated protein kinase kinase kinase 7	chr6q16.1-q16.3	211537_x_at	NM_003188 /// NM_145331 /// NM_145332 /// NM_145333
3.81	4.07	0.26	1.98E-01	5.71E-01	---	---	---	239060_at	---
6.56	7.16	0.60	1.98E-01	5.71E-01	MBD4	methyl-CpG binding domain protein 4	chr3q21-q22	209579_s_at	NM_003925
2.02	2.22	0.19	1.98E-01	5.71E-01	OR7D2	olfactory receptor, family 7, subfamily D, member 2	chr19p13.2	1562337_at	NM_175883
5.11	5.67	0.56	1.98E-01	5.71E-01	---	---	---	238883_at	---
3.27	3.52	0.25	1.98E-01	5.71E-01	---	---	---	241488_at	---
3.55	3.79	0.24	1.98E-01	5.71E-01	---	---	---	222323_at	---
2.59	2.79	0.20	1.98E-01	5.71E-01	SIM1	single-minded homolog 1 (Drosophila)	chr6q16.3-q21	206876_at	NM_005068
6.33	7.26	0.93	1.98E-01	5.71E-01	PCM1	pericentriolar material 1	chr8p22-p21.3	202174_s_at	NM_006197
4.95	5.09	0.14	1.98E-01	5.71E-01	FAM104B	family with sequence similarity 104, member B	chrXp11.21	227869_at	NM_138362
6.43	6.94	0.51	1.98E-01	5.71E-01	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	chr14q23.3	201142_at	NM_004094
2.88	3.10	0.22	1.98E-01	5.71E-01	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	chr3q26.1	231524_at	NM_003471 /// NM_172159 /// NM_172160
8.77	9.35	0.58	1.98E-01	5.71E-01	CCT8	chaperonin containing TCP1, subunit 8 (theta)	chr21q22.11	200873_s_at	NM_006585
7.04	7.54	0.50	1.98E-01	5.71E-01	AZIN1	antizyme inhibitor 1	chr8q22.3	212461_at	NM_015878 /// NM_148174
6.72	7.18	0.46	1.98E-01	5.71E-01	41339	membrane-associated ring finger (C3HC4) 6	chr5p15.2	201737_s_at	NM_005885
3.19	3.46	0.26	1.98E-01	5.71E-01	---	---	---	241630_at	---
4.86	5.10	0.24	1.98E-01	5.71E-01	CTSZ	Cathepsin Z	chr20q13	212562_s_at	NM_001336
3.03	3.19	0.15	1.98E-01	5.71E-01	---	---	---	244160_at	---
3.91	4.18	0.27	1.98E-01	5.71E-01	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	chr3q24-q25	229760_at	NM_024621
2.36	2.55	0.19	1.98E-01	5.71E-01	---	---	---	1556505_at	---
2.57	2.76	0.18	1.98E-01	5.71E-01	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	chr21q22.1-q22.2|21q22.11	1564482_at	NM_001697
2.70	2.92	0.21	1.98E-01	5.72E-01	---	---	---	238882_at	---
2.26	2.45	0.19	1.98E-01	5.72E-01	---	---	---	1562864_at	---
2.29	2.48	0.19	1.98E-01	5.72E-01	COBL	cordon-bleu homolog (mouse)	chr7p12.1	213050_at	NM_015198
2.35	2.53	0.17	1.98E-01	5.72E-01	LOC399900	hypothetical gene supported by AK093779	chr11q12.3	1560058_at	XR_040387
2.00	2.17	0.16	1.98E-01	5.72E-01	---	---	---	235952_at	---
1.95	2.10	0.16	1.98E-01	5.72E-01	PRO0471	hypothetical LOC28994	chr3p13-q26.1	224231_at	---
6.45	6.65	0.20	1.98E-01	5.72E-01	ITGB1BP1	integrin beta 1 binding protein 1	chr2p25.2	203336_s_at	NM_004763 /// NM_022334
2.08	2.29	0.21	1.98E-01	5.72E-01	LOC100131317	similar to hCG1781072	---	239997_at	XM_001722446
3.71	4.00	0.29	1.99E-01	5.72E-01	TOR2A	Torsin family 2, member A	chr9q34.11	244155_x_at	NM_001085347 /// NM_001134430 /// NM_001134431 /// NM_130459
2.10	2.33	0.23	1.99E-01	5.72E-01	KRTAP4-11	keratin associated protein 4-11	chr17q12-q21	234633_at	NM_033059
2.84	3.04	0.20	1.99E-01	5.72E-01	AQP12A /// AQP12B	aquaporin 12A /// aquaporin 12B	chr2q37.3	1559575_a_at	NM_001102467 /// NM_198998
2.22	2.41	0.19	1.99E-01	5.72E-01	---	---	---	1564510_at	---
2.49	2.70	0.21	1.99E-01	5.72E-01	LOC339524	hypothetical protein LOC339524	chr1p22.3	233673_at	XR_039940 /// XR_039941 /// XR_039942
6.46	6.90	0.45	1.99E-01	5.72E-01	DENND4C	DENN/MADD domain containing 4C	chr9p22.1	226867_at	NM_017925
3.84	4.13	0.29	1.99E-01	5.72E-01	LOC138948	BPR	chr9q34.2	230488_s_at	NR_002783
3.48	3.74	0.26	1.99E-01	5.72E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	216852_x_at	---
2.35	2.57	0.22	1.99E-01	5.72E-01	OR5I1	olfactory receptor, family 5, subfamily I, member 1	chr11q11	208521_at	NM_006637
2.54	2.76	0.22	1.99E-01	5.72E-01	FMO5	flavin containing monooxygenase 5	chr1q21.1	215300_s_at	NM_001461
2.20	2.42	0.22	1.99E-01	5.72E-01	---	---	---	228734_at	---

2.79	3.00	0.21	1.99E-01	5.72E-01	LOC100128552	Similar to hCG1986848	chr2q12.1	244797_at	XM_001715075 /// XM_001715316 /// XM_001715317
2.89	3.06	0.17	1.99E-01	5.72E-01	FLJ21408	hypothetical gene supported by AK025061	chr16p12.1	234627_at	---
2.45	2.60	0.16	1.99E-01	5.72E-01	LAG3	lymphocyte-activation gene 3	chr12p13.32	206486_at	NM_002286
3.01	3.51	0.50	1.99E-01	5.72E-01	---	---	---	1565566_a_at	---
2.71	3.20	0.48	1.99E-01	5.72E-01	FBXW2	F-box and WD repeat domain containing 2	chr9q34	235195_at	NM_012164
5.51	5.80	0.29	1.99E-01	5.72E-01	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	chr9p11.1	209645_s_at	NM_000692
3.45	3.68	0.23	1.99E-01	5.72E-01	---	---	---	241552_at	---
3.06	3.29	0.23	1.99E-01	5.72E-01	AMZ1	archaelysin family metallopeptidase 1	chr7p22.2	1562261_at	NM_133463
4.78	5.01	0.23	1.99E-01	5.72E-01	ZNF777	zinc finger protein 777	chr7q36.1	237855_at	NM_015694
2.14	2.34	0.20	1.99E-01	5.72E-01	---	---	---	244042_x_at	---
2.28	2.46	0.18	1.99E-01	5.72E-01	TGFA	transforming growth factor, alpha	chr2p13	205016_at	NM_001099691 /// NM_003236
2.95	3.12	0.17	1.99E-01	5.72E-01	---	---	---	233135_at	---
2.72	2.89	0.17	1.99E-01	5.72E-01	MAN1A2	Mannosidase, alpha, class 1A, member 2	chr1p13	214242_at	NM_006699
2.21	2.38	0.16	1.99E-01	5.72E-01	SNORA74A	small nucleolar RNA, H/ACA box 74A	chr5q31.2	1567682_x_at	NR_002915
2.04	2.18	0.14	1.99E-01	5.72E-01	LOC284926	hypothetical protein LOC284926	chr22q13.31	1556065_at	---
7.66	8.22	0.56	1.99E-01	5.73E-01	CUL3	cullin 3	chr2q36.2	201371_s_at	NM_003590
5.77	6.25	0.48	1.99E-01	5.73E-01	---	---	---	237895_at	---
2.95	3.32	0.37	1.99E-01	5.73E-01	ZNF616	zinc finger protein 616	chr19q13.33	232137_at	NM_178523
5.77	6.01	0.24	1.99E-01	5.73E-01	ZNF264	zinc finger protein 264	chr19q13.4	230063_at	NM_003417
2.76	2.95	0.19	1.99E-01	5.73E-01	FAM81A	Family with sequence similarity 81, member A	chr15q22.2	241481_at	NM_152450
2.38	2.57	0.19	1.99E-01	5.73E-01	PRLHR	prolactin releasing hormone receptor	chr10q26.13	231805_at	NM_004248
3.14	3.38	0.24	1.99E-01	5.73E-01	SLC13A4	solute carrier family 13 (sodium/sulfate symporters), member 4	chr7q33	219824_at	NM_012450
3.97	4.39	0.43	1.99E-01	5.73E-01	MYCT1	myc target 1	chr6q25.2	231947_at	NM_025107
3.61	3.92	0.31	1.99E-01	5.73E-01	MMP11	matrix metallopeptidase 11 (stromelysin 3)	chr22q11.2|22q11.23	203876_s_at	NM_005940
1.80	1.93	0.14	1.99E-01	5.73E-01	---	---	---	1564192_at	---
3.70	4.03	0.32	1.99E-01	5.73E-01	SOCS3	suppressor of cytokine signaling 3	chr17q25.3	214105_at	NM_003955
2.36	2.52	0.16	1.99E-01	5.73E-01	---	---	---	240842_at	---
2.28	2.51	0.23	1.99E-01	5.73E-01	EGFL6	EGF-like-domain, multiple 6	chrXp22	219454_at	NM_015507
3.29	3.56	0.27	1.99E-01	5.73E-01	---	---	---	241445_at	---
6.46	7.19	0.73	1.99E-01	5.73E-01	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	chr11q13.2	218242_s_at	NM_016028 /// NM_017635
1.93	2.13	0.20	1.99E-01	5.73E-01	---	---	---	236219_at	---
8.71	9.38	0.67	2.00E-01	5.73E-01	DDR2	discoidin domain receptor tyrosine kinase 2	chr1q23.3	225442_at	NM_001014796 /// NM_006182
5.73	6.26	0.52	1.99E-01	5.73E-01	IL1R2	interleukin 1 receptor, type II	chr2q12-q22	205403_at	NM_004633 /// NM_173343
7.40	7.81	0.41	2.00E-01	5.73E-01	DICER1	dicer 1, ribonuclease type III	chr14q32.13	213229_at	NM_030621 /// NM_177438
2.11	2.43	0.32	2.00E-01	5.73E-01	---	---	---	1562848_at	---
5.59	5.85	0.26	2.00E-01	5.73E-01	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	chr16p13.3	213177_at	NM_001040439 /// NM_015133
2.91	3.15	0.24	1.99E-01	5.73E-01	MPRIP	Myosin phosphatase Rho interacting protein	chr17p11.2	238330_s_at	NM_015134 /// NM_201274
2.12	2.30	0.18	2.00E-01	5.73E-01	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	chr5q11.1	1555057_at	NM_002495
5.94	6.70	0.76	2.00E-01	5.73E-01	RHOU	ras homolog gene family, member U	chr1q42.11-q42.3	223168_at	NM_021205
5.04	5.23	0.19	2.00E-01	5.73E-01	LOC654780	SFPQ	chr16q24.1	1562428_at	XR_040611 /// XR_040612 /// XR_040613
3.06	3.24	0.17	2.00E-01	5.73E-01	---	---	---	221148_at	---
2.80	3.01	0.21	2.00E-01	5.73E-01	CD6	CD6 molecule	chr11q13	1566099_at	NM_006725
2.17	2.69	0.52	2.00E-01	5.73E-01	SLC38A4	solute carrier family 38, member 4	chr12q13	1555345_at	NM_018018
8.07	8.77	0.70	2.00E-01	5.73E-01	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	chr2p24	201241_at	NM_004939
6.96	7.49	0.53	2.00E-01	5.73E-01	GSPT1	G1 to S phase transition 1	chr16p13.1	225276_at	NM_001130006 /// NM_001130007 /// NM_002094
5.13	5.44	0.32	2.00E-01	5.73E-01	LOC100133432 /// MUC6	similar to Mucin-6 precursor (Gastric mucin-6) /// mucin 6, oligomeric mucus/gel-forming	chr11p15.5-p15.4	214133_at	NM_005961 /// XM_001714734
7.52	7.77	0.25	2.00E-01	5.73E-01	AATF	apoptosis antagonizing transcription factor	chr17q11.2-q12	209165_at	NM_012138
2.38	2.60	0.22	2.00E-01	5.73E-01	---	---	---	1556963_at	---

2.51	2.73	0.21	2.00E-01	5.73E-01	CPEB1	cytoplasmic polyadenylation element binding protein 1	chr15q25.2	222903_s_at	NM_001079533 /// NM_001079534 /// NM_001079535 /// NM_030594
3.07	3.26	0.19	2.00E-01	5.73E-01	IL28A /// IL28B	interleukin 28A (interferon, lambda 2) /// interleukin 28B (interferon, lambda 3)	chr19q13.13	1552609_s_at	NM_172138 /// NM_172139
2.08	2.26	0.18	2.00E-01	5.73E-01	CNBD1	cyclic nucleotide binding domain containing 1	chr8q21.3	1552588_a_at	NM_173538
2.26	2.43	0.17	2.00E-01	5.73E-01	---	---	---	1566809_a_at	---
1.96	2.10	0.14	2.00E-01	5.73E-01	---	---	---	230356_at	---
5.61	5.89	0.27	2.00E-01	5.73E-01	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	chr11q24	208397_x_at	NM_000890
5.84	6.40	0.57	2.00E-01	5.73E-01	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	chr10q24	229450_at	NM_001031683 /// NM_001549
2.25	2.48	0.23	2.00E-01	5.73E-01	---	---	---	241885_at	---
2.15	2.35	0.21	2.00E-01	5.73E-01	C9orf96	chromosome 9 open reading frame 96	chr9q34.2	1554787_at	NM_153710
5.37	5.87	0.49	2.00E-01	5.73E-01	DCP1A	DCP1 decapping enzyme homolog A (S. cerevisiae)	chr3p21.1	218508_at	NM_018403
2.34	2.54	0.20	2.00E-01	5.73E-01	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	chr7q32	215850_s_at	NM_005000
3.11	3.30	0.19	2.00E-01	5.73E-01	---	---	---	234152_at	---
2.17	2.32	0.15	2.00E-01	5.73E-01	GAB3	GRB2-associated binding protein 3	chrXq28	241259_at	NM_001081573 /// NM_080612
2.84	3.15	0.32	2.00E-01	5.74E-01	GRSF1	G-rich RNA sequence binding factor 1	chr4q13	221917_s_at	NM_001098477 /// NM_002092
2.53	2.78	0.24	2.00E-01	5.74E-01	LOC728613	programmed cell death 6 pseudogene	chr5p15.33	229283_at	NR_003713
2.68	2.92	0.24	2.00E-01	5.74E-01	ZNF107	Zinc finger protein 107	chr7q11.2	243312_at	NM_001013746 /// NM_016220
2.37	2.53	0.17	2.00E-01	5.74E-01	ALDOB	Aldolase B, fructose-bisphosphate	chr9q21.3-q22.2	241280_at	NM_000035
5.19	5.43	0.24	2.00E-01	5.74E-01	FLJ11710	hypothetical protein FLJ11710	chr17q23.2	220529_at	---
7.28	7.45	0.18	2.00E-01	5.74E-01	PGF	Placental growth factor	chr14q24-q31	215179_x_at	NM_002632
4.79	5.46	0.67	2.00E-01	5.74E-01	FNDC3B	Fibronectin type III domain containing 3B	chr3q26.31	242029_at	NM_022763
2.71	2.95	0.25	2.00E-01	5.74E-01	ATXN7L1	ataxin 7-like 1	chr7q22.2	214342_at	NM_020725 /// NM_152749
2.72	2.92	0.20	2.00E-01	5.74E-01	ELAC2	elaC homolog 2 (E. coli)	chr17p11.2	201766_at	NM_018127
2.46	2.66	0.19	2.00E-01	5.74E-01	DAO	D-amino-acid oxidase	chr12q24	206878_at	NM_001917
2.36	2.63	0.27	2.01E-01	5.74E-01	SLC39A9	Solute carrier family 39 (zinc transporter), member 9	chr14q24.1	216011_at	NM_018375
3.23	3.42	0.19	2.01E-01	5.74E-01	CST9	cystatin 9 (testatin)	chr20p11.21	1554386_at	NM_001008693
4.33	4.51	0.18	2.01E-01	5.74E-01	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	chr12q13	1563252_at	NM_001005915 /// NM_001982
2.65	2.92	0.27	2.01E-01	5.74E-01	SLC25A27	Solute carrier family 25, member 27	chr6p11.2-q12	229361_at	NM_004277
2.98	3.20	0.22	2.01E-01	5.74E-01	---	---	---	1566183_at	---
4.57	5.12	0.54	2.01E-01	5.74E-01	RBL2	retinoblastoma-like 2 (p130)	chr16q12.2	212332_at	NM_005611
4.98	5.25	0.27	2.01E-01	5.74E-01	ITGB4	integrin, beta 4	chr17q25	204990_s_at	NM_000213 /// NM_001005619 /// NM_001005731
3.02	3.24	0.22	2.01E-01	5.74E-01	---	---	---	233152_x_at	---
2.48	2.66	0.18	2.01E-01	5.74E-01	---	---	---	242156_at	---
4.74	5.04	0.30	2.01E-01	5.74E-01	LOC492311	similar to bovine IgA regulatory protein	chr5q31	241874_at	NM_001007189
3.81	4.08	0.27	2.01E-01	5.74E-01	CHADL	chondroadherin-like	chr22q13.2	1557123_a_at	NM_138481 /// XM_377720 /// XM_940422
2.80	3.11	0.30	2.01E-01	5.74E-01	ZNF688	zinc finger protein 688	chr16p11.2	235951_s_at	NM_001024683 /// NM_145271
4.05	4.32	0.27	2.01E-01	5.74E-01	ACTL8	actin-like 8	chr1p36.2-p35	214957_at	NM_030812
2.52	2.68	0.16	2.01E-01	5.74E-01	---	---	---	241505_at	---
2.28	2.44	0.15	2.01E-01	5.74E-01	SPRR2C	small proline-rich protein 2C (pseudogene)	chr1q21-q22	220664_at	NR_003062
3.15	3.44	0.29	2.01E-01	5.74E-01	ST7L	suppression of tumorigenicity 7 like	chr1p13.2	233141_s_at	NM_017744 /// NM_138727 /// NM_138728 /// NM_138729
2.68	2.86	0.18	2.01E-01	5.74E-01	TTN	titin	chr2q31	1557994_at	NM_003319 /// NM_133378 /// NM_133379 /// NM_133432 /// NM_133437

2.26	2.48	0.22	2.01E-01	5.75E-01	LOC441383 /// ZNF252	hypothetical gene supported by AF086559; BC065734 /// zinc finger protein 252	chr8q24.3	1558722_at	NR_023392 /// XM_001714325 /// XM_001714728 /// XM_001714801																				
4.31	4.51	0.20	2.01E-01	5.75E-01	COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	chr10q24	235855_at	NM_004376 /// NM_078470																				
2.90	3.08	0.18	2.01E-01	5.75E-01	---	---	---	244810_at	---																				
6.68	7.68	1.00	2.01E-01	5.75E-01	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	chr5q31-q34	224963_at	NM_000112																				
3.99	4.72	0.73	2.01E-01	5.75E-01	TPSAB1 /// TPSB2	tryptase alpha/beta 1 /// tryptase beta 2	chr16p13.3	217023_x_at	NM_003294 /// NM_024164 /// XM_001720738 /// XM_001720740																				
3.60	3.87	0.26	2.01E-01	5.75E-01	CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6	chr19q13.2	1494_f_at	NM_000762																				
1.97	2.28	0.31	2.01E-01	5.75E-01	CLEC4C	C-type lectin domain family 4, member C	chr12p13.2-p12.3	1555687_a_at	NM_130441 /// NM_203503																				
2.96	3.23	0.27	2.01E-01	5.75E-01	LOC653786	otoancorin pseudogene	chr16p12.1	242114_at	NR_003676 /// XR_017362																				
1.92	2.18	0.26	2.01E-01	5.75E-01	CHD5	chromodomain helicase DNA binding protein 5	chr1p36.31	217250_s_at	NM_015557																				
3.12	3.33	0.21	2.01E-01	5.75E-01	---	---	---	243187_at	---																				
3.12	3.44	0.31	2.01E-01	5.75E-01	FAM33A	family with sequence similarity 33, member A	chr17q22	225686_at	NM_001100595 /// NM_182620																				
2.80	3.11	0.31	2.01E-01	5.75E-01	LOC284865	hypothetical protein LOC284865	chr22q11.21	1564109_at	---																				
2.18	2.34	0.15	2.01E-01	5.75E-01	---	---	---	234217_at	---																				
1.89	2.04	0.15	2.01E-01	5.75E-01	ARPP-21	cyclic AMP-regulated phosphoprotein, 21 kD	chr3p22.3	1552722_at	NM_001025068 /// NM_001025069 /// NM_016300 /// NM_198399																				
3.31	3.54	0.23	2.01E-01	5.75E-01	---	---	---	216655_s_at	---																				
2.47	2.66	0.19	2.01E-01	5.75E-01	TMCO3	Transmembrane and coiled-coil domains 3	chr13q34	230317_x_at	NM_017905																				
8.62	8.92	0.30	2.01E-01	5.75E-01	TKT	transketolase	chr3p14.3	208699_x_at	NM_001064																				
1.82	1.96	0.14	2.02E-01	5.75E-01	USP53	ubiquitin specific peptidase 53	chr4q26	216775_at	NM_019050																				
2.63	2.84	0.20	2.02E-01	5.75E-01	DENND2C	DENN/MADD domain containing 2C	chr1p13.2	233294_at	NM_198459																				
2.54	2.82	0.28	2.02E-01	5.75E-01	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	chr18q21.3-q22	211362_s_at	NM_012397																				
5.31	5.88	0.57	2.02E-01	5.75E-01	OSTM1	osteopetrosis associated transmembrane protein 1	chr6q21	218196_at	NM_014028																				
2.82	3.03	0.20	2.02E-01	5.75E-01	MAP3K7IP1	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1	chr22q13.1	235480_at	NM_006116 /// NM_153497																				
2.94	3.13	0.19	2.02E-01	5.75E-01	CD59	CD59 molecule, complement regulatory protein	chr11p13	228748_at	NM_000611 /// NM_001127223 /// NM_001127225 /// NM_001127226 /// NM_001127227 /// NM_203329 /// NM_203330 /// NM_203331																				
2.57	2.73	0.16	2.02E-01	5.75E-01	---	---	---	1560844_at	---																				
4.44	4.85	0.40	2.02E-01	5.75E-01	CSRP2BP	CSRP2 binding protein	chr20p11.23	225432_s_at	NM_020536 /// NM_177926																				
7.13	7.37	0.24	2.02E-01	5.75E-01	MRPS18A	mitochondrial ribosomal protein S18A	chr6p21.3	218385_at	NM_018135																				
2.15	2.44	0.29	2.02E-01	5.75E-01	INSM1	insulinoma-associated 1	chr20p11.2	206502_s_at	NM_002196																				
2.66	2.93	0.27	2.02E-01	5.75E-01	---	---	---	1570349_at	---																				
2.23	2.41	0.18	2.02E-01	5.75E-01	---	---	---	242827_x_at	---																				
2.18	2.39	0.21	2.02E-01	5.76E-01	HRNBP3 /// LOC100130312 /// LOC100133332	hexaribonucleotide binding protein 3 /// hypothetical protein LOC100130312 /// hypothetical protein LOC100133332	chr17q25.3	235468_at	NM_001082575 /// XM_001713646 /// XM_001713647																				
5.45	5.67	0.22	2.02E-01	5.76E-01	MED13L	mediator complex subunit 13-like	chr12q24.21	212207_at	NM_015335																				
1.81	1.96	0.15	2.02E-01	5.76E-01	LOC338862	hypothetical protein LOC338862	chr13q21.33	1557717_at	---																				
3.27	3.60	0.33	2.02E-01	5.76E-01	---	---	---	238420_at	---																				
4.69	5.50	0.81	2.02E-01	5.76E-01	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	chr16q24.1	204613_at	NM_002661																				
2.14	2.33	0.19	2.02E-01	5.76E-01	---	---	---	243625_at	---																				
3.05	3.24	0.19	2.02E-01	5.76E-01	---	---	---	208144_s_at	---																				
5.94	6.27	0.33	2.02E-01	5.76E-01	BRAP	BRCA1 associated protein	chr12q24	213473_at	NM_006768																				
5.43	5.97	0.54	2.02E-01	5.76E-01	ZFAND1	zinc finger, AN1-type domain 1	chr8q21.13	218919_at	NM_024699																				

2.28	2.46	0.18	2.02E-01	5.76E-01	AK5	adenylate kinase 5	chr1p31	219308_s_at	NM_012093 /// NM_174858
4.92	5.19	0.27	2.02E-01	5.76E-01	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	chr12q	219634_at	NM_018413
2.83	3.02	0.20	2.02E-01	5.76E-01	ZNF461	zinc finger protein 461	chr19q13.12	232391_at	NM_153257
5.48	5.91	0.43	2.02E-01	5.76E-01	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	chr2p21	202551_s_at	NM_016441
1.99	2.15	0.16	2.02E-01	5.76E-01	---	---	---	231063_at	---
2.11	2.28	0.16	2.02E-01	5.76E-01	---	---	---	1556655_s_at	---
5.19	5.45	0.26	2.02E-01	5.76E-01	EFNB1	ephrin-B1	chrXq12	202711_at	NM_004429
7.15	7.38	0.23	2.02E-01	5.76E-01	---	---	---	235084_x_at	---
1.92	2.09	0.17	2.02E-01	5.76E-01	---	---	---	244688_at	---
1.95	2.11	0.16	2.02E-01	5.76E-01	CNGA3	cyclic nucleotide gated channel alpha 3	chr2q11.2	207261_at	NM_001079878 /// NM_001298
2.09	2.25	0.16	2.02E-01	5.76E-01	---	---	---	237573_at	---
7.34	7.56	0.22	2.03E-01	5.76E-01	RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	chr2cen-q13	202100_at	NM_002881
1.75	1.93	0.19	2.03E-01	5.76E-01	---	---	---	1566439_at	---
3.30	3.48	0.17	2.03E-01	5.76E-01	SAA3P	serum amyloid A3 pseudogene	chr11p15.1-p14	222226_at	---
3.52	3.75	0.23	2.03E-01	5.76E-01	---	---	---	241409_at	---
2.20	2.39	0.19	2.03E-01	5.76E-01	---	---	---	1566767_at	---
2.05	2.20	0.15	2.03E-01	5.76E-01	---	---	---	233351_at	---
4.12	4.34	0.22	2.03E-01	5.77E-01	---	---	---	240535_at	---
2.36	2.55	0.19	2.03E-01	5.77E-01	ADCK4	aarF domain containing kinase 4	chr19q13.2	220434_at	NM_024876
3.04	3.25	0.21	2.03E-01	5.77E-01	---	---	---	237621_at	---
2.52	3.04	0.53	2.03E-01	5.77E-01	---	---	---	233799_at	---
7.24	8.22	0.98	2.03E-01	5.77E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	1553678_a_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376
1.84	2.01	0.16	2.03E-01	5.77E-01	RAB27B	RAB27B, member RAS oncogene family	chr18q21.2	207018_s_at	NM_004163
2.32	2.51	0.19	2.03E-01	5.77E-01	ZSWIM4	zinc finger, SWIM-type containing 4	chr19p13.13-p13.12	231915_at	NM_023072
5.57	5.78	0.22	2.03E-01	5.77E-01	C1orf113	chromosome 1 open reading frame 113	chr1p34.3	220193_at	NM_024676
3.98	4.16	0.18	2.03E-01	5.77E-01	HOXC8	homeobox C8	chr12q13.3	221350_at	NM_022658
3.17	3.39	0.23	2.03E-01	5.77E-01	ADPRHL1	ADP-ribosylhydrolase like 1	chr13q34	1553163_at	NM_138430 /// NM_199162
2.32	2.77	0.44	2.03E-01	5.77E-01	TCEAL2	transcription elongation factor A (SII)-like 2	chrXq22.1-q22.3	211276_at	NM_080390
2.97	3.22	0.25	2.03E-01	5.77E-01	---	---	---	238879_at	---
3.80	4.02	0.22	2.03E-01	5.77E-01	LOC100129026	hypothetical protein LOC100129026	chr5q35.1	226578_s_at	XM_001715125 /// XM_001715856 /// XM_001718088
3.57	3.87	0.30	2.03E-01	5.77E-01	EGLN2	Egl nine homolog 2 (C. elegans)	chr19q13.2	227147_s_at	NM_053046 /// NM_080732
2.13	2.27	0.14	2.03E-01	5.77E-01	CR2	complement component (3d/Epstein Barr virus) receptor 2	chr1q32	205544_s_at	NM_001006658 /// NM_001877
4.31	4.57	0.26	2.03E-01	5.77E-01	SIGLEC7	sialic acid binding Ig-like lectin 7	chr19q13.3	216537_s_at	NM_014385 /// NM_016543
7.32	7.94	0.62	2.03E-01	5.77E-01	COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	chr8q13.2	201652_at	NM_006837
2.17	2.41	0.24	2.03E-01	5.77E-01	---	---	---	1559780_at	---
2.33	2.79	0.46	2.03E-01	5.77E-01	CALB1	calbindin 1, 28kDa	chr8q21.3-q22.1	205625_s_at	NM_004929
2.64	2.85	0.22	2.03E-01	5.77E-01	---	---	---	243869_at	---
9.80	9.98	0.18	2.03E-01	5.77E-01	PSAP	prosaposin	chr10q21-q22	200866_s_at	NM_001042465 /// NM_001042466 /// NM_002778
2.84	3.05	0.21	2.03E-01	5.77E-01	RBMY3AP	RNA binding motif protein, Y-linked, family 3, member A pseudogene	chrYp11.2	1565132_at	NR_001573
2.38	2.53	0.15	2.03E-01	5.77E-01	KCNJ12 /// LOC100131509 /// LOC100134444	potassium inwardly-rectifying channel, subfamily J, member 12 /// similar to inward rectifying K+ channel negative regulator Kir2.2v /// similar to hkir2.2x	chr17p11.2	208567_s_at	NM_021012 /// XM_001718636 /// XM_001720057

7.14	7.63	0.49	2.03E-01	5.78E-01	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	chr8q11.23	226119_at	NM_052937
2.40	2.66	0.26	2.03E-01	5.78E-01	KLRG2	killer cell lectin-like receptor subfamily G, member 2	chr7q34	244264_at	NM_198508
2.65	2.83	0.18	2.03E-01	5.78E-01	LMOD2	leiomodin 2 (cardiac)	chr7q31.32	239057_at	NM_207163
2.90	3.07	0.17	2.04E-01	5.78E-01	---	---	---	240169_at	---
5.37	5.65	0.27	2.04E-01	5.78E-01	PDE3B	Phosphodiesterase 3B, cGMP-inhibited	chr11p15.1	231276_at	NM_000922
3.04	3.30	0.25	2.04E-01	5.78E-01	HOXD11	homeobox D11	chr2q31.1	214604_at	NM_021192
7.57	7.85	0.28	2.04E-01	5.78E-01	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	chr2q21.3	213531_s_at	NM_012233
5.98	6.24	0.26	2.04E-01	5.78E-01	C17orf96	chromosome 17 open reading frame 96	chr17q12	228066_at	NM_001130677
5.05	5.29	0.24	2.04E-01	5.78E-01	CTXN1	cortexin 1	chr19p13.2	228126_x_at	NM_206833
2.38	2.58	0.19	2.04E-01	5.78E-01	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	chr3q29	240926_at	NM_032773
2.53	2.72	0.18	2.04E-01	5.78E-01	---	---	---	232795_at	---
7.03	7.20	0.17	2.04E-01	5.78E-01	RTN3	reticulon 3	chr11q13	224564_s_at	NM_006054 /// NM_201428 /// NM_201429 /// NM_201430
4.13	4.37	0.24	2.04E-01	5.78E-01	CREBBP	CREB binding protein	chr16p13.3	235858_at	NM_001079846 /// NM_004380
8.30	8.55	0.25	2.04E-01	5.78E-01	---	---	---	230958_s_at	---
8.24	8.90	0.66	2.04E-01	5.78E-01	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	229353_s_at	NM_022731
6.03	6.45	0.41	2.04E-01	5.78E-01	HEG1	HEG homolog 1 (zebrafish)	chr3q21.2	213069_at	NM_020733
3.06	3.24	0.18	2.04E-01	5.78E-01	C1orf65	chromosome 1 open reading frame 65	chr1q41	1552391_at	NM_152610
3.96	4.94	0.98	2.04E-01	5.78E-01	IGKC /// IGKV1-5 /// LOC100130100 /// LOC647506 /// LOC650405 /// LOC652493 /// LOC652694	immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5 /// similar to hCG26659 /// similar to Ig kappa chain V-I region HK101 precursor /// similar to Ig kappa chain V-I region HK102 precursor /// similar to Ig kappa chain V-I region HK102 precursor /// similar to Ig kappa chain V-I region HK102 precursor	chr2p12 /// chr2q14.1	216207_x_at	XM_001713938 /// XM_001715827 /// XM_001716310 /// XM_001716615 /// XM_001724425 /// XM_942302
2.68	2.90	0.22	2.04E-01	5.78E-01	RPL7	ribosomal protein L7	chr8q21.11	239493_at	NM_000971
5.51	5.84	0.33	2.04E-01	5.78E-01	TRIM62	tripartite motif-containing 62	chr1p35.1	236845_at	NM_018207
2.51	2.81	0.30	2.04E-01	5.78E-01	LOC202181	hypothetical protein LOC202181	chr5q35.3	220609_at	XR_015120 /// XR_015544 /// XR_040243
1.93	2.07	0.15	2.04E-01	5.78E-01	ALS2CR11	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	chr2q33.1	1553260_s_at	NM_152525
3.19	3.50	0.31	2.04E-01	5.78E-01	OR10D1P	olfactory receptor, family 10, subfamily D, member 1 pseudogene	chr11q24.2	1567255_at	---
2.73	3.09	0.36	2.04E-01	5.78E-01	---	---	---	235784_at	---
4.23	4.49	0.26	2.04E-01	5.78E-01	C22orf34	chromosome 22 open reading frame 34	chr22q13.33	235839_at	XR_040809 /// XR_040810 /// XR_040811
2.11	2.28	0.18	2.04E-01	5.78E-01	---	---	---	243060_at	---
2.08	2.25	0.17	2.04E-01	5.78E-01	FKSG83	FKSG83	chr6p22.1	224289_s_at	NM_032030
2.24	2.43	0.18	2.04E-01	5.78E-01	DCX	doublecortin	chrXq22.3|Xq22.3-q23	204850_s_at	NM_000555 /// NM_178151 /// NM_178152 /// NM_178153
3.56	3.78	0.22	2.04E-01	5.78E-01	C17orf67	chromosome 17 open reading frame 67	chr17q22	236863_at	NM_001085430
2.25	2.41	0.16	2.04E-01	5.78E-01	---	---	---	232496_at	---
6.96	7.13	0.16	2.04E-01	5.78E-01	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	chr20p12	201206_s_at	NM_001042576 /// NM_004587
3.47	3.73	0.25	2.04E-01	5.78E-01	DTX3	deltex 3 homolog (Drosophila)	chr12q13.3	221835_at	NM_178502
3.09	3.31	0.22	2.04E-01	5.79E-01	FAM173B	family with sequence similarity 173, member B	chr5p15.2	225668_at	NM_199133
5.30	6.09	0.79	2.05E-01	5.79E-01	---	---	---	226587_at	---
6.64	7.15	0.51	2.05E-01	5.79E-01	NT5C3	5'-nucleotidase, cytosolic III	chr7p14.3	223298_s_at	NM_001002009 /// NM_001002010 /// NM_016489
2.11	2.29	0.18	2.04E-01	5.79E-01	XG	Xg blood group	chrXp22.33	1554062_at	NM_175569
1.99	2.16	0.17	2.04E-01	5.79E-01	LOC100129973	Hypothetical protein LOC100129973	chr15q21.2	215229_at	XM_001722457 /// XM_001726190 /// XM_001726320
2.09	2.26	0.17	2.05E-01	5.79E-01	PGGT1B	Protein geranylgeranyltransferase type I, beta subunit	chr5q22.3	244684_at	NM_005023

2.65	2.91	0.26	2.05E-01	5.79E-01	---	---	---	237740_at	---
2.53	2.73	0.21	2.05E-01	5.79E-01	---	---	---	237769_at	---
1.90	2.08	0.17	2.05E-01	5.79E-01	CCDC141	coiled-coil domain containing 141	chr2q31.2	1553645_at	NM_173648
1.92	2.07	0.16	2.05E-01	5.79E-01	KIAA1659	KIAA1659 protein	---	215674_at	XM_001723799 /// XM_001725435 /// XM_001726785
3.63	3.83	0.20	2.05E-01	5.79E-01	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	chr21q22.11	208395_s_at	NM_014825
8.92	9.38	0.46	2.05E-01	5.79E-01	HSPA9	heat shock 70kDa protein 9 (mortalin)	chr5q31.1	200691_s_at	NM_004134
2.49	2.68	0.19	2.05E-01	5.79E-01	DTL	denticleless homolog (Drosophila)	chr1q32.1-q32.2	222680_s_at	NM_016448
5.48	6.48	1.00	2.05E-01	5.79E-01	---	---	---	236545_at	---
3.24	3.42	0.18	2.05E-01	5.79E-01	---	---	---	235785_at	---
2.15	2.30	0.15	2.05E-01	5.79E-01	IQCH	IQ motif containing H	chr15q23	239812_s_at	NM_001031715 /// NM_022784
2.74	2.91	0.17	2.05E-01	5.79E-01	---	---	---	241677_x_at	---
2.54	2.73	0.19	2.05E-01	5.79E-01	---	---	---	1568685_at	---
2.39	2.56	0.17	2.05E-01	5.79E-01	---	---	---	234658_at	---
2.01	2.15	0.14	2.05E-01	5.79E-01	DKFZp686O1327	hypothetical gene supported by BC043549; BX648102	chr2q22.3	1562475_at	XM_379141
3.06	3.24	0.18	2.05E-01	5.79E-01	POFUT2	protein O-fucosyltransferase 2	chr21q22.3	207448_at	NM_015227 /// NM_133634 /// NM_133635 /// NR_004858
2.66	2.82	0.16	2.05E-01	5.79E-01	---	---	---	220859_at	---
5.40	5.71	0.31	2.05E-01	5.79E-01	SLAIN2	SLAIN motif family, member 2	chr4p12	224844_at	NM_020846
2.57	2.83	0.27	2.05E-01	5.79E-01	IGHA1 /// IGHD /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM /// IGHV4-31 /// LOC652494	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// similar to Ig heavy chain V-III region VH26 precursor	chr14q32.33	216558_x_at	XM_001717586 /// XM_001719484
2.63	2.77	0.15	2.05E-01	5.79E-01	---	---	---	230074_s_at	---
4.04	4.54	0.50	2.05E-01	5.79E-01	GTDC1	glycosyltransferase-like domain containing 1	chr2q22.2-q22.3	238585_at	NM_001006636 /// NM_024659
2.78	3.05	0.27	2.05E-01	5.79E-01	ZNF239	zinc finger protein 239	chr10q11.22-q11.23	206261_at	NM_001099282 /// NM_001099283 /// NM_001099284 /// NM_005674
3.53	3.76	0.23	2.05E-01	5.79E-01	---	---	---	1556416_s_at	---
2.11	2.27	0.16	2.05E-01	5.80E-01	FGF2	fibroblast growth factor 2 (basic)	chr4q26-q27	204422_s_at	NM_002006
2.10	2.25	0.15	2.05E-01	5.80E-01	---	---	---	1562058_at	---
3.62	4.35	0.73	2.05E-01	5.80E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	217258_x_at	---
2.46	2.75	0.29	2.05E-01	5.80E-01	---	---	---	1556851_at	---
3.47	3.79	0.33	2.05E-01	5.80E-01	MAPK4	mitogen-activated protein kinase 4	chr18q12-q21	204707_s_at	NM_002747
2.35	2.54	0.19	2.05E-01	5.80E-01	---	---	---	237569_at	---
4.33	4.55	0.22	2.05E-01	5.80E-01	RARB	retinoic acid receptor, beta	chr3p24	208412_s_at	NM_000965 /// NM_016152
3.57	4.04	0.47	2.06E-01	5.80E-01	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	chr9q31.1	1570279_at	NM_005502
3.51	3.95	0.44	2.05E-01	5.80E-01	NCALD	neurocalcin delta	chr8q22.2	211685_s_at	NM_001040624 /// NM_001040625 /// NM_001040626 /// NM_001040627 /// NM_001040628 /// NM_001040629 /// NM_001040630 /// NM_032041
3.67	4.03	0.36	2.06E-01	5.80E-01	TLN1	Talin 1	chr9p13	232763_at	NM_006289
7.09	7.43	0.34	2.06E-01	5.80E-01	NSFL1C	NSFL1 (p97) cofactor (p47)	chr20p13	217831_s_at	NM_016143 /// NM_018839 /// NM_182483
3.74	3.99	0.25	2.06E-01	5.80E-01	PIGM	phosphatidylinositol glycan anchor biosynthesis, class M	chr1q23.2	235168_at	NM_145167

2.64	2.85	0.22	2.06E-01	5.80E-01	TGS1	Trimethylguanosine synthase homolog (S. cerevisiae)	chr8q11	236371_s_at	NM_024831
2.72	2.91	0.20	2.06E-01	5.80E-01	HRASLS	HRAS-like suppressor	chr3q29	219984_s_at	NM_020386
7.31	7.49	0.19	2.06E-01	5.80E-01	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	chr19p13.3	203926_x_at	NM_001001975 /// NM_001687
1.90	2.05	0.15	2.06E-01	5.80E-01	C1orf96	chromosome 1 open reading frame 96	chr1q42.13	1553697_at	NM_145257
2.76	3.02	0.26	2.06E-01	5.80E-01	PVT1	Pvt1 oncogene (non-protein coding)	chr8q24	216249_at	NR_003367
1.90	2.06	0.16	2.06E-01	5.80E-01	---	---	---	237978_at	---
2.16	2.33	0.17	2.06E-01	5.80E-01	SNTG2	syntrophin, gamma 2	chr2p25.3	220487_at	NM_018968
2.69	2.85	0.16	2.06E-01	5.80E-01	---	---	---	239563_at	---
5.27	5.78	0.50	2.06E-01	5.80E-01	NCK1	NCK adaptor protein 1	chr3q21	204725_s_at	NM_006153
2.61	2.90	0.28	2.06E-01	5.80E-01	---	---	---	239164_at	---
3.13	3.36	0.23	2.06E-01	5.80E-01	---	---	---	241187_at	---
1.91	2.08	0.17	2.06E-01	5.80E-01	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	chr9q32	1553129_at	NM_153366
3.21	3.36	0.16	2.06E-01	5.80E-01	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)	chr9p23-p22	221378_at	NM_005454
6.52	7.07	0.55	2.06E-01	5.80E-01	SHC3	SHC (Src homology 2 domain containing) transforming protein 3	chr9q22.1	206330_s_at	NM_016848
2.40	2.70	0.30	2.06E-01	5.80E-01	---	---	---	1557238_s_at	---
3.09	3.34	0.25	2.06E-01	5.80E-01	LEPR	leptin receptor	chr1p31	209894_at	NM_001003679 /// NM_001003680 /// NM_002303
7.88	8.55	0.67	2.06E-01	5.80E-01	TUBB4	tubulin, beta 4	chr19p13.3	212664_at	NM_006087
7.94	8.48	0.54	2.06E-01	5.81E-01	ETFA	electron-transfer-flavoprotein, alpha polypeptide	chr15q23-q25	201931_at	NM_000126 /// NM_001127716
8.75	9.09	0.33	2.06E-01	5.81E-01	RPL22	ribosomal protein L22	chr1p36.3-p36.2	214042_s_at	NM_000983
5.38	5.66	0.27	2.06E-01	5.81E-01	SIAE	sialic acid acetylesterase	chr11q24	224391_s_at	NM_170601
2.02	2.23	0.21	2.06E-01	5.81E-01	---	---	---	1560798_at	---
3.27	3.47	0.20	2.06E-01	5.81E-01	C15orf55	chromosome 15 open reading frame 55	chr15q14	1564603_at	NM_175741
2.45	2.63	0.18	2.06E-01	5.81E-01	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	chr13q34	207546_at	NM_000705
2.04	2.18	0.14	2.06E-01	5.81E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	216803_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257
8.02	8.56	0.54	2.06E-01	5.81E-01	PDK4	pyruvate dehydrogenase kinase, isozyme 4	chr7q21.3	225207_at	NM_002612
3.22	3.45	0.23	2.06E-01	5.81E-01	---	---	---	237846_at	---
4.77	4.98	0.21	2.06E-01	5.81E-01	TMC6	transmembrane channel-like 6	chr17q25.3	214958_s_at	NM_001127198 /// NM_007267
3.74	4.28	0.54	2.06E-01	5.81E-01	KIAA1604	KIAA1604 protein	chr2q31.3	226588_at	NM_020943
8.88	9.38	0.51	2.06E-01	5.81E-01	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	chr20pter-q12	208726_s_at	NM_003908
2.45	2.60	0.15	2.06E-01	5.81E-01	FBXO16	F-box protein 16	chr8p21.1	228427_at	NM_172366
2.69	2.84	0.15	2.07E-01	5.81E-01	MCM3AP	minichromosome maintenance complex component 3 associated protein	chr21q22.3	215580_at	NM_003906
3.36	3.54	0.19	2.07E-01	5.81E-01	CXCR6	chemokine (C-X-C motif) receptor 6	chr3p21	211469_s_at	NM_006564
4.48	4.65	0.16	2.07E-01	5.81E-01	FOXP3	forkhead box P3	chrXp11.23	221334_s_at	NM_001114377 /// NM_014009
3.98	4.26	0.27	2.07E-01	5.81E-01	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	chr16q24.3	222234_s_at	NM_001042610 /// NM_024043
1.86	2.06	0.20	2.07E-01	5.81E-01	C6orf174 /// KIAA0408	chromosome 6 open reading frame 174 /// KIAA0408	chr6q22.33	233050_at	NM_001012279 /// NM_014702
2.28	2.47	0.19	2.07E-01	5.81E-01	TAS2R50	taste receptor, type 2, member 50	chr12p13.2	1553561_at	NM_176890
1.84	1.99	0.15	2.07E-01	5.81E-01	ERAP2	endoplasmic reticulum aminopeptidase 2	chr5q15	1554272_at	NM_001130140 /// NM_022350
2.55	2.72	0.17	2.07E-01	5.81E-01	FAM38B	Family with sequence similarity 38, member B	chr18p11.22	1565775_at	NM_022068
6.69	7.56	0.87	2.07E-01	5.81E-01	KIAA0368	KIAA0368	chr9q31.3	212428_at	NM_001080398
3.94	4.24	0.30	2.07E-01	5.81E-01	ZNF462	zinc finger protein 462	chr9q31.2	244007_at	NM_021224
2.94	3.18	0.24	2.07E-01	5.81E-01	---	---	---	233395_at	---
3.43	3.64	0.21	2.07E-01	5.81E-01	---	---	---	239274_at	---
4.24	4.62	0.38	2.07E-01	5.81E-01	VANGL1	vang-like 1 (van gogh, Drosophila)	chr1p11-p13.1	229492_at	NM_138959

3.93	4.22	0.30	2.07E-01	5.81E-01	C18orf1	chromosome 18 open reading frame 1	chr18p11.2	209573_s_at	NM_001003674 /// NM_001003675 /// NM_004338 /// NM_181481 /// NM_181482 /// NM_181483
1.93	2.11	0.18	2.07E-01	5.81E-01	MIST	mast cell immunoreceptor signal transducer	chr4p16.1	1562587_at	NM_052964
3.08	3.31	0.23	2.07E-01	5.81E-01	KRTCAP3	keratinocyte associated protein 3	chr2p23.3	235148_at	NM_173853
2.99	3.20	0.21	2.07E-01	5.81E-01	---	---	---	1562016_at	---
4.51	5.05	0.54	2.07E-01	5.82E-01	PLXNC1	plexin C1	chr12q23.3	213241_at	NM_005761
2.37	2.54	0.17	2.07E-01	5.82E-01	---	---	---	242311_x_at	---
5.19	5.84	0.65	2.07E-01	5.82E-01	COG5	component of oligomeric golgi complex 5	chr7q22-q31	203630_s_at	NM_006348 /// NM_181733
6.86	7.26	0.40	2.07E-01	5.82E-01	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	chr22q13.2	208666_s_at	NM_003932
3.72	3.96	0.24	2.07E-01	5.82E-01	---	---	---	235393_at	---
2.58	2.77	0.19	2.07E-01	5.82E-01	---	---	---	243667_at	---
2.45	2.63	0.18	2.07E-01	5.82E-01	C13orf16	chromosome 13 open reading frame 16	chr13q34	236853_at	NM_152324
1.88	2.05	0.16	2.07E-01	5.82E-01	---	---	---	1557533_at	---
2.69	3.42	0.73	2.07E-01	5.82E-01	ADAMDEC1	ADAM-like, decysin 1	chr8p21.2	206134_at	NM_014479
2.44	2.73	0.29	2.07E-01	5.82E-01	VKORC1L1	vitamin K epoxide reductase complex, subunit 1-like 1	chr7q11.21	1553679_s_at	NM_173517
2.15	2.39	0.24	2.07E-01	5.82E-01	---	---	---	236280_at	---
2.47	2.70	0.23	2.07E-01	5.82E-01	DGKI	diacylglycerol kinase, iota	chr7q32.3-q33	206806_at	NM_004717
2.18	2.35	0.17	2.07E-01	5.82E-01	PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	chr20q13.13	235165_at	NM_032521
2.00	2.13	0.13	2.07E-01	5.82E-01	---	---	---	AFFX-LysX-3_at	---
4.85	5.52	0.66	2.07E-01	5.82E-01	DNM1L	dynamin 1-like	chr12p11.21	203105_s_at	NM_005690 /// NM_012062 /// NM_012063
3.48	3.83	0.35	2.07E-01	5.82E-01	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	chr16p11.2	219722_s_at	NM_024307
4.07	4.41	0.34	2.08E-01	5.82E-01	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	chr10p14-p13	1554376_s_at	NM_014241
3.29	3.62	0.34	2.08E-01	5.82E-01	LIPE	lipase, hormone-sensitive	chr19q13.2	213855_s_at	NM_005357
5.49	5.82	0.33	2.08E-01	5.82E-01	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	chr3p21.3	201904_s_at	NM_001008392 /// NM_005808
4.79	5.08	0.30	2.07E-01	5.82E-01	TMPRSS2	transmembrane protease, serine 2	chr21q22.3	205102_at	NM_005656 /// XM_001717226 /// XM_001722209 /// XM_001726078
3.72	3.98	0.26	2.08E-01	5.82E-01	NRL	neural retina leucine zipper	chr14q11.1-q11.2	206597_at	NM_006177
2.29	2.52	0.23	2.07E-01	5.82E-01	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	chr21q22.2	210119_at	NM_002243 /// NM_170736 /// NM_170737
3.16	3.38	0.22	2.07E-01	5.82E-01	ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	chr17q23.3	209749_s_at	NM_000789 /// NM_152830
2.18	2.40	0.22	2.08E-01	5.82E-01	---	---	---	243783_at	---
5.73	5.94	0.22	2.08E-01	5.82E-01	CHRNB2	cholinergic receptor, nicotinic, beta 2 (neuronal)	chr1q21.3	206635_at	NM_000748
2.62	2.83	0.21	2.07E-01	5.82E-01	---	---	---	230785_at	---
2.49	2.70	0.21	2.08E-01	5.82E-01	LOC732275	similar to hCG1645603	chr16q24.1	234925_at	XM_001713925 /// XM_001718279 /// XM_001719678
1.93	2.10	0.17	2.07E-01	5.82E-01	---	---	---	1565840_at	---
2.08	2.24	0.16	2.08E-01	5.82E-01	---	---	---	1565888_at	---
6.89	7.15	0.26	2.08E-01	5.82E-01	MRC2	mannose receptor, C type 2	chr17q23.2	209280_at	NM_006039
4.49	5.36	0.86	2.08E-01	5.82E-01	IGHM	immunoglobulin heavy constant mu	chr14q32.33	209374_s_at	---
4.50	4.74	0.24	2.08E-01	5.82E-01	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	chr19p13.1	204856_at	NM_014256
3.29	3.53	0.24	2.08E-01	5.82E-01	DGCR7	DiGeorge syndrome critical region gene 7	chr22q11	1566038_at	---
3.67	3.88	0.21	2.08E-01	5.82E-01	PRKCB	Protein kinase C, beta	chr16p11.2	227817_at	NM_002738 /// NM_212535
2.57	2.78	0.21	2.08E-01	5.82E-01	---	---	---	1569041_at	---
2.38	2.58	0.20	2.08E-01	5.82E-01	---	---	---	1564545_a_at	---
1.84	1.98	0.14	2.08E-01	5.82E-01	ZNF208	zinc finger protein 208	chr19p12	1568644_at	NM_007153
7.31	8.15	0.84	2.08E-01	5.82E-01	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	chr8p22-p21.3	1555419_a_at	NM_001127505 /// NM_004315 /// NM_177924
4.77	5.39	0.62	2.08E-01	5.82E-01	ARHGAP29	Rho GTPase activating protein 29	chr1p22.1	203910_at	NM_004815

5.66	6.11	0.45	2.08E-01	5.82E-01	F11R	F11 receptor	chr1q21.2-q21.3	224097_s_at	NM_016946 /// NM_144503																					
5.65	6.04	0.40	2.08E-01	5.82E-01	C10orf58	chromosome 10 open reading frame 58	chr10q23.1	232662_x_at	NM_032333																					
2.99	3.38	0.39	2.08E-01	5.82E-01	---	---	---	1555617_x_at	---																					
7.02	7.26	0.25	2.08E-01	5.82E-01	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	chr10p12.31	218409_s_at	NM_022365																					
2.98	3.20	0.22	2.08E-01	5.82E-01	---	---	---	237852_at	---																					
2.44	2.64	0.20	2.08E-01	5.82E-01	PLEKHA7	pleckstrin homology domain containing, family A member 7	chr11p15.1	228450_at	NM_175058																					
4.18	4.38	0.20	2.08E-01	5.82E-01	SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	chr17p13.2	207567_at	NM_003984																					
5.40	5.76	0.36	2.08E-01	5.82E-01	SFRS18	splicing factor, arginine/serine-rich 18	chr6q16.3	226412_at	NM_015491 /// NM_032870																					
3.48	3.75	0.27	2.08E-01	5.82E-01	KRT74	keratin 74	chr12q13.13	1553539_at	NM_175053																					
2.43	2.64	0.21	2.08E-01	5.82E-01	LOC136242	Peptidase S1 domain-containing protein LOC136242	chr7q34	231572_at	NM_001008270																					
2.17	2.38	0.22	2.08E-01	5.82E-01	C3orf51	chromosome 3 open reading frame 51	---	208247_at	XR_041400 /// XR_041401 /// XR_041402																					
8.24	8.69	0.45	2.08E-01	5.82E-01	CNOT7	CCR4-NOT transcription complex, subunit 7	chr8p22-p21.3	218250_s_at	NM_013354 /// NM_054026																					
5.65	6.06	0.41	2.08E-01	5.82E-01	HIST1H2BD	histone cluster 1, H2bd	chr6p21.3	209911_x_at	NM_021063 /// NM_138720																					
2.65	2.89	0.25	2.08E-01	5.82E-01	SEC14L3	SEC14-like 3 (S. cerevisiae)	chr22q12.2	241221_at	NM_174975																					
2.77	3.01	0.24	2.08E-01	5.82E-01	WDR32	WD repeat domain 32	chr9p13.2	230679_at	NM_024345																					
2.58	2.80	0.22	2.08E-01	5.82E-01	LYPD4	LY6/PLAUR domain containing 4	chr19q13.2	231266_at	NM_173506																					
3.42	3.60	0.18	2.08E-01	5.82E-01	PYGO1	pygopus homolog 1 (Drosophila)	chr15q21.1	215517_at	NM_015617																					
6.45	7.10	0.65	2.08E-01	5.82E-01	VCL	vinculin	chr10q22.2	200931_s_at	NM_003373 /// NM_014000																					
6.86	7.37	0.50	2.08E-01	5.82E-01	TCF4	transcription factor 4	chr18q21.1	222146_s_at	NM_001083962 /// NM_003199																					
3.60	3.85	0.25	2.09E-01	5.82E-01	IL17B	interleukin 17B	chr5q32-q34	220273_at	NM_014443																					
2.56	2.78	0.22	2.09E-01	5.83E-01	---	---	---	227953_at	---																					
4.51	4.69	0.18	2.09E-01	5.83E-01	MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	chr22q13.1	209764_at	NM_001098270 /// NM_002409																					
6.12	6.76	0.64	2.09E-01	5.83E-01	GLUD2	glutamate dehydrogenase 2	chrXq24-q25	215794_x_at	NM_012084																					
3.28	3.52	0.24	2.09E-01	5.83E-01	KIAA0644	KIAA0644 gene product	chr7p15.1	205150_s_at	NM_014817																					
2.11	2.28	0.17	2.09E-01	5.83E-01	CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	chr1p32	1570533_at	NM_016308																					
2.30	2.53	0.22	2.09E-01	5.83E-01	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	chr13q13.3	1555401_at	NM_017826																					
2.31	2.47	0.16	2.09E-01	5.83E-01	---	---	---	1561488_at	---																					
4.19	4.73	0.53	2.09E-01	5.83E-01	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	chr10q24	207691_x_at	NM_001098175 /// NM_001776																					
7.04	7.50	0.46	2.09E-01	5.83E-01	BGN	biglycan	chrXq28	201261_x_at	NM_001711																					
3.13	3.37	0.23	2.09E-01	5.83E-01	ZNF710	zinc finger protein 710	chr15q26.1	239700_at	NM_198526																					
2.24	2.45	0.21	2.09E-01	5.83E-01	FGF10	fibroblast growth factor 10	chr5p13-p12	231762_at	NM_004465																					
2.11	2.30	0.19	2.09E-01	5.83E-01	---	---	---	243676_at	---																					
2.13	2.31	0.17	2.09E-01	5.83E-01	---	---	---	243557_at	---																					
2.43	2.58	0.15	2.09E-01	5.83E-01	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	chr10p11.23	1564308_a_at	NM_173496																					
5.96	6.63	0.67	2.09E-01	5.83E-01	GFM1	G elongation factor, mitochondrial 1	chr3q25.1-q26.2	225161_at	NM_024996																					
1.87	2.04	0.18	2.09E-01	5.83E-01	---	---	---	241200_x_at	---																					
2.08	2.28	0.20	2.09E-01	5.83E-01	---	---	---	1560002_at	---																					
4.09	4.41	0.32	2.09E-01	5.83E-01	NMNAT1	nicotinamide nucleotide adenylyltransferase 1	chr1p32-p35	223692_at	NM_022787																					
3.47	3.79	0.33	2.09E-01	5.83E-01	---	---	---	226615_at	---																					
2.74	2.97	0.22	2.09E-01	5.83E-01	SMAD5OS	SMAD family member 5 opposite strand	chr5q31.1	220263_at	XR_041121 /// XR_041122 /// XR_041123																					
4.68	5.36	0.69	2.09E-01	5.83E-01	PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	chr2q14.2	205171_at	NM_002830																					
2.66	2.81	0.15	2.09E-01	5.83E-01	---	---	---	237267_at	---																					
3.22	3.42	0.21	2.09E-01	5.83E-01	---	---	---	217572_at	---																					
1.87	2.01	0.14	2.09E-01	5.83E-01	POU1F1	POU class 1 homeobox 1	chr3p11	207846_at	NM_000306 /// NM_001122757																					
5.53	6.31	0.78	2.09E-01	5.83E-01	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	chr2p14	200727_s_at	NM_001005386 /// NM_005722																					
4.08	4.30	0.22	2.09E-01	5.83E-01	STX1A	syntaxin 1A (brain)	chr7q11.23	204729_s_at	NM_004603																					
2.06	2.25	0.19	2.09E-01	5.83E-01	---	---	---	207481_at	---																					
2.41	2.60	0.18	2.09E-01	5.83E-01	CMA1	chymase 1, mast cell	chr14q11.2	214533_at	NM_001836																					
6.77	7.09	0.31	2.09E-01	5.83E-01	FAF1	Fas (TNFRSF6) associated factor 1	chr1p33	218080_x_at	NM_007051																					
5.46	5.71	0.25	2.09E-01	5.83E-01	ARL4D	ADP-ribosylation factor-like 4D	chr17q12-q21	203586_s_at	NM_001661																					
4.04	4.23	0.19	2.09E-01	5.83E-01	CABP2	calcium binding protein 2	chr11q13.1	207745_at	NM_016366 /// NM_031204																					
3.09	3.31	0.23	2.09E-01	5.84E-01	MGC16384	hypothetical protein MGC16384	chr12q24.32	234011_at	XM_001726755																					

2.22	2.39	0.17	2.09E-01	5.84E-01	---	---	---	239768_x_at	---
2.73	2.92	0.20	2.10E-01	5.84E-01	GLIS3	GLIS family zinc finger 3	chr9p24.2	230258_at	NM_001042413 /// NM_152629
2.88	3.14	0.26	2.10E-01	5.84E-01	---	---	---	233993_at	---
9.13	9.31	0.17	2.10E-01	5.84E-01	UBE2L3	ubiquitin-conjugating enzyme E2L 3	chr22q11.21	200682_s_at	NM_003347 /// NM_198157
2.38	2.67	0.29	2.10E-01	5.84E-01	ADRA1A	adrenergic, alpha-1A-, receptor	chr8p21-p11.2	211490_at	NM_000680 /// NM_033302 /// NM_033303 /// NM_033304
1.92	2.09	0.17	2.10E-01	5.84E-01	CXCL11	chemokine (C-X-C motif) ligand 11	chr4q21.2	210163_at	NM_005409
4.26	4.66	0.40	2.10E-01	5.84E-01	ZNF268	zinc finger protein 268	chr12q24.33	209989_at	NM_003415
3.44	3.68	0.24	2.10E-01	5.84E-01	LOC339666	hypothetical protein LOC339666	chr22q12.3	1562841_at	---
3.37	3.58	0.21	2.10E-01	5.84E-01	---	---	---	215675_at	---
3.75	3.97	0.22	2.10E-01	5.84E-01	---	---	---	1569426_at	---
3.52	3.95	0.43	2.10E-01	5.84E-01	AASDH	aminoadipate-semialdehyde dehydrogenase	chr4q12	235435_at	NM_181806
3.60	3.83	0.23	2.10E-01	5.84E-01	DOK3	docking protein 3	chr5q35.3	220320_at	NM_024872
5.58	6.06	0.48	2.10E-01	5.84E-01	MIA3	melanoma inhibitory activity family, member 3	chr1q41	212305_s_at	NM_198551
6.54	6.96	0.42	2.10E-01	5.84E-01	KPNA3	karyopherin alpha 3 (importin alpha 4)	chr13q14.3	221502_at	NM_002267
4.90	5.27	0.37	2.10E-01	5.84E-01	C11orf57	chromosome 11 open reading frame 57	chr11q23.1	1555803_a_at	NM_001082969 /// NM_001082970 /// NM_018195
4.30	4.66	0.36	2.10E-01	5.84E-01	ARHGAP1	Rho GTPase activating protein 1	chr11p12-q12	216689_x_at	NM_004308
5.20	5.55	0.35	2.10E-01	5.84E-01	TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	chr1q23.2	1554351_a_at	NM_001031800 /// NM_152902
5.73	5.96	0.24	2.10E-01	5.84E-01	ZNF853	zinc finger protein 853	chr7p22.1	227170_at	XM_001715278 /// XM_001716278 /// XM_001716628 /// XM_001723503
2.88	3.11	0.22	2.10E-01	5.84E-01	---	---	---	1561598_at	---
2.73	2.95	0.22	2.10E-01	5.84E-01	GPR12	G protein-coupled receptor 12	chr13q12	214558_at	NM_005288
2.03	2.19	0.17	2.10E-01	5.84E-01	MOG	myelin oligodendrocyte glycoprotein	chr6p22.1	205989_s_at	NM_001008228 /// NM_001008229 /// NM_002433 /// NM_206809 /// NM_206810 /// NM_206811 /// NM_206812 /// NM_206813 /// NM_206814
1.93	2.08	0.16	2.10E-01	5.84E-01	FLJ37786	hypothetical LOC642691	chr2p11.1	1558579_at	XR_041472 /// XR_041473
1.95	2.09	0.14	2.10E-01	5.84E-01	---	---	---	237489_at	---
2.22	2.36	0.14	2.10E-01	5.84E-01	---	---	---	1553310_at	---
7.03	7.80	0.77	2.10E-01	5.84E-01	ZNF24	zinc finger protein 24	chr18q12	203247_s_at	NM_006965
7.07	7.50	0.44	2.10E-01	5.84E-01	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	chr13q14.3	223329_x_at	NM_001130912 /// NM_006704
3.95	4.27	0.32	2.10E-01	5.84E-01	ZNF253	zinc finger protein 253	chr19p13.11	242919_at	NM_021047
7.58	8.01	0.43	2.11E-01	5.85E-01	SSR1	signal sequence receptor, alpha	chr6p24.3	201894_s_at	NM_003144
4.96	5.27	0.31	2.11E-01	5.85E-01	USP32	ubiquitin specific peptidase 32	chr17q23.2	211702_s_at	NM_032582
2.99	3.21	0.22	2.11E-01	5.85E-01	IKZF2	IKAROS family zinc finger 2 (Helios)	chr2q34	1555060_a_at	NM_001079526 /// NM_016260
2.34	2.51	0.18	2.11E-01	5.85E-01	ZNF704	zinc finger protein 704	chr8q21.13	1558941_at	NM_001033723
6.26	6.72	0.46	2.11E-01	5.85E-01	EIF3J	eukaryotic translation initiation factor 3, subunit J	chr15q15.3	208985_s_at	NM_003758
2.42	2.82	0.40	2.11E-01	5.85E-01	---	---	---	1565863_at	---
5.32	5.73	0.40	2.11E-01	5.85E-01	MINA	MYC induced nuclear antigen	chr3q11.2	213188_s_at	NM_001042533 /// NM_032778 /// NM_153182
4.95	5.16	0.20	2.11E-01	5.85E-01	FLJ40142	FLJ40142 protein	chr12q24.11	226583_at	NM_207435

3.24	3.44	0.20	2.11E-01	5.85E-01	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	chr19p13.3	229834_at	NM_002501
2.02	2.21	0.19	2.11E-01	5.85E-01	C7orf38	chromosome 7 open reading frame 38	chr7q22.1	1566865_at	NM_145111
4.18	4.85	0.67	2.11E-01	5.85E-01	CAB39	calcium binding protein 39	chr2q37.1	224311_s_at	NM_001130849 /// NM_001130850 /// NM_016289
5.57	5.84	0.27	2.11E-01	5.85E-01	ZC3H13	zinc finger CCCH-type containing 13	chr13q14.12	227536_at	NM_015070
3.12	3.33	0.21	2.11E-01	5.85E-01	ZNF607	zinc finger protein 607	chr19q13.1	223680_at	NM_032689
2.28	2.44	0.16	2.11E-01	5.85E-01	SNORA37	small nucleolar RNA, H/ACA box 37	chr18q21.2	236130_at	NR_002970
2.95	3.11	0.15	2.11E-01	5.85E-01	ZC3H12B	zinc finger CCCH-type containing 12B	chrXq11.1	234878_at	NM_001010888
2.02	2.20	0.18	2.11E-01	5.85E-01	---	---	---	237548_at	---
3.14	3.37	0.23	2.11E-01	5.86E-01	---	---	---	239411_at	---
1.93	2.10	0.17	2.11E-01	5.86E-01	---	---	---	222308_x_at	---
5.18	5.51	0.33	2.11E-01	5.86E-01	CDGAP	Cdc42 GTPase-activating protein	chr3q13.32-q13.33	226056_at	NM_020754
2.89	3.13	0.24	2.11E-01	5.86E-01	RFX1	regulatory factor X, 1 (influences HLA class II expression)	chr19p13.1	206321_at	NM_002918
3.18	3.44	0.26	2.11E-01	5.86E-01	---	---	---	243947_s_at	---
2.60	2.79	0.19	2.11E-01	5.86E-01	E2F7	E2F transcription factor 7	chr12q21.2	241725_at	NM_203394
5.72	6.52	0.80	2.11E-01	5.86E-01	PRSS23	protease, serine, 23	chr11q14.1	226279_at	NM_007173
7.12	7.67	0.55	2.11E-01	5.86E-01	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	chr15q25.1	203396_at	NM_001102667 /// NM_001102668 /// NM_002789
2.26	2.52	0.26	2.11E-01	5.86E-01	---	---	---	239765_at	---
2.51	2.71	0.21	2.11E-01	5.86E-01	DPY19L1	Dpy-19-like 1 (C. elegans)	chr7p14.3	215433_at	NM_015283
2.00	2.21	0.20	2.11E-01	5.86E-01	DISC1	disrupted in schizophrenia 1	chr1q42.1	207759_s_at	NM_001012957 /// NM_001012958 /// NM_001012959 /// NM_018662
2.67	2.87	0.20	2.11E-01	5.86E-01	SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila)	chr19q13.42	1570058_at	NM_032701
3.29	3.47	0.18	2.11E-01	5.86E-01	TEKT1	tektin 1	chr17p13.2	239216_at	NM_053285
3.60	3.88	0.28	2.11E-01	5.86E-01	SAA4	serum amyloid A4, constitutive	chr11p15.1-p14	207096_at	NM_006512
3.00	3.23	0.23	2.11E-01	5.86E-01	---	---	---	1563949_at	---
2.97	3.17	0.21	2.11E-01	5.86E-01	---	---	---	240945_at	---
3.29	3.46	0.17	2.11E-01	5.86E-01	CHN2	chimerin (chimaerin) 2	chr7p15.3	211419_s_at	NM_001039936 /// NM_004067
1.83	2.01	0.17	2.12E-01	5.86E-01	---	---	---	1569941_at	---
5.24	6.16	0.93	2.12E-01	5.86E-01	ZBTB38	zinc finger and BTB domain containing 38	chr3q23	1558733_at	NM_001080412
1.95	2.16	0.21	2.12E-01	5.86E-01	---	---	---	240107_at	---
3.76	3.92	0.16	2.12E-01	5.86E-01	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	chr15q23	222539_at	NM_017882
3.10	3.31	0.21	2.12E-01	5.86E-01	LDLR	low density lipoprotein receptor	chr19p13.3	217005_at	NM_000527
2.19	2.36	0.17	2.12E-01	5.86E-01	---	---	---	210918_at	---
2.16	2.33	0.18	2.12E-01	5.86E-01	SPAG4L	sperm associated antigen 4-like	chr20q11.21	234504_at	NM_080675
3.33	4.29	0.96	2.12E-01	5.86E-01	TPSAB1 /// TPSB2	tryptase alpha/beta 1 /// tryptase beta 2	chr16p13.3	216474_x_at	NM_003294 /// NM_024164 /// XM_001720738 /// XM_001720740
3.38	3.69	0.31	2.12E-01	5.87E-01	IFLTD1	intermediate filament tail domain containing 1	chr12p12.1	1552865_a_at	NM_152590
2.14	2.29	0.15	2.12E-01	5.87E-01	---	---	---	237645_at	---
3.37	3.64	0.27	2.12E-01	5.87E-01	---	---	---	229844_at	---
4.82	5.04	0.22	2.12E-01	5.87E-01	OBP2A	odorant binding protein 2A	chr9q34	234436_x_at	NM_014582
2.01	2.15	0.14	2.12E-01	5.87E-01	ATP13A5	ATPase type 13A5	chr3q29	243585_at	NM_198505
6.08	6.32	0.24	2.12E-01	5.87E-01	SAPS1	SAPS domain family, member 1	chr19q13.42	209229_s_at	NM_014931
3.97	4.22	0.25	2.12E-01	5.87E-01	MMP28	matrix metallopeptidase 28	chr17q11-q21.1	222937_s_at	NM_001032278 /// NM_024302
2.41	2.65	0.25	2.12E-01	5.87E-01	---	---	---	1562826_at	---
3.18	3.39	0.21	2.12E-01	5.87E-01	SLC22A15	solute carrier family 22, member 15	chr1p13.1	228497_at	NM_018420
2.32	2.63	0.31	2.12E-01	5.87E-01	ANGPT2	angiopoietin 2	chr8p23.1	237261_at	NM_001118887 /// NM_001118888 /// NM_001147

2.67	2.94	0.27	2.12E-01	5.87E-01	TDRD12	tudor domain containing 12	chr19q13.11	215356_at	NM_001110822 /// XM_001713629 /// XM_001713630 /// XM_001713631
2.66	2.82	0.16	2.12E-01	5.87E-01	---	---	---	239926_at	---
5.18	5.38	0.20	2.12E-01	5.87E-01	PPARD	peroxisome proliferator-activated receptor delta	chr6p21.2-p21.1	208044_s_at	NM_006238
2.03	2.20	0.16	2.12E-01	5.87E-01	---	---	---	1566703_at	---
2.40	2.56	0.16	2.12E-01	5.87E-01	TAS1R2	taste receptor, type 1, member 2	chr1p36.13	1553529_at	NM_152232
3.39	3.66	0.27	2.13E-01	5.88E-01	LOC100129444	Hypothetical protein LOC100129444	chr12q24.31	243545_at	XM_001716666 /// XM_001719053
3.80	4.04	0.24	2.12E-01	5.88E-01	C1orf94	chromosome 1 open reading frame 94	chr1p34.3	231514_at	NM_001134734 /// NM_032884
3.10	3.32	0.22	2.13E-01	5.88E-01	C10orf25	chromosome 10 open reading frame 25	chr10q11.21	1552422_at	NM_001039380
3.26	3.47	0.22	2.13E-01	5.88E-01	---	---	---	241000_at	---
2.36	2.53	0.18	2.13E-01	5.88E-01	UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1	chr5p13.2	235904_at	NM_152404
3.02	3.23	0.21	2.13E-01	5.88E-01	RAD54L	RAD54-like (S. cerevisiae)	chr1p32	204558_at	NM_003579
2.37	2.57	0.20	2.13E-01	5.88E-01	---	---	---	241169_at	---
5.73	6.19	0.46	2.13E-01	5.88E-01	SASH1	SAM and SH3 domain containing 1	chr6q24.3	213236_at	NM_015278
2.25	2.44	0.20	2.13E-01	5.88E-01	PRKCB	Protein kinase C, beta	chr16p11.2	227824_at	NM_002738 /// NM_212535
6.24	6.63	0.39	2.13E-01	5.88E-01	CLEC14A	C-type lectin domain family 14, member A	chr14q21.1	226244_at	NM_175060
2.75	2.98	0.23	2.13E-01	5.88E-01	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	chr1p36.1	210232_at	NM_001039802 /// NM_001791 /// NM_044472
5.63	6.06	0.43	2.13E-01	5.88E-01	RFC1	replication factor C (activator 1) 1, 145kDa	chr4p14-p13	209085_x_at	NM_002913
5.29	5.50	0.21	2.13E-01	5.88E-01	CD70	CD70 molecule	chr19p13	206508_at	NM_001252
2.56	2.76	0.20	2.13E-01	5.88E-01	CCDC45	Coiled-coil domain containing 45	chr17q24.1	223815_at	NM_138363
3.27	3.47	0.19	2.13E-01	5.88E-01	KLK11	kallikrein-related peptidase 11	chr19q13.3-q13.4	205470_s_at	NM_006853 /// NM_144947
1.94	2.10	0.16	2.13E-01	5.88E-01	C1orf62	chromosome 1 open reading frame 62	chr1p13.3	1552933_at	NM_152763
4.21	4.63	0.43	2.13E-01	5.88E-01	---	---	---	227227_at	---
4.82	5.04	0.22	2.13E-01	5.88E-01	---	---	---	215502_at	---
2.54	2.72	0.18	2.13E-01	5.88E-01	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	chr7p14.2	233100_at	NM_030636
4.55	4.79	0.24	2.13E-01	5.88E-01	BAIAP2	BAI1-associated protein 2	chr17q25	207832_at	NM_006340 /// NM_017450 /// NM_017451
6.27	6.55	0.28	2.13E-01	5.88E-01	ZNF205	zinc finger protein 205	chr16p13.3	206416_at	NM_001042428 /// NM_003456
3.28	3.53	0.25	2.13E-01	5.88E-01	NUDT16P	nudix (nucleoside diphosphate linked moiety X)-type motif 16 pseudogene	chr3q22.1	1568593_a_at	NR_002949
2.13	2.34	0.21	2.13E-01	5.88E-01	---	---	---	1562653_at	---
2.05	2.22	0.17	2.13E-01	5.88E-01	---	---	---	1568615_a_at	---
2.84	3.05	0.21	2.13E-01	5.88E-01	LAMA4	laminin, alpha 4	chr6q21	216081_at	NM_001105206 /// NM_001105207 /// NM_001105208 /// NM_001105209 /// NM_002290
2.20	2.38	0.18	2.13E-01	5.88E-01	CCDC13	coiled-coil domain containing 13	chr3p22.1	1554022_at	NM_144719
4.09	4.35	0.26	2.13E-01	5.88E-01	FAM181B	family with sequence similarity 181, member B	chr11q14.1	230994_at	NM_175885
3.54	3.77	0.23	2.13E-01	5.88E-01	FBXO10	F-box protein 10	chr9p13.2	237036_at	NM_012166
2.55	2.78	0.23	2.13E-01	5.88E-01	NT5C2	5'-nucleotidase, cytosolic II	chr10q24.32-q24.33	241778_at	NM_001134373 /// NM_012229
3.71	3.94	0.23	2.13E-01	5.88E-01	---	---	---	216078_at	---
2.55	2.72	0.17	2.13E-01	5.88E-01	---	---	---	235611_at	---
5.98	6.20	0.22	2.13E-01	5.89E-01	TGOLN2	trans-golgi network protein 2	chr2p11.2	203834_s_at	NM_006464
4.11	4.32	0.21	2.13E-01	5.89E-01	CCL24	chemokine (C-C motif) ligand 24	chr7q11.23	221463_at	NM_002991
3.06	3.31	0.25	2.13E-01	5.89E-01	FAM171A2	family with sequence similarity 171, member A2	chr17q21.31	235544_x_at	XM_001715615 /// XM_001717269 /// XM_208993
2.50	2.73	0.23	2.14E-01	5.89E-01	---	---	---	240234_at	---
2.09	2.28	0.19	2.14E-01	5.89E-01	---	---	---	241039_at	---

1.75	1.90	0.14	2.14E-01	5.89E-01	---	---	---	242522_at	---
3.23	3.48	0.25	2.14E-01	5.89E-01	MAP2K5	mitogen-activated protein kinase kinase 5	chr15q23	211371_at	NM_002757 /// NM_145160
4.40	5.32	0.92	2.14E-01	5.89E-01	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	chr2p14	1558015_s_at	NM_001005386 /// NM_005722
5.00	5.45	0.44	2.14E-01	5.89E-01	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	chr16q22.1	208003_s_at	NM_001113178 /// NM_006599 /// NM_138713 /// NM_138714 /// NM_173214
4.50	4.93	0.43	2.14E-01	5.89E-01	---	---	---	232501_at	---
3.56	3.76	0.20	2.14E-01	5.89E-01	SYT8	synaptotagmin VIII	chr11p15.5	232802_at	NM_138567
1.95	2.13	0.18	2.14E-01	5.89E-01	SNIP	SNAP25-interacting protein	chr17q12	232547_at	NM_025248
2.93	3.07	0.14	2.14E-01	5.89E-01	---	---	---	243229_at	---
1.89	2.03	0.13	2.14E-01	5.89E-01	LOC339788	hypothetical LOC339788	chr2p25.1	1560413_at	---
4.99	5.80	0.82	2.14E-01	5.89E-01	EMCN	endomucin	chr4q23	219436_s_at	NM_016242
3.05	3.23	0.18	2.14E-01	5.89E-01	---	---	---	242489_at	---
3.77	3.93	0.16	2.14E-01	5.89E-01	PPP1R12C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	chr19q13.42	234265_at	NM_017607
5.45	5.88	0.43	2.14E-01	5.89E-01	SLC46A1	solute carrier family 46 (folate transporter), member 1	chr17q11.2	1552278_a_at	NM_080669
3.65	3.97	0.32	2.14E-01	5.89E-01	IGHA1 /// IGHG1 /// IGHV@	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy variable group	chr14q32.33	216542_x_at	---
3.74	4.01	0.27	2.14E-01	5.89E-01	---	---	---	238161_at	---
4.32	4.57	0.25	2.14E-01	5.89E-01	CRYBB3	crystallin, beta B3	chr22q11.2-q12.1|22q11.23	207685_at	NM_004076
2.57	2.81	0.24	2.14E-01	5.89E-01	FLJ40243	hypothetical protein FLJ40243	chr5p13.1	1569730_at	NM_173489
3.68	3.92	0.24	2.14E-01	5.89E-01	EHMT2	Euchromatic histone-lysine N-methyltransferase 2	chr6p21.31	229079_at	NM_006709 /// NM_025256
2.57	2.79	0.22	2.14E-01	5.89E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	1567378_x_at	NM_015512
2.75	2.94	0.18	2.14E-01	5.89E-01	LOC441601	septin 7 pseudogene	chr11p11.12	214381_at	NR_003034
4.44	4.63	0.18	2.14E-01	5.89E-01	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	chr6p21	201187_s_at	NM_002224
2.74	2.91	0.17	2.14E-01	5.89E-01	CGN	cingulin	chr1q21	223233_s_at	NM_020770
2.90	3.06	0.16	2.14E-01	5.89E-01	C21orf88 /// LOC100131337	chromosome 21 open reading frame 88 /// similar to C21orf88 protein	chr21q22.2	1555231_a_at	XM_001715878 /// XM_001715888 /// XR_040123 /// XR_040124 /// XR_040125 /// XR_040126 /// XR_040127 /// XR_040128 /// XR_040129
2.10	2.24	0.14	2.14E-01	5.89E-01	---	---	---	1562281_at	---
1.91	2.03	0.12	2.14E-01	5.89E-01	ZNF678	zinc finger protein 678	chr1q42.13	1554922_at	NM_178549
3.43	4.18	0.75	2.14E-01	5.89E-01	ITGA6	integrin, alpha 6	chr2q31.1	215177_s_at	NM_000210 /// NM_001079818
5.24	5.92	0.68	2.14E-01	5.89E-01	MAP3K7	mitogen-activated protein kinase kinase kinase 7	chr6q16.1-q16.3	206854_s_at	NM_003188 /// NM_145331 /// NM_145332 /// NM_145333
7.06	7.71	0.65	2.14E-01	5.89E-01	C9orf5	chromosome 9 open reading frame 5	chr9q31	223005_s_at	NM_001099734 /// NM_032012
5.07	5.64	0.57	2.14E-01	5.89E-01	PROS1	protein S (alpha)	chr3q11.2	207808_s_at	NM_000313
6.43	6.99	0.56	2.15E-01	5.89E-01	VAMP7	vesicle-associated membrane protein 7	chrXq28 and Yq12	202829_s_at	NM_005638
3.14	3.67	0.52	2.14E-01	5.89E-01	COL12A1	collagen, type XII, alpha 1	chr6q12-q13	231766_s_at	NM_004370 /// NM_080645
4.63	5.09	0.47	2.15E-01	5.89E-01	ELMOD2	ELMO/CED-12 domain containing 2	chr4q31.1	1553928_at	NM_153702
6.21	6.64	0.43	2.14E-01	5.89E-01	SMAD2	SMAD family member 2	chr18q21.1	226563_at	NM_001003652 /// NM_005901
5.56	5.94	0.38	2.14E-01	5.89E-01	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	chr11p11.2	222403_at	NM_014342
3.64	4.00	0.36	2.14E-01	5.89E-01	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	chr3p14.3	1555993_at	NM_000720 /// NM_001128839 /// NM_001128840

6.32	6.66	0.35	2.14E-01	5.89E-01	ECHDC1	enoyl Coenzyme A hydratase domain containing 1	chr6q22.33	223088_x_at	NM_001002030 /// NM_001105544 /// NM_001105545 /// NM_018479																				
5.76	6.09	0.33	2.14E-01	5.89E-01	ZNF398	zinc finger protein 398	chr7q36.1	228145_s_at	NM_020781 /// NM_170686																				
2.79	3.11	0.32	2.14E-01	5.89E-01	FAM134B	family with sequence similarity 134, member B	chr5p15.1	218510_x_at	NM_001034850 /// NM_019000																				
3.87	4.14	0.27	2.14E-01	5.89E-01	---	---	---	231672_at	---																				
3.08	3.35	0.27	2.14E-01	5.89E-01	GTPBP1	GTP binding protein 1	chr22q13.1	205274_at	NM_004286																				
2.89	3.16	0.27	2.14E-01	5.89E-01	MSRB2	methionine sulfoxide reductase B2	chr10p12	230575_at	NM_012228																				
4.23	4.50	0.26	2.14E-01	5.89E-01	CBS	cystathionine-beta-synthase	chr21q22.3	240517_at	NM_000071																				
2.72	2.97	0.26	2.15E-01	5.89E-01	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	chr17q11.1-q12	207519_at	NM_001045																				
3.33	3.58	0.25	2.14E-01	5.89E-01	TMIE	transmembrane inner ear	chr3p21	1553600_at	NM_147196																				
4.45	4.70	0.25	2.14E-01	5.89E-01	SNX25	sorting nexin 25	chr4q35.1	227408_s_at	NM_031953																				
3.80	4.04	0.24	2.14E-01	5.89E-01	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	chr7q21.1	210726_at	NM_017460																				
3.17	3.40	0.24	2.15E-01	5.89E-01	ATXN3	ataxin 3	chr14q24.3-q32.2	205416_s_at	NM_001127696 /// NM_001127697 /// NM_004993 /// NM_030660																				
3.44	3.67	0.23	2.15E-01	5.89E-01	KLK12	kallikrein-related peptidase 12	chr19q13.3-q13.4	220782_x_at	NM_019598 /// NM_145894 /// NM_145895																				
3.96	4.18	0.22	2.14E-01	5.89E-01	BARX2	BARX homeobox 2	chr11q25	210419_at	NM_003658																				
6.25	6.46	0.21	2.15E-01	5.89E-01	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	chr8p23.1	202561_at	NM_003747																				
3.32	3.53	0.21	2.14E-01	5.89E-01	---	---	---	233762_at	---																				
2.16	2.36	0.20	2.14E-01	5.89E-01	CHRNB3	cholinergic receptor, nicotinic, beta 3	chr8p11.2	217086_at	NM_000749																				
2.24	2.43	0.19	2.14E-01	5.89E-01	LOC100130135	hypothetical protein LOC100130135	chr3p21.31	234743_at	XM_001717607 /// XM_001718419																				
3.39	3.57	0.19	2.14E-01	5.89E-01	C21orf62	chromosome 21 open reading frame 62	chr21q22.11	223923_at	NM_019596																				
3.04	3.22	0.19	2.14E-01	5.89E-01	DLX3	distal-less homeobox 3	chr17q21	231778_at	NM_005220																				
2.42	2.61	0.18	2.15E-01	5.89E-01	---	---	---	1558687_a_at	---																				
2.07	2.25	0.18	2.14E-01	5.89E-01	---	---	---	234275_at	---																				
2.58	2.76	0.18	2.14E-01	5.89E-01	LOC606495	hypothetical protein LOC606495	chr1p32.3	238280_at	NM_001031672																				
3.12	3.29	0.17	2.14E-01	5.89E-01	---	---	---	216597_at	---																				
2.31	2.48	0.17	2.14E-01	5.89E-01	hCG_2036596	HCG2036596	chr1p36.32	1566737_at	XM_001132281 /// XM_001134291 /// XM_001134292 /// XM_001724323																				
2.09	2.25	0.16	2.14E-01	5.89E-01	---	---	---	1557733_a_at	---																				
3.03	3.19	0.16	2.14E-01	5.89E-01	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	chr16p11.2	205785_at	NM_000632																				
2.17	2.33	0.16	2.14E-01	5.89E-01	TMEM75	transmembrane protein 75	chr8q24.21	1559611_at	XR_040740 /// XR_040741 /// XR_040742																				
2.64	2.79	0.16	2.15E-01	5.89E-01	PATL2	protein associated with topoisomerase II homolog 2 (yeast)	chr15q21.1	230753_at	XR_015477 /// XR_040922 /// XR_040923																				
2.10	2.25	0.15	2.14E-01	5.89E-01	NRG1	neuregulin 1	chr8p12	206343_s_at	NM_004495 /// NM_013956 /// NM_013957 /// NM_013958 /// NM_013959 /// NM_013960 /// NM_013961 /// NM_013962 /// NM_013964																				
4.66	5.48	0.82	2.15E-01	5.89E-01	LIMA1	LIM domain and actin binding 1	chr12q13	222457_s_at	NM_001113546 /// NM_001113547 /// NM_016357																				
5.39	6.01	0.63	2.15E-01	5.89E-01	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	chr12q21.2	203202_at	NM_007043																				

4.33	4.52	0.19	2.15E-01	5.89E-01	CD9	CD9 molecule	chr12p13.3	233322_at	NM_001769
2.28	2.45	0.16	2.15E-01	5.89E-01	LOC400831	hypothetical LOC400831	chr20p13	1556265_at	NM_001009612 /// XM_001724704 /// XM_930959 /// XM_943808
1.93	2.09	0.15	2.15E-01	5.89E-01	RAB7A	RAB7A, member RAS oncogene family	chr3q21.3	217268_at	NM_004637
3.31	3.58	0.26	2.15E-01	5.89E-01	FIGNL1	fidgetin-like 1	chr7p12.2	1552921_a_at	NM_001042762 /// NM_022116
3.34	3.70	0.36	2.15E-01	5.90E-01	---	---	---	244496_at	---
3.10	3.30	0.20	2.15E-01	5.90E-01	---	---	---	1557024_at	---
2.71	2.88	0.17	2.15E-01	5.90E-01	P2RX3	purinergic receptor P2X, ligand-gated ion channel, 3	chr11q12	208338_at	NM_002559
3.17	3.54	0.38	2.15E-01	5.90E-01	C20orf74	chromosome 20 open reading frame 74	chr20p11.22	239660_at	NM_020343
2.03	2.22	0.19	2.15E-01	5.90E-01	TNMD	tenomodulin	chrXq21.33-q23	220065_at	NM_022144
2.81	3.06	0.24	2.15E-01	5.90E-01	---	---	---	1559295_at	---
2.87	3.19	0.32	2.15E-01	5.90E-01	RAB2A	RAB2A, member RAS oncogene family	chr8q12.1	208733_at	NM_002865
2.99	3.27	0.28	2.15E-01	5.90E-01	DKFZp686E2433	similar to hypothetical protein 9630041N07	chr5q35.3	230421_at	XM_001714318 /// XM_001715681 /// XM_001717115
2.65	2.90	0.25	2.15E-01	5.90E-01	---	---	---	236612_at	---
2.85	3.05	0.20	2.15E-01	5.90E-01	LOC158863	Hypothetical protein LOC158863	chrXq13.1	232179_at	---
1.90	2.05	0.15	2.15E-01	5.90E-01	ZNF99	zinc finger protein 99	chr19p12	1553883_at	NM_001080409
2.14	2.29	0.15	2.15E-01	5.90E-01	HSFY1 /// HSFY2	heat shock transcription factor, Y-linked 1 /// heat shock transcription factor, Y linked 2	chrYq11.222	224052_at	NM_001001877 /// NM_033108 /// NM_152584 /// NM_153716 /// NR_003509 /// NR_003510
2.26	2.46	0.19	2.15E-01	5.90E-01	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	chr2p25.1-p24.1	244526_at	NM_170672
4.48	5.07	0.60	2.15E-01	5.90E-01	TMED5	Transmembrane emp24 protein transport domain containing 5	chr1pter-q31.3	242263_at	NM_016040
3.67	4.35	0.69	2.15E-01	5.90E-01	CHPT1	Choline phosphotransferase 1	chr12q	1559739_at	NM_020244
4.57	4.97	0.40	2.15E-01	5.90E-01	---	---	---	1558836_at	---
3.49	3.76	0.28	2.15E-01	5.90E-01	---	---	---	239160_at	---
2.95	3.22	0.28	2.15E-01	5.90E-01	FCRL5	Fc receptor-like 5	chr1q21	224406_s_at	NM_031281
3.28	3.56	0.28	2.15E-01	5.90E-01	TMEM5	transmembrane protein 5	chr12q14.2	204807_at	NM_014254
5.06	5.33	0.27	2.15E-01	5.90E-01	ZNF358	zinc finger protein 358	---	226260_x_at	NM_018083
3.33	3.55	0.21	2.15E-01	5.90E-01	ANKRD50	ankyrin repeat domain 50	chr4q28.1	225735_at	NM_020337
6.31	6.52	0.21	2.15E-01	5.90E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	209508_x_at	NM_001127183 /// NM_001127184 /// NM_003879
2.94	3.15	0.20	2.16E-01	5.90E-01	ITPKB	Inositol 1,4,5-trisphosphate 3-kinase B	chr1q42.13	235213_at	NM_002221
2.21	2.41	0.20	2.15E-01	5.90E-01	SLCO1C1	solute carrier organic anion transporter family, member 1C1	chr12p12.2	220460_at	NM_017435
2.28	2.43	0.15	2.15E-01	5.90E-01	CENPN	centromere protein N	chr16q23.2	234811_at	NM_001100624 /// NM_001100625 /// NM_018455
1.90	2.04	0.15	2.15E-01	5.90E-01	---	---	---	240563_at	---
2.35	2.49	0.14	2.15E-01	5.90E-01	TLX3	T-cell leukemia homeobox 3	chr5q35.1	208495_at	NM_021025
4.85	5.35	0.50	2.16E-01	5.90E-01	CLIP1	CAP-GLY domain containing linker protein 1	chr12q24.3	210716_s_at	NM_002956 /// NM_198240
2.52	2.76	0.24	2.16E-01	5.90E-01	CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	chr2q35	204920_at	NM_001122633 /// NM_001122634 /// NM_001875
2.22	2.38	0.16	2.16E-01	5.90E-01	---	---	---	238466_at	---
3.53	3.84	0.31	2.16E-01	5.90E-01	GPR173	G protein-coupled receptor 173	chrXp11	244877_at	NM_018969
1.98	2.13	0.15	2.16E-01	5.90E-01	TRPM7	transient receptor potential cation channel, subfamily M, member 7	chr15q21	237884_x_at	NM_017672
3.48	3.68	0.20	2.16E-01	5.90E-01	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	chr19p13.13	216454_at	NM_017722
2.59	2.76	0.16	2.16E-01	5.90E-01	---	---	---	1559508_at	---
2.20	2.41	0.21	2.16E-01	5.90E-01	HMX2	H6 family homeobox 2	chr10q25.2-q26.3	244565_at	NM_005519
2.38	2.56	0.18	2.16E-01	5.90E-01	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7	chr2q24.2	224099_at	NM_033272 /// NM_173162

2.68	2.82	0.14	2.16E-01	5.90E-01	C6orf150	chromosome 6 open reading frame 150	chr6q13	242077_x_at	NM_138441
2.19	2.35	0.16	2.16E-01	5.90E-01	---	---	---	244393_x_at	---
1.87	2.03	0.16	2.16E-01	5.90E-01	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	chr10p13	219262_at	NM_024670
4.42	4.62	0.20	2.16E-01	5.90E-01	C8orf58	chromosome 8 open reading frame 58	chr8p21	236296_x_at	NM_001013842
4.17	4.66	0.49	2.16E-01	5.91E-01	KIAA2018	KIAA2018	chr3q13.2	227435_at	NM_001009899
3.10	3.37	0.27	2.16E-01	5.91E-01	HSPA12A	heat shock 70kDa protein 12A	chr10q26.12	220763_at	NM_025015
2.40	2.61	0.21	2.16E-01	5.91E-01	---	---	---	208043_at	---
2.32	2.50	0.18	2.16E-01	5.91E-01	PVALB	parvalbumin	chr22q12-q13.1|22q13.1	205336_at	NM_002854
5.46	6.05	0.59	2.16E-01	5.91E-01	SSR1	signal sequence receptor, alpha	chr6p24.3	200890_s_at	NM_003144
3.73	4.07	0.34	2.16E-01	5.91E-01	SLC28A1	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	chr15q25-q26	207560_at	NM_004213 /// NM_201651
2.10	2.28	0.18	2.16E-01	5.91E-01	---	---	---	243915_at	---
3.38	3.53	0.15	2.16E-01	5.91E-01	---	---	---	231190_at	---
3.04	3.25	0.21	2.16E-01	5.91E-01	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	chr17q21.32	204628_s_at	NM_000212
5.68	6.33	0.64	2.16E-01	5.91E-01	EBAG9	estrogen receptor binding site associated, antigen, 9	chr8q23	204278_s_at	NM_004215 /// NM_198120
3.06	3.29	0.23	2.16E-01	5.91E-01	EML4	Echinoderm microtubule associated protein like 4	chr2p22-p21	228673_s_at	NM_019063
2.82	3.04	0.22	2.16E-01	5.91E-01	HYDIN2	hydrocephalus inducing homolog 2 (mouse)	chr1q21.1	1563529_at	XM_001717859
1.88	2.10	0.22	2.16E-01	5.91E-01	---	---	---	240427_at	---
4.01	4.22	0.21	2.16E-01	5.91E-01	SMC2	structural maintenance of chromosomes 2	chr9q31.1	213253_at	NM_001042550 /// NM_001042551 /// NM_006444
2.32	2.51	0.19	2.16E-01	5.91E-01	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	chr18p11.31-p11.21	210917_at	NM_005433
4.87	5.06	0.19	2.16E-01	5.91E-01	---	---	---	213818_x_at	---
1.95	2.11	0.15	2.16E-01	5.91E-01	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	chr17q21.32	216966_at	NM_000419
8.64	8.92	0.28	2.16E-01	5.91E-01	YY1	YY1 transcription factor	chr14q	201901_s_at	NM_003403
3.98	4.15	0.17	2.16E-01	5.91E-01	YTHDC1	YTH domain containing 1	chr4q13.2	228556_at	NM_001031732 /// NM_133370
2.00	2.15	0.15	2.16E-01	5.91E-01	---	---	---	1569971_at	---
3.02	3.28	0.25	2.16E-01	5.91E-01	VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	chr20q13.33	202549_at	NM_004738
5.93	6.77	0.84	2.17E-01	5.91E-01	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	chr6q14-q15	209024_s_at	NM_006372
2.62	2.96	0.33	2.17E-01	5.91E-01	NMUR1	neuromedin U receptor 1	chr2q37.1	221383_at	NM_006056
7.67	7.82	0.16	2.17E-01	5.91E-01	PPCS	phosphopantothenoylcysteine synthetase	chr1p34.2	218341_at	NM_001077447 /// NM_024664
2.73	3.03	0.30	2.17E-01	5.91E-01	---	---	---	215635_at	---
2.05	2.21	0.16	2.17E-01	5.91E-01	---	---	---	1564685_a_at	---
3.16	3.78	0.62	2.17E-01	5.91E-01	PELO	Pelota homolog (Drosophila)	chr5q11.2	214660_at	NM_015946
7.96	8.43	0.47	2.17E-01	5.91E-01	MRPL47	mitochondrial ribosomal protein L47	chr3q26.33	223480_s_at	NM_020409 /// NM_177988
3.48	3.83	0.34	2.17E-01	5.91E-01	TMOD3	tropomodulin 3 (ubiquitous)	chr15q21.1-q21.2	223078_s_at	NM_014547
2.44	2.59	0.15	2.17E-01	5.91E-01	---	---	---	1560386_at	---
7.07	7.45	0.38	2.17E-01	5.91E-01	RHOQ	ras homolog gene family, member Q	chr2p21	212117_at	NM_012249
3.80	4.18	0.38	2.17E-01	5.91E-01	BRAF	v-raf murine sarcoma viral oncogene homolog B1	chr7q34	243829_at	NM_004333
3.98	4.25	0.27	2.17E-01	5.91E-01	B4GALNT3	beta-1,4-N-acetyl-galactosaminyl transferase 3	chr12p13.33	1553727_at	NM_173593
2.89	3.13	0.25	2.17E-01	5.91E-01	CD24	CD24 molecule	chr6q21	209772_s_at	NM_013230 /// XM_001725629
3.06	3.29	0.23	2.17E-01	5.91E-01	SYT15	Synaptotagmin XV	chr10q11.1	244307_s_at	NM_031912 /// NM_181519 /// XM_001720092
2.63	2.77	0.14	2.17E-01	5.92E-01	FGF18	fibroblast growth factor 18	chr5q34	211029_x_at	NM_003862
8.76	9.01	0.24	2.17E-01	5.92E-01	RAB10	RAB10, member RAS oncogene family	chr2p23.3	222980_at	NM_016131
4.90	5.13	0.22	2.17E-01	5.92E-01	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	chr19p13.3	214893_x_at	NM_001194
4.37	4.79	0.42	2.17E-01	5.92E-01	DACT3	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	chr19q13.32	228228_at	NM_145056
2.22	2.41	0.19	2.17E-01	5.92E-01	---	---	---	236759_at	---
2.99	3.15	0.16	2.17E-01	5.92E-01	FLJ39080	hypothetical gene supported by AK096399	chr8q21.11	1561371_at	XM_001721483 /// XM_499117 /// XM_943975
6.12	6.59	0.46	2.17E-01	5.92E-01	KIDINS220	kinase D-interacting substrate of 220 kDa	chr2p24	212162_at	NM_020738
6.06	6.30	0.24	2.17E-01	5.92E-01	CLSTN3	calsyntenin 3	chr12p13.31	204375_at	NM_014718
4.56	4.96	0.41	2.17E-01	5.92E-01	MAN1A2	mannosidase, alpha, class 1A, member 2	chr1p13	217920_at	NM_006699

2.18	2.41	0.22	2.17E-01	5.92E-01	---	---	---	237332_at	---
2.53	2.71	0.18	2.17E-01	5.92E-01	ANKRD5	ankyrin repeat domain 5	chr20pter-q11.23	222951_s_at	NM_022096 /// NM_198798
7.52	8.00	0.48	2.17E-01	5.92E-01	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	chr8p21	221478_at	NM_004331
4.41	4.70	0.29	2.17E-01	5.92E-01	---	---	---	227187_at	---
6.44	7.02	0.57	2.17E-01	5.92E-01	KIAA1012	KIAA1012	chr18q12.1	207305_s_at	NM_014939
2.92	3.17	0.25	2.17E-01	5.92E-01	---	---	---	244099_at	---
2.33	2.48	0.15	2.17E-01	5.92E-01	---	---	---	235636_at	---
3.65	3.87	0.23	2.17E-01	5.92E-01	P4HA3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III	chr11q13.4	228703_at	NM_182904
2.89	3.05	0.16	2.17E-01	5.92E-01	MYBL1	V-myb myeloblastosis viral oncogene homolog (avian)-like 1	chr8q22	237014_at	NM_001080416
2.78	3.05	0.27	2.17E-01	5.92E-01	LEPR	leptin receptor	chr1p31	211355_x_at	NM_001003679 /// NM_001003680 /// NM_002303
3.84	4.05	0.21	2.17E-01	5.92E-01	---	---	---	216564_at	---
1.84	1.98	0.15	2.17E-01	5.92E-01	---	---	---	1555263_at	---
2.28	2.50	0.22	2.17E-01	5.92E-01	ZNF763	zinc finger protein 763	chr19p13.2	1558755_x_at	NM_001012753
2.62	2.85	0.23	2.18E-01	5.92E-01	LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	chr1p13.1	242165_at	NM_014813
3.68	3.91	0.23	2.18E-01	5.92E-01	CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	chr15q24	207609_s_at	NM_000761
2.42	2.62	0.20	2.18E-01	5.92E-01	---	---	---	233225_at	---
1.92	2.10	0.18	2.17E-01	5.92E-01	FCRL4	Fc receptor-like 4	chr1q21	224402_s_at	NM_031282
4.80	5.29	0.49	2.18E-01	5.92E-01	ZCCHC7	Zinc finger, CCHC domain containing 7	chr9p13.2	230332_at	NM_032226
2.61	2.96	0.35	2.18E-01	5.92E-01	CHRNA3	cholinergic receptor, nicotinic, alpha 3	chr15q24	211772_x_at	NM_000743
3.84	4.07	0.22	2.18E-01	5.92E-01	---	---	---	230770_at	---
2.83	3.08	0.25	2.18E-01	5.92E-01	IRF4	interferon regulatory factor 4	chr6p25-p23	204562_at	NM_002460
4.55	4.78	0.23	2.18E-01	5.92E-01	---	---	---	237792_at	---
4.14	4.33	0.18	2.18E-01	5.92E-01	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	chr8p21.3	204077_x_at	NM_001128930 /// NM_004901
2.30	2.46	0.16	2.18E-01	5.92E-01	---	---	---	242914_at	---
4.12	4.67	0.55	2.18E-01	5.92E-01	---	---	---	244341_at	---
2.99	3.17	0.17	2.18E-01	5.92E-01	AKR1A1	Aldo-keto reductase family 1, member A1 (aldehyde reductase)	chr1p33-p32	241978_at	NM_006066 /// NM_153326
4.53	4.71	0.18	2.18E-01	5.92E-01	MARCKS	myristoylated alanine-rich protein kinase C substrate	chr6q22.2	201668_x_at	NM_002356
7.07	7.77	0.70	2.18E-01	5.92E-01	---	---	---	226252_at	---
3.48	3.79	0.32	2.18E-01	5.92E-01	---	---	---	1557099_at	---
3.84	4.07	0.23	2.18E-01	5.92E-01	---	---	---	244607_at	---
2.87	3.06	0.19	2.18E-01	5.92E-01	---	---	---	1568974_at	---
1.90	2.08	0.18	2.18E-01	5.92E-01	FLJ39739	hypothetical FLJ39739	chr1q21.1	1556457_s_at	XR_039904 /// XR_039905
3.86	4.04	0.18	2.18E-01	5.92E-01	---	---	---	244798_at	---
1.87	2.04	0.17	2.18E-01	5.92E-01	C17orf77	chromosome 17 open reading frame 77	chr17q25.1	1553298_at	NM_152460
1.97	2.12	0.15	2.18E-01	5.92E-01	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	chr15q15-q21.1	1555103_s_at	NM_002009
2.25	2.39	0.14	2.18E-01	5.92E-01	---	---	---	1564851_at	---
5.65	5.89	0.24	2.18E-01	5.93E-01	CCDC22	coiled-coil domain containing 22	chrXp11.23	214037_s_at	NM_014008
2.65	2.84	0.20	2.18E-01	5.93E-01	---	---	---	240690_at	---
2.88	3.12	0.24	2.18E-01	5.93E-01	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	chr21q22.3	241926_s_at	NM_004449 /// NM_182918
1.93	2.05	0.13	2.18E-01	5.93E-01	---	---	---	217220_at	---
2.23	2.41	0.18	2.18E-01	5.93E-01	---	---	---	238395_at	---
5.57	6.14	0.57	2.18E-01	5.93E-01	SOCS5	suppressor of cytokine signaling 5	chr2p21	209647_s_at	NM_014011 /// NM_144949
5.44	5.98	0.54	2.18E-01	5.93E-01	CREB1	cAMP responsive element binding protein 1	chr2q34	204313_s_at	NM_004379 /// NM_134442
5.20	5.66	0.46	2.18E-01	5.93E-01	ZNF302	zinc finger protein 302	chr19q13.11	228392_at	NM_001012320 /// NM_018443
7.92	8.28	0.37	2.18E-01	5.93E-01	MBOAT7	membrane bound O-acyltransferase domain containing 7	chr19q13.4	209179_s_at	NM_024298
2.63	2.88	0.25	2.18E-01	5.93E-01	---	---	---	1566994_at	---
2.08	2.22	0.14	2.18E-01	5.93E-01	LOC642236	similar to FRG1 protein (FSHD region gene 1 protein)	chr9q12	242135_at	XR_041084 /// XR_041085 /// XR_041086 /// XR_041087
9.01	9.57	0.56	2.18E-01	5.93E-01	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	chr7p15	200977_s_at	NM_001079864 /// NM_006024
5.29	5.83	0.54	2.18E-01	5.93E-01	CYBB	cytochrome b-245, beta polypeptide	chrXp21.1	203922_s_at	NM_000397
6.20	6.48	0.28	2.18E-01	5.93E-01	C11orf74	chromosome 11 open reading frame 74	chr11p12	228249_at	NM_138787
5.67	5.89	0.22	2.18E-01	5.93E-01	RARA	retinoic acid receptor, alpha	chr17q21	216300_x_at	NM_000964 /// NM_001024809
2.02	2.15	0.13	2.18E-01	5.93E-01	---	---	---	242102_at	---

2.00	2.20	0.20	2.18E-01	5.93E-01	LOC100130155	Hypothetical protein LOC100130155	chr8q12.3	238661_at	XM_001720201 /// XM_001720202 /// XM_001720219																				
5.41	5.65	0.24	2.19E-01	5.93E-01	HSPC072	HSPC072 protein	chr20p11.23	220747_at	XR_017886 /// XR_017985 /// XR_041836																				
2.54	2.75	0.21	2.19E-01	5.93E-01	NFYC	Nuclear transcription factor Y, gamma	chr1p32|1p32	238231_at	NM_014223																				
2.30	2.51	0.21	2.19E-01	5.93E-01	C9orf144	chromosome 9 open reading frame 144	chr9p13.2	241690_at	XR_040555 /// XR_040556 /// XR_040557																				
4.57	4.75	0.18	2.19E-01	5.93E-01	---	---	---	237199_at	---																				
2.55	2.71	0.16	2.18E-01	5.93E-01	MAGEA5	melanoma antigen family A, 5	chrXq28	1553585_a_at	NM_021049																				
2.00	2.15	0.15	2.19E-01	5.93E-01	---	---	---	240208_at	---																				
8.62	8.99	0.37	2.19E-01	5.93E-01	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	chr3q13.2-q13.31	201972_at	NM_001690																				
5.19	5.61	0.42	2.19E-01	5.93E-01	NFIB	nuclear factor I/B	chr9p24.1	213033_s_at	NM_005596																				
2.91	3.24	0.32	2.19E-01	5.93E-01	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	chr20q11.22-q11.23	209743_s_at	NM_031483																				
2.40	2.63	0.23	2.19E-01	5.93E-01	LOC26010	viral DNA polymerase-transactivated protein 6	chr2q33.1	215617_at	NM_001100422 /// NM_001100423 /// NM_001100424 /// NM_015535																				
2.48	2.69	0.21	2.19E-01	5.93E-01	---	---	---	237524_at	---																				
3.35	3.55	0.20	2.19E-01	5.93E-01	TGFA	transforming growth factor, alpha	chr2p13	211258_s_at	NM_001099691 /// NM_003236																				
2.59	2.77	0.19	2.19E-01	5.93E-01	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	chr3q25.31	1556829_at	NM_015508																				
3.64	3.93	0.29	2.19E-01	5.93E-01	---	---	---	228987_at	---																				
2.97	3.22	0.25	2.19E-01	5.93E-01	RNF138	ring finger protein 138	chr18q12.1	239143_x_at	NM_016271 /// NM_198128																				
2.08	2.24	0.16	2.19E-01	5.93E-01	GPR155	G protein-coupled receptor 155	chr2q31.1	239533_at	NM_001033045 /// NM_152529																				
4.50	4.96	0.46	2.19E-01	5.93E-01	C6orf130	chromosome 6 open reading frame 130	chr6p21.1	238860_at	NM_145063																				
2.33	2.52	0.18	2.19E-01	5.93E-01	---	---	---	233099_at	---																				
2.81	3.12	0.31	2.19E-01	5.93E-01	FBXO7	F-box protein 7	chr22q12-q13	243649_at	NM_001033024 /// NM_012179																				
3.38	3.61	0.23	2.19E-01	5.93E-01	DHRS9	dehydrogenase/reductase (SDR family) member 9	chr2q31.1	219799_s_at	NM_005771 /// NM_199204																				
4.75	5.87	1.12	2.19E-01	5.93E-01	RANBP2	RAN binding protein 2	chr2q12.3	201711_x_at	NM_006267																				
5.88	6.21	0.33	2.19E-01	5.93E-01	DUSP26	dual specificity phosphatase 26 (putative)	chr8p12	219144_at	NM_024025																				
2.25	2.46	0.21	2.19E-01	5.93E-01	SNAP91	synaptosomal-associated protein, 91kDa homolog (mouse)	chr6q14.2	204953_at	NM_014841																				
4.40	4.80	0.39	2.19E-01	5.93E-01	APLP1	amyloid beta (A4) precursor-like protein 1	chr19q13.1	209462_at	NM_001024807 /// NM_005166																				
5.41	5.69	0.28	2.19E-01	5.93E-01	TMEM59L	transmembrane protein 59-like	chr19p12	219005_at	NM_012109																				
6.20	6.43	0.22	2.19E-01	5.93E-01	---	---	---	226719_at	---																				
2.03	2.23	0.19	2.19E-01	5.93E-01	FRMPD2 /// FRMPD2L1 /// FRMPD2L2	FERM and PDZ domain containing 2 /// FERM and PDZ domain containing 2 like 1 /// FERM and PDZ domain containing 2 like 2	chr10q11.21 /// chr10q11.22	239275_at	NM_001017929 /// NM_001018071 /// NM_001042512 /// NM_001042515 /// NM_001042516 /// NM_001042524 /// NM_001042525 /// NM_152428 /// XM_001714608 /// XM_001714969																				
2.66	2.84	0.19	2.19E-01	5.93E-01	---	---	---	1560872_at	---																				
2.29	2.45	0.16	2.19E-01	5.93E-01	CHRM3	cholinergic receptor, muscarinic 3	chr1q43	1559633_a_at	NM_000740																				

4.60	4.91	0.30	2.19E-01	5.94E-01	CNTROB	centrobin, centrosomal BRCA2 interacting protein	chr17p13.1	234694_at	NM_001037144 /// NM_053051
4.07	4.29	0.23	2.19E-01	5.94E-01	---	---	---	233696_at	---
1.96	2.10	0.15	2.19E-01	5.94E-01	---	---	---	236187_s_at	---
6.46	6.75	0.29	2.19E-01	5.94E-01	LIFR	leukemia inhibitory factor receptor alpha	chr5p13-p12	225575_at	NM_001127671 /// NM_002310
3.84	4.07	0.23	2.19E-01	5.94E-01	MKL1	megakaryoblastic leukemia (translocation) 1	chr22q13	1559902_at	NM_020831
5.37	6.22	0.86	2.19E-01	5.94E-01	GULP1	GULP, engulfment adaptor PTB domain containing 1	chr2q32.3-q33	215913_s_at	NM_016315
3.17	3.47	0.30	2.19E-01	5.94E-01	---	---	---	220689_at	---
2.14	2.32	0.17	2.19E-01	5.94E-01	CASR	calcium-sensing receptor	chr3q13	242744_s_at	NM_000388
4.27	4.68	0.41	2.20E-01	5.94E-01	---	---	---	239794_at	---
4.99	5.37	0.38	2.20E-01	5.94E-01	---	---	---	242968_at	---
4.18	4.44	0.26	2.20E-01	5.94E-01	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	chr2q33.3	228411_at	NM_057177 /// NM_152526 /// NM_205863
2.30	2.52	0.23	2.20E-01	5.94E-01	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	chr13q32.1	1555561_a_at	NM_020121
3.00	3.22	0.22	2.20E-01	5.94E-01	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	chr20p13	236012_at	NM_006814 /// NM_178578
1.90	2.07	0.18	2.20E-01	5.94E-01	---	---	---	244346_at	---
5.03	5.19	0.16	2.20E-01	5.94E-01	C1RL	complement component 1, r subcomponent-like	chr12p13.31	233645_s_at	NM_016546
3.59	3.75	0.16	2.20E-01	5.94E-01	MADCAM1	mucosal vascular addressin cell adhesion molecule 1	chr19p13.3	208037_s_at	NM_130760 /// NM_130762
2.18	2.33	0.15	2.20E-01	5.94E-01	NPAL2	NIPA-like domain containing 2	chr8q22.2	222950_at	NM_024759
3.81	4.00	0.19	2.20E-01	5.94E-01	DUOXA1	dual oxidase maturation factor 1	chr15q21.1	1555404_a_at	NM_144565
3.32	3.92	0.59	2.20E-01	5.94E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	215214_at	---
4.72	5.13	0.41	2.20E-01	5.94E-01	PRKCDBP	protein kinase C, delta binding protein	chr11p15.4	213010_at	NM_145040
2.00	2.20	0.19	2.20E-01	5.94E-01	TRIB1	Tribbles homolog 1 (Drosophila)	chr8q24.13	235641_at	NM_025195
1.85	1.98	0.13	2.20E-01	5.94E-01	---	---	---	1566673_at	---
5.68	5.90	0.22	2.20E-01	5.94E-01	EPHB3	EPH receptor B3	chr3q21-qter	204600_at	NM_004443
2.38	2.60	0.22	2.20E-01	5.94E-01	P704P	prostate-specific P704P	chr14q11.2	242912_at	XR_040579 /// XR_040580
4.57	4.84	0.27	2.20E-01	5.94E-01	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	chr14q11.2	214523_at	NM_001805
5.88	6.09	0.22	2.20E-01	5.94E-01	BCL2	B-cell CLL/lymphoma 2	chr18q21.33|18q21.3	207004_at	NM_000633 /// NM_000657
5.62	6.15	0.52	2.20E-01	5.94E-01	CAND1	cullin-associated and neddylation-dissociated 1	chr12q14	208839_s_at	NM_018448
2.13	2.30	0.17	2.20E-01	5.94E-01	DEPDC1	DEP domain containing 1	chr1p31.2	222958_s_at	NM_001114120 /// NM_017779
3.85	4.27	0.42	2.20E-01	5.94E-01	IGHA1 /// IGHG1 /// LOC100133862	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// similar to hCG1773549	chr14q32.33	211640_x_at	XM_001720441
2.77	2.95	0.18	2.20E-01	5.94E-01	---	---	---	236084_at	---
5.88	6.17	0.29	2.20E-01	5.94E-01	COL6A2	collagen, type VI, alpha 2	chr21q22.3	213290_at	NM_001849 /// NM_058174 /// NM_058175
6.13	6.34	0.21	2.20E-01	5.94E-01	KANK2	KN motif and ankyrin repeat domains 2	chr19p13.2	221068_at	NM_015493
1.99	2.14	0.15	2.20E-01	5.94E-01	PTK6	PTK6 protein tyrosine kinase 6	chr20q13.3	206482_at	NM_005975
2.40	2.54	0.15	2.20E-01	5.94E-01	GRM8	glutamate receptor, metabotropic 8	chr7q31.3-q32.1	216992_s_at	NM_000845 /// NM_001127323 /// NM_001127326
2.21	2.34	0.13	2.20E-01	5.94E-01	DBT	dihydrolipoamide branched chain transacylase E2	chr1p31	211196_at	NM_001918
3.87	4.16	0.29	2.20E-01	5.94E-01	LOC100132832 /// LOC441259 /// LOC730324 /// PMS2L1 /// PMS2L2 /// PMS2L5	similar to postmeiotic segregation increased 2-like 5 /// PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like /// similar to postmeiotic segregation increased 2-like 2 /// postmeiotic segregation increased 2-like 1 pseudogene /// postmeiotic segregation increased 2-like 2 pseudogene /// postmeiotic segregation increased 2-like 5	chr7q11-q22 /// chr7q11.23 /// chr7q22.1	215410_at	NM_001129851 /// NM_174930 /// NR_003613 /// NR_003614 /// XM_001713820 /// XM_001722095 /// XM_001722503 /// XR_042144 /// XR_042161 /// XR_042167
4.56	4.72	0.16	2.20E-01	5.94E-01	---	---	---	239728_at	---
3.90	4.40	0.50	2.20E-01	5.95E-01	LRPPRC	leucine-rich PPR-motif containing	chr2p21	1557360_at	NM_133259
3.79	3.95	0.16	2.20E-01	5.95E-01	ADAMTSL5	ADAMTS-like 5	chr19p13.3	242200_at	NM_213604
2.70	2.90	0.20	2.20E-01	5.95E-01	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	chr22q12.2	1555632_at	NM_052880
2.16	2.91	0.75	2.20E-01	5.95E-01	PAH	phenylalanine hydroxylase	chr12q22-q24.2	205719_s_at	NM_000277
4.11	4.63	0.52	2.20E-01	5.95E-01	GAB1	GRB2-associated binding protein 1	chr4q31.21	226002_at	NM_002039 /// NM_207123

4.40	4.90	0.50	2.20E-01	5.95E-01	ITGB1BP1	integrin beta 1 binding protein 1	chr2p25.2	203337_x_at	NM_004763 /// NM_022334
6.11	6.52	0.41	2.20E-01	5.95E-01	WAPAL	wings apart-like homolog (Drosophila)	chr10q23.2	212267_at	NM_015045
5.52	5.82	0.30	2.20E-01	5.95E-01	MOSC2	MOCO sulphurase C-terminal domain containing 2	chr1q41	221636_s_at	NM_017898
2.03	2.19	0.16	2.20E-01	5.95E-01	FLJ32955	hypothetical protein FLJ32955	chr2q23.3	1553472_at	NM_153041
4.71	5.33	0.62	2.20E-01	5.95E-01	KIAA0485	hypothetical LOC57235	---	214295_at	---
1.92	2.15	0.24	2.20E-01	5.95E-01	MGAT4C	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme C (putative)	chr12q21	207447_s_at	NM_013244
2.98	3.18	0.19	2.20E-01	5.95E-01	CLUAP1	clusterin associated protein 1	chr16p13.3	204577_s_at	NM_015041 /// NM_024793
2.11	2.35	0.25	2.21E-01	5.95E-01	---	---	---	234112_at	---
2.26	2.47	0.21	2.21E-01	5.95E-01	CDC25C	cell division cycle 25 homolog C (S. pombe)	chr5q31	217010_s_at	NM_001790 /// NM_022809
2.77	2.97	0.20	2.21E-01	5.95E-01	WNT2B	wingless-type MMTV integration site family, member 2B	chr1p13	206459_s_at	NM_004185 /// NM_024494
4.75	5.06	0.31	2.21E-01	5.95E-01	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	chrXq28	221196_x_at	NM_001018055 /// NM_024332
3.85	4.14	0.29	2.21E-01	5.95E-01	SARM1	sterile alpha and TIR motif containing 1	chr17q11	213257_at	NM_015077
5.39	5.60	0.21	2.21E-01	5.95E-01	---	---	---	236923_x_at	---
5.25	6.02	0.77	2.21E-01	5.95E-01	LAMB1	laminin, beta 1	chr7q22	211651_s_at	NM_002291
7.35	8.08	0.73	2.21E-01	5.95E-01	CSDE1	cold shock domain containing E1, RNA-binding	chr1p22	222975_s_at	NM_001007553 /// NM_001130523 /// NM_007158
5.24	5.77	0.54	2.21E-01	5.95E-01	GNG12	guanine nucleotide binding protein (G protein), gamma 12	chr1p31.3	222834_s_at	NM_018841
4.35	4.83	0.47	2.21E-01	5.95E-01	KIAA2026	KIAA2026	chr9p24.1	238490_at	NM_001017969
2.79	2.99	0.20	2.21E-01	5.95E-01	OXCT2	3-oxoacid CoA transferase 2	chr1p34	233301_at	NM_022120
4.10	4.29	0.20	2.21E-01	5.95E-01	---	---	---	236479_at	---
2.66	2.85	0.19	2.21E-01	5.95E-01	---	---	---	1559622_at	---
2.58	2.80	0.22	2.21E-01	5.95E-01	---	---	---	240916_x_at	---
3.16	3.32	0.16	2.21E-01	5.95E-01	SYT3	synaptotagmin III	chr19q13.33	223901_at	NM_032298
4.01	4.30	0.28	2.21E-01	5.95E-01	SEC14L2	SEC14-like 2 (S. cerevisiae)	chr22q12.2	204541_at	NM_012429
5.81	6.30	0.49	2.21E-01	5.95E-01	KIAA0564	KIAA0564	chr13q14.11	212946_at	NM_001009814 /// NM_015058
2.75	2.99	0.24	2.21E-01	5.95E-01	---	---	---	1559597_at	---
7.16	7.40	0.24	2.21E-01	5.95E-01	SCAMP2	secretory carrier membrane protein 2	chr15q23-q25	224921_at	NM_005697
3.72	3.96	0.24	2.21E-01	5.95E-01	POL3S	polyserase 3	chr16p11.2	214226_at	NM_001039503
2.73	2.93	0.20	2.21E-01	5.95E-01	PVT1	Pvt1 oncogene (non-protein coding)	chr8q24	216240_at	NR_003367
2.30	2.44	0.14	2.21E-01	5.95E-01	---	---	---	234149_at	---
4.60	4.96	0.36	2.21E-01	5.95E-01	MAN1C1	mannosidase, alpha, class 1C, member 1	chr1p35	214180_at	NM_020379
2.64	2.97	0.33	2.21E-01	5.95E-01	---	---	---	1556744_a_at	---
3.16	3.40	0.24	2.21E-01	5.95E-01	KIAA1632	KIAA1632	chr18q12.3-q21.1	232031_s_at	NM_020964
2.11	2.24	0.13	2.21E-01	5.96E-01	---	---	---	244679_at	---
1.98	2.15	0.17	2.21E-01	5.96E-01	PDC	phosducin	chr1q25.2	211496_s_at	NM_002597 /// NM_022576
4.32	4.70	0.38	2.21E-01	5.96E-01	ZUFSP	zinc finger with UFM1-specific peptidase domain	chr6q22.1	228330_at	NM_145062
2.55	2.77	0.22	2.21E-01	5.96E-01	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	chr22q13.32	229655_at	NM_001082967 /// NM_015381
2.69	3.02	0.33	2.21E-01	5.96E-01	C21orf34	Chromosome 21 open reading frame 34	chr21q21.1	239999_at	NM_001005732 /// NM_001005733 /// NM_001005734
1.98	2.17	0.19	2.21E-01	5.96E-01	---	---	---	1561166_a_at	---
4.78	5.12	0.34	2.21E-01	5.96E-01	NAAA	N-acylethanolamine acid amidase	chr4q21.1	227135_at	NM_001042402 /// NM_014435
3.89	4.22	0.34	2.22E-01	5.96E-01	TREX2 /// UCHL5IP	three prime repair exonuclease 2 /// UCHL5 interacting protein	chrXq28	207891_s_at	NM_017518 /// NM_080701 /// NM_207107
2.88	3.09	0.22	2.22E-01	5.96E-01	---	---	---	240917_at	---
2.36	2.57	0.21	2.22E-01	5.96E-01	---	---	---	235286_at	---
2.06	2.25	0.19	2.21E-01	5.96E-01	---	---	---	1563277_at	---
2.23	2.40	0.17	2.22E-01	5.96E-01	---	---	---	240819_at	---
6.40	6.71	0.31	2.22E-01	5.96E-01	BTN3A2	butyrophilin, subfamily 3, member A2	chr6p22.1	212613_at	NM_007047
5.06	5.44	0.38	2.22E-01	5.96E-01	---	---	---	229885_at	---
2.90	3.14	0.24	2.22E-01	5.96E-01	ARSB	arylsulfatase B	chr5q11-q13	206129_s_at	NM_000046 /// NM_198709

3.09	3.28	0.19	2.22E-01	5.96E-01	NFASC	neurofascin homolog (chicken)	chr1q32.1	243645_at	NM_015090
2.65	2.80	0.15	2.22E-01	5.96E-01	RGS8	regulator of G-protein signaling 8	chr1q25	224390_s_at	NM_001102450 /// NM_033345
3.21	3.42	0.21	2.22E-01	5.96E-01	---	---	---	238566_at	---
2.16	2.32	0.16	2.22E-01	5.96E-01	---	---	---	243907_at	---
3.44	3.99	0.55	2.22E-01	5.96E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM /// IGHV4-31 /// LOC100126583 /// LOC100133739 /// LOC652494	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical LOC100126583 /// similar to hCG2038920 /// similar to Ig heavy chain V-III region VH26 precursor	chr14q32.33	217281_x_at	XM_001717586 /// XM_001718220 /// XM_001719484
6.77	7.00	0.23	2.22E-01	5.96E-01	---	---	---	235671_at	---
2.79	3.01	0.22	2.22E-01	5.96E-01	ST14	suppression of tumorigenicity 14 (colon carcinoma)	chr11q24-q25	216905_s_at	NM_021978
4.99	5.50	0.51	2.22E-01	5.96E-01	IDE	insulin-degrading enzyme	chr10q23-q25	203328_x_at	NM_004969
2.48	2.71	0.23	2.22E-01	5.96E-01	SOX18	SRY (sex determining region Y)-box 18	chr20q13.33	219568_x_at	NM_018419
6.60	6.79	0.19	2.22E-01	5.96E-01	PQBP1	polyglutamine binding protein 1	chrXp11.23	210499_s_at	NM_001032381 /// NM_001032382 /// NM_001032383 /// NM_001032384 /// NM_005710
5.62	5.96	0.34	2.22E-01	5.96E-01	FBXW7	F-box and WD repeat domain containing 7	chr4q31.3	218751_s_at	NM_001013415 /// NM_018315 /// NM_033632
4.86	5.21	0.35	2.22E-01	5.96E-01	---	---	---	229470_at	---
2.11	2.28	0.17	2.22E-01	5.96E-01	PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	chr8q21.12	226864_at	NM_006823 /// NM_181839
3.15	3.39	0.23	2.22E-01	5.96E-01	BRSK2	BR serine/threonine kinase 2	chr11p15.5	223715_at	NM_003957
3.35	3.59	0.24	2.22E-01	5.96E-01	TUBA8	tubulin, alpha 8	chr22q11.1	220069_at	NM_018943
7.07	7.62	0.55	2.22E-01	5.96E-01	UQCRC2	ubiquinol-cytochrome c reductase core protein II	chr16p12	200883_at	NM_003366
3.62	3.89	0.28	2.22E-01	5.96E-01	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	chr1q23.3	238056_at	NM_001035511 /// NM_001035512 /// NM_001035513 /// NM_003001
3.77	3.99	0.22	2.22E-01	5.96E-01	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	chr5q33-q34	210329_s_at	NM_000337 /// NM_001128209 /// NM_172244
2.85	3.07	0.22	2.22E-01	5.96E-01	---	---	---	217293_at	---
2.67	2.85	0.18	2.22E-01	5.96E-01	PLA2G10	phospholipase A2, group X	chr16p13.1-p12	207222_at	NM_003561
1.89	2.07	0.17	2.22E-01	5.96E-01	---	---	---	1556392_a_at	---
2.17	2.33	0.15	2.22E-01	5.96E-01	---	---	---	236792_at	---
2.30	2.42	0.13	2.22E-01	5.96E-01	---	---	---	231025_at	---
5.91	7.01	1.09	2.22E-01	5.96E-01	RDX	radixin	chr11q23	204969_s_at	NM_002906
5.46	5.82	0.35	2.22E-01	5.96E-01	CEP170	centrosomal protein 170kDa	chr1q44	212746_s_at	NM_001042404 /// NM_001042405 /// NM_014812
2.79	3.02	0.22	2.22E-01	5.96E-01	FAM102A	Family with sequence similarity 102, member A	chr9q34.11	228428_at	NM_001035254 /// NM_203305
3.66	3.88	0.22	2.22E-01	5.96E-01	LIMD2	LIM domain containing 2	chr17q23.3	218600_at	NM_030576
3.38	3.57	0.19	2.22E-01	5.96E-01	LOC285943	Hypothetical protein LOC285943	chr7p15.2	230080_at	XR_040113 /// XR_040114 /// XR_040115 /// XR_040116
2.85	3.03	0.18	2.22E-01	5.96E-01	---	---	---	1560512_at	---
3.30	4.08	0.78	2.22E-01	5.96E-01	TPSB2	tryptase beta 2	chr16p13.3	207134_x_at	NM_024164
4.30	4.83	0.53	2.22E-01	5.96E-01	GPR124	G protein-coupled receptor 124	chr8p12	221814_at	NM_032777
5.16	5.66	0.50	2.22E-01	5.96E-01	AGPS	alkylglycerone phosphate synthase	chr2q31.2	225108_at	NM_003659
7.15	7.57	0.41	2.22E-01	5.96E-01	IFI16	interferon, gamma-inducible protein 16	chr1q22	206332_s_at	NM_005531
5.60	6.00	0.41	2.22E-01	5.96E-01	---	---	---	230740_at	---
3.94	4.26	0.32	2.23E-01	5.96E-01	---	---	---	241458_at	---
5.06	5.36	0.30	2.23E-01	5.96E-01	---	---	---	234572_at	---

4.21	4.45	0.24	2.22E-01	5.96E-01	---	---	---	229986_at	---
5.44	5.67	0.23	2.22E-01	5.96E-01	SPN	sialophorin	chr16p11.2	216980_s_at	NM_001030288 /// NM_003123
3.17	3.39	0.22	2.23E-01	5.96E-01	RPLP1	Ribosomal protein, large, P1	chr15q22	244191_at	NM_001003 /// NM_213725
2.03	2.25	0.22	2.23E-01	5.96E-01	HIST1H2BO	histone cluster 1, H2bo	chr6p22-p21.3	214540_at	NM_003527
3.54	3.75	0.22	2.23E-01	5.96E-01	BOK	BCL2-related ovarian killer	chr2q37.3	221454_at	NM_032515
2.30	2.51	0.21	2.23E-01	5.96E-01	FLJ32810	Hypothetical protein FLJ32810	chr11q22.1	233923_at	XM_001127597 /// XM_001725431 /// XM_001726122
2.14	2.34	0.20	2.22E-01	5.96E-01	PAPPA2	pappalysin 2	chr1q23-q25	228237_at	NM_020318 /// NM_021936
3.45	3.65	0.19	2.22E-01	5.96E-01	SHOX2	short stature homeobox 2	chr3q25-q26.1	210134_x_at	NM_003030 /// NM_006884
3.04	3.23	0.19	2.22E-01	5.96E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	230150_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844
3.06	3.23	0.18	2.22E-01	5.96E-01	C15orf42	chromosome 15 open reading frame 42	chr15q26.1	230021_at	NM_152259
2.90	3.08	0.17	2.23E-01	5.96E-01	CNIH4	Cornichon homolog 4 (Drosophila)	chr1q42.11	243051_at	NM_014184
2.03	2.20	0.17	2.22E-01	5.96E-01	CDCA7	cell division cycle associated 7	chr2q31	230060_at	NM_031942 /// NM_145810
3.79	3.95	0.16	2.22E-01	5.96E-01	CACYBP	calcyclin binding protein	chr1q24-q25	201382_at	NM_001007214 /// NM_014412
1.96	2.10	0.14	2.22E-01	5.96E-01	---	---	---	1561368_at	---
5.64	5.88	0.23	2.23E-01	5.96E-01	---	---	---	230929_s_at	---
5.62	5.80	0.18	2.23E-01	5.96E-01	---	---	---	233128_at	---
4.76	5.41	0.66	2.23E-01	5.96E-01	VTA1	Vps20-associated 1 homolog (S. cerevisiae)	chr6q24.1	223021_x_at	NM_016485
5.06	5.67	0.61	2.23E-01	5.96E-01	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	chr20p11.2	219913_s_at	NM_016652
6.65	7.00	0.35	2.23E-01	5.96E-01	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	chr7p14-p13	201282_at	NM_001003941 /// NM_002541
3.70	3.95	0.26	2.23E-01	5.96E-01	PURB	purine-rich element binding protein B	chr7p13	235711_at	NM_033224
3.58	3.82	0.24	2.23E-01	5.96E-01	FLJ22184	hypothetical protein FLJ22184	chr19p13.2	220584_at	XM_001717591 /// XM_001719253 /// XM_001719282
2.81	3.05	0.24	2.23E-01	5.96E-01	---	---	---	233207_at	---
4.30	4.53	0.23	2.23E-01	5.96E-01	MAPT	microtubule-associated protein tau	chr17q21.1	225379_at	NM_001123066 /// NM_001123067 /// NM_005910 /// NM_016834 /// NM_016835 /// NM_016841
1.94	2.15	0.21	2.23E-01	5.96E-01	---	---	---	1562780_at	---
4.88	5.09	0.21	2.23E-01	5.96E-01	BMP1	bone morphogenetic protein 1	chr8p21.3	1569001_at	NM_001199 /// NM_006128 /// NM_006129
2.47	2.66	0.19	2.23E-01	5.96E-01	MOGAT3	monoacylglycerol O-acyltransferase 3	chr7q22.1	234850_at	NM_178176
2.19	2.37	0.18	2.23E-01	5.96E-01	---	---	---	240719_at	---
2.09	2.26	0.18	2.23E-01	5.96E-01	BLID	BH3-like motif containing, cell death inducer	chr11q24.1	1555675_at	NM_001001786
2.03	2.19	0.17	2.23E-01	5.96E-01	---	---	---	237951_at	---
2.18	2.32	0.15	2.23E-01	5.96E-01	---	---	---	232998_at	---
1.96	2.15	0.19	2.23E-01	5.97E-01	TOX3	TOX high mobility group box family member 3	chr16q12.1	216623_x_at	NM_001080430
2.01	2.17	0.17	2.23E-01	5.97E-01	---	---	---	1562687_x_at	---
3.50	3.73	0.23	2.23E-01	5.97E-01	TSKS	testis-specific kinase substrate	chr19q13.3	220544_at	NM_021733

5.19	5.43	0.24	2.23E-01	5.97E-01	LOC100131218 /// LOC648245 /// NDOR1	similar to NADPH-dependent FMN and FAD containing oxidoreductase /// hypothetical LOC648245 /// NADPH dependent diflavin oxidoreductase 1	chr9q34.3	234318_x_at	NM_014434 /// XM_001714467 /// XM_001715437 /// XM_001716570 /// XM_001720502 /// XM_001723031
8.07	8.34	0.27	2.23E-01	5.97E-01	SERINC3	serine incorporator 3	chr20q13.1-q13.3	221472_at	NM_006811 /// NM_198941
2.31	2.49	0.18	2.23E-01	5.97E-01	LHFPL3	lipoma HMGIC fusion partner-like 3	chr7q22.1	236761_at	NM_199000
1.81	1.94	0.13	2.23E-01	5.97E-01	LOC401097	Similar to LOC166075	chr3q26.1	236738_at	XM_001717103 /// XM_001718562 /// XM_001718743
4.86	5.08	0.22	2.23E-01	5.97E-01	---	---	---	240374_at	---
2.08	2.43	0.35	2.23E-01	5.97E-01	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	chr1q31	217452_s_at	NM_003783
2.49	2.71	0.22	2.23E-01	5.97E-01	---	---	---	238953_at	---
3.64	3.80	0.16	2.23E-01	5.97E-01	IGL@	Immunoglobulin lambda locus	chr22q11.1-q11.2	217193_x_at	---
4.52	4.72	0.21	2.23E-01	5.97E-01	DUSP18	dual specificity phosphatase 18	chr22q12.2	1553701_a_at	NM_152511
4.03	4.26	0.23	2.23E-01	5.97E-01	PRSS3	protease, serine, 3	chr9p11.2	207463_x_at	NM_002771 /// NM_007343
2.00	2.16	0.17	2.23E-01	5.97E-01	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)	chr5q31.2	1565325_at	NR_003141
1.97	2.13	0.16	2.23E-01	5.97E-01	WDR21C	WD repeat domain 21C	chr8q21.3	1553197_at	NM_152418
4.41	4.70	0.29	2.23E-01	5.97E-01	---	---	---	233323_at	---
3.98	4.24	0.27	2.23E-01	5.97E-01	GPR26	G protein-coupled receptor 26	chr10q26.2	244617_at	NM_153442
2.83	3.08	0.25	2.23E-01	5.97E-01	PIGX	phosphatidylinositol glycan anchor biosynthesis, class X	chr3q29	1552291_at	NM_017861
1.95	2.15	0.20	2.23E-01	5.97E-01	---	---	---	241079_at	---
2.67	2.87	0.19	2.23E-01	5.97E-01	EDA	ectodysplasin A	chrXq12-q13.1|Xq12	211128_at	NM_001005609 /// NM_001005610 /// NM_001005611 /// NM_001005612 /// NM_001005615 /// NM_001399
3.74	3.91	0.17	2.23E-01	5.97E-01	FXYD2	FXYD domain containing ion transport regulator 2	chr11q23	205674_x_at	NM_001127489 /// NM_001680 /// NM_021603
2.21	2.42	0.21	2.24E-01	5.97E-01	TTBK2	tau tubulin kinase 2	chr15q15.2	213922_at	NM_173500
2.37	2.52	0.15	2.24E-01	5.97E-01	ZNF29	zinc finger protein 29 pseudogene	chr17p13-p12	1567856_x_at	---
2.63	2.78	0.15	2.24E-01	5.97E-01	FANCD2	Fanconi anemia, complementation group D2	chr3p26	242560_at	NM_001018115 /// NM_033084
6.63	6.98	0.35	2.24E-01	5.97E-01	ATRN	attractin	chr20p13	211852_s_at	NM_139321 /// NM_139322
3.28	3.48	0.20	2.24E-01	5.97E-01	DRD4	dopamine receptor D4	chr11p15.5	208215_x_at	NM_000797
4.19	4.37	0.18	2.24E-01	5.97E-01	---	---	---	216745_x_at	---
2.06	2.22	0.16	2.24E-01	5.97E-01	---	---	---	243654_at	---
1.90	2.06	0.15	2.24E-01	5.97E-01	---	---	---	234247_at	---
2.70	2.85	0.15	2.24E-01	5.97E-01	SENP8	SUMO/sentrin specific peptidase family member 8	chr15q23	1552684_a_at	NM_145204
2.63	2.80	0.17	2.24E-01	5.97E-01	HORMAD2	HORMA domain containing 2	chr22q12.2	244442_at	NM_152510
6.18	7.16	0.98	2.24E-01	5.97E-01	PNPLA8	patatin-like phospholipase domain containing 8	chr7q31	223309_x_at	NM_015723
2.14	2.56	0.42	2.24E-01	5.97E-01	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	chr12q22-q23	213880_at	NM_003667
5.53	6.11	0.58	2.24E-01	5.98E-01	YIPF5	Yip1 domain family, member 5	chr5q32	224949_at	NM_001024947 /// NM_030799
4.47	4.95	0.48	2.24E-01	5.98E-01	BARD1	BRCA1 associated RING domain 1	chr2q34-q35	205345_at	NM_000465
2.59	2.83	0.24	2.24E-01	5.98E-01	---	---	---	239025_at	---
2.20	2.41	0.20	2.24E-01	5.98E-01	---	---	---	1559813_at	---
2.96	3.15	0.19	2.24E-01	5.98E-01	DHH	desert hedgehog homolog (Drosophila)	chr12q12-q13.1	1552730_at	NM_021044
2.06	2.22	0.16	2.24E-01	5.98E-01	IL5	interleukin 5 (colony-stimulating factor, eosinophil)	chr5q31.1	207952_at	NM_000879
2.20	2.35	0.15	2.24E-01	5.98E-01	---	---	---	1559102_at	---
2.62	2.77	0.15	2.24E-01	5.98E-01	---	---	---	231347_at	---

7.14	7.80	0.66	2.24E-01	5.98E-01	SCP2	sterol carrier protein 2	chr1p32	201339_s_at	NM_001007098 /// NM_001007099 /// NM_001007100 /// NM_001007250 /// NM_002979
2.31	2.51	0.20	2.24E-01	5.98E-01	SYNE2	spectrin repeat containing, nuclear envelope 2	chr14q23.2	243841_at	NM_015180 /// NM_182910 /// NM_182913 /// NM_182914
5.09	5.35	0.26	2.24E-01	5.98E-01	---	---	---	242402_x_at	---
1.95	2.11	0.16	2.24E-01	5.98E-01	---	---	---	1558871_at	---
2.26	2.42	0.16	2.24E-01	5.98E-01	TRADD	TNFRSF1A-associated via death domain	chr16q22	213443_at	NM_003789
9.54	9.89	0.35	2.24E-01	5.98E-01	MGST1	microsomal glutathione S-transferase 1	chr12p12.3-p12.1	1565162_s_at	NM_020300 /// NM_145764 /// NM_145791 /// NM_145792
3.52	3.72	0.21	2.24E-01	5.98E-01	NMNAT1	nicotinamide nucleotide adenylyltransferase 1	chr1p32-p35	1569631_at	NM_022787
2.14	2.26	0.12	2.24E-01	5.98E-01	---	---	---	241529_at	---
4.73	5.12	0.39	2.24E-01	5.98E-01	MAP1A	microtubule-associated protein 1A	chr15q13-qter	203151_at	NM_002373
4.85	5.16	0.30	2.24E-01	5.98E-01	TSPAN32	tetraspanin 32	chr11p15.5	220558_x_at	NM_005705 /// NM_139022
2.22	2.38	0.17	2.24E-01	5.98E-01	---	---	---	1570100_at	---
2.92	3.10	0.18	2.24E-01	5.98E-01	FAM123C	family with sequence similarity 123C	chr2q21.1	244709_at	NM_001105193 /// NM_001105194 /// NM_001105195 /// NM_152698
2.91	3.09	0.17	2.24E-01	5.98E-01	EPX	eosinophil peroxidase	chr17q23.1	214627_at	NM_000502
5.96	6.37	0.42	2.24E-01	5.98E-01	KLHL20	kelch-like 20 (Drosophila)	chr1q24.1-q24.3	204177_s_at	NM_014458
3.38	3.68	0.30	2.24E-01	5.98E-01	---	---	---	230663_at	---
2.05	2.21	0.16	2.24E-01	5.98E-01	AAK1	AP2 associated kinase 1	chr2p14	214998_at	NM_014911
2.55	2.72	0.17	2.24E-01	5.98E-01	CLOCK	clock homolog (mouse)	chr4q12	217563_at	NM_004898
2.32	2.48	0.15	2.24E-01	5.98E-01	PRTN3	proteinase 3	chr19p13.3	207341_at	NM_002777
2.97	3.12	0.15	2.24E-01	5.98E-01	LOC219731	hypothetical protein LOC219731	chr10p14	1569722_s_at	---
2.35	2.49	0.14	2.24E-01	5.98E-01	MOG	myelin oligodendrocyte glycoprotein	chr6p22.1	211836_s_at	NM_001008228 /// NM_001008229 /// NM_002433 /// NM_206809 /// NM_206810 /// NM_206811 /// NM_206812 /// NM_206813 /// NM_206814
1.86	1.99	0.13	2.24E-01	5.98E-01	IKZF3	IKAROS family zinc finger 3 (Aiolos)	chr17q21	221092_at	NM_012481 /// NM_183228 /// NM_183229 /// NM_183230 /// NM_183231 /// NM_183232
4.48	4.70	0.22	2.25E-01	5.98E-01	SYT5	synaptotagmin V	chr19q|11p	206162_x_at	NM_003180
3.90	4.15	0.25	2.25E-01	5.98E-01	CHRD	chordin	chr3q27	211248_s_at	NM_003741
3.01	3.16	0.15	2.25E-01	5.98E-01	---	---	---	242710_at	---
5.59	6.05	0.46	2.25E-01	5.98E-01	SYNPO2	synaptopodin 2	chr4q26	225721_at	NM_001128933 /// NM_001128934 /// NM_133477
2.02	2.44	0.43	2.25E-01	5.98E-01	PAX6	paired box 6	chr11p13	235795_at	NM_000280 /// NM_001127612 /// NM_001604
4.88	5.19	0.31	2.25E-01	5.98E-01	MED7	mediator complex subunit 7	chr5q33.3	204349_at	NM_001100816 /// NM_004270

2.13	2.30	0.17	2.25E-01	5.98E-01	C5orf44	chromosome 5 open reading frame 44	chr5q12.3	1559369_at	NM_001093755 /// NM_001093756 /// NM_024941 /// NR_003545
2.41	2.59	0.18	2.25E-01	5.98E-01	---	---	---	1557606_at	---
1.85	2.01	0.16	2.25E-01	5.98E-01	MGC39900	thymosin beta15b	chrXq22.2	1570039_at	NM_194324 /// XR_042096 /// XR_042097 /// XR_042098
4.73	5.32	0.58	2.25E-01	5.98E-01	IGLJ3	immunoglobulin lambda joining 3	chr22q11.1-q11.2	211881_x_at	---
3.49	3.67	0.18	2.25E-01	5.98E-01	KIAA0913 /// SAT1	KIAA0913 /// spermidine/spermine N1-acetyltransferase 1	chr10q22.2 /// chrXp22.1	210593_at	NM_002970 /// NM_015037
6.39	7.00	0.61	2.25E-01	5.98E-01	UBXN4	UBX domain protein 4	chr2q21.3	212006_at	NM_014607
6.06	6.78	0.72	2.25E-01	5.99E-01	C1S	complement component 1, s subcomponent	chr12p13	1555229_a_at	NM_001734 /// NM_201442
2.68	2.95	0.27	2.25E-01	5.99E-01	---	---	---	215376_at	---
2.05	2.24	0.19	2.25E-01	5.99E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	232188_at	NM_006738 /// NM_007200 /// NM_144767
4.61	5.38	0.77	2.25E-01	5.99E-01	BRWD2	bromodomain and WD repeat domain containing 2	chr10q26	229694_at	NM_018117
2.39	2.58	0.19	2.25E-01	5.99E-01	---	---	---	242759_at	---
2.29	2.45	0.16	2.25E-01	5.99E-01	ANGPTL3	Angiopoietin-like 3	chr1p31.1-p22.3	231684_at	NM_014495
7.05	7.31	0.26	2.25E-01	5.99E-01	AGRN	agrin	chr1p36.33	217410_at	NM_198576
5.29	5.94	0.65	2.25E-01	5.99E-01	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	chr1p34.3	201948_at	NM_013285
4.34	4.71	0.37	2.25E-01	5.99E-01	DOCK4	dedicator of cytokinesis 4	chr7q31.1	244840_x_at	NM_014705
11.92	12.29	0.36	2.25E-01	5.99E-01	RPL7	ribosomal protein L7	chr8q21.11	200717_x_at	NM_000971
2.22	2.39	0.17	2.25E-01	5.99E-01	---	---	---	241338_at	---
5.08	5.24	0.16	2.25E-01	5.99E-01	---	---	---	1563946_at	---
1.98	2.10	0.13	2.25E-01	5.99E-01	---	---	---	1559377_at	---
2.42	2.54	0.12	2.25E-01	5.99E-01	---	---	---	241559_at	---
5.96	6.48	0.52	2.25E-01	5.99E-01	PCNX	pecanex homolog (Drosophila)	chr14q24.2	229287_at	NM_014982
2.79	2.95	0.16	2.25E-01	5.99E-01	LOC285954	hypothetical protein LOC285954	chr7p13	1557850_at	---
3.00	3.42	0.42	2.25E-01	5.99E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	238546_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
12.55	12.74	0.19	2.25E-01	5.99E-01	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	chr6q14.1	213477_x_at	NM_001402
4.19	5.44	1.25	2.25E-01	5.99E-01	CST2	cystatin SA	chr20p11.21	208555_x_at	NM_001322
9.16	9.49	0.33	2.25E-01	5.99E-01	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	chr2q33.1	205133_s_at	NM_002157
5.13	5.39	0.26	2.25E-01	5.99E-01	---	---	---	242862_x_at	---
2.51	2.68	0.17	2.25E-01	5.99E-01	SCARB1	scavenger receptor class B, member 1	chr12q24.31	215835_at	NM_001082959 /// NM_005505
4.46	4.67	0.20	2.25E-01	5.99E-01	SERPINF2	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2	chr17p13	205075_at	NM_000934
7.92	8.69	0.77	2.25E-01	5.99E-01	IDI1	isopentenyl-diphosphate delta isomerase 1	chr10p15.3	208881_x_at	NM_004508
2.19	2.40	0.20	2.25E-01	5.99E-01	SNX16	sorting nexin 16	chr8q21.13	219793_at	NM_022133 /// NM_152836 /// NM_152837
2.72	2.92	0.20	2.25E-01	5.99E-01	FBXO24	F-box protein 24	chr7q22	221157_s_at	NM_012172 /// NM_033506
1.89	2.03	0.14	2.25E-01	5.99E-01	LOC283432	hypothetical protein LOC283432	chr12q23.2	1561222_at	XM_378379 /// XM_944966
1.87	2.03	0.16	2.26E-01	5.99E-01	RHOA	Ras homolog gene family, member A	chr3p21.3	240337_at	NM_001664
3.13	3.46	0.33	2.26E-01	5.99E-01	---	---	---	1555303_at	---
3.82	4.06	0.24	2.26E-01	5.99E-01	---	---	---	241633_x_at	---
3.15	3.30	0.16	2.26E-01	5.99E-01	---	---	---	244719_at	---
5.73	6.64	0.91	2.26E-01	5.99E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	223940_x_at	NR_002819
4.48	4.73	0.26	2.26E-01	5.99E-01	ADD2	adducin 2 (beta)	chr2p14-p13	206807_s_at	NM_001617 /// NM_017482 /// NM_017483 /// NM_017484 /// NM_017488
3.08	3.30	0.22	2.26E-01	5.99E-01	---	---	---	228481_at	---
4.15	4.32	0.17	2.26E-01	5.99E-01	MGC44328	hypothetical gene supported by BC033985	chr20p11.23	231447_at	XR_040561 /// XR_040562 /// XR_040563
1.94	2.08	0.15	2.26E-01	5.99E-01	SFRS4	Splicing factor, arginine/serine-rich 4	chr1p35.3	241245_at	NM_005626
2.42	2.55	0.13	2.26E-01	5.99E-01	---	---	---	213929_at	---
2.85	3.01	0.15	2.26E-01	5.99E-01	---	---	---	241293_x_at	---
2.11	2.24	0.13	2.26E-01	5.99E-01	ACMSD	aminocarboxymuconate semialdehyde decarboxylase	chr2q21.3	230602_at	NM_138326

4.02	4.70	0.68	2.26E-01	5.99E-01	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	chr21q21.2	222486_s_at	NM_006988
3.07	3.28	0.21	2.26E-01	5.99E-01	NOS1	nitric oxide synthase 1 (neuronal)	chr12q24.2-q24.31	207309_at	NM_000620
2.23	2.41	0.18	2.26E-01	5.99E-01	---	---	---	240747_at	---
4.50	4.68	0.18	2.26E-01	5.99E-01	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	chr17q21.33	234465_at	NM_152463
1.82	1.95	0.13	2.26E-01	5.99E-01	---	---	---	231512_at	---
3.97	4.15	0.18	2.26E-01	5.99E-01	---	---	---	238742_x_at	---
2.35	2.53	0.18	2.26E-01	5.99E-01	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	chr17q21-q22	1552713_a_at	NM_000342
4.74	5.26	0.51	2.26E-01	5.99E-01	---	---	---	228218_at	---
2.83	3.06	0.23	2.26E-01	5.99E-01	NLRP1	NLR family, pyrin domain containing 1	chr17p13.2	1562257_x_at	NM_001033053 /// NM_014922 /// NM_033004 /// NM_033006 /// NM_033007
3.09	3.31	0.22	2.26E-01	6.00E-01	GHRL	ghrelin/obestatin prepropeptide	chr3p26-p25	223862_at	NM_016362
3.76	3.93	0.17	2.26E-01	6.00E-01	LY6G6D	lymphocyte antigen 6 complex, locus G6D	chr6p21.3	207457_s_at	NM_021246
2.28	2.49	0.21	2.26E-01	6.00E-01	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3	chr15q12	216895_at	NM_033223
2.80	2.92	0.12	2.26E-01	6.00E-01	---	---	---	237921_at	---
4.68	5.17	0.49	2.26E-01	6.00E-01	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	chr17q21-q23	202631_s_at	NM_006380
3.52	3.84	0.32	2.26E-01	6.00E-01	---	---	---	215191_at	---
2.14	3.10	0.96	2.26E-01	6.00E-01	ORM1 /// ORM2	orosomucoid 1 /// orosomucoid 2	chr9q31-q32 /// chr9q32	205041_s_at	NM_000607 /// NM_000608
2.41	2.66	0.25	2.26E-01	6.00E-01	EN1	engrailed homeobox 1	chr2q13-q21	220559_at	NM_001426
4.28	5.03	0.76	2.26E-01	6.00E-01	SLC30A5	solute carrier family 30 (zinc transporter), member 5	chr5q12.1	1555334_s_at	NM_022902 /// NM_024055
1.81	1.98	0.16	2.26E-01	6.00E-01	---	---	---	1563054_at	---
5.22	5.54	0.32	2.26E-01	6.00E-01	ATP7A /// LOC644732	ATPase, Cu++ transporting, alpha polypeptide /// similar to ATPase, Cu++ transporting, alpha polypeptide	chrXq13.2-q13.3	205197_s_at	NM_000052 /// XM_001717231
2.65	2.92	0.27	2.26E-01	6.00E-01	LIPA	Lipase A, lysosomal acid, cholesterol esterase	chr10q23.2-q23.3	1561557_at	NM_000235 /// NM_001127605
3.22	3.48	0.26	2.26E-01	6.00E-01	CD244	CD244 molecule, natural killer cell receptor 2B4	chr1q23.3	220307_at	NM_016382
2.25	2.46	0.21	2.26E-01	6.00E-01	LOC644246	Hypothetical protein LOC644246	chr17q21.31	229857_s_at	XM_927427
2.19	2.39	0.20	2.26E-01	6.00E-01	MARK1	MAP/microtubule affinity-regulating kinase 1	chr1q41	226653_at	NM_018650
3.04	3.24	0.20	2.26E-01	6.00E-01	FLJ25917	hypothetical gene supported by AK098783	chrXp11.3	1564295_at	---
3.08	3.31	0.23	2.26E-01	6.00E-01	---	---	---	244356_at	---
3.29	3.45	0.16	2.26E-01	6.00E-01	TEX13A	testis expressed 13A	chrXq22.3	221429_x_at	NM_031274
2.78	2.97	0.19	2.27E-01	6.00E-01	GPR135	G protein-coupled receptor 135	chr14q23.1	217641_at	NM_022571
4.42	4.94	0.52	2.27E-01	6.00E-01	AGPS	alkylglycerone phosphate synthase	chr2q31.2	225113_at	NM_003659
4.79	5.15	0.36	2.27E-01	6.00E-01	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	chr11p15	202586_at	NM_021128
2.56	2.89	0.33	2.27E-01	6.00E-01	EXOC6	exocyst complex component 6	chr10q23.33	232599_at	NM_001013848 /// NM_019053
2.43	2.57	0.14	2.27E-01	6.00E-01	GRIN2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	chr12p12	210412_at	NM_000834
3.25	3.70	0.45	2.27E-01	6.00E-01	TLR7	toll-like receptor 7	chrXp22.3	220146_at	NM_016562
7.72	7.97	0.26	2.27E-01	6.01E-01	ESD	esterase D/formylglutathione hydrolase	chr13q14.1-q14.2	215096_s_at	NM_001984
2.87	3.03	0.16	2.27E-01	6.01E-01	OR6W1P	olfactory receptor, family 6, subfamily W, member 1 pseudogene	chr7q34	1553061_at	NR_002140
2.32	2.46	0.14	2.27E-01	6.01E-01	FLJ34077 /// LOC728558	weakly similar to zinc finger protein 195 /// hypothetical LOC728558	chr10q23-q24 /// chr10q23.33	232502_at	XM_001130206 /// XM_001130313 /// XM_001718401
2.08	2.23	0.15	2.27E-01	6.01E-01	PCDH11Y	protocadherin 11 Y-linked	chrYp11.2	217049_x_at	NM_032971 /// NM_032972 /// NM_032973
4.51	4.82	0.31	2.27E-01	6.01E-01	RAMP1	receptor (G protein-coupled) activity modifying protein 1	chr2q36-q37.1	204916_at	NM_005855
3.30	3.56	0.26	2.27E-01	6.01E-01	---	---	---	229242_at	---
2.38	2.58	0.20	2.27E-01	6.01E-01	TNK2	tyrosine kinase, non-receptor, 2	chr3q29	1555557_a_at	NM_001010938 /// NM_005781

2.42	2.59	0.17	2.27E-01	6.01E-01	KALRN	Kalirin, RhoGEF kinase	chr3q21.1-q21.2	232717_at	NM_001024660 /// NM_003947 /// NM_007064
2.42	2.66	0.24	2.27E-01	6.01E-01	---	---	---	1562044_at	---
2.64	2.84	0.20	2.27E-01	6.01E-01	---	---	---	228620_at	---
2.19	2.35	0.16	2.27E-01	6.01E-01	---	---	---	237924_at	---
1.84	1.98	0.13	2.27E-01	6.01E-01	ZNF605	zinc finger protein 605	chr12q24.33	1559849_at	NM_183238
6.99	7.67	0.68	2.27E-01	6.01E-01	GSTA3	glutathione S-transferase A3	chr6p12.1	222102_at	NM_000847
4.88	5.28	0.41	2.27E-01	6.01E-01	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	chr5p13.2	235032_at	NM_001012339 /// NM_194283
2.16	2.39	0.22	2.27E-01	6.01E-01	---	---	---	1562307_at	---
2.73	2.98	0.26	2.27E-01	6.01E-01	KCNIP4	Kv channel interacting protein 4	chr4p15.31	236783_at	NM_001035003 /// NM_001035004 /// NM_025221 /// NM_147181 /// NM_147182 /// NM_147183
3.02	3.30	0.28	2.27E-01	6.01E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	216430_x_at	---
5.24	5.49	0.25	2.27E-01	6.01E-01	ADAM11	ADAM metallopeptidase domain 11	chr17q21.3	239837_at	NM_002390
6.93	7.46	0.53	2.27E-01	6.02E-01	SKAP2	src kinase associated phosphoprotein 2	chr7p21-p15	204362_at	NM_003930
3.85	4.23	0.38	2.27E-01	6.02E-01	---	---	---	1556412_at	---
1.78	1.93	0.15	2.27E-01	6.02E-01	PHF14	PHD finger protein 14	chr7p21.3	204525_at	NM_001007157 /// NM_014660
1.92	2.10	0.18	2.27E-01	6.02E-01	---	---	---	215993_at	---
2.07	2.24	0.17	2.27E-01	6.02E-01	---	---	---	234634_at	---
2.70	2.93	0.23	2.28E-01	6.02E-01	ACTL6B	actin-like 6B	chr7q22	206013_s_at	NM_016188
2.79	2.95	0.16	2.28E-01	6.02E-01	---	---	---	1569961_at	---
6.21	6.87	0.66	2.28E-01	6.02E-01	SCFD1	sec1 family domain containing 1	chr14q12	215548_s_at	NM_016106 /// NM_182835
6.08	6.37	0.29	2.28E-01	6.02E-01	TMEM48	transmembrane protein 48	chr1p32.3	234672_s_at	NM_018087
5.44	6.30	0.87	2.28E-01	6.02E-01	SNX2	sorting nexin 2	chr5q23	202113_s_at	NM_003100
2.15	2.33	0.18	2.28E-01	6.02E-01	DAB1	disabled homolog 1 (Drosophila)	chr1p32-p31	228329_at	NM_021080
7.91	8.46	0.55	2.28E-01	6.02E-01	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	chr13q22.2	204616_at	NM_006002
7.83	8.20	0.37	2.28E-01	6.02E-01	SETD7	SET domain containing (lysine methyltransferase) 7	chr4q28	224928_at	NM_030648
6.05	6.32	0.27	2.28E-01	6.02E-01	LOC283378	hypothetical protein LOC283378	chr12q24.31	229528_at	---
2.94	3.13	0.20	2.28E-01	6.02E-01	---	---	---	240255_at	---
2.42	2.59	0.17	2.28E-01	6.02E-01	C15orf62	chromosome 15 open reading frame 62	chr15q15.1	1569064_at	NM_001130448 /// XR_041736 /// XR_041737 /// XR_041738
2.38	2.54	0.16	2.28E-01	6.02E-01	HIST1H2AD /// HIST1H2BN /// HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	histone cluster 1, H2ad /// histone cluster 1, H2bn /// histone cluster 1, H3a /// histone cluster 1, H3b /// histone cluster 1, H3c /// histone cluster 1, H3d /// histone cluster 1, H3e /// histone cluster 1, H3f /// histone cluster 1, H3g /// histone cluster 1, H3h /// histone cluster 1, H3i /// histone cluster 1, H3j	chr6p21.3 /// chr6p22-p21.3 /// chr6p22.1	208576_s_at	NM_003520 /// NM_003529 /// NM_003530 /// NM_003531 /// NM_003532 /// NM_003533 /// NM_003534 /// NM_003535 /// NM_003536 /// NM_003537 /// NM_021018 /// NM_021065
3.22	3.96	0.73	2.28E-01	6.02E-01	C10orf82	chromosome 10 open reading frame 82	chr10q25.3	231609_at	NM_144661
5.60	6.31	0.71	2.28E-01	6.02E-01	---	---	---	232144_at	---
3.50	4.06	0.56	2.28E-01	6.02E-01	---	---	---	233648_at	---
3.29	3.73	0.43	2.28E-01	6.02E-01	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	chr7q32	242984_at	NM_013255
3.67	3.96	0.29	2.28E-01	6.02E-01	TNS4	tensin 4	chr17q21.2	222265_at	NM_032865
2.44	2.65	0.20	2.28E-01	6.02E-01	MED13L	Mediator complex subunit 13-like	chr12q24.21	216109_at	NM_015335
2.81	3.01	0.20	2.28E-01	6.02E-01	---	---	---	1564379_at	---
2.40	2.56	0.16	2.28E-01	6.02E-01	---	---	---	240487_at	---
4.03	4.37	0.34	2.28E-01	6.02E-01	RBM6	RNA binding motif protein 6	chr3p21.3	1556672_a_at	NM_005777
3.79	3.97	0.18	2.28E-01	6.02E-01	DBF4B	DBF4 homolog B (S. cerevisiae)	chr17q21.31|17q21	1555378_at	NM_025104 /// NM_145663

3.97	4.13	0.16	2.28E-01	6.02E-01	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	chr12q23.2	220398_at	NM_024312																					
3.49	4.06	0.57	2.28E-01	6.02E-01	FABP5 /// FABP5L2 /// FABP5L7	fatty acid binding protein 5 (psoriasis-associated) /// fatty acid binding protein 5-like 2 /// fatty acid binding protein 5-like 7	chr11q12.1 /// chr13q14.3 /// chr8q21.13	202345_s_at	NM_001444 /// XM_001127657 /// XM_001128089 /// XM_001132811 /// XM_001134012 /// XM_001718375 /// XM_001721172																						
3.04	3.28	0.24	2.28E-01	6.02E-01	GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	chr17p13.1	207884_at	NM_000180																					
6.68	6.92	0.23	2.28E-01	6.02E-01	ADCK4	aarF domain containing kinase 4	chr19q13.2	227324_at	NM_024876																					
2.70	2.93	0.23	2.28E-01	6.02E-01	SLC46A2	solute carrier family 46, member 2	chr9q32	223816_at	NM_033051																					
3.51	3.73	0.22	2.28E-01	6.02E-01	---	---	---	238926_at	---																					
4.75	4.96	0.21	2.28E-01	6.02E-01	KCNF1	potassium voltage-gated channel, subfamily F, member 1	chr2p25	210263_at	NM_002236																					
3.05	3.25	0.20	2.28E-01	6.02E-01	TAF4	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	chr20q13.33	208545_x_at	NM_003185																					
2.47	2.65	0.18	2.28E-01	6.02E-01	C1QTNF6	C1q and tumor necrosis factor related protein 6	chr22q13.1	242444_at	NM_031910 /// NM_182486																					
2.26	2.42	0.16	2.28E-01	6.02E-01	ANKIB1	ankyrin repeat and IBR domain containing 1	chr7q21.2	243181_at	NM_019004																					
2.37	2.52	0.15	2.28E-01	6.02E-01	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	chr10p11.23	216651_s_at	NM_000818 /// NM_001134366																					
2.36	2.53	0.17	2.28E-01	6.02E-01	GRIK1	glutamate receptor, ionotropic, kainate 1	chr21q22.11	207242_s_at	NM_000830 /// NM_175611																					
2.80	3.00	0.20	2.28E-01	6.02E-01	RNF213	ring finger protein 213	chr17q25.3	233880_at	NM_020914																					
2.72	2.93	0.21	2.28E-01	6.02E-01	TDRKH	tudor and KH domain containing	chr1q21	223530_at	NM_001083963 /// NM_001083964 /// NM_001083965 /// NM_006862																					
3.98	4.20	0.21	2.28E-01	6.02E-01	NCOA7	nuclear receptor coactivator 7	chr6q22.31-q22.32	243807_at	NM_001122842 /// NM_181782																					
2.57	2.76	0.19	2.28E-01	6.02E-01	---	---	---	215995_x_at	---																					
2.13	2.28	0.15	2.28E-01	6.02E-01	---	---	---	234382_x_at	---																					
5.91	6.58	0.67	2.28E-01	6.02E-01	C6orf62	chromosome 6 open reading frame 62	chr6p22.2	213875_x_at	NM_030939																					
2.16	2.33	0.16	2.28E-01	6.02E-01	OR10A5	olfactory receptor, family 10, subfamily A, member 5	chr11p15.4	1555651_at	NM_178168																					
4.58	4.90	0.32	2.29E-01	6.02E-01	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	---	222754_at	NM_182916																					
2.78	2.97	0.19	2.29E-01	6.02E-01	MED31	mediator complex subunit 31	chr17p13.2	219318_x_at	NM_016060																					
2.57	2.73	0.17	2.29E-01	6.02E-01	---	---	---	215132_at	---																					
2.20	2.34	0.14	2.29E-01	6.02E-01	NANS	N-acetylneuraminic acid synthase	chr9p24.1-p23	241923_x_at	NM_018946																					
2.15	2.31	0.16	2.29E-01	6.02E-01	ZNRD1	zinc ribbon domain containing 1	chr6p21.3	234115_s_at	NM_014596 /// NM_170783																					
5.54	5.86	0.32	2.29E-01	6.02E-01	VAMP4	vesicle-associated membrane protein 4	chr1q24-q25	213480_at	NM_003762																					
10.04	10.33	0.29	2.29E-01	6.02E-01	C7	complement component 7	chr5p13	202992_at	NM_000587																					
3.36	3.58	0.22	2.29E-01	6.02E-01	C9orf85	chromosome 9 open reading frame 85	chr9q21.13	235866_at	NM_182505																					
2.47	2.67	0.20	2.29E-01	6.02E-01	SCN2B	sodium channel, voltage-gated, type II, beta	chr11q23	210363_s_at	NM_004588																					
2.28	2.45	0.17	2.29E-01	6.02E-01	---	---	---	1566550_at	---																					
6.10	6.52	0.42	2.29E-01	6.02E-01	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	chr11q12.1	232724_at	NM_022349 /// NM_152851 /// NM_152852																					
2.83	3.00	0.17	2.29E-01	6.02E-01	ROPN1	ropporin, rhophilin associated protein 1	chr3q21.1	224191_x_at	NM_017578																					
7.44	7.74	0.30	2.29E-01	6.02E-01	HIPK1	homeodomain interacting protein kinase 1	chr1p13.2	212291_at	NM_152696 /// NM_181358 /// NM_198268 /// NM_198269																					
2.67	2.89	0.22	2.29E-01	6.02E-01	NEUROD2	neurogenic differentiation 2	chr17q12	210271_at	NM_006160																					
6.15	6.41	0.26	2.29E-01	6.02E-01	GOLGA2	golgi autoantigen, golgin subfamily a, 2	chr9q34.11	211059_s_at	NM_004486																					
2.88	3.12	0.24	2.29E-01	6.02E-01	C10orf72	chromosome 10 open reading frame 72	chr10q11.22	1553458_at	NM_001031746 /// NM_144984																					
4.68	4.87	0.18	2.29E-01	6.02E-01	C17orf68	chromosome 17 open reading frame 68	chr17p13.1	240875_at	NM_025099																					
6.30	7.37	1.07	2.29E-01	6.02E-01	CPEB4	cytoplasmic polyadenylation element binding protein 4	chr5q21	224828_at	NM_030627																					
5.23	5.78	0.55	2.29E-01	6.02E-01	FBLIM1	filamin binding LIM protein 1	chr1p36.21	225258_at	NM_001024215 /// NM_001024216 /// NM_017556																					
2.08	2.31	0.23	2.29E-01	6.02E-01	TOX3	TOX high mobility group box family member 3	chr16q12.1	214774_x_at	NM_001080430																					

4.51	4.73	0.22	2.29E-01	6.02E-01	DAB2IP	DAB2 interacting protein	chr9q33.1-q33.3	235966_at	NM_032552 /// NM_138709
5.71	5.92	0.21	2.29E-01	6.02E-01	FLJ42709	hypothetical gene supported by AK124699	chr5q15	229014_at	NR_015369 /// NR_021490 /// NR_021491 /// XM_499008 /// XM_943794
2.71	2.91	0.20	2.29E-01	6.02E-01	MAK	male germ cell-associated kinase	chr6p24	220302_at	NM_005906
2.51	2.71	0.20	2.29E-01	6.02E-01	---	---	---	237491_at	---
2.56	2.72	0.16	2.29E-01	6.02E-01	TNFRSF18	tumor necrosis factor receptor superfamily, member 18	chr1p36.3	223851_s_at	NM_004195 /// NM_148901 /// NM_148902
2.43	2.59	0.15	2.29E-01	6.02E-01	LSAMP	Limbic system-associated membrane protein	chr3q13.2-q21	1570190_at	NM_002338
1.79	1.94	0.14	2.29E-01	6.02E-01	---	---	---	244125_at	---
2.13	2.28	0.15	2.29E-01	6.03E-01	PDK3	pyruvate dehydrogenase kinase, isozyme 3	chrXp22.11	206347_at	NM_005391
4.89	5.08	0.19	2.29E-01	6.03E-01	CYTH2	cytohesin 2	chr19q13.3	237234_at	NM_004228 /// NM_017457
2.19	2.35	0.16	2.29E-01	6.03E-01	---	---	---	236818_at	---
3.58	4.06	0.48	2.29E-01	6.03E-01	---	---	---	1560082_at	---
6.19	6.42	0.23	2.29E-01	6.03E-01	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	chr7q31	227153_at	NM_032549
2.20	2.41	0.21	2.29E-01	6.03E-01	RIMBP2	RIMS binding protein 2	chr12q24.33	214811_at	NM_015347
2.04	2.19	0.14	2.29E-01	6.03E-01	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	chr3q25.2	222121_at	NM_015595
2.99	3.47	0.49	2.29E-01	6.03E-01	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	chr14q24.1	242998_at	NM_152443
3.20	3.36	0.16	2.29E-01	6.03E-01	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	chr8p23.1	1552669_at	NM_024607
2.16	2.33	0.17	2.29E-01	6.03E-01	GAP43	growth associated protein 43	chr3q13.1-q13.2	216967_at	NM_001130064 /// NM_002045
8.53	8.89	0.36	2.29E-01	6.03E-01	CMTM6	CKLF-like MARVEL transmembrane domain containing 6	chr3p22.3	217947_at	NM_017801
3.16	3.39	0.22	2.29E-01	6.03E-01	LOC731602 /// METT11D1	similar to methyltransferase 11 domain containing 1 isoform 2 /// methyltransferase 11 domain containing 1	chr14q11.2	1558590_at	NM_001029991 /// NM_022734 /// XR_037376
7.98	8.28	0.30	2.30E-01	6.03E-01	EIF5A	eukaryotic translation initiation factor 5A	chr17p13-p12	213753_x_at	NM_001970 /// XM_001724572
4.31	4.57	0.26	2.30E-01	6.03E-01	---	---	---	235862_at	---
2.34	2.56	0.23	2.30E-01	6.03E-01	---	---	---	241845_at	---
3.30	3.52	0.22	2.30E-01	6.03E-01	---	---	---	225345_s_at	---
3.34	3.53	0.19	2.30E-01	6.03E-01	NPAS2	neuronal PAS domain protein 2	chr2q11.2	205460_at	NM_002518
3.86	4.46	0.60	2.30E-01	6.03E-01	RGNEF	Rho-guanine nucleotide exchange factor	chr5q13.2	1559706_at	NM_001080479
3.85	4.25	0.40	2.30E-01	6.03E-01	---	---	---	1554948_at	---
2.43	2.67	0.24	2.30E-01	6.03E-01	TTTY15	testis-specific transcript, Y-linked 15	chrYq11.1	214983_at	NR_001545
3.81	4.04	0.22	2.30E-01	6.03E-01	---	---	---	216630_at	---
3.02	3.24	0.22	2.30E-01	6.03E-01	ZNF256	zinc finger protein 256	chr19q13.43	223714_at	NM_005773
2.75	2.94	0.19	2.30E-01	6.03E-01	PKP2	plakophilin 2	chr12p11	214154_s_at	NM_001005242 /// NM_004572
2.15	2.31	0.15	2.30E-01	6.03E-01	LOC340090	hypothetical protein LOC340090	chr5q13.3	1562492_at	---
6.73	6.97	0.24	2.30E-01	6.03E-01	PRR11	proline rich 11	chr17q22	219392_x_at	NM_018304
6.49	6.88	0.39	2.30E-01	6.03E-01	CEP57	centrosomal protein 57kDa	chr11q21	203494_s_at	NM_014679
3.58	3.94	0.36	2.30E-01	6.03E-01	SAMHD1	SAM domain and HD domain 1	chr20pter-q12	1559883_s_at	NM_015474
6.72	7.04	0.31	2.30E-01	6.03E-01	NSF	N-ethylmaleimide-sensitive factor	chr17q21	202395_at	NM_006178
2.73	2.93	0.21	2.30E-01	6.03E-01	RASAL2	RAS protein activator like 2	chr1q24	219026_s_at	NM_004841 /// NM_170692
2.15	2.34	0.19	2.30E-01	6.03E-01	ADH6	alcohol dehydrogenase 6 (class V)	chr4q23	207544_s_at	NM_000672 /// NM_001102470
6.69	7.76	1.07	2.30E-01	6.03E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	1553530_a_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376
4.33	4.56	0.23	2.30E-01	6.03E-01	---	---	---	239427_at	---
2.83	3.03	0.20	2.30E-01	6.03E-01	FLJ38359	hypothetical protein FLJ38359	chr2q13	235083_at	XR_041916 /// XR_041917 /// XR_041918

11.40	11.69	0.29	2.30E-01	6.03E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	207243_s_at	NM_001743 /// NM_005184 /// NM_006888																				
2.57	2.84	0.27	2.30E-01	6.03E-01	PLK4	polo-like kinase 4 (Drosophila)	chr4q28	204887_s_at	NM_014264																				
2.27	2.45	0.18	2.30E-01	6.03E-01	FLJ40243	hypothetical protein FLJ40243	chr5p13.1	240411_at	NM_173489																				
6.37	7.16	0.80	2.30E-01	6.03E-01	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	chr4q21-q24	202457_s_at	NM_000944 /// NM_001130691 /// NM_001130692																				
5.28	5.81	0.53	2.30E-01	6.03E-01	CASP4	caspase 4, apoptosis-related cysteine peptidase	chr11q22.2-q22.3	209310_s_at	NM_001225 /// NM_033306																				
3.68	4.13	0.45	2.30E-01	6.03E-01	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	chr1p31.1-p22.1	215039_at	NM_001134492 /// NM_012262																				
4.24	4.64	0.40	2.30E-01	6.03E-01	ELN	elastin	chr7q11.23	212670_at	NM_000501 /// NM_001081752 /// NM_001081753 /// NM_001081754 /// NM_001081755																				
2.65	2.89	0.25	2.30E-01	6.03E-01	---	---	---	237838_at	---																				
4.58	4.78	0.20	2.30E-01	6.03E-01	HEATR6	HEAT repeat containing 6	chr17q23.1	65493_at	NM_022070																				
2.41	2.70	0.29	2.30E-01	6.04E-01	---	---	---	239344_at	---																				
3.03	3.29	0.26	2.30E-01	6.04E-01	ICA1	islet cell autoantigen 1, 69kDa	chr7p22	204002_s_at	NM_004968 /// NM_022307																				
6.73	7.02	0.28	2.30E-01	6.04E-01	COG2	component of oligomeric golgi complex 2	chr1q42.2	203073_at	NM_007357																				
2.24	2.42	0.18	2.30E-01	6.04E-01	TTBK2	Tau tubulin kinase 2	chr15q15.2	231610_at	NM_173500																				
6.15	6.51	0.36	2.30E-01	6.04E-01	NPEPPS	aminopeptidase puromycin sensitive	chr17q21	201454_s_at	NM_006310																				
2.45	2.67	0.22	2.30E-01	6.04E-01	---	---	---	1563057_at	---																				
2.20	2.41	0.21	2.30E-01	6.04E-01	NRXN3	neurexin 3	chr14q31	205795_at	NM_001105250 /// NM_004796 /// NM_138970																				
2.56	2.75	0.19	2.30E-01	6.04E-01	BMP6	bone morphogenetic protein 6	chr6p24-p23	215042_at	NM_001718																				
2.20	2.46	0.27	2.30E-01	6.04E-01	---	---	---	244502_at	---																				
3.96	4.18	0.22	2.30E-01	6.04E-01	IWS1	IWS1 homolog (S. cerevisiae)	chr2q14.3	224775_at	NM_017969																				
6.37	6.57	0.20	2.30E-01	6.04E-01	NT5C	5', 3'-nucleotidase, cytosolic	chr17q25.1	219214_s_at	NM_014595																				
3.29	4.08	0.78	2.30E-01	6.04E-01	HHIP	hedgehog interacting protein	chr4q28-q32	237466_s_at	NM_022475																				
5.09	5.54	0.46	2.30E-01	6.04E-01	RAI14	retinoic acid induced 14	chr5p13.3-p13.2	202052_s_at	NM_015577																				
2.78	2.99	0.21	2.31E-01	6.04E-01	TMPRSS6	transmembrane protease, serine 6	chr22q12.3	234367_x_at	NM_153609																				
4.00	4.18	0.19	2.31E-01	6.04E-01	PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	chr1p36	205233_s_at	NM_000437																				
1.82	1.96	0.14	2.30E-01	6.04E-01	---	---	---	217524_x_at	---																				
6.26	6.84	0.58	2.31E-01	6.04E-01	N4BP2L2	NEDD4 binding protein 2-like 2	chr13q13.1	214753_at	NM_014887 /// NM_033111																				
2.02	2.21	0.19	2.31E-01	6.04E-01	CASZ1	castor zinc finger 1	chr1p36.22	230420_at	NM_001079843 /// NM_017766																				
3.45	3.63	0.18	2.31E-01	6.04E-01	---	---	---	237097_at	---																				
6.40	6.93	0.53	2.31E-01	6.04E-01	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	chr10p15-p14	204151_x_at	NM_001353 /// XM_001724839																				
4.70	5.15	0.45	2.31E-01	6.04E-01	MED1	mediator complex subunit 1	chr17q12-q21.1	225452_at	NM_004774																				
2.42	2.77	0.35	2.31E-01	6.04E-01	---	---	---	242650_at	---																				
3.65	3.84	0.19	2.31E-01	6.04E-01	---	---	---	212029_s_at	---																				
1.91	2.03	0.12	2.31E-01	6.04E-01	C8orf47	chromosome 8 open reading frame 47	chr8q22.2	1552390_a_at	NM_173549																				
4.68	4.91	0.24	2.31E-01	6.04E-01	COX19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr7p22.3	231831_at	NM_001031617																				
2.11	2.25	0.14	2.31E-01	6.04E-01	---	---	---	216566_at	---																				
3.33	3.63	0.30	2.31E-01	6.04E-01	---	---	---	236016_at	---																				
8.37	8.60	0.23	2.31E-01	6.04E-01	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	chr22q11.23	202567_at	NM_004175																				
2.09	2.21	0.12	2.31E-01	6.04E-01	---	---	---	1562093_at	---																				
2.64	2.83	0.19	2.31E-01	6.04E-01	---	---	---	242055_at	---																				
5.00	5.40	0.40	2.31E-01	6.04E-01	CLIP3	CAP-GLY domain containing linker protein 3	chr19q13.12	212358_at	NM_015526																				
7.95	8.19	0.24	2.31E-01	6.04E-01	LOC550643	hypothetical LOC550643	chrXp11.1	225029_at	NR_015367 /// XM_001718993 /// XM_001720195 /// XM_001721066																				
4.80	5.03	0.23	2.31E-01	6.04E-01	HOXB5	homeobox B5	chr17q21.3	205601_s_at	NM_002147																				

2.05	2.24	0.19	2.31E-01	6.04E-01	---	---	---	231494_at	---
2.50	2.66	0.16	2.31E-01	6.04E-01	---	---	---	1557117_at	---
4.08	4.26	0.18	2.31E-01	6.04E-01	KIAA1614	KIAA1614	chr1q25.3	215367_at	NM_020950
2.54	2.79	0.25	2.31E-01	6.04E-01	LOC100128361	similar to hCG1985411	chr9q22.31	242207_at	XM_001721550 /// XM_001722316 /// XM_001723807
1.91	2.08	0.17	2.31E-01	6.05E-01	CAPS2	calcyphosine 2	chr12q21.1	1560458_s_at	NM_032606
3.86	4.12	0.26	2.31E-01	6.05E-01	LOC253962	hypothetical protein LOC253962	chr17q21.33	1559061_at	---
4.47	4.83	0.36	2.31E-01	6.05E-01	ATP2A3	ATPase, Ca++ transporting, ubiquitous	chr17p13.3	213036_x_at	NM_005173 /// NM_174953 /// NM_174954 /// NM_174955 /// NM_174956 /// NM_174957 /// NM_174958
3.73	3.92	0.19	2.31E-01	6.05E-01	WWC1	WW and C2 domain containing 1	chr5q35.1	229180_at	NM_015238
2.20	2.38	0.19	2.31E-01	6.05E-01	---	---	---	233581_at	---
2.19	2.36	0.17	2.31E-01	6.05E-01	---	---	---	244838_at	---
1.97	2.14	0.17	2.31E-01	6.05E-01	CCDC122	coiled-coil domain containing 122	chr13q14.11	1553894_at	NM_144974
4.98	5.17	0.19	2.31E-01	6.05E-01	SAMD14	Sterile alpha motif domain containing 14	chr17q21.33	1559997_x_at	NM_174920
2.36	2.54	0.18	2.31E-01	6.05E-01	---	---	---	1561642_at	---
3.08	3.24	0.16	2.31E-01	6.05E-01	---	---	---	1566549_at	---
2.17	2.32	0.16	2.31E-01	6.05E-01	CHEK1	CHK1 checkpoint homolog (S. pombe)	chr11q24-q24	205394_at	NM_001114121 /// NM_001114122 /// NM_001274
2.12	2.25	0.14	2.31E-01	6.05E-01	---	---	---	1561073_at	---
6.36	6.69	0.33	2.31E-01	6.05E-01	MDK	midkine (neurite growth-promoting factor 2)	chr11p11.2	209035_at	NM_001012333 /// NM_001012334 /// NM_002391
3.17	3.39	0.22	2.31E-01	6.05E-01	---	---	---	230014_at	---
4.03	4.80	0.76	2.32E-01	6.05E-01	---	---	---	243462_s_at	---
2.27	2.44	0.17	2.32E-01	6.05E-01	FCRL3	Fc receptor-like 3	chr1q21-q22	231093_at	NM_052939
2.51	3.10	0.59	2.32E-01	6.05E-01	GPM6B	glycoprotein M6B	chrXp22.2	209170_s_at	NM_001001994 /// NM_001001995 /// NM_001001996 /// NM_005278
2.32	2.48	0.17	2.32E-01	6.05E-01	---	---	---	1560429_at	---
5.74	6.28	0.54	2.32E-01	6.05E-01	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	chr4q23-q25	229905_at	NM_001100426 /// NM_001100427 /// NM_001100428 /// NM_001100429 /// NM_001100430 /// NM_021159
8.53	8.88	0.35	2.32E-01	6.05E-01	CWC15	CWC15 homolog (S. cerevisiae)	chr11q21	223067_at	NM_016403
4.05	4.25	0.20	2.32E-01	6.05E-01	---	---	---	1561542_at	---
2.21	3.08	0.86	2.32E-01	6.05E-01	TMEM178	transmembrane protein 178	chr2p22.1	229302_at	NM_152390
4.57	4.97	0.40	2.32E-01	6.05E-01	---	---	---	224005_at	---
4.28	4.51	0.24	2.32E-01	6.05E-01	GPR97	G protein-coupled receptor 97	chr16q13	220404_at	NM_170776
2.05	2.22	0.17	2.32E-01	6.05E-01	---	---	---	1565833_at	---
2.05	2.20	0.15	2.32E-01	6.05E-01	DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1	chr7q21.3-q22.1	1569843_at	NM_004411
1.99	2.13	0.14	2.32E-01	6.05E-01	C15orf33	chromosome 15 open reading frame 33	chr15q21.1-q21.2	1557429_s_at	NM_152647
2.26	2.39	0.13	2.32E-01	6.05E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	211390_at	NM_001079691 /// NM_052818

5.42	5.72	0.30	2.32E-01	6.05E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	234411_x_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392
2.38	2.65	0.27	2.32E-01	6.05E-01	RERGL	RERG/RAS-like	chr12p12.3	220276_at	NM_024730
2.88	3.12	0.24	2.32E-01	6.05E-01	CASKIN1	CASK interacting protein 1	chr16p13.3	239189_at	NM_020764
2.41	2.62	0.21	2.32E-01	6.05E-01	---	---	---	1570314_at	---
2.16	2.30	0.15	2.32E-01	6.05E-01	---	---	---	1560867_a_at	---
4.14	4.39	0.26	2.32E-01	6.06E-01	GAL3ST2	galactose-3-O-sulfotransferase 2	chr2q37.3	1553046_s_at	NM_022134
1.97	2.15	0.19	2.32E-01	6.06E-01	SCN1A	sodium channel, voltage-gated, type I, alpha subunit	chr2q24.3	1555246_a_at	NM_006920
2.21	2.38	0.16	2.32E-01	6.06E-01	---	---	---	1554825_at	---
3.18	3.48	0.30	2.32E-01	6.06E-01	RIMS3	regulating synaptic membrane exocytosis 3	chr1pter-p22.2	204730_at	NM_014747
2.82	2.98	0.16	2.32E-01	6.06E-01	GOT1L1	glutamic-oxaloacetic transaminase 1-like 1	chr8p12	1553879_a_at	NM_152413
12.33	12.64	0.31	2.32E-01	6.06E-01	RPS24	ribosomal protein S24	chr10q22-q23	200061_s_at	NM_001026 /// NM_033022
2.37	2.58	0.20	2.32E-01	6.06E-01	---	---	---	240691_at	---
2.28	2.44	0.16	2.32E-01	6.06E-01	---	---	---	242395_at	---
8.65	9.17	0.51	2.33E-01	6.07E-01	GLO1	glyoxalase I	chr6p21.3-p21.1	200681_at	NM_006708
7.81	8.11	0.29	2.33E-01	6.07E-01	C2orf12	chromosome 2 open reading frame 12	chr2q24.3	225269_s_at	XM_938663 /// XM_944033
2.15	2.36	0.20	2.33E-01	6.07E-01	---	---	---	240706_at	---
2.14	2.34	0.20	2.33E-01	6.07E-01	CASP3	Caspase 3, apoptosis-related cysteine peptidase	chr4q34	236729_at	NM_004346 /// NM_032991
3.05	3.21	0.15	2.33E-01	6.07E-01	---	---	---	222365_at	---
2.55	2.79	0.24	2.33E-01	6.07E-01	---	---	---	232626_at	---
2.10	2.25	0.15	2.33E-01	6.07E-01	---	---	---	243641_at	---
6.14	6.42	0.27	2.33E-01	6.07E-01	UBTD2	ubiquitin domain containing 2	chr5q35.1	224834_at	NM_152277
4.05	4.43	0.38	2.33E-01	6.07E-01	CCDC82	coiled-coil domain containing 82	chr11q21	223300_s_at	NM_024725
3.33	3.58	0.25	2.33E-01	6.07E-01	SLC7A10	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10	chr19q13.1	220868_s_at	NM_019849
2.06	2.25	0.19	2.33E-01	6.07E-01	PLP1	proteolipid protein 1	chrXq22	210198_s_at	NM_000533 /// NM_001128834 /// NM_199478
2.82	2.99	0.18	2.33E-01	6.07E-01	KCNJ10	potassium inwardly-rectifying channel, subfamily J, member 10	chr1q22-q23	228581_at	NM_002241
2.02	2.17	0.15	2.33E-01	6.07E-01	CPB2	carboxypeptidase B2 (plasma)	chr13q14.11	206651_s_at	NM_001872 /// NM_016413
2.45	2.59	0.14	2.33E-01	6.07E-01	LOC143381	Hypothetical protein LOC143381	chr10q26.11	230163_at	---
5.99	6.50	0.51	2.33E-01	6.07E-01	ZMYM4	zinc finger, MYM-type 4	chr1p32-p34	202051_s_at	NM_005095
2.97	3.24	0.27	2.33E-01	6.07E-01	---	---	---	237697_at	---
2.39	2.61	0.22	2.33E-01	6.08E-01	---	---	---	1557878_at	---
2.02	2.17	0.15	2.33E-01	6.08E-01	C1orf150	chromosome 1 open reading frame 150	chr1q44	1552908_at	NM_145278
2.65	2.81	0.16	2.33E-01	6.08E-01	SPTLC3	serine palmitoyltransferase, long chain base subunit 3	chr20p12.1	220456_at	NM_018327
2.19	2.35	0.16	2.33E-01	6.08E-01	BRUNOL4	bruno-like 4, RNA binding protein (Drosophila)	chr18q12	238966_at	NM_001025087 /// NM_001025088 /// NM_001025089 /// NM_020180
6.06	6.83	0.77	2.33E-01	6.08E-01	---	---	---	241457_at	---
2.14	2.31	0.17	2.33E-01	6.08E-01	LARGE	like-glycosyltransferase	chr22q12.3	204414_at	NM_004737 /// NM_133642
4.24	4.46	0.22	2.33E-01	6.08E-01	---	---	---	244284_at	---
5.24	5.82	0.58	2.33E-01	6.08E-01	TSPAN12	tetraspanin 12	chr7q31.31	230625_s_at	NM_012338
2.33	2.58	0.24	2.33E-01	6.08E-01	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	chr4p15.2	231730_at	NM_016955 /// NM_153825
2.30	2.47	0.16	2.33E-01	6.08E-01	---	---	---	1561232_at	---
5.57	6.04	0.46	2.34E-01	6.08E-01	---	---	---	235716_at	---
5.81	6.22	0.42	2.34E-01	6.08E-01	PHF17	PHD finger protein 17	chr4q26-q27	225816_at	NM_024900 /// NM_199320
2.81	3.13	0.32	2.34E-01	6.08E-01	---	---	---	235835_at	---
8.04	8.39	0.35	2.34E-01	6.08E-01	CADM1	cell adhesion molecule 1	chr11q23.2	209030_s_at	NM_001098517 /// NM_014333
3.52	3.72	0.20	2.34E-01	6.08E-01	B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	chr11q25	219521_at	NM_018644 /// NM_054025
3.20	3.38	0.17	2.34E-01	6.08E-01	TEX101	testis expressed 101	chr19q13.31	223906_s_at	NM_001130011 /// NM_031451

6.16	6.39	0.22	2.34E-01	6.08E-01	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	chr3q22.1	209633_at	NM_002718 /// NM_181897
5.32	6.12	0.79	2.34E-01	6.08E-01	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	226210_s_at	NR_002766 /// NR_003530 /// NR_003531
5.39	6.16	0.77	2.34E-01	6.08E-01	DPH3	DPH3, KTI11 homolog (S. cerevisiae)	chr3p24.3	225200_at	NM_001047434 /// NM_206831
2.35	2.52	0.17	2.34E-01	6.08E-01	BBS5	Bardet-Biedl syndrome 5	chr2q31.1	230697_at	NM_152384
9.25	9.80	0.55	2.34E-01	6.08E-01	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	chr6p12	1557910_at	NM_007355
7.30	7.53	0.23	2.34E-01	6.08E-01	KIAA0100	KIAA0100	chr17q11.2	201729_s_at	NM_014680
3.10	3.52	0.42	2.34E-01	6.09E-01	KIF3A	kinesin family member 3A	chr5q31	213623_at	NM_007054
5.07	5.41	0.34	2.34E-01	6.09E-01	CIR	CBF1 interacting corepressor	chr2q31.1	209571_at	NM_004882
2.27	2.46	0.19	2.34E-01	6.09E-01	LOC643714	hypothetical protein LOC643714	chr16q12.1	238211_at	XM_001721908 /// XM_931757 /// XM_944020
2.24	2.43	0.18	2.34E-01	6.09E-01	MAP3K6	mitogen-activated protein kinase kinase kinase 6	chr1p36.11	229960_at	NM_004672
1.92	2.08	0.16	2.34E-01	6.09E-01	MMP8	matrix metallopeptidase 8 (neutrophil collagenase)	chr11q22.3	231688_at	NM_002424
1.87	1.99	0.12	2.34E-01	6.09E-01	C2orf67 /// RPE	Chromosome 2 open reading frame 67 /// Ribulose-5-phosphate-3-epimerase	chr2q32-q33.3 /// chr2q34	1558519_at	NM_006916 /// NM_152519 /// NM_199229
6.51	6.88	0.37	2.34E-01	6.09E-01	TMEM30A	transmembrane protein 30A	chr6q14.1	222391_at	NM_018247
2.26	2.43	0.17	2.34E-01	6.09E-01	GK5	glycerol kinase 5 (putative)	chr3q23	1553772_at	NM_001039547
3.77	3.94	0.17	2.34E-01	6.09E-01	HMCN2	Hemicentin 2	chr9q34.11	235797_x_at	XM_001715154 /// XM_001726942
4.58	5.46	0.88	2.34E-01	6.09E-01	---	---	---	239723_at	---
4.09	4.75	0.66	2.34E-01	6.09E-01	---	---	---	232628_at	---
2.13	2.29	0.16	2.34E-01	6.09E-01	TEKT3	tektin 3	chr17p12	223867_at	NM_031898
3.27	3.42	0.15	2.34E-01	6.09E-01	AHSG	alpha-2-HS-glycoprotein	chr3q27	204551_s_at	NM_001622
7.51	8.21	0.69	2.34E-01	6.09E-01	EIF3A	eukaryotic translation initiation factor 3, subunit A	chr10q26	200596_s_at	NM_003750
6.55	6.83	0.28	2.34E-01	6.09E-01	UROS	uroporphyrinogen III synthase	chr10q25.2-q26.3	203031_s_at	NM_000375
2.24	2.47	0.23	2.34E-01	6.09E-01	ZNF566	zinc finger protein 566	chr19q13.12	240239_at	NM_032838
6.24	7.04	0.80	2.35E-01	6.09E-01	MTF2	metal response element binding transcription factor 2	chr1p22.1	203345_s_at	NM_007358
4.50	5.01	0.51	2.34E-01	6.09E-01	SLAIN2	SLAIN motif family, member 2	chr4p12	233874_at	NM_020846
5.47	5.70	0.23	2.34E-01	6.09E-01	TEX261	testis expressed 261	chr2p13.3	212084_at	NM_144582
3.72	3.95	0.22	2.34E-01	6.09E-01	tcag7.1177	opposite strand transcription unit to STAG3	chr7q22.1	227321_at	NM_178831
2.96	3.17	0.21	2.34E-01	6.09E-01	---	---	---	1555904_at	---
2.75	2.96	0.21	2.35E-01	6.09E-01	SIGLEC8	sialic acid binding Ig-like lectin 8	chr19q13.33-q13.41	216328_at	NM_014442
2.03	2.22	0.19	2.35E-01	6.09E-01	---	---	---	1561210_at	---
2.09	2.26	0.17	2.35E-01	6.09E-01	LOC648691	hypothetical protein LOC648691	---	1561252_at	XM_001722311 /// XM_001725966
2.13	2.29	0.16	2.35E-01	6.09E-01	THPO	thrombopoietin	chr3q27	211155_s_at	NM_000460
1.99	2.14	0.15	2.34E-01	6.09E-01	LOC349160	Hypothetical protein LOC349160	chr7q34	233934_at	---
2.08	2.22	0.15	2.35E-01	6.09E-01	---	---	---	1569023_a_at	---
2.16	2.30	0.14	2.35E-01	6.09E-01	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	chr13q12	207302_at	NM_000231
2.21	2.43	0.22	2.35E-01	6.09E-01	KAP2.1B /// KRTAP2-1 /// KRTAP2-4 /// LOC644350 /// LOC728285 /// LOC728934 /// LOC730755	keratin associated protein 2.1B /// keratin associated protein 2-1 /// keratin associated protein 2-4 /// hypothetical LOC644350 /// similar to keratin associated protein /// hypothetical LOC728934 /// similar to keratin associated protein 2-4	chr17q12-q21 /// chr17q21.2	1555673_at	NM_001123387 /// NM_033184 /// XM_001127070 /// XM_001127094 /// XM_001128836 /// XM_001714716 /// XM_001725764 /// XM_927511
3.05	3.26	0.21	2.35E-01	6.09E-01	ZRSR1	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 1	chr5q22	206512_at	---
2.39	2.58	0.18	2.35E-01	6.09E-01	LOC728114	hypothetical protein LOC728114	chr12q13.11	1569842_at	XR_040708 /// XR_040709 /// XR_040710

3.57	3.80	0.23	2.35E-01	6.09E-01	CLTA	clathrin, light chain (Lca)	chr9p13	216296_at	NM_001076677 /// NM_001833 /// NM_007096
3.13	3.30	0.17	2.35E-01	6.09E-01	FAM167A	Family with sequence similarity 167, member A	chr8p23-p22	233641_s_at	NM_053279
2.21	2.36	0.15	2.35E-01	6.09E-01	---	---	---	234534_at	---
2.08	2.22	0.14	2.35E-01	6.09E-01	---	---	---	1560548_at	---
3.62	3.79	0.17	2.35E-01	6.09E-01	---	---	---	239795_at	---
3.29	3.49	0.20	2.35E-01	6.09E-01	---	---	---	1555415_at	---
6.05	6.32	0.27	2.35E-01	6.09E-01	---	---	---	228605_at	---
2.29	2.48	0.19	2.35E-01	6.09E-01	LRRC4B	leucine rich repeat containing 4B	chr19q13.33	239320_at	NM_001080457
4.37	4.57	0.20	2.35E-01	6.09E-01	SGK269	NKF3 kinase family member	chr15q24.3	220008_at	NM_024776
4.73	4.92	0.19	2.35E-01	6.09E-01	LNP1	leukemia NUP98 fusion partner 1	chr3q12.2	227181_at	NM_001085451
2.78	2.96	0.19	2.35E-01	6.09E-01	VENTX	VENT homeobox homolog (Xenopus laevis)	chr10q26.3	207376_at	NM_014468
7.03	7.30	0.28	2.35E-01	6.10E-01	CKAP5	cytoskeleton associated protein 5	chr11p11.2	212832_s_at	NM_001008938 /// NM_014756
2.02	2.18	0.16	2.35E-01	6.10E-01	---	---	---	241177_at	---
2.07	2.25	0.18	2.35E-01	6.10E-01	GRID1	glutamate receptor, ionotropic, delta 1	chr10q22	231977_at	NM_017551
4.37	4.61	0.24	2.35E-01	6.10E-01	C6orf64	chromosome 6 open reading frame 64	chr6p21.2	218784_s_at	NM_018322
2.42	2.59	0.17	2.35E-01	6.10E-01	KCNK9	potassium channel, subfamily K, member 9	chr8q24.3	224072_s_at	NM_016601
2.31	2.44	0.13	2.35E-01	6.10E-01	---	---	---	1567008_at	---
4.99	5.58	0.59	2.35E-01	6.10E-01	IGF2 /// INS-IGF2	insulin-like growth factor 2 (somatomedin A) /// INS-IGF2	chr11p15.5	202410_x_at	NM_000612 /// NM_001007139 /// NM_001042376 /// NM_001127598 /// NR_003512
4.71	4.89	0.18	2.35E-01	6.10E-01	TLX2	T-cell leukemia homeobox 2	chr2p13.1-p12	211049_at	NM_016170
5.03	5.28	0.25	2.35E-01	6.10E-01	PLEK	pleckstrin	chr2p14	203470_s_at	NM_002664
1.91	2.04	0.13	2.35E-01	6.10E-01	C14orf174	chromosome 14 open reading frame 174	chr14q24.3	1557681_s_at	NM_001010860
4.91	5.11	0.21	2.36E-01	6.10E-01	DGCR8	DiGeorge syndrome critical region gene 8	chr22q11.2	219811_at	NM_022720
6.37	6.79	0.42	2.36E-01	6.10E-01	FAM175B	family with sequence similarity 175, member B	chr10q26.13	212837_at	NM_032182
3.78	4.17	0.39	2.36E-01	6.10E-01	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	chr4p14	227945_at	NM_015173
7.66	7.97	0.31	2.36E-01	6.10E-01	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	chr1p34.2	213798_s_at	NM_001105530 /// NM_006367
2.67	2.84	0.17	2.36E-01	6.10E-01	PPM1H	protein phosphatase 1H (PP2C domain containing)	chr12q14.1-q14.2	233911_s_at	NM_020700
2.33	2.52	0.19	2.36E-01	6.10E-01	GFER	Growth factor, augmenter of liver regeneration	chr16p13.3-p13.12	228514_at	NM_005262
6.62	6.80	0.18	2.36E-01	6.10E-01	---	---	---	217679_x_at	---
3.27	3.44	0.17	2.36E-01	6.10E-01	---	---	---	236578_at	---
3.13	3.31	0.17	2.36E-01	6.10E-01	GHSR	growth hormone secretagogue receptor	chr3q26.31	224554_at	NM_004122 /// NM_198407
2.41	2.59	0.18	2.36E-01	6.10E-01	LOC283174	Hypothetical LOC283174	chr11q25	229734_at	XR_017873 /// XR_017972 /// XR_039979
5.99	6.23	0.24	2.36E-01	6.10E-01	DPP9	dipeptidyl-peptidase 9	chr19p13.3	226916_x_at	NM_139159
1.97	2.12	0.15	2.36E-01	6.10E-01	---	---	---	234075_at	---
4.77	5.20	0.44	2.36E-01	6.10E-01	LYPLAL1	lysophospholipase-like 1	chr1q41	230174_at	NM_138794
3.18	3.81	0.64	2.36E-01	6.10E-01	CAV2	caveolin 2	chr7q31.1	203324_s_at	NM_001233 /// NM_198212
3.15	3.54	0.39	2.36E-01	6.10E-01	GJB4	gap junction protein, beta 4, 30.3kDa	chr1p34.3	216579_at	NM_153212
2.95	3.20	0.25	2.36E-01	6.10E-01	HSAJ2425	p65 protein	---	207882_at	---
2.65	2.81	0.16	2.36E-01	6.10E-01	---	---	---	244541_x_at	---
7.95	8.82	0.87	2.36E-01	6.10E-01	RDX	radixin	chr11q23	212398_at	NM_002906
5.52	5.97	0.46	2.36E-01	6.10E-01	ARMC8	armadillo repeat containing 8	chr3q22.3	203486_s_at	NM_014154 /// NM_015396 /// NM_213654
4.21	4.50	0.29	2.36E-01	6.10E-01	LOC100132999	hypothetical protein LOC100132999	chr1q21.1	229264_at	XM_001722799
2.45	3.04	0.59	2.36E-01	6.10E-01	CYorf15B	chromosome Y open reading frame 15B	chrYq11.222	214131_at	NM_032576
1.92	2.05	0.13	2.36E-01	6.10E-01	---	---	---	1567303_at	---
7.38	7.82	0.43	2.36E-01	6.10E-01	ITGA9	integrin, alpha 9	chr3p21.3	227297_at	NM_002207
7.26	8.31	1.05	2.36E-01	6.10E-01	CPEB4	cytoplasmic polyadenylation element binding protein 4	chr5q21	224829_at	NM_030627
10.94	11.42	0.48	2.36E-01	6.10E-01	RPL15	ribosomal protein L15	chr3p24.2	221476_s_at	NM_002948
4.14	4.38	0.24	2.36E-01	6.10E-01	ZNF84	zinc finger protein 84	chr12q24.33	228630_at	NM_001127372 /// NM_003428

2.54	2.75	0.21	2.36E-01	6.10E-01	LOC100133946 /// MTCP1	similar to mature T-cell proliferations 1 /// mature T-cell proliferation 1	chrXq28	244790_at	NM_001018024 /// NM_001018025 /// NM_014221 /// XM_001719446
3.10	3.33	0.22	2.36E-01	6.10E-01	RFXAP	regulatory factor X-associated protein	chr13q14	208492_at	NM_000538
6.71	7.00	0.29	2.36E-01	6.10E-01	PBRM1	polybromo 1	chr3p21	220355_s_at	NM_018165 /// NM_018313 /// NM_181042
2.01	2.17	0.15	2.36E-01	6.10E-01	TRPM1	transient receptor potential cation channel, subfamily M, member 1	chr15q13-q14	237069_s_at	NM_002420
2.34	2.54	0.20	2.36E-01	6.10E-01	ANO6	anoctamin 6	chr12q12	240947_at	NM_001025356
4.28	4.70	0.42	2.36E-01	6.11E-01	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	chr9p24.1	228561_at	NM_017913
2.37	2.61	0.24	2.36E-01	6.11E-01	PNPLA3	patatin-like phospholipase domain containing 3	chr22q13.31	233030_at	NM_025225
9.71	9.95	0.24	2.36E-01	6.11E-01	MRCL3 /// MRLC2	myosin regulatory light chain MRCL3 /// myosin regulatory light chain MRLC2	chr18p11.31	201318_s_at	NM_006471 /// NM_033546
2.33	2.51	0.18	2.37E-01	6.11E-01	CDC27	Cell division cycle 27 homolog (S. cerevisiae)	chr17q12-q23.2	214236_at	NM_001114091 /// NM_001256
2.23	2.46	0.24	2.37E-01	6.11E-01	ZNF718	zinc finger protein 718	chr4p16.3	1569479_at	NM_001039127
2.88	3.17	0.29	2.37E-01	6.11E-01	---	---	---	244791_at	---
4.60	4.84	0.24	2.37E-01	6.11E-01	---	---	---	240229_at	---
2.46	2.71	0.25	2.37E-01	6.11E-01	---	---	---	236404_at	---
2.29	2.48	0.18	2.37E-01	6.11E-01	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	chr17q24.2	239185_at	NM_080283
2.13	2.30	0.17	2.37E-01	6.11E-01	LIN28	lin-28 homolog (C. elegans)	chr1p36.11	219823_at	NM_024674
5.51	6.16	0.65	2.37E-01	6.11E-01	IGLL3	immunoglobulin lambda-like polypeptide 3	chr22q11.2|22q11.23	215946_x_at	NM_001013618
2.74	2.97	0.23	2.37E-01	6.11E-01	KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2	chr8q22	232401_at	NM_020697
4.36	4.88	0.52	2.37E-01	6.11E-01	NT5DC1	5'-nucleotidase domain containing 1	chr6q22.1	223178_s_at	NM_152729
3.63	3.95	0.32	2.37E-01	6.11E-01	PRKCH	protein kinase C, eta	chr14q22-q23	206099_at	NM_006255
6.28	6.55	0.26	2.37E-01	6.11E-01	UBE2L3	ubiquitin-conjugating enzyme E2L 3	chr22q11.21	200684_s_at	NM_003347 /// NM_198157
3.86	4.07	0.21	2.37E-01	6.11E-01	---	---	---	1556909_at	---
2.04	2.20	0.16	2.37E-01	6.11E-01	---	---	---	234399_at	---
2.12	2.27	0.14	2.37E-01	6.11E-01	LOC728245	hypothetical LOC728245	chr2q37.3	243647_at	XM_001714315 /// XM_001715678 /// XM_001717075
6.18	6.64	0.46	2.37E-01	6.12E-01	CPSF3	cleavage and polyadenylation specific factor 3, 73kDa	chr2p25.1	225082_at	NM_016207
4.33	4.71	0.38	2.37E-01	6.12E-01	FGFR1OP	FGFR1 oncogene partner	chr6q27	205588_s_at	NM_007045 /// NM_194429
2.25	2.43	0.18	2.37E-01	6.12E-01	---	---	---	1567011_at	---
2.24	2.42	0.18	2.37E-01	6.12E-01	LOC145837	hypothetical protein LOC145837	chr15q23	239594_at	XR_040650 /// XR_040651 /// XR_040652
4.32	4.78	0.47	2.37E-01	6.12E-01	C9orf61	chromosome 9 open reading frame 61	chr9q13-q21	213900_at	NM_001127608 /// NM_004816
6.03	6.57	0.54	2.37E-01	6.12E-01	MTIF2	mitochondrial translational initiation factor 2	chr2p14-p16	203095_at	NM_001005369 /// NM_002453
3.18	3.48	0.31	2.37E-01	6.12E-01	---	---	---	242373_at	---
2.29	2.54	0.25	2.37E-01	6.12E-01	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	chr12q13	37512_at	NM_003725
4.96	5.18	0.21	2.37E-01	6.12E-01	RP11-265F14.2	elastase 2B	chr1p36.21	207077_at	NM_015849
2.82	3.00	0.18	2.37E-01	6.12E-01	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	chr5q33.1	207613_s_at	NM_015981 /// NM_171825
2.77	2.92	0.15	2.37E-01	6.12E-01	LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	chr19q13.4	215839_at	NM_021250 /// NM_181879 /// NM_181985 /// NM_181986
4.73	5.75	1.02	2.37E-01	6.12E-01	FABP4	fatty acid binding protein 4, adipocyte	chr8q21	203980_at	NM_001442
4.78	5.11	0.33	2.37E-01	6.12E-01	PDIA3	protein disulfide isomerase family A, member 3	chr15q15	227033_at	NM_005313
2.63	2.92	0.29	2.37E-01	6.12E-01	---	---	---	232876_at	---
2.15	2.37	0.22	2.37E-01	6.12E-01	ZNF551	zinc finger protein 551	chr19q13.43	243194_at	NM_138347
2.62	2.81	0.20	2.37E-01	6.12E-01	ZYG11A	zyg-11 homolog A (C. elegans)	chr1p32.3	231517_at	XM_001133615 /// XM_001718774 /// XM_941659
1.78	1.92	0.15	2.37E-01	6.12E-01	---	---	---	220787_at	---
3.28	3.46	0.19	2.38E-01	6.12E-01	LOC284408	Hypothetical protein LOC284408	chr19q13.13	235779_at	---
3.66	3.87	0.21	2.38E-01	6.12E-01	KCTD19	potassium channel tetramerisation domain containing 19	chr16q22.1	244538_at	NM_001100915

3.12	3.28	0.16	2.38E-01	6.12E-01	MYO10	myosin X	chr5p15.1-p14.3	216222_s_at	NM_012334
2.69	2.84	0.15	2.38E-01	6.12E-01	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	chr1q42.13	232526_at	NM_002221
3.32	3.46	0.14	2.38E-01	6.12E-01	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	chr7p14.2	225631_at	NM_030636
1.97	2.10	0.13	2.38E-01	6.12E-01	TCEB3B	transcription elongation factor B polypeptide 3B (elongin A2)	chr18q21.1	220844_at	NM_016427
2.23	2.47	0.24	2.38E-01	6.12E-01	BCL2L10	BCL2-like 10 (apoptosis facilitator)	chr15q21	236491_at	NM_020396
4.09	4.55	0.45	2.38E-01	6.12E-01	---	---	---	239131_at	---
3.49	3.74	0.26	2.38E-01	6.12E-01	ANKRD23	ankyrin repeat domain 23	chr2q11.2	1553366_s_at	NM_144994
2.82	3.07	0.25	2.38E-01	6.12E-01	---	---	---	1564821_at	---
3.78	4.02	0.24	2.38E-01	6.12E-01	---	---	---	241391_at	---
2.86	3.05	0.19	2.38E-01	6.12E-01	FAM108B1	family with sequence similarity 108, member B1	chr9q21.13	228872_at	NM_001025780 /// NM_016014
2.01	2.19	0.19	2.38E-01	6.12E-01	DRD1	dopamine receptor D1	chr5q35.1	214652_at	NM_000794
2.64	2.82	0.18	2.38E-01	6.12E-01	---	---	---	232093_at	---
2.39	2.65	0.26	2.38E-01	6.13E-01	---	---	---	241095_at	---
1.96	2.10	0.14	2.38E-01	6.13E-01	---	---	---	1561912_at	---
2.56	2.74	0.18	2.38E-01	6.13E-01	PDGFA	platelet-derived growth factor alpha polypeptide	chr7p22	216867_s_at	NM_002607 /// NM_033023
5.01	5.25	0.24	2.38E-01	6.13E-01	RALBP1	ralA binding protein 1	chr18p11.3	226957_x_at	NM_006788
5.70	6.23	0.53	2.38E-01	6.13E-01	PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein	chr8p21.3	205325_at	NM_001099335 /// NM_014759
2.43	2.62	0.19	2.38E-01	6.13E-01	PAP2D	phosphatidic acid phosphatase type 2	chr1p21.3	242825_at	NM_001010861 /// NM_001037317
10.51	10.89	0.37	2.38E-01	6.13E-01	---	---	---	213048_s_at	---
3.31	3.64	0.33	2.38E-01	6.13E-01	MAGED4 /// MAGED4B	melanoma antigen family D, 4 /// melanoma antigen family D, 4B	chrXp11.22	223313_s_at	NM_001098800 /// NM_030801 /// NM_177535 /// NM_177537
3.73	4.03	0.31	2.38E-01	6.13E-01	ANO1	anoctamin 1, calcium activated chloride channel	chr11q13.3	1555269_a_at	NM_018043
3.00	3.28	0.29	2.38E-01	6.13E-01	---	---	---	215526_at	---
1.96	2.13	0.17	2.38E-01	6.13E-01	---	---	---	240101_at	---
2.28	2.43	0.15	2.38E-01	6.13E-01	---	---	---	1561631_at	---
4.71	4.90	0.19	2.38E-01	6.13E-01	LOC100130872	hypothetical protein LOC100130872	chr4p16.3	1569496_s_at	XM_001717439 /// XM_001720019 /// XM_001721454
3.03	3.39	0.35	2.38E-01	6.13E-01	PCDHA1 /// PCDHA10 /// PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2	protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	chr5q31	224212_s_at	NM_014005 /// NM_018898 /// NM_018899 /// NM_018900 /// NM_018901 /// NM_018902 /// NM_018903 /// NM_018904 /// NM_018905 /// NM_018906 /// NM_018907 /// NM_018908 /// NM_018909 /// NM_018910 /// NM_018911 /// NM_031410 /// NM_031411 /// NM_031495 /// NM_031496 /// NM_031497 /// NM_031500 /// NM_031501 /// NM_031848 /// NM_031849 /// NM_031852 /// NM_031856 /// NM_031857 /// NM_031859 /// NM_031860 /// NM_031861 /// NM_031864 /// NM_031865 /// NM_031882 /// NM_031883

2.48	2.70	0.22	2.38E-01	6.13E-01	NIN	ninein (GSK3B interacting protein)	chr14q22.1	234299_s_at	NM_016350 /// NM_020921 /// NM_182944 /// NM_182946
5.12	5.55	0.43	2.38E-01	6.13E-01	MIA3	melanoma inhibitory activity family, member 3	chr1q41	1569057_s_at	NM_198551
4.65	4.89	0.24	2.38E-01	6.13E-01	XPO5	exportin 5	chr6p21.1	223055_s_at	NM_020750
10.17	10.42	0.25	2.39E-01	6.13E-01	EIF3C /// EIF3CL	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation initiation factor 3, subunit C-like	chr16p11.2	210949_s_at	NM_001037808 /// NM_001099661 /// NM_003752
4.50	4.72	0.22	2.38E-01	6.13E-01	TPD52L3	tumor protein D52-like 3	chr9p24.1	240051_at	NM_001001874 /// NM_001001875 /// NM_033516
2.13	2.34	0.21	2.39E-01	6.13E-01	DENND2A	DENN/MADD domain containing 2A	chr7q34	221886_at	NM_015689
4.04	4.25	0.21	2.39E-01	6.13E-01	TLE6	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)	chr19p13.3	222219_s_at	NM_024760
2.03	2.23	0.20	2.39E-01	6.13E-01	---	---	---	1561576_a_at	---
2.09	2.27	0.18	2.39E-01	6.13E-01	---	---	---	232569_at	---
3.81	4.04	0.23	2.39E-01	6.13E-01	---	---	---	237965_at	---
2.77	2.99	0.22	2.39E-01	6.13E-01	FOXB1	forkhead box B1	chr15q21-q26	208513_at	NM_012182
2.09	2.29	0.19	2.39E-01	6.13E-01	LOC284263	hypothetical protein LOC284263	chr18q21.1	1562585_at	---
2.79	2.95	0.16	2.39E-01	6.13E-01	---	---	---	237089_at	---
7.12	7.62	0.50	2.39E-01	6.13E-01	BGN	biglycan	chrXq28	213905_x_at	NM_001711
3.33	3.57	0.24	2.39E-01	6.13E-01	TES	testis derived transcript (3 LIM domains)	chr7q31.2	244870_at	NM_015641 /// NM_152829
2.92	3.13	0.21	2.39E-01	6.13E-01	WNT5B	wingless-type MMTV integration site family, member 5B	chr12p13.3	221029_s_at	NM_030775 /// NM_032642
3.46	3.66	0.20	2.39E-01	6.13E-01	---	---	---	244373_at	---
8.88	9.08	0.19	2.39E-01	6.13E-01	C5orf32	chromosome 5 open reading frame 32	chr5q31.3	224707_at	NM_032412
2.61	2.79	0.18	2.39E-01	6.13E-01	HTR5A	5-hydroxytryptamine (serotonin) receptor 5A	chr7q36.1	221362_at	NM_024012
1.90	2.08	0.18	2.39E-01	6.13E-01	---	---	---	1557348_at	---
2.26	2.43	0.17	2.39E-01	6.13E-01	---	---	---	1559843_s_at	---
2.06	2.23	0.17	2.39E-01	6.13E-01	C4orf45	chromosome 4 open reading frame 45	chr4q32.1	1553838_at	NM_152543
1.99	2.16	0.17	2.39E-01	6.13E-01	---	---	---	237390_at	---
6.72	6.88	0.16	2.39E-01	6.13E-01	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	chr22q13.2-q13.31	202000_at	NM_002490
2.07	2.23	0.16	2.39E-01	6.13E-01	---	---	---	1566725_at	---
1.99	2.13	0.14	2.39E-01	6.13E-01	---	---	---	242893_at	---
2.02	2.15	0.13	2.39E-01	6.13E-01	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	chr2q36.1	1555734_x_at	NM_001039569
3.40	3.70	0.29	2.39E-01	6.13E-01	---	---	---	238064_at	---
3.52	3.75	0.23	2.39E-01	6.13E-01	LOC100131043	hypothetical LOC100131043	chr6p21.2	244029_at	XM_001722081 /// XM_001722152 /// XM_001725057
5.56	5.78	0.22	2.39E-01	6.13E-01	FLJ90757	hypothetical protein LOC440465	chr17q25.3	1558147_a_at	XR_017883 /// XR_017982 /// XR_040055
2.75	2.97	0.22	2.39E-01	6.13E-01	---	---	---	243704_at	---
3.45	3.64	0.20	2.39E-01	6.13E-01	---	---	---	236060_at	---
5.26	5.45	0.19	2.39E-01	6.13E-01	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	chr11q13	227795_at	NM_007103
2.81	2.97	0.16	2.39E-01	6.13E-01	---	---	---	236825_at	---
1.91	2.04	0.13	2.39E-01	6.13E-01	FMR1NB	fragile X mental retardation 1 neighbor	chrXq27.3-q28	1552906_at	NM_152578
1.89	2.07	0.18	2.39E-01	6.13E-01	---	---	---	240132_at	---
2.72	2.95	0.23	2.39E-01	6.13E-01	C1orf217	chromosome 1 open reading frame 217	chr1q32.1	210711_at	XR_040168 /// XR_040169 /// XR_040170
8.46	8.77	0.31	2.39E-01	6.13E-01	C20orf199	chromosome 20 open reading frame 199	chr20q13.13	224915_x_at	NR_003604 /// NR_003605 /// NR_003606
4.93	5.14	0.21	2.39E-01	6.13E-01	---	---	---	242793_at	---
2.78	2.96	0.18	2.39E-01	6.13E-01	---	---	---	1566854_at	---
5.65	5.99	0.33	2.39E-01	6.13E-01	SNX2	sorting nexin 2	chr5q23	202114_at	NM_003100
3.11	3.32	0.21	2.39E-01	6.13E-01	MAP6	microtubule-associated protein 6	chr11q13.5	235672_at	NM_033063 /// NM_207577
3.47	3.66	0.19	2.39E-01	6.13E-01	LOC441476	hypothetical protein LOC441476	chr9q34.3	1566908_at	NM_001004353
2.72	2.90	0.18	2.39E-01	6.13E-01	---	---	---	232928_at	---
1.86	2.01	0.15	2.39E-01	6.13E-01	IL12B	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	chr5q31.1-q33.1	207901_at	NM_002187
3.07	3.27	0.20	2.39E-01	6.13E-01	---	---	---	226397_s_at	---
2.93	3.09	0.16	2.39E-01	6.13E-01	NOS3	nitric oxide synthase 3 (endothelial cell)	chr7q36	229093_at	NM_000603

2.94	3.13	0.19	2.39E-01	6.14E-01	KCNN3 /// LOC100133958	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 /// similar to small conductance calcium-activated potassium channel protein 3	chr1q21.3	205902_at	NM_002249 /// NM_170782 /// XM_001722033
4.58	5.14	0.56	2.40E-01	6.14E-01	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1	chr1p33-p32	219134_at	NM_022159
7.31	7.75	0.45	2.40E-01	6.14E-01	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	chr16q12	222388_s_at	NM_018206
2.85	3.04	0.19	2.39E-01	6.14E-01	---	---	---	238094_at	---
2.83	3.01	0.18	2.40E-01	6.14E-01	---	---	---	233790_at	---
2.70	2.86	0.16	2.40E-01	6.14E-01	---	---	---	244813_at	---
2.99	3.15	0.15	2.39E-01	6.14E-01	GP2	glycoprotein 2 (zymogen granule membrane)	chr16p12	214324_at	NM_001007240 /// NM_001007241 /// NM_001007242 /// NM_001502
2.03	2.15	0.13	2.40E-01	6.14E-01	RPL22	Ribosomal protein L22	chr1p36.3-p36.2	238375_at	NM_000983
2.39	2.65	0.25	2.40E-01	6.14E-01	ZNF479	zinc finger protein 479	chr7p11.2	1555368_x_at	NM_033273 /// XM_001714591 /// XM_001719979
2.18	2.32	0.14	2.40E-01	6.14E-01	LOC100128081	Similar to hCG2033532	chr7p15.1	1559650_at	XM_001716238 /// XM_001717474 /// XM_001717737
2.57	2.82	0.24	2.40E-01	6.14E-01	---	---	---	237347_at	---
4.32	4.56	0.23	2.40E-01	6.14E-01	KLHL18	kelch-like 18 (Drosophila)	chr3p21.31	1557165_s_at	NM_025010
4.79	5.03	0.23	2.40E-01	6.14E-01	ICOSLG	inducible T-cell co-stimulator ligand	chr21q22.3	213450_s_at	NM_015259
3.29	3.48	0.19	2.40E-01	6.14E-01	ZNF551	zinc finger protein 551	chr19q13.43	243195_s_at	NM_138347
2.25	2.45	0.20	2.40E-01	6.14E-01	MAGEC3	melanoma antigen family C, 3	chrXq27.2	216592_at	NM_138702 /// NM_177456
2.30	2.51	0.21	2.40E-01	6.14E-01	DNASE1	deoxyribonuclease I	chr16p13.3	240144_at	NM_005223
2.36	2.55	0.19	2.40E-01	6.14E-01	---	---	---	205800_at	---
2.27	2.43	0.16	2.40E-01	6.14E-01	---	---	---	239867_at	---
1.91	2.05	0.14	2.40E-01	6.14E-01	LOC100127980	Hypothetical protein LOC100127980	chr19q13.12	1557046_x_at	XM_001720119 /// XM_001722650
3.22	3.39	0.17	2.40E-01	6.14E-01	LHFPL4	lipoma HMGIC fusion partner-like 4	chr3p25.3	228422_at	NM_198560
1.89	2.17	0.28	2.40E-01	6.14E-01	---	---	---	1557838_at	---
2.96	3.24	0.28	2.40E-01	6.14E-01	---	---	---	1556657_at	---
2.34	2.56	0.22	2.40E-01	6.14E-01	---	---	---	234531_at	---
3.36	3.58	0.21	2.40E-01	6.14E-01	---	---	---	229602_at	---
2.27	2.44	0.17	2.40E-01	6.14E-01	---	---	---	1561718_at	---
1.98	2.12	0.15	2.40E-01	6.14E-01	ALS2CR11	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	chr2q33.1	1554831_x_at	NM_152525
2.03	2.20	0.17	2.40E-01	6.14E-01	---	---	---	236103_at	---
3.66	4.22	0.56	2.40E-01	6.14E-01	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	chr1q25	210145_at	NM_024420
3.07	3.35	0.27	2.40E-01	6.14E-01	---	---	---	243298_at	---
2.20	2.34	0.14	2.40E-01	6.14E-01	---	---	---	237545_at	---
2.64	2.89	0.25	2.40E-01	6.14E-01	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	231235_at	NM_005385
2.38	2.97	0.59	2.40E-01	6.14E-01	ORM1 /// ORM2	orosomucoid 1 /// orosomucoid 2	chr9q31-q32 /// chr9q32	214465_at	NM_000607 /// NM_000608
6.63	7.14	0.51	2.40E-01	6.14E-01	---	---	---	235138_at	---
3.01	3.18	0.16	2.40E-01	6.14E-01	LRRC48	leucine rich repeat containing 48	chr17p11.2	1554584_at	NM_001130090 /// NM_001130091 /// NM_001130092 /// NM_031294
4.42	4.82	0.40	2.40E-01	6.14E-01	---	---	---	235152_at	---
4.31	4.48	0.17	2.40E-01	6.14E-01	---	---	---	1557453_at	---
2.68	2.89	0.21	2.40E-01	6.14E-01	---	---	---	234814_at	---
3.00	3.21	0.21	2.40E-01	6.15E-01	---	---	---	1557335_at	---
5.45	5.95	0.50	2.41E-01	6.15E-01	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	chr6p21.1-p12.2	218856_at	NM_014452
8.39	8.74	0.34	2.41E-01	6.15E-01	TM9SF2	transmembrane 9 superfamily member 2	chr13q32.3	201078_at	NM_004800
3.22	3.44	0.21	2.41E-01	6.15E-01	MLLT1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	chr19p13.3	214477_at	NM_005934
2.57	2.73	0.16	2.41E-01	6.15E-01	CCDC36	coiled-coil domain containing 36	chr3p21.31	1569690_at	NM_178173

3.83	4.09	0.26	2.41E-01	6.15E-01	---	---	---	1563902_at	---
2.08	2.33	0.25	2.41E-01	6.15E-01	ST6GAL2	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	chr2q11.2-q12.1	1555123_at	NM_032528
2.50	2.64	0.14	2.41E-01	6.15E-01	RRBP1	Ribosome binding protein 1 homolog 180kDa (dog)	chr20p12	213495_s_at	NM_001042576 /// NM_004587
6.05	6.45	0.40	2.41E-01	6.15E-01	FICD	FIC domain containing	chr12q24.1	219910_at	NM_007076
6.07	6.49	0.42	2.41E-01	6.15E-01	TMEM37	transmembrane protein 37	chr2q14.2	227190_at	NM_183240
1.98	2.20	0.22	2.41E-01	6.15E-01	ABHD7	abhydrolase domain containing 7	chr1p22.1	239579_at	NM_173567
3.05	3.26	0.21	2.41E-01	6.15E-01	KHK	ketohexokinase (fructokinase)	chr2p23.3	205175_s_at	NM_000221 /// NM_006488
3.90	4.10	0.20	2.41E-01	6.15E-01	SPTB	spectrin, beta, erythrocytic	chr14q23-q24.2	208416_s_at	NM_000347 /// NM_001024858
2.50	2.64	0.15	2.41E-01	6.15E-01	GUCY1B2	guanylate cyclase 1, soluble, beta 2	chr13q14.2-q14.3	220506_at	NR_003923
3.80	4.02	0.22	2.41E-01	6.15E-01	LOC645634	Hypothetical LOC645634	chr1p36.13	244379_at	XM_001714143 /// XR_016998 /// XR_019624
2.03	2.20	0.17	2.41E-01	6.15E-01	---	---	---	1559788_at	---
2.45	2.64	0.19	2.41E-01	6.15E-01	OR2K2	olfactory receptor, family 2, subfamily K, member 2	chr9q31.3	1567272_at	NM_205859
3.21	3.80	0.59	2.41E-01	6.15E-01	---	---	---	240772_at	---
3.62	3.83	0.22	2.41E-01	6.15E-01	LOC728288	hypothetical LOC728288	chr15q14	236925_at	XM_001128351 /// XM_001128438 /// XM_001724283
2.25	2.42	0.17	2.41E-01	6.15E-01	ZNF782	Zinc finger protein 782	chr9q22.33	235290_at	NM_001001662
2.20	2.33	0.12	2.41E-01	6.15E-01	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	chr11p11.2	1554122_a_at	NM_016142
2.99	3.49	0.50	2.41E-01	6.15E-01	MRAP	melanocortin 2 receptor accessory protein	chr21q22.1	1555741_at	NM_178817 /// NM_206898
6.01	6.33	0.32	2.41E-01	6.15E-01	ANKRD17	ankyrin repeat domain 17	chr4q13.3	212211_at	NM_032217 /// NM_198889
2.81	3.05	0.24	2.41E-01	6.15E-01	B3GALT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	chr1p36.33	226427_s_at	NM_080605
3.29	3.50	0.21	2.41E-01	6.15E-01	---	---	---	230095_at	---
2.05	2.19	0.14	2.41E-01	6.15E-01	MUC15	mucin 15, cell surface associated	chr11p14.3	227241_at	NM_145650
2.15	2.34	0.19	2.41E-01	6.15E-01	---	---	---	239715_at	---
2.94	3.20	0.26	2.41E-01	6.15E-01	---	---	---	244598_at	---
2.25	2.45	0.20	2.41E-01	6.15E-01	EPHA10	EPH receptor A10	chr1p34.3	1553371_at	NM_001099439 /// NM_173641
3.47	3.67	0.20	2.41E-01	6.15E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	201982_s_at	NM_002581
1.96	2.10	0.14	2.41E-01	6.15E-01	TRA@	T cell receptor alpha locus	chr14q11.2	234849_at	---
7.37	7.79	0.42	2.41E-01	6.16E-01	IFI16	interferon, gamma-inducible protein 16	chr1q22	208966_x_at	NM_005531
4.84	5.08	0.24	2.41E-01	6.16E-01	GGTLC1	gamma-glutamyltransferase light chain 1	chr20p11.1	209918_at	NM_080920 /// NM_178311 /// NM_178312
7.46	7.69	0.23	2.42E-01	6.16E-01	COX16	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr14q24.2	223191_at	NM_016468
2.43	2.61	0.18	2.42E-01	6.16E-01	LOC221272	hypothetical protein LOC221272	chr6q22.1	232772_at	---
2.26	2.43	0.17	2.42E-01	6.16E-01	PCDH11X	protocadherin 11 X-linked	chrXq21.3	208366_at	NM_014522 /// NM_032967 /// NM_032968 /// NM_032969
6.17	6.68	0.51	2.42E-01	6.16E-01	C8orf83	chromosome 8 open reading frame 83	chr8q22.1	225603_s_at	NR_015339 /// XR_041349 /// XR_041350 /// XR_041351
4.23	4.56	0.33	2.42E-01	6.16E-01	C2orf43	chromosome 2 open reading frame 43	chr2p24.1	222193_at	NM_021925
4.30	4.54	0.24	2.42E-01	6.16E-01	WDR53	WD repeat domain 53	chr3q29	227814_at	NM_182627
5.52	5.75	0.24	2.42E-01	6.16E-01	RUSC2	RUN and SH3 domain containing 2	chr9p13.3	213066_at	NM_014806
1.84	1.97	0.13	2.42E-01	6.16E-01	---	---	---	1559652_at	---
5.78	6.36	0.58	2.42E-01	6.16E-01	AKAP2 /// PALM2 /// PALM2-AKAP2	A kinase (PRKA) anchor protein 2 /// paralemmin 2 /// PALM2-AKAP2	chr9q31-q33	202759_s_at	NM_001004065 /// NM_001037293 /// NM_007203 /// NM_053016 /// NM_147150
3.13	3.57	0.44	2.42E-01	6.16E-01	---	---	---	234649_at	---
5.82	6.13	0.31	2.42E-01	6.16E-01	TMEM57	transmembrane protein 57	chr1p36.11|1p36.11	218562_s_at	NM_018202

2.54	2.74	0.21	2.42E-01	6.16E-01	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	215375_x_at	NM_004735
2.02	2.21	0.19	2.42E-01	6.16E-01	---	---	---	1558739_at	---
2.48	2.65	0.17	2.42E-01	6.16E-01	KLRD1	killer cell lectin-like receptor subfamily D, member 1	chr12p13	207795_s_at	NM_001114396 /// NM_002262 /// NM_007334
2.02	2.18	0.16	2.42E-01	6.16E-01	CPA6	carboxypeptidase A6	chr8q13.2	1552511_a_at	NM_001127445 /// NM_020361
4.90	5.28	0.38	2.42E-01	6.16E-01	PAPOLA	poly(A) polymerase alpha	chr14q32.31	228569_at	NM_032632
2.02	2.15	0.13	2.42E-01	6.16E-01	CNGB3	cyclic nucleotide gated channel beta 3	chr8q21-q22	222959_at	NM_019098
2.71	2.92	0.20	2.42E-01	6.16E-01	CABP4	calcium binding protein 4	chr11q13.1	1552890_a_at	NM_145200
2.95	3.12	0.17	2.42E-01	6.16E-01	NRP2	Neuropilin 2	chr2q33.3	228102_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279
3.55	3.75	0.20	2.42E-01	6.16E-01	LOC100132707	Hypothetical LOC100132707	chr7q36.2	1558527_at	XM_001719292 /// XM_001720302 /// XM_001721385
3.95	4.12	0.17	2.42E-01	6.16E-01	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	chr15q15-q21.1	1554842_at	NM_000338
6.17	6.88	0.71	2.42E-01	6.16E-01	PGGT1B	Protein geranylgeranyltransferase type I, beta subunit	chr5q22.3	242844_at	NM_005023
8.58	8.95	0.37	2.42E-01	6.16E-01	hCG_1757335 /// RAP1B	hCG1757335 /// RAP1B, member of RAS oncogene family	chr12q14 /// chr5q13.3	200833_s_at	NM_001010942 /// NM_001089704 /// NM_015646
2.91	3.21	0.30	2.42E-01	6.16E-01	LCK	lymphocyte-specific protein tyrosine kinase	chr1p34.3	204891_s_at	NM_001042771 /// NM_005356
2.96	3.18	0.22	2.42E-01	6.16E-01	GPR101	G protein-coupled receptor 101	chrXq25-q27.1	1553544_at	NM_054021
4.87	5.49	0.62	2.42E-01	6.17E-01	IDE	insulin-degrading enzyme	chr10q23-q25	217496_s_at	NM_004969
7.43	7.71	0.28	2.42E-01	6.17E-01	RAB14	RAB14, member RAS oncogene family	chr9q32-q34.11	211503_s_at	NM_016322
3.51	3.72	0.21	2.42E-01	6.17E-01	SSX3	synovial sarcoma, X breakpoint 3	chrXp11.23	211670_x_at	NM_021014 /// NM_175711
4.59	4.80	0.20	2.42E-01	6.17E-01	SPATA7	spermatogenesis associated 7	chr14q31.3	234929_s_at	NM_001040428 /// NM_018418
4.49	4.68	0.19	2.42E-01	6.17E-01	LOC100128074	hypothetical protein LOC100128074	chr11q13.1	228203_at	XM_001716218 /// XM_001716221 /// XM_001716711
2.02	2.20	0.18	2.42E-01	6.17E-01	GIT2	G protein-coupled receptor kinase interactor 2	chr12q24.1	1556912_at	NM_014776 /// NM_057169 /// NM_057170 /// NM_139201
2.51	2.66	0.15	2.42E-01	6.17E-01	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	chr3q27-q28	214970_s_at	NM_003032 /// NM_173216 /// NM_173217
1.97	2.10	0.13	2.42E-01	6.17E-01	hCG_1806964	hCG1806964	chr3q25.1	232298_at	XR_041581 /// XR_041582 /// XR_041583
3.27	3.73	0.47	2.42E-01	6.17E-01	C9orf4	chromosome 9 open reading frame 4	chr9q31	1558414_at	NM_014334
2.62	2.83	0.21	2.42E-01	6.17E-01	---	---	---	242741_x_at	---
2.38	2.54	0.17	2.42E-01	6.17E-01	---	---	---	1569516_at	---
7.69	7.88	0.19	2.42E-01	6.17E-01	LRRC40	leucine rich repeat containing 40	chr1p31.1	215063_x_at	NM_017768
2.40	2.53	0.13	2.42E-01	6.17E-01	---	---	---	217695_x_at	---
12.22	12.64	0.42	2.43E-01	6.17E-01	RPS3A	ribosomal protein S3A	chr4q31.2-q31.3	212391_x_at	NM_001006
7.08	7.49	0.42	2.43E-01	6.17E-01	HSPH1	heat shock 105kDa/110kDa protein 1	chr13q12.3	206976_s_at	NM_006644
2.76	3.09	0.33	2.43E-01	6.17E-01	ARSG	arylsulfatase G	chr17q24.2	1552632_a_at	NM_014960
3.42	3.73	0.31	2.43E-01	6.17E-01	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	chr6q21	238736_at	NM_002912
7.81	8.10	0.30	2.43E-01	6.17E-01	CSDE1	cold shock domain containing E1, RNA-binding	chr1p22	202646_s_at	NM_001007553 /// NM_001130523 /// NM_007158
5.31	5.58	0.27	2.43E-01	6.17E-01	KIAA0586	KIAA0586	chr14q23.1	205631_at	NM_014749
4.58	4.83	0.25	2.43E-01	6.17E-01	C1orf186	chromosome 1 open reading frame 186	chr1q32.1	230381_at	NM_001007544
2.71	2.96	0.25	2.43E-01	6.17E-01	---	---	---	236785_at	---

2.50	2.74	0.24	2.43E-01	6.17E-01	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	chr12q13	226213_at	NM_001005915 /// NM_001982
2.09	2.32	0.24	2.43E-01	6.17E-01	C2orf27	Chromosome 2 open reading frame 27	chr2q21.1-q21.2	242418_at	NM_013310
3.16	3.39	0.23	2.43E-01	6.17E-01	MAPK8	mitogen-activated protein kinase 8	chr10q11.22	210477_x_at	NM_002750 /// NM_139046 /// NM_139047 /// NM_139049
2.51	2.72	0.21	2.43E-01	6.17E-01	TPM1	tropomyosin 1 (alpha)	chr15q22.1	1558532_at	NM_000366 /// NM_001018004 /// NM_001018005 /// NM_001018006 /// NM_001018007 /// NM_001018008 /// NM_001018020
2.48	2.67	0.19	2.43E-01	6.17E-01	---	---	---	244879_at	---
3.30	3.48	0.18	2.43E-01	6.17E-01	STOX2	storkhead box 2	chr4q35.1	234319_at	NM_020225
3.32	3.50	0.18	2.43E-01	6.17E-01	---	---	---	229330_at	---
9.73	9.90	0.17	2.43E-01	6.17E-01	GNS	glucosamine (N-acetyl)-6-sulfatase	chr12q14	212334_at	NM_002076
4.79	4.94	0.15	2.43E-01	6.17E-01	ZNF175	zinc finger protein 175	chr19q13.4	205497_at	NM_007147
2.11	2.26	0.15	2.43E-01	6.17E-01	CLK4	CDC-like kinase 4	chr5q35	1568836_at	NM_020666
1.79	1.94	0.14	2.43E-01	6.17E-01	---	---	---	244039_x_at	---
4.59	4.77	0.18	2.43E-01	6.17E-01	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	chr6p21.3	208523_x_at	NM_003518 /// NM_003522 /// NM_003523 /// NM_003525 /// NM_003526
2.21	2.35	0.15	2.43E-01	6.17E-01	---	---	---	1557857_a_at	---
5.17	5.32	0.15	2.43E-01	6.17E-01	---	---	---	216784_at	---
3.19	3.42	0.23	2.43E-01	6.17E-01	CREBBP	CREB binding protein	chr16p13.3	211808_s_at	NM_001079846 /// NM_004380
2.23	2.42	0.19	2.43E-01	6.17E-01	---	---	---	1561152_a_at	---
3.05	3.26	0.21	2.43E-01	6.17E-01	---	---	---	237500_at	---
2.50	2.69	0.18	2.43E-01	6.17E-01	ANXA13	annexin A13	chr8q24.13	208323_s_at	NM_001003954 /// NM_004306
2.12	2.27	0.16	2.43E-01	6.17E-01	---	---	---	234051_at	---
3.38	3.67	0.29	2.43E-01	6.17E-01	C20orf132	chromosome 20 open reading frame 132	chr20q11.22	232185_at	NM_152503 /// NM_213631 /// NM_213632
1.98	2.10	0.12	2.43E-01	6.17E-01	FLJ23834	Hypothetical protein FLJ23834	chr7q22.2	231582_at	NM_152750
5.17	5.66	0.49	2.43E-01	6.17E-01	CEP63	centrosomal protein 63kDa	chr3q22.1-q22.2	219242_at	NM_001042383 /// NM_001042384 /// NM_001042400 /// NM_025180
4.30	4.51	0.20	2.43E-01	6.17E-01	---	---	---	231355_at	---
5.82	6.05	0.23	2.43E-01	6.17E-01	NPAL3	NIPA-like domain containing 3	chr1p36.12-p35.1	225875_s_at	NM_020448
3.49	3.68	0.19	2.43E-01	6.17E-01	POFUT2	protein O-fucosyltransferase 2	chr21q22.3	207449_s_at	NM_015227 /// NM_133634 /// NM_133635 /// NR_004858
3.33	3.55	0.22	2.43E-01	6.17E-01	CHRNA6	cholinergic receptor, nicotinic, alpha 6	chr8p11.21	207568_at	NM_004198
2.37	2.57	0.20	2.43E-01	6.17E-01	KIAA1109	KIAA1109	chr4q27	1553793_a_at	NM_015312
2.06	2.20	0.14	2.43E-01	6.17E-01	GP5	glycoprotein V (platelet)	chr3q29	207926_at	NM_004488
2.88	3.13	0.25	2.43E-01	6.17E-01	LYZL1 /// LYZL2	lysozyme-like 1 /// lysozyme-like 2	chr10p11.23	230514_s_at	NM_032517 /// NM_183058
3.68	3.88	0.20	2.43E-01	6.17E-01	CBLC	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	chr19q13.2	220638_s_at	NM_001130852 /// NM_012116
2.28	2.42	0.14	2.43E-01	6.17E-01	TMEM87A	Transmembrane protein 87A	chr15q15.1	223771_at	NM_001110503 /// NM_015497
1.92	2.05	0.13	2.43E-01	6.17E-01	---	---	---	236502_at	---
2.42	2.61	0.19	2.44E-01	6.18E-01	C9orf14	Chromosome 9 open reading frame 14	chr9p21	1559293_x_at	XM_376821 /// XM_938938

2.98	3.21	0.23	2.44E-01	6.18E-01	ANXA8 /// ANXA8L1 /// ANXA8L2	annexin A8 /// annexin A8-like 1 /// annexin A8-like 2	chr10q11.22	203074_at	NM_001040084 /// NM_001098845 /// NM_001630																				
2.07	2.24	0.17	2.44E-01	6.18E-01	LOC730051	similar to hCG2044798	chr19q13.43	222135_at	XM_001725674 /// XM_001725708 /// XM_001726286																				
4.01	4.18	0.17	2.44E-01	6.18E-01	TMEM177	Transmembrane protein 177	chr2q14.2	237506_at	NM_001105198 /// NM_001105199 /// NM_030577																				
2.32	2.51	0.19	2.44E-01	6.18E-01	IL28A	interleukin 28A (interferon, lambda 2)	chr19q13.13	1552915_at	NM_172138																				
2.34	2.48	0.14	2.44E-01	6.18E-01	CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B subunit	chr9q34	235781_at	NM_000718																				
4.65	4.86	0.21	2.44E-01	6.18E-01	CSF3	colony stimulating factor 3 (granulocyte)	chr17q11.2-q12	207442_at	NM_000759 /// NM_172219 /// NM_172220																				
2.88	3.05	0.17	2.44E-01	6.18E-01	EMILIN2	elastin microfibril interfacer 2	chr18p11.3	242288_s_at	NM_032048																				
1.90	2.07	0.16	2.44E-01	6.18E-01	HORMAD1	HORMA domain containing 1	chr1q21.2	223861_at	NM_032132																				
2.49	2.64	0.15	2.44E-01	6.18E-01	---	---	---	237295_at	---																				
2.34	2.47	0.13	2.44E-01	6.18E-01	---	---	---	1565741_at	---																				
5.69	6.02	0.33	2.44E-01	6.18E-01	KPNB1	Karyopherin (importin) beta 1	chr17q21.32	213803_at	NM_002265																				
3.57	3.81	0.25	2.44E-01	6.18E-01	---	---	---	1562852_at	---																				
7.48	7.97	0.50	2.44E-01	6.18E-01	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	chr4q21-q24	202429_s_at	NM_000944 /// NM_001130691 /// NM_001130692																				
2.58	2.75	0.17	2.44E-01	6.18E-01	HTR1E	5-hydroxytryptamine (serotonin) receptor 1E	chr6q14-q15	207404_s_at	NM_000865																				
2.59	2.74	0.15	2.44E-01	6.18E-01	---	---	---	230113_at	---																				
2.46	2.67	0.21	2.44E-01	6.18E-01	IGHD	immunoglobulin heavy constant delta	chr14q32.33	222285_at	---																				
2.04	2.19	0.15	2.44E-01	6.18E-01	---	---	---	243163_at	---																				
2.14	2.28	0.13	2.44E-01	6.18E-01	---	---	---	1564149_at	---																				
6.79	7.38	0.59	2.44E-01	6.18E-01	CSE1L	CSE1 chromosome segregation 1-like (yeast)	chr20q13	210766_s_at	NM_001316																				
4.59	4.83	0.24	2.44E-01	6.18E-01	PTPRS	protein tyrosine phosphatase, receptor type, S	chr19p13.3	210823_s_at	NM_002850 /// NM_130853 /// NM_130854 /// NM_130855																				
2.08	2.22	0.15	2.44E-01	6.18E-01	LOC100129597	hypothetical protein LOC100129597	chr13q14.2	240058_at	XM_001720616 /// XM_001722755 /// XM_001725592																				
4.11	4.36	0.25	2.44E-01	6.18E-01	TAL2	T-cell acute lymphocytic leukemia 2	chr9q32	231759_at	NM_005421																				
4.08	4.31	0.23	2.44E-01	6.18E-01	---	---	---	220713_at	---																				
7.22	7.38	0.17	2.44E-01	6.18E-01	CCDC152	coiled-coil domain containing 152	chr5p12	237475_x_at	XM_001714967 /// XM_001716661 /// XM_001717416																				
8.92	9.26	0.34	2.44E-01	6.18E-01	SERINC3	serine incorporator 3	chr20q13.1-q13.3	221473_x_at	NM_006811 /// NM_198941																				
5.93	7.42	1.49	2.44E-01	6.18E-01	IGL@ /// IGLC2 /// IGLV2-14	immunoglobulin lambda locus /// immunoglobulin lambda constant 2 (Kern-Oz- marker) /// immunoglobulin lambda variable 2-14	chr22q11.1-q11.2 /// chr22q11.2	215379_x_at	---																				
3.39	3.55	0.16	2.44E-01	6.18E-01	GDF1 /// LASS1	growth differentiation factor 1 /// LAG1 homolog, ceramide synthase 1	chr19p12	206397_x_at	NM_001492 /// NM_021267 /// NM_198207																				
3.80	3.95	0.15	2.44E-01	6.18E-01	---	---	---	236647_at	---																				
6.01	6.39	0.39	2.44E-01	6.18E-01	NSDHL	NAD(P) dependent steroid dehydrogenase-like	chrXq28	215093_at	NM_001129765 /// NM_015922																				
5.07	5.32	0.25	2.44E-01	6.18E-01	LYSMD1	LysM, putative peptidoglycan-binding, domain containing 1	chr1q21.2	232283_at	NM_212551																				
2.42	2.62	0.20	2.44E-01	6.18E-01	---	---	---	241543_at	---																				
3.80	3.98	0.19	2.44E-01	6.18E-01	EPS8L1	EPS8-like 1	chr19q13.42	218779_x_at	NM_017729 /// NM_133180																				
8.33	8.74	0.41	2.44E-01	6.18E-01	PAPOLA	poly(A) polymerase alpha	chr14q32.31	212718_at	NM_032632																				
6.76	7.26	0.50	2.44E-01	6.19E-01	SP100	SP100 nuclear antigen	chr2q37.1	202864_s_at	NM_001080391 /// NM_003113																				

2.51	2.71	0.20	2.45E-01	6.19E-01	GP2	glycoprotein 2 (zymogen granule membrane)	chr16p12	214325_at	NM_001007240 /// NM_001007241 /// NM_001007242 /// NM_001502																				
4.30	4.61	0.31	2.45E-01	6.19E-01	ZFHX3	zinc finger homeobox 3	chr16q22.3-q23.1	208033_s_at	NM_006885																				
2.12	2.31	0.19	2.45E-01	6.19E-01	KLRC1 /// KLRC2	killer cell lectin-like receptor subfamily C, member 1 /// killer cell lectin-like receptor subfamily C, member 2	chr12p13	206785_s_at	NM_002259 /// NM_002260 /// NM_007328 /// NM_213657 /// NM_213658 /// XM_001713685 /// XM_001713701																				
5.14	6.03	0.89	2.45E-01	6.19E-01	FAS	Fas (TNF receptor superfamily, member 6)	chr10q24.1	215719_x_at	NM_000043 /// NM_152871 /// NM_152872 /// NM_152873 /// NM_152874 /// NM_152875 /// NM_152876 /// NM_152877																				
2.49	2.78	0.28	2.45E-01	6.19E-01	LOC128102	3-beta-hydroxysteroid dehydrogenase, tissue-type heart	chr1p12	216819_at	---																				
2.42	2.70	0.29	2.45E-01	6.19E-01	---	---	---	1557833_at	---																				
4.02	4.19	0.17	2.45E-01	6.19E-01	ZFP57	zinc finger protein 57 homolog (mouse)	chr6p22.1	231236_at	NM_001109809																				
6.61	7.18	0.57	2.45E-01	6.19E-01	SNRK	SNF related kinase	chr3p22.1	209481_at	NM_001100594 /// NM_017719																				
4.49	4.76	0.27	2.45E-01	6.19E-01	TNNC2	troponin C type 2 (fast)	chr20q12-q13.11	205388_at	NM_003279																				
3.07	3.22	0.15	2.45E-01	6.19E-01	TRIM31	tripartite motif-containing 31	chr6p21.3	215444_s_at	NM_007028																				
3.35	3.54	0.18	2.45E-01	6.19E-01	UBE3B	ubiquitin protein ligase E3B	chr12q24.11	228860_at	NM_130466 /// NM_183415																				
2.42	2.55	0.12	2.45E-01	6.19E-01	---	---	---	240262_at	---																				
1.99	2.21	0.22	2.45E-01	6.19E-01	---	---	---	228692_at	---																				
4.85	5.07	0.22	2.45E-01	6.19E-01	---	---	---	244814_at	---																				
1.99	2.14	0.14	2.45E-01	6.19E-01	---	---	---	234800_at	---																				
2.42	2.64	0.23	2.45E-01	6.19E-01	LOC442240	similar to zinc finger protein 259	chr6q21	217186_at	XR_016496 /// XR_019092 /// XR_040401																				
2.69	2.87	0.19	2.45E-01	6.19E-01	C6orf159	chromosome 6 open reading frame 159	chr6q14.2	236771_at	NM_001009994																				
7.17	7.42	0.24	2.45E-01	6.19E-01	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	chr10q21-q22	202432_at	NM_021132																				
3.11	3.30	0.19	2.45E-01	6.19E-01	NOVA2	neuro-oncological ventral antigen 2	chr19q13.3	206476_s_at	NM_002516																				
1.94	2.09	0.15	2.45E-01	6.19E-01	MITF	microphthalmia-associated transcription factor	chr3p14.2-p14.1	1554874_at	NM_000248 /// NM_006722 /// NM_198158 /// NM_198159 /// NM_198177 /// NM_198178																				
3.60	4.10	0.50	2.45E-01	6.19E-01	FBXO38	F-box protein 38	chr5q33.1	219608_s_at	NM_030793 /// NM_205836																				
3.73	3.94	0.21	2.45E-01	6.19E-01	TROAP	trophinin associated protein (tastin)	chr12q13.12	204649_at	NM_001100620 /// NM_005480																				
4.28	4.55	0.27	2.45E-01	6.19E-01	PRSS22	protease, serine, 22	chr16p13.3	205847_at	NM_022119																				
3.28	3.44	0.15	2.45E-01	6.19E-01	---	---	---	237260_at	---																				
1.98	2.15	0.17	2.45E-01	6.19E-01	CDH19	cadherin 19, type 2	chr18q22-q23	1555403_a_at	NM_021153																				
1.93	2.08	0.14	2.45E-01	6.19E-01	---	---	---	240250_at	---																				
3.06	3.44	0.39	2.45E-01	6.19E-01	PTPRT	protein tyrosine phosphatase, receptor type, T	chr20q12-q13	205948_at	NM_007050 /// NM_133170																				
4.43	4.64	0.20	2.45E-01	6.19E-01	---	---	---	237518_at	---																				
1.99	2.17	0.17	2.45E-01	6.19E-01	MAK	male germ cell-associated kinase	chr6p24	1555315_a_at	NM_005906																				
4.71	5.08	0.37	2.45E-01	6.19E-01	ZFR	zinc finger RNA binding protein	chr5p13.3	213286_at	NM_016107																				
2.97	3.13	0.17	2.45E-01	6.20E-01	---	---	---	215593_at	---																				

5.73	6.43	0.70	2.46E-01	6.20E-01	GPBP1	GC-rich promoter binding protein 1	chr5q11.2	224648_at	NM_001127235 /// NM_001127236 /// NM_022913																				
2.32	2.85	0.53	2.46E-01	6.20E-01	GUCY1A3	Guanylate cyclase 1, soluble, alpha 3	chr4q31.3-q33|4q31.1-q31.2	239580_at	NM_000856 /// NM_001130682 /// NM_001130683 /// NM_001130684 /// NM_001130685 /// NM_001130686 /// NM_001130687																				
2.19	2.39	0.20	2.46E-01	6.20E-01	RP5-1000E10.4	suppressor of IKK epsilon	chr1p13.2	204665_at	NM_001102396 /// NM_025073																				
2.24	2.45	0.20	2.46E-01	6.20E-01	---	---	---	231460_at	---																				
3.41	3.61	0.20	2.46E-01	6.20E-01	PCNX	pecanex homolog (Drosophila)	chr14q24.2	239100_x_at	NM_014982																				
3.29	3.47	0.19	2.46E-01	6.20E-01	---	---	---	234909_at	---																				
2.17	2.34	0.17	2.46E-01	6.20E-01	---	---	---	233778_at	---																				
1.92	2.07	0.15	2.46E-01	6.20E-01	ZBTB1	zinc finger and BTB domain containing 1	chr14q23.3	205092_x_at	NM_001123329 /// NM_014950																				
1.93	2.07	0.14	2.46E-01	6.20E-01	STARD6	StAR-related lipid transfer (START) domain containing 6	chr18q21.2	1553084_at	NM_139171																				
2.80	3.08	0.27	2.46E-01	6.20E-01	---	---	---	1562280_at	---																				
2.10	2.27	0.17	2.46E-01	6.20E-01	---	---	---	239951_at	---																				
6.61	7.14	0.54	2.46E-01	6.20E-01	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	chr17p13.3	202226_s_at	NM_005206 /// NM_016823																				
2.24	2.40	0.16	2.46E-01	6.20E-01	OR8G2	olfactory receptor, family 8, subfamily G, member 2	chr11q24.2	1567058_at	NM_001007249																				
4.25	4.47	0.21	2.46E-01	6.20E-01	---	---	---	230762_at	---																				
2.90	3.05	0.15	2.46E-01	6.20E-01	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	chr20p11.2-p11.22	234946_at	NM_001114089 /// NM_001247																				
2.08	2.21	0.13	2.46E-01	6.20E-01	---	---	---	234081_at	---																				
8.34	8.68	0.33	2.46E-01	6.20E-01	TMEM106B	transmembrane protein 106B	chr7p21.3	226529_at	NM_001134232 /// NM_018374																				
2.57	2.79	0.22	2.46E-01	6.20E-01	---	---	---	234422_at	---																				
4.99	5.48	0.49	2.46E-01	6.20E-01	SLC22A18	solute carrier family 22, member 18	chr11p15.5	204981_at	NM_002555 /// NM_183233																				
2.44	2.56	0.13	2.46E-01	6.20E-01	MMD	monocyte to macrophage differentiation-associated	chr17q	244523_at	NM_012329																				
2.88	3.17	0.30	2.46E-01	6.20E-01	SEC62	SEC62 homolog (S. cerevisiae)	chr3q26.2	1552789_at	NM_003262																				
2.20	2.39	0.19	2.46E-01	6.20E-01	---	---	---	1561966_at	---																				
3.22	3.40	0.18	2.46E-01	6.20E-01	CCDC116	coiled-coil domain containing 116	chr22q11.21	1555792_a_at	NM_152612																				
3.51	3.68	0.17	2.46E-01	6.20E-01	SLC5A9	solute carrier family 5 (sodium/glucose cotransporter), member 9	chr1p33	232378_at	NM_001011547																				
4.17	4.33	0.16	2.46E-01	6.20E-01	FGF6	fibroblast growth factor 6	chr12p13	208417_at	NM_020996																				
2.54	2.74	0.20	2.46E-01	6.20E-01	---	---	---	1561453_at	---																				
2.15	2.35	0.20	2.46E-01	6.20E-01	---	---	---	232742_at	---																				
2.08	2.24	0.16	2.46E-01	6.20E-01	---	---	---	243275_at	---																				
2.51	2.66	0.15	2.46E-01	6.20E-01	TLR8	toll-like receptor 8	chrXp22	220832_at	NM_138636																				
4.10	4.36	0.26	2.46E-01	6.20E-01	PCDHB11	protocadherin beta 11	chr5q31	208504_x_at	NM_018931																				
6.34	6.57	0.23	2.46E-01	6.20E-01	ASPH	aspartate beta-hydroxylase	chr8q12.1	209135_at	NM_004318 /// NM_020164 /// NM_032466 /// NM_032467 /// NM_032468																				
3.05	3.20	0.16	2.46E-01	6.20E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	1555711_x_at	---																				
4.14	4.45	0.31	2.46E-01	6.20E-01	---	---	---	233511_at	---																				
4.46	4.73	0.28	2.46E-01	6.20E-01	KIF3C	kinesin family member 3C	chr2p23	203389_at	NM_002254																				
4.48	4.75	0.27	2.46E-01	6.20E-01	---	---	---	236066_at	---																				
3.69	3.96	0.27	2.47E-01	6.21E-01	---	---	---	1557007_a_at	---																				
2.19	2.34	0.14	2.47E-01	6.21E-01	---	---	---	241870_at	---																				
3.99	4.45	0.46	2.47E-01	6.21E-01	---	---	---	232701_at	---																				
5.54	5.90	0.36	2.47E-01	6.21E-01	FHOD3	formin homology 2 domain containing 3	chr18q12	218980_at	NM_025135																				
2.49	2.75	0.26	2.47E-01	6.21E-01	---	---	---	244422_at	---																				
2.24	2.46	0.22	2.47E-01	6.21E-01	---	---	---	1562358_at	---																				
2.18	2.37	0.19	2.47E-01	6.21E-01	SPINLW1	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	chr20q12-q13.2	206319_s_at	NM_020398 /// NM_181502																				

2.60	2.79	0.19	2.47E-01	6.21E-01	---	---	---	234196_at	---
2.56	2.72	0.16	2.47E-01	6.21E-01	---	---	---	237526_at	---
2.82	2.97	0.15	2.47E-01	6.21E-01	GATA5	GATA binding protein 5	chr20q13.33	238095_at	NM_080473
2.18	2.34	0.15	2.47E-01	6.21E-01	RTP1	receptor (chemosensory) transporter protein 1	chr3q27.3	1553823_a_at	NM_153708
2.08	2.23	0.15	2.47E-01	6.21E-01	LOC340094	hypothetical LOC340094	chr5p15.32	1557876_at	XR_040086 /// XR_040087 /// XR_040088
1.95	2.10	0.15	2.47E-01	6.21E-01	KIAA1432	KIAA1432	chr9p24.1	223825_at	NM_020829
4.40	4.96	0.55	2.47E-01	6.21E-01	TWSG1	twisted gastrulation homolog 1 (Drosophila)	chr18p11.3	219201_s_at	NM_020648
2.35	2.62	0.26	2.47E-01	6.21E-01	ZNF684	zinc finger protein 684	chr1p34.2	232563_at	NM_152373
2.89	3.12	0.23	2.47E-01	6.21E-01	ABHD9	abhydrolase domain containing 9	chr19p13.12	220013_at	NM_024794
2.88	3.06	0.17	2.47E-01	6.21E-01	---	---	---	234781_at	---
2.62	2.75	0.13	2.47E-01	6.21E-01	GH2	growth hormone 2	chr17q24.2	206195_x_at	NM_002059 /// NM_022556 /// NM_022557 /// NM_022558
2.02	2.19	0.16	2.47E-01	6.21E-01	GYS2	glycogen synthase 2 (liver)	chr12p12.2	214621_at	NM_021957
1.88	2.05	0.18	2.47E-01	6.21E-01	MED14	mediator complex subunit 14	chrXp11.4-p11.2	202612_s_at	NM_004229
7.00	7.70	0.70	2.47E-01	6.21E-01	hCG_1644608 /// SET	SET translocation (myeloid leukemia-associated) pseudogene /// SET nuclear oncogene	chr9q34 /// chrXq21.1	215780_s_at	NM_001122821 /// NM_003011
6.46	6.84	0.38	2.47E-01	6.21E-01	SHOC2	soc-2 suppressor of clear homolog (C. elegans)	chr10q25	202777_at	NM_007373
4.88	5.07	0.19	2.47E-01	6.21E-01	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	chr19q13.4	207697_x_at	NM_001080978 /// NM_005874
2.18	2.33	0.14	2.47E-01	6.21E-01	KRTAP2-1	keratin associated protein 2-1	chr17q12-q21	234691_at	NM_001123387 /// XM_001725764
4.86	5.20	0.34	2.47E-01	6.21E-01	SETMAR	SET domain and mariner transposase fusion gene	chr3p26.2	206554_x_at	NM_006515 /// NR_024022
5.72	5.99	0.26	2.47E-01	6.21E-01	APLN	Apelin	chrXq25-q26.3	244166_at	NM_017413
6.59	6.81	0.22	2.47E-01	6.21E-01	---	---	---	214223_at	---
2.36	2.51	0.15	2.47E-01	6.21E-01	---	---	---	1562730_a_at	---
2.34	2.47	0.13	2.47E-01	6.21E-01	---	---	---	1565890_at	---
4.88	5.16	0.28	2.47E-01	6.21E-01	TGM6	transglutaminase 6	chr20p13	233983_at	NM_198994
9.29	9.59	0.30	2.47E-01	6.21E-01	RHOA	ras homolog gene family, member A	chr3p21.3	1555814_a_at	NM_001664
3.38	3.59	0.22	2.47E-01	6.21E-01	FNDC8	fibronectin type III domain containing 8	chr17q12	220499_at	NM_017559
3.21	3.41	0.21	2.47E-01	6.21E-01	CRYAA	crystallin, alpha A	chr21q22.3	210199_at	NM_000394
2.18	2.34	0.16	2.47E-01	6.21E-01	FLJ37035	FLJ37035 protein	chr10q26.13	1560714_at	XR_000880 /// XR_000881 /// XR_001301 /// XR_001302
2.72	2.85	0.14	2.47E-01	6.21E-01	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	chr8p23.1	217121_at	NM_003747
4.60	4.74	0.14	2.47E-01	6.21E-01	SSPO	SCO-spondin homolog (Bos taurus)	chr7q36.1	234349_at	NM_198455
4.29	4.71	0.42	2.47E-01	6.21E-01	LPP	LIM domain containing preferred translocation partner in lipoma	chr3q28	243874_at	NM_005578
3.99	4.34	0.35	2.48E-01	6.21E-01	---	---	---	227293_at	---
4.09	4.65	0.56	2.48E-01	6.21E-01	CDK8	cyclin-dependent kinase 8	chr13q12	1553112_s_at	NM_001260
6.43	6.95	0.52	2.48E-01	6.21E-01	---	---	---	229858_at	---
7.73	8.13	0.40	2.48E-01	6.21E-01	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	chr4q21-q23	209613_s_at	NM_000668
4.52	4.69	0.17	2.48E-01	6.21E-01	---	---	---	224438_at	---
2.12	2.29	0.16	2.48E-01	6.21E-01	ATP1A4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	chr1q21-q23	1564241_at	NM_001001734 /// NM_144699
2.93	3.08	0.15	2.48E-01	6.21E-01	FLJ22662	hypothetical protein FLJ22662	chr12p13.1	222639_s_at	NM_024829
2.95	3.16	0.20	2.48E-01	6.22E-01	DOHH	Deoxyhypusine hydroxylase/monooxygenase	chr19p13.3	213949_s_at	NM_031304
6.54	7.09	0.55	2.48E-01	6.22E-01	IDE	insulin-degrading enzyme	chr10q23-q25	203327_at	NM_004969
2.54	2.72	0.18	2.48E-01	6.22E-01	C14orf106	chromosome 14 open reading frame 106	chr14q21.3	206500_s_at	NM_018353
4.95	5.21	0.26	2.48E-01	6.22E-01	CCDC75	coiled-coil domain containing 75	chr2p22.2	228495_at	NM_174931
2.67	2.90	0.23	2.48E-01	6.22E-01	HAND1	heart and neural crest derivatives expressed 1	chr5q33	220138_at	NM_004821
2.09	2.24	0.15	2.48E-01	6.22E-01	CHD9	Chromodomain helicase DNA binding protein 9	chr16q12.2	243660_at	NM_025134
2.03	2.16	0.14	2.48E-01	6.22E-01	LOC145837	hypothetical protein LOC145837	chr15q23	240838_s_at	XR_040650 /// XR_040651 /// XR_040652
4.49	4.70	0.21	2.48E-01	6.22E-01	---	---	---	240598_at	---
2.30	2.68	0.37	2.48E-01	6.22E-01	GNG4	guanine nucleotide binding protein (G protein), gamma 4	chr1q42.3	1555867_at	NM_001098721 /// NM_001098722 /// NM_004485
8.08	8.64	0.56	2.48E-01	6.22E-01	UBE3A	ubiquitin protein ligase E3A	chr15q11-q13	211285_s_at	NM_000462 /// NM_130838 /// NM_130839
7.71	8.36	0.65	2.48E-01	6.22E-01	COL4A1	collagen, type IV, alpha 1	chr13q34	211980_at	NM_001845

2.40	2.87	0.48	2.48E-01	6.22E-01	GNG4	guanine nucleotide binding protein (G protein), gamma 4	chr1q42.3	1555765_a_at	NM_001098721 /// NM_001098722 /// NM_004485
4.34	4.66	0.31	2.48E-01	6.22E-01	---	---	---	1558822_at	---
2.89	3.15	0.27	2.48E-01	6.22E-01	---	---	---	234645_at	---
6.81	7.06	0.25	2.48E-01	6.22E-01	MAPK14	mitogen-activated protein kinase 14	chr6p21.3-p21.2	202530_at	NM_001315 /// NM_139012 /// NM_139013 /// NM_139014
2.34	2.58	0.24	2.48E-01	6.22E-01	---	---	---	241917_at	---
3.22	3.44	0.22	2.48E-01	6.22E-01	KCMF1	potassium channel modulatory factor 1	chr2p11.2	240430_at	NM_020122
3.00	3.22	0.22	2.48E-01	6.22E-01	---	---	---	239560_at	---
2.65	2.87	0.21	2.48E-01	6.22E-01	KREMEN1	kringle containing transmembrane protein 1	chr22q12.1	224534_at	NM_001039570 /// NM_001039571
3.10	3.30	0.20	2.48E-01	6.22E-01	C16orf42	chromosome 16 open reading frame 42	chr16p13.3	214067_at	NM_001001410
6.48	6.68	0.20	2.48E-01	6.22E-01	KCTD17	potassium channel tetramerisation domain containing 17	chr22q12.3	205561_at	NM_024681
2.69	2.89	0.20	2.48E-01	6.22E-01	---	---	---	1562482_at	---
2.03	2.22	0.19	2.48E-01	6.22E-01	HTN3	histatin 3	chr4q13	206786_at	NM_000200
3.75	3.94	0.19	2.48E-01	6.22E-01	C19orf42	chromosome 19 open reading frame 42	chr19p13.11	1559382_at	NM_024104
2.53	2.71	0.17	2.48E-01	6.22E-01	---	---	---	237077_at	---
3.20	3.38	0.17	2.48E-01	6.22E-01	---	---	---	216776_at	---
2.88	3.06	0.17	2.48E-01	6.22E-01	ASCL1	achaete-scute complex homolog 1 (Drosophila)	chr12q23.2	213768_s_at	NM_004316
3.72	3.89	0.17	2.48E-01	6.22E-01	CEP170 /// CEP170L	centrosomal protein 170kDa /// centrosomal protein 170kDa-like	chr1q44 /// chr4q26	1552717_s_at	NM_001042404 /// NM_001042405 /// NM_014812 /// NR_003135 /// XR_042148 /// XR_042173
2.20	2.35	0.14	2.48E-01	6.22E-01	---	---	---	240492_at	---
2.18	2.31	0.13	2.48E-01	6.22E-01	---	---	---	1557336_at	---
1.89	2.03	0.13	2.48E-01	6.22E-01	C6orf103	chromosome 6 open reading frame 103	chr6q24.3	220614_s_at	NM_024694 /// XM_001716966 /// XM_929679 /// XM_941958
2.28	2.42	0.13	2.48E-01	6.22E-01	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	chr11p13-p12	1558010_s_at	NM_004171
1.85	1.98	0.13	2.48E-01	6.22E-01	---	---	---	1557683_at	---
2.42	2.55	0.13	2.48E-01	6.22E-01	---	---	---	238414_at	---
2.00	2.17	0.17	2.48E-01	6.22E-01	---	---	---	1558661_at	---
2.37	2.54	0.17	2.49E-01	6.22E-01	HLA-C /// IGKC /// IGKV1-5 /// LOC100130100 /// LOC647506 /// LOC650405 /// LOC652493 /// LOC652694	major histocompatibility complex, class I, C /// immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5 /// similar to hCG26659 /// similar to Ig kappa chain V-I region HK101 precursor /// similar to Ig kappa chain V-I region HK102 precursor /// similar to Ig kappa chain V-I region HK102 precursor /// similar to Ig kappa chain V-I region HK102 precursor	chr2p12 /// chr2q14.1 /// chr6p21.3	216517_at	NM_002117 /// XM_001713938 /// XM_001715827 /// XM_001715881 /// XM_001716310 /// XM_001716615 /// XM_001717045 /// XM_001719879 /// XM_001724425 /// XM_942302
2.15	2.28	0.13	2.49E-01	6.22E-01	DTYMK	Deoxythymidylate kinase (thymidylate kinase)	chr2q37.3	1565693_at	NM_012145
2.62	2.83	0.22	2.49E-01	6.22E-01	LOC100129296	hypothetical protein LOC100129296	chr2p24.3	242026_at	XM_001715416
3.72	4.12	0.40	2.49E-01	6.22E-01	CCDC128	coiled-coil domain containing 128	chr2p16.3	1554145_a_at	NM_152994
5.08	5.36	0.28	2.49E-01	6.22E-01	NIN	ninein (GSK3B interacting protein)	chr14q22.1	225921_at	NM_016350 /// NM_020921 /// NM_182944 /// NM_182946
2.38	2.56	0.17	2.49E-01	6.22E-01	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	chr4q31.22	242702_at	NM_172250
1.97	2.13	0.15	2.49E-01	6.22E-01	LOC285965	hypothetical protein LOC285965	chr7q35	1562249_at	---
1.92	2.07	0.15	2.49E-01	6.22E-01	ERICH1	Glutamate-rich 1	chr8p23.3	242003_at	NM_207332
2.08	2.22	0.15	2.49E-01	6.22E-01	---	---	---	215422_at	---
2.30	2.44	0.14	2.49E-01	6.22E-01	---	---	---	238371_s_at	---
2.96	3.10	0.14	2.49E-01	6.22E-01	C7orf34	chromosome 7 open reading frame 34	chr7q34	1555757_at	NM_178829

2.91	3.04	0.14	2.49E-01	6.22E-01	---	---	---	216528_at	---
1.93	2.10	0.16	2.49E-01	6.22E-01	---	---	---	243666_at	---
2.81	2.99	0.18	2.49E-01	6.23E-01	CHRNA10	cholinergic receptor, nicotinic, alpha 10	chr11p15.5	220210_at	NM_020402
6.34	6.98	0.64	2.49E-01	6.23E-01	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	chr4q31.1-q31.2	202303_x_at	NM_003601
4.49	5.23	0.74	2.49E-01	6.23E-01	---	---	---	241509_at	---
10.96	11.33	0.38	2.49E-01	6.23E-01	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	chr10p15.1	208870_x_at	NM_001001973 /// NM_005174
3.49	3.76	0.26	2.49E-01	6.23E-01	ATG16L1	ATG16 autophagy related 16-like 1 (S. cerevisiae)	chr2q37.1	220521_s_at	NM_017974 /// NM_030803
3.56	3.80	0.24	2.49E-01	6.23E-01	ZDHHC18	Zinc finger, DHHC-type containing 18	chr1p36.11	231900_at	NM_032283
4.01	4.21	0.20	2.49E-01	6.23E-01	---	---	---	1566974_at	---
2.07	2.27	0.19	2.49E-01	6.23E-01	---	---	---	234957_at	---
3.36	3.53	0.17	2.49E-01	6.23E-01	---	---	---	1560353_at	---
2.22	2.39	0.17	2.49E-01	6.23E-01	LOC729298 /// PCNP	similar to PEST proteolytic signal containing nuclear protein /// PEST proteolytic signal containing nuclear protein	chr12q14.3 /// chr3q12.3	237577_at	NM_020357 /// XR_015503 /// XR_015556 /// XR_039124
4.08	4.25	0.17	2.49E-01	6.23E-01	HEMK1	HemK methyltransferase family member 1	chr3p21.3	1556092_s_at	NM_016173
2.06	2.23	0.17	2.49E-01	6.23E-01	---	---	---	217697_at	---
1.88	2.04	0.15	2.49E-01	6.23E-01	LOC729806	similar to hCG1725380	chr1q44	217544_at	XR_037671 /// XR_037682 /// XR_037719
2.47	2.62	0.15	2.49E-01	6.23E-01	C20orf114	chromosome 20 open reading frame 114	chr20q11.21	226067_at	NM_033197
1.74	1.89	0.15	2.49E-01	6.23E-01	ZNF80	zinc finger protein 80	chr3q13.3	207272_at	NM_007136
5.18	5.43	0.25	2.49E-01	6.23E-01	HHLA1	HERV-H LTR-associating 1	chr8q24	221162_at	XR_040231 /// XR_040232 /// XR_040233
2.35	2.56	0.21	2.49E-01	6.23E-01	---	---	---	1556676_a_at	---
3.91	4.08	0.16	2.49E-01	6.23E-01	ADPRH	ADP-ribosylarginine hydrolase	chr3q13.31-q13.33	238505_at	NM_001125
2.05	2.20	0.15	2.49E-01	6.23E-01	IFNA2	interferon, alpha 2	chr9p22	211338_at	NM_000605
8.92	9.33	0.41	2.49E-01	6.23E-01	SDCBP	syndecan binding protein (syntenin)	chr8q12	200958_s_at	NM_001007067 /// NM_001007068 /// NM_001007069 /// NM_001007070 /// NM_005625
5.81	6.17	0.36	2.49E-01	6.23E-01	SLC35B4	solute carrier family 35, member B4	chr7q33	238418_at	NM_032826
5.47	5.88	0.42	2.50E-01	6.23E-01	41528	septin 11	chr4q21.1	201307_at	NM_018243
3.48	3.78	0.31	2.50E-01	6.23E-01	RICTOR	rapamycin-insensitive companion of mTOR	chr5p13.1	226310_at	NM_152756
8.13	8.67	0.54	2.50E-01	6.23E-01	SUB1	SUB1 homolog (S. cerevisiae)	chr5p13.3	214512_s_at	NM_006713
5.34	5.54	0.21	2.50E-01	6.23E-01	HMGA1	high mobility group AT-hook 1	chr6p21	210457_x_at	NM_002131 /// NM_145899 /// NM_145901 /// NM_145902 /// NM_145903 /// NM_145904 /// NM_145905
2.70	2.87	0.17	2.50E-01	6.23E-01	---	---	---	242860_at	---
2.98	3.26	0.27	2.50E-01	6.23E-01	PCM1	pericentriolar material 1	chr8p22-p21.3	209996_x_at	NM_006197
3.22	3.37	0.15	2.50E-01	6.23E-01	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	chr10q24.31	221000_s_at	NM_030929
5.55	6.08	0.54	2.50E-01	6.23E-01	ECHDC1	enoyl Coenzyme A hydratase domain containing 1	chr6q22.33	219974_x_at	NM_001002030 /// NM_001105544 /// NM_001105545 /// NM_018479
2.78	3.01	0.23	2.50E-01	6.23E-01	CYP3A4	Cytochrome P450, family 3, subfamily A, polypeptide 4	chr7q21.1	231704_at	NM_017460
5.57	6.43	0.87	2.50E-01	6.23E-01	---	---	---	240120_at	---
3.98	4.30	0.32	2.50E-01	6.23E-01	HPX	hemopexin	chr11p15.5-p15.4	210013_at	NM_000613
2.84	3.03	0.18	2.50E-01	6.23E-01	LASS3	LAG1 homolog, ceramide synthase 3	chr15q26.3	1554253_a_at	NM_178842
2.31	2.45	0.14	2.50E-01	6.23E-01	---	---	---	243226_at	---
3.63	4.03	0.40	2.50E-01	6.23E-01	FLI1	Friend leukemia virus integration 1	chr11q24.1-q24.3	204236_at	NM_002017
6.97	7.58	0.60	2.50E-01	6.24E-01	SYAP1	synapse associated protein 1, SAP47 homolog (Drosophila)	chrXp22.2	225154_at	NM_032796
2.34	2.57	0.23	2.50E-01	6.24E-01	LOC285628	hypothetical protein LOC285628	chr5q34	232504_at	---
2.40	2.61	0.20	2.50E-01	6.24E-01	FLJ13744	hypothetical protein FLJ13744	chr6q14	1553413_at	---
2.23	2.38	0.14	2.50E-01	6.24E-01	KIF6	kinesin family member 6	chr6p21.2	232695_at	NM_145027
7.37	7.72	0.35	2.50E-01	6.24E-01	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	chr17q21.2	211988_at	NM_003079
4.73	5.16	0.43	2.50E-01	6.24E-01	---	---	---	232929_at	---

2.27	2.45	0.18	2.50E-01	6.24E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	229221_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392
1.95	2.09	0.13	2.50E-01	6.24E-01	ADAM22	ADAM metallopeptidase domain 22	chr7q21	1555024_at	NM_004194 /// NM_016351 /// NM_021721 /// NM_021722 /// NM_021723
3.17	3.44	0.27	2.51E-01	6.24E-01	ADCY8 /// LOC100134077	adenylate cyclase 8 (brain) /// similar to adenylyl cyclase	chr8q24	206811_at	NM_001115 /// XM_001713841
2.28	2.44	0.16	2.51E-01	6.25E-01	MAP3K2	mitogen-activated protein kinase kinase kinase 2	chr2q14.3	1565130_at	NM_006609
8.27	8.87	0.59	2.51E-01	6.25E-01	EBP	emopamil binding protein (sterol isomerase)	chrXp11.23-p11.22	213787_s_at	NM_006579
2.09	2.24	0.16	2.51E-01	6.25E-01	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	chr2q33.1	1555284_at	NM_020919
2.70	2.86	0.16	2.51E-01	6.25E-01	ANGPTL7	angiopoietin-like 7	chr1p36.3-p36.2	206423_at	NM_021146
2.11	2.28	0.17	2.51E-01	6.25E-01	LOC100129266	Hypothetical protein LOC100129266	chr15q15.1	1557863_at	XM_001715005 /// XM_001717532 /// XM_001719008
3.90	4.20	0.30	2.51E-01	6.25E-01	---	---	---	234723_x_at	---
2.42	2.54	0.11	2.51E-01	6.25E-01	---	---	---	237574_at	---
7.09	7.32	0.23	2.51E-01	6.25E-01	CCDC107	coiled-coil domain containing 107	chr9p13.3	229063_s_at	NM_174923
2.96	3.13	0.17	2.51E-01	6.25E-01	ZNRF2	zinc and ring finger 2	chr7p15.1	226261_at	NM_147128
2.54	2.70	0.17	2.51E-01	6.25E-01	MC4R	melanocortin 4 receptor	chr18q22	221467_at	NM_005912
2.17	2.34	0.17	2.51E-01	6.25E-01	---	---	---	243923_at	---
2.09	2.24	0.15	2.51E-01	6.25E-01	DGKE	diacylglycerol kinase, epsilon 64kDa	chr17q22	207518_at	NM_003647
3.21	3.44	0.23	2.51E-01	6.25E-01	VAV3	vav 3 guanine nucleotide exchange factor	chr1p13.3	218807_at	NM_001079874 /// NM_006113
2.01	2.22	0.22	2.51E-01	6.25E-01	PRO2012	hypothetical protein PRO2012	chr1q42.13	220883_at	---
2.95	3.14	0.18	2.51E-01	6.25E-01	LMTK3	lemur tyrosine kinase 3	chr19q13.32	1557103_a_at	NM_001080434
2.10	2.29	0.19	2.51E-01	6.25E-01	LOC401134	hypothetical gene supported by BC040544	chr4q13.1	1557823_s_at	---
2.02	2.14	0.12	2.51E-01	6.25E-01	SHANK2	SH3 and multiple ankyrin repeat domains 2	chr11q13.3	243681_at	NM_012309 /// NM_133266
4.53	4.99	0.45	2.51E-01	6.25E-01	NCOA2	Nuclear receptor coactivator 2	chr8q13.3	215605_at	NM_006540
2.50	2.76	0.26	2.51E-01	6.25E-01	KRT40 /// LOC728760	keratin 40 /// similar to type I hair keratin KA36	chr17q21.2	1562629_a_at	NM_182497 /// XM_001722603
3.88	4.08	0.20	2.51E-01	6.25E-01	IHH	Indian hedgehog homolog (Drosophila)	chr2q33-q35	229358_at	NM_002181
3.53	3.68	0.15	2.51E-01	6.25E-01	CP110	CP110 protein	chr16p12.3	204662_at	NM_014711
2.71	2.86	0.15	2.51E-01	6.25E-01	SNX18	sorting nexin 18	chr5q11.2	1552828_at	NM_001102575 /// NM_052870
2.62	2.77	0.15	2.51E-01	6.25E-01	---	---	---	1559437_at	---
2.26	2.41	0.14	2.51E-01	6.25E-01	LOC642587	NPC-A-5	chr1q32.2	226755_at	NM_001104548
2.83	2.94	0.12	2.51E-01	6.25E-01	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	chr19pter-p13.11	210452_x_at	NM_001082
3.06	3.26	0.20	2.51E-01	6.25E-01	TBC1D21	TBC1 domain family, member 21	chr15q24.1	231475_at	NM_153356
9.05	9.55	0.50	2.52E-01	6.26E-01	CCNG1	cyclin G1	chr5q32-q34	208796_s_at	NM_004060 /// NM_199246
2.44	2.65	0.21	2.52E-01	6.26E-01	MCF2	MCF.2 cell line derived transforming sequence	chrXq27	214884_at	NM_001099855 /// NM_005369
2.60	2.83	0.22	2.52E-01	6.26E-01	---	---	---	240956_at	---
5.65	5.89	0.24	2.52E-01	6.26E-01	C1orf86	chromosome 1 open reading frame 86	chr1p36.33	236499_at	NM_182533 /// XM_001718861
2.80	2.99	0.19	2.52E-01	6.26E-01	MIAT	myocardial infarction associated transcript (non-protein coding)	chr22q12.1	228658_at	NR_003491
3.68	3.90	0.21	2.52E-01	6.26E-01	BTRC	beta-transducin repeat containing	chr10q24.32	216091_s_at	NM_003939 /// NM_033637
4.13	4.33	0.20	2.52E-01	6.26E-01	---	---	---	241058_at	---
9.10	9.68	0.58	2.52E-01	6.26E-01	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	chr12q24.2-q24.3	200599_s_at	NM_003299
2.04	2.22	0.18	2.52E-01	6.26E-01	---	---	---	1554232_a_at	---
3.55	3.79	0.24	2.52E-01	6.26E-01	METTL7B	methyltransferase like 7B	chr12q13.2	227055_at	NM_152637
4.82	5.02	0.20	2.52E-01	6.26E-01	UBTD1	ubiquitin domain containing 1	chr10q24.1	219172_at	NM_024954

2.05	2.24	0.19	2.52E-01	6.26E-01	CCNA1	cyclin A1	chr13q12.3-q13	205899_at	NM_001111045 /// NM_001111046 /// NM_001111047 /// NM_003914
1.84	2.00	0.16	2.52E-01	6.26E-01	EAF2	ELL associated factor 2	chr3q13.33	1568672_at	NM_018456
4.51	4.74	0.23	2.52E-01	6.26E-01	MPZL1	myelin protein zero-like 1	chr1q24.2	210210_at	NM_003953 /// NM_024569
2.03	2.18	0.15	2.52E-01	6.26E-01	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	chr17q11.1-q11.2	234168_at	NM_003487 /// NM_139215
2.01	2.28	0.26	2.52E-01	6.26E-01	FAM40B	family with sequence similarity 40, member B	chr7q32.1	1555292_at	NM_001134336 /// NM_020704
5.16	5.41	0.25	2.52E-01	6.26E-01	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	chr11q13.3	202065_s_at	NM_003626 /// NM_177423
3.77	4.00	0.22	2.52E-01	6.27E-01	ELN	elastin	chr7q11.23	216269_s_at	NM_000501 /// NM_001081752 /// NM_001081753 /// NM_001081754 /// NM_001081755
2.97	3.29	0.32	2.52E-01	6.27E-01	RNPC3	RNA-binding region (RNP1, RRM) containing 3	chr1p21	226999_at	NM_017619
3.06	3.30	0.24	2.52E-01	6.27E-01	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	chr2q33.3	1557719_at	NM_015040 /// NM_152671
3.39	3.58	0.19	2.52E-01	6.27E-01	---	---	---	231125_at	---
4.78	5.14	0.37	2.53E-01	6.27E-01	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	chr5q31.3	201866_s_at	NM_000176 /// NM_001018074 /// NM_001018075 /// NM_001018076 /// NM_001018077 /// NM_001020825 /// NM_001024094
7.48	7.82	0.34	2.53E-01	6.27E-01	LYRM5	LYR motif containing 5	chr12p12.1	225469_at	NM_001001660
3.25	3.59	0.34	2.52E-01	6.27E-01	FLJ41603	FLJ41603 protein	chr5q33.1	227717_at	NM_001001669
3.41	3.65	0.25	2.53E-01	6.27E-01	RNF12	Ring finger protein 12	chrXq13-q21	244470_at	NM_016120 /// NM_183353
3.41	3.62	0.22	2.53E-01	6.27E-01	TTC17	Tetratricopeptide repeat domain 17	chr11p12-p11.2	232646_at	NM_018259
2.75	2.97	0.22	2.53E-01	6.27E-01	---	---	---	237185_at	---
3.00	3.19	0.19	2.52E-01	6.27E-01	---	---	---	234857_at	---
2.30	2.49	0.19	2.53E-01	6.27E-01	---	---	---	1562229_at	---
4.00	4.18	0.17	2.53E-01	6.27E-01	KCNK16	potassium channel, subfamily K, member 16	chr6p21.2-p21.1	234554_at	NM_032115
2.30	2.47	0.17	2.53E-01	6.27E-01	C6orf138	chromosome 6 open reading frame 138	chr6p12.3	234689_at	NM_001013732
2.25	2.41	0.17	2.52E-01	6.27E-01	FAM18A	family with sequence similarity 18, member A	chr16p13.13	1563638_at	NM_001079512
1.73	1.87	0.14	2.53E-01	6.27E-01	---	---	---	237937_x_at	---
2.31	2.44	0.12	2.52E-01	6.27E-01	---	---	---	1565918_a_at	---
3.65	3.93	0.28	2.53E-01	6.27E-01	---	---	---	215147_at	---
2.01	2.15	0.13	2.53E-01	6.27E-01	ZNF214	zinc finger protein 214	chr11p15.4	220497_at	NM_013249
5.87	6.17	0.30	2.53E-01	6.27E-01	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	chr3q21.1	212640_at	NM_198402
2.87	3.12	0.25	2.53E-01	6.27E-01	KNDC1	kinase non-catalytic C-lobe domain (KIND) containing 1	chr10q26.3	233146_at	NM_152643
2.28	2.43	0.15	2.53E-01	6.27E-01	CNTLN	centlein, centrosomal protein	chr9p22.2	241696_at	NM_001114395 /// NM_017738
6.22	6.41	0.19	2.53E-01	6.27E-01	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	chr5q31.1	210228_at	NM_000758
3.97	4.58	0.61	2.53E-01	6.27E-01	---	---	---	215206_at	---
1.95	2.08	0.14	2.53E-01	6.27E-01	ADAM3A	ADAM metallopeptidase domain 3A (cyritestin 1)	chr8p11.23	216276_s_at	NR_001569 /// NR_024106 /// NR_024107
4.10	4.31	0.21	2.53E-01	6.27E-01	GAS2L1	growth arrest-specific 2 like 1	chr22q12.2	208258_s_at	NM_006478 /// NM_152236 /// NM_152237
2.29	2.45	0.15	2.53E-01	6.27E-01	PDSS1	Prenyl (decaprenyl) diphosphate synthase, subunit 1	chr10p12.1	236298_at	NM_014317
4.35	4.55	0.20	2.53E-01	6.27E-01	NOX1	NADPH oxidase 1	chrXq22	210808_s_at	NM_007052 /// NM_013955
2.13	2.31	0.17	2.53E-01	6.27E-01	---	---	---	216732_at	---

2.16	2.30	0.14	2.53E-01	6.27E-01	---	---	---	236253_at	---
2.00	2.12	0.12	2.53E-01	6.27E-01	HSD17B12	Hydroxysteroid (17-beta) dehydrogenase 12	chr11p11.2	1559518_at	NM_016142
6.18	6.69	0.51	2.53E-01	6.27E-01	PURB	purine-rich element binding protein B	chr7p13	225120_at	NM_033224
3.30	3.57	0.27	2.53E-01	6.27E-01	---	---	---	235394_at	---
2.25	2.43	0.18	2.53E-01	6.27E-01	C1orf87	chromosome 1 open reading frame 87	chr1p32.1	236710_at	NM_152377
1.97	2.12	0.15	2.53E-01	6.27E-01	---	---	---	1560349_at	---
3.42	3.57	0.14	2.53E-01	6.27E-01	RBM9	RNA binding motif protein 9	chr22q13.1	213898_at	NM_001031695 /// NM_001082576 /// NM_001082577 /// NM_001082578 /// NM_001082579 /// NM_014309
1.97	2.10	0.13	2.53E-01	6.27E-01	SYT1	synaptotagmin I	chr12cen-q21	203998_s_at	NM_005639
5.73	5.93	0.20	2.53E-01	6.27E-01	LOC645431	hypothetical LOC645431	chr14q23.3	242889_x_at	XR_015289 /// XR_015673 /// XR_040487
4.73	4.96	0.23	2.53E-01	6.27E-01	TCP11L1	t-complex 11 (mouse)-like 1	chr11p13	205797_s_at	NM_018393
3.71	3.93	0.22	2.53E-01	6.27E-01	CLP1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	chr11q12	229496_at	NM_006831
2.99	3.20	0.21	2.53E-01	6.27E-01	C17orf88	chromosome 17 open reading frame 88	chr17q21.31	221129_at	XR_017759 /// XR_017911 /// XR_041640
3.72	3.92	0.20	2.53E-01	6.27E-01	---	---	---	237146_at	---
3.38	3.57	0.19	2.53E-01	6.27E-01	---	---	---	1562728_at	---
5.05	5.24	0.19	2.53E-01	6.27E-01	---	---	---	243629_x_at	---
2.86	3.05	0.18	2.53E-01	6.27E-01	---	---	---	222145_at	---
3.35	3.51	0.16	2.53E-01	6.27E-01	C21orf134	chromosome 21 open reading frame 134	chr21q22.3	1562034_at	---
2.18	2.34	0.15	2.53E-01	6.27E-01	FRYL	FRY-like	chr4p12	1562650_at	NM_015030
1.76	1.88	0.13	2.53E-01	6.27E-01	CENPI	centromere protein I	chrXq22.1	1555046_at	NM_006733
6.38	6.65	0.27	2.53E-01	6.27E-01	ZDHHC24	zinc finger, DHHC-type containing 24	chr11q13.1	205634_x_at	NM_207340
2.55	2.75	0.20	2.53E-01	6.27E-01	---	---	---	1569670_at	---
4.42	4.90	0.48	2.53E-01	6.27E-01	ZCCHC6	Zinc finger, CCHC domain containing 6	chr9q21	236243_at	NM_024617
2.33	2.52	0.19	2.53E-01	6.27E-01	MTL5	Metallothionein-like 5, testis-specific (tesmin)	chr11q13.2-q13.3	238246_at	NM_001039656 /// NM_004923
2.82	2.99	0.17	2.53E-01	6.27E-01	---	---	---	239306_at	---
3.00	3.15	0.15	2.53E-01	6.27E-01	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	211882_x_at	NM_000150 /// NM_001040701
1.60	1.73	0.12	2.53E-01	6.27E-01	---	---	---	1562916_at	---
2.18	2.33	0.16	2.53E-01	6.27E-01	LOC100130855	hypothetical protein LOC100130855	chr15q22.31	1562738_a_at	XM_001719369 /// XM_001723958 /// XM_001725745
5.95	6.18	0.23	2.54E-01	6.27E-01	KLC3	kinesin light chain 3	chr19q13.2-q13.3	1552749_a_at	NM_177417
6.36	7.49	1.13	2.54E-01	6.28E-01	RGS5	regulator of G-protein signaling 5	chr1q23.1	1555725_a_at	NM_003617
4.18	4.36	0.19	2.54E-01	6.28E-01	AKNA	AT-hook transcription factor	chr9q32	237715_at	NM_030767
3.09	3.39	0.30	2.54E-01	6.28E-01	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	chr1p34.1	211580_s_at	NM_001114172 /// NM_003629
2.80	3.07	0.27	2.54E-01	6.28E-01	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	chr3q26.1	210471_s_at	NM_003471 /// NM_172159 /// NM_172160
5.65	5.86	0.21	2.54E-01	6.28E-01	C1orf92	chromosome 1 open reading frame 92	chr1q23.1	237251_at	NM_144702
6.17	6.43	0.27	2.54E-01	6.28E-01	---	---	---	AFFX-r2-Ec-bioB-5_at	---
2.99	3.20	0.21	2.54E-01	6.28E-01	---	---	---	240761_at	---
1.81	1.95	0.14	2.54E-01	6.28E-01	LOC100130423 /// SUGT1L1	similar to SGT1, suppressor of G2 allele of SKP1 like 1 (S. cerevisiae) /// SGT1, suppressor of G2 allele of SKP1 like 1 (S. cerevisiae)	chr13q14.11	1554142_at	NR_003365 /// XM_001718775 /// XM_001721699 /// XM_001725074
2.20	2.36	0.17	2.54E-01	6.28E-01	---	---	---	242007_at	---
3.89	4.12	0.24	2.54E-01	6.28E-01	C1orf183	chromosome 1 open reading frame 183	chr1p13.2	229382_at	NM_019099 /// NM_198926
3.03	3.21	0.18	2.54E-01	6.28E-01	DKFZp434E1119	hypothetical protein DKFZp434E1119	chr11q14.1	1565771_at	XM_001717558 /// XM_495888

6.32	6.81	0.49	2.54E-01	6.28E-01	COX11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	chr17q22	211727_s_at	NM_004375
6.40	6.65	0.25	2.54E-01	6.28E-01	C9orf6	chromosome 9 open reading frame 6	chr9q31.3	218998_at	NM_017832
2.40	2.55	0.15	2.54E-01	6.28E-01	C12orf66	chromosome 12 open reading frame 66	chr12q14.2	1554068_s_at	NM_152440
1.83	1.96	0.13	2.54E-01	6.28E-01	LOC158381	ATPase, Class I, type 8B family pseudogene	chr9p13.3	1568686_at	NR_003581 /// NR_003582
3.28	3.88	0.60	2.54E-01	6.28E-01	IGL@ /// IGLC1 /// IGLV2-11 /// IGLV2-18 /// IGLV2-23	immunoglobulin lambda locus /// immunoglobulin lambda constant 1 (Mcg marker) /// immunoglobulin lambda variable 2-11 /// immunoglobulin lambda variable 2-18 /// immunoglobulin lambda variable 2-23	chr22q11.1-q11.2 /// chr22q11.2	217235_x_at	---
4.30	4.48	0.18	2.54E-01	6.28E-01	CCDC61	coiled-coil domain containing 61	chr19q13.32	228887_x_at	NM_001080402
3.32	3.50	0.17	2.54E-01	6.28E-01	CHRM3	cholinergic receptor, muscarinic 3	chr1q43	1564339_a_at	NM_000740
2.57	2.68	0.11	2.54E-01	6.28E-01	COL6A1	collagen, type VI, alpha 1	chr21q22.3	216904_at	NM_001848
6.82	7.30	0.48	2.54E-01	6.28E-01	---	---	---	229713_at	---
6.05	6.66	0.61	2.55E-01	6.28E-01	HAT1	histone acetyltransferase 1	chr2q31.2-q33.1	203138_at	NM_001033085 /// NM_003642
3.80	4.09	0.29	2.55E-01	6.28E-01	---	---	---	1558467_a_at	---
3.45	3.70	0.25	2.54E-01	6.28E-01	LTB	Lymphotoxin beta (TNF superfamily, member 3)	chr6p21.3	1559754_at	NM_002341 /// NM_009588
2.79	3.01	0.22	2.55E-01	6.28E-01	MYO15A	myosin XVA	chr17p11.2	220288_at	NM_016239
3.00	3.22	0.22	2.54E-01	6.28E-01	UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)	chr2q31.1	235265_at	NM_172070
2.23	2.45	0.21	2.54E-01	6.28E-01	NUP62CL	nucleoporin 62kDa C-terminal like	chrXq22.3	232960_at	NM_017681
2.71	2.91	0.19	2.55E-01	6.28E-01	LOC650794	Similar to FRAS1 related extracellular matrix protein 2	chr13q12.11	240436_at	XM_001716126 /// XM_370711 /// XM_939879
8.38	8.57	0.19	2.55E-01	6.28E-01	C15orf24	chromosome 15 open reading frame 24	chr15q14	217898_at	NM_020154
1.97	2.14	0.17	2.54E-01	6.28E-01	CASP8AP2	CASP8 associated protein 2	chr6q15	1570001_at	NM_012115
2.41	2.57	0.16	2.54E-01	6.28E-01	LOC728099	hypothetical protein LOC728099	chr13q12.11	1561218_s_at	XR_015256
2.16	2.32	0.16	2.55E-01	6.28E-01	---	---	---	1564882_at	---
1.93	2.08	0.14	2.55E-01	6.28E-01	---	---	---	1570633_at	---
1.86	1.99	0.14	2.55E-01	6.28E-01	---	---	---	1562082_at	---
3.70	3.99	0.29	2.55E-01	6.29E-01	TRPM7	transient receptor potential cation channel, subfamily M, member 7	chr15q21	223323_x_at	NM_017672
2.76	2.97	0.21	2.55E-01	6.29E-01	SCFD1	sec1 family domain containing 1	chr14q12	233229_at	NM_016106 /// NM_182835
2.16	2.33	0.17	2.55E-01	6.29E-01	---	---	---	1570191_at	---
5.73	6.00	0.27	2.55E-01	6.29E-01	GCDH	glutaryl-Coenzyme A dehydrogenase	chr19p13.2	208369_s_at	NM_000159 /// NM_013976
2.46	2.62	0.16	2.55E-01	6.29E-01	---	---	---	241284_at	---
1.93	2.10	0.17	2.55E-01	6.29E-01	NBLA00301	Nbla00301	chr4q34.1	236141_at	NR_003679
7.18	7.57	0.38	2.55E-01	6.29E-01	NRIP1	nuclear receptor interacting protein 1	chr21q11.2	202599_s_at	NM_003489
2.31	2.46	0.14	2.55E-01	6.29E-01	GFAP	glial fibrillary acidic protein	chr17q21	229259_at	NM_001131019 /// NM_002055
5.76	6.52	0.76	2.55E-01	6.29E-01	HSPA4	heat shock 70kDa protein 4	chr5q31.1-q31.2	211015_s_at	NM_002154
8.74	9.11	0.37	2.55E-01	6.29E-01	TCF4	transcription factor 4	chr18q21.1	212386_at	NM_001083962 /// NM_003199
4.06	4.40	0.34	2.55E-01	6.29E-01	SLC36A4	solute carrier family 36 (proton/amino acid symporter), member 4	chr11q21	234978_at	NM_152313
3.21	3.43	0.23	2.55E-01	6.29E-01	RP11-93B14.6	hypothetical protein FLJ32154	chr20q13.33	235933_at	XM_001724364 /// XM_928933 /// XM_940524
3.26	3.49	0.22	2.55E-01	6.29E-01	KIAA1683	KIAA1683	chr19p13.1	223600_s_at	NM_025249
4.39	4.58	0.18	2.55E-01	6.29E-01	U2AF1	U2 small nuclear RNA auxiliary factor 1	chr21q22.3	232141_at	NM_001025203 /// NM_001025204 /// NM_006758
2.72	2.89	0.18	2.55E-01	6.29E-01	LOC153346	hypothetical protein LOC153346	chr5q33.1	232181_at	---
3.06	3.23	0.17	2.55E-01	6.29E-01	BCORL1	BCL6 co-repressor-like 1	chrXq25-q26.1	234711_s_at	NM_021946
4.14	4.31	0.17	2.55E-01	6.29E-01	PIP	prolactin-induced protein	chr7q34	206509_at	NM_002652
2.48	2.63	0.15	2.55E-01	6.29E-01	GLRA3	glycine receptor, alpha 3	chr4q33-q34	216021_s_at	NM_001042543 /// NM_006529
2.98	3.13	0.15	2.55E-01	6.29E-01	LOC284379	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 pseudogene	chr19q13.41	1569006_at	NR_002938
2.32	2.51	0.18	2.55E-01	6.29E-01	---	---	---	1557514_a_at	---
2.96	3.14	0.19	2.55E-01	6.29E-01	---	---	---	229780_at	---
2.02	2.19	0.17	2.55E-01	6.29E-01	---	---	---	233793_at	---
2.79	3.25	0.46	2.55E-01	6.29E-01	ILDR1	immunoglobulin-like domain containing receptor 1	chr3q13.33	235583_at	NM_175924
2.22	2.40	0.18	2.55E-01	6.29E-01	UNC5A	unc-5 homolog A (C. elegans)	chr5q35.2	236448_at	NM_133369

2.31	2.54	0.23	2.55E-01	6.29E-01	---	---	---	240829_at	---
3.23	3.41	0.18	2.55E-01	6.29E-01	ESRRB	estrogen-related receptor beta	chr14q24.3	223858_at	NM_004452
1.82	2.00	0.17	2.55E-01	6.29E-01	---	---	---	1562286_at	---
2.91	3.08	0.17	2.55E-01	6.29E-01	---	---	---	243408_at	---
2.07	2.22	0.15	2.55E-01	6.29E-01	LMO3	LIM domain only 3 (rhombotin-like 2)	chr12p12.3	1565937_a_at	NM_001001395 /// NM_018640
3.90	4.08	0.18	2.55E-01	6.29E-01	---	---	---	242619_x_at	---
3.04	3.31	0.27	2.56E-01	6.30E-01	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	chr15q24	1554992_at	NM_002891 /// NM_153815
1.80	1.93	0.13	2.56E-01	6.30E-01	SLC30A5	solute carrier family 30 (zinc transporter), member 5	chr5q12.1	243166_at	NM_022902 /// NM_024055
3.48	3.75	0.27	2.56E-01	6.30E-01	---	---	---	239861_at	---
5.80	6.49	0.68	2.56E-01	6.30E-01	MTF2	metal response element binding transcription factor 2	chr1p22.1	203346_s_at	NM_007358
3.70	3.90	0.20	2.56E-01	6.30E-01	PGA3	Pepsinogen 3, group I (pepsinogen A)	chr11q12.2	240514_at	NM_001079807
4.39	4.84	0.45	2.56E-01	6.30E-01	---	---	---	235493_at	---
5.05	5.92	0.87	2.56E-01	6.30E-01	PECAM1	platelet/endothelial cell adhesion molecule	chr17q23	208983_s_at	NM_000442
3.81	4.39	0.58	2.56E-01	6.30E-01	GUCY1B3	guanylate cyclase 1, soluble, beta 3	chr4q31.3-q33	203817_at	NM_000857
5.15	5.42	0.27	2.56E-01	6.30E-01	C22orf9	chromosome 22 open reading frame 9	chr22q13.31	212421_at	NM_001009880 /// NM_015264
5.28	5.54	0.26	2.56E-01	6.30E-01	SLC38A10	Solute carrier family 38, member 10	chr17q25.3	238345_at	NM_001037984 /// NM_138570
2.40	2.64	0.24	2.56E-01	6.30E-01	EXT1	exostoses (multiple) 1	chr8q24.11-q24.13	214985_at	NM_000127
2.96	3.20	0.23	2.56E-01	6.30E-01	MXRA8	Matrix-remodelling associated 8	chr1p36.33	228576_s_at	NM_032348
2.74	2.93	0.19	2.56E-01	6.30E-01	LOC643923	hypothetical protein LOC643923	chr11q22.3	1564787_at	NM_001039772
2.21	2.39	0.18	2.56E-01	6.30E-01	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4	deleted in azoospermia 1 /// deleted in azoospermia 2 /// deleted in azoospermia 3 /// deleted in azoospermia 4	chrYq11.223	208281_x_at	NM_001005375 /// NM_001005785 /// NM_001005786 /// NM_004081 /// NM_020363 /// NM_020364 /// NM_020420 /// XM_001718583
3.92	4.10	0.18	2.56E-01	6.30E-01	PAIP2B	poly(A) binding protein interacting protein 2B	chr2p13.3	221868_at	NM_020459
3.40	3.57	0.17	2.56E-01	6.30E-01	SORBS1	sorbin and SH3 domain containing 1	chr10q23.3-q24.1	211819_s_at	NM_001034954 /// NM_001034955 /// NM_001034956 /// NM_001034957 /// NM_006434 /// NM_015385 /// NM_024991
2.12	2.28	0.15	2.56E-01	6.30E-01	GCNT7	glucosaminyl (N-acetyl) transferase family member 7	chr20q13.2	234540_at	NM_001128614 /// NM_080615 /// XM_001723312 /// XM_001723344 /// XM_001723681
1.97	2.09	0.12	2.56E-01	6.30E-01	---	---	---	1558905_at	---
6.32	6.67	0.35	2.56E-01	6.30E-01	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	chr14q32	200702_s_at	NM_020414
3.20	3.48	0.28	2.56E-01	6.30E-01	PAPD4	PAP associated domain containing 4	chr5q14.1	1556277_a_at	NM_001114393 /// NM_001114394 /// NM_173797
3.78	4.02	0.24	2.56E-01	6.30E-01	---	---	---	234877_x_at	---
2.86	3.07	0.21	2.56E-01	6.30E-01	MAP7D3	MAP7 domain containing 3	chrXq26.3	237842_at	NM_024597

2.64	2.82	0.18	2.56E-01	6.30E-01	H2BFM	H2B histone family, member M	chrXq22.2	234899_at	XM_001714135 /// XM_001723437 /// XM_936705																				
2.22	2.40	0.18	2.56E-01	6.30E-01	ARPP-21	cyclic AMP-regulated phosphoprotein, 21 kD	chr3p22.3	231935_at	NM_001025068 /// NM_001025069 /// NM_016300 /// NM_198399																				
2.79	2.93	0.14	2.56E-01	6.30E-01	RNH1	ribonuclease/angiogenin inhibitor 1	chr11p15.5	1555529_at	NM_002939 /// NM_203383 /// NM_203384 /// NM_203385 /// NM_203386 /// NM_203387 /// NM_203388 /// NM_203389																				
1.85	1.99	0.13	2.56E-01	6.30E-01	---	---	---	230225_x_at	---																				
2.92	3.06	0.14	2.56E-01	6.30E-01	SLIT1	Slit homolog 1 (Drosophila)	chr10q23.3-q24	1557615_a_at	NM_003061																				
2.81	3.04	0.23	2.56E-01	6.30E-01	---	---	---	1562383_at	---																				
5.24	5.89	0.65	2.56E-01	6.30E-01	CROP	cisplatin resistance-associated overexpressed protein	chr17q21.33	208835_s_at	NM_006107 /// NM_016424																				
7.73	8.06	0.33	2.56E-01	6.30E-01	ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	chr3p21-p13	218501_at	NM_001128615 /// NM_001128616 /// NM_019555																				
5.87	6.17	0.30	2.56E-01	6.30E-01	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF3 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.12 /// chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	1562063_x_at	NM_001037675 /// NM_001039703 /// NM_001101663 /// NM_001102663 /// NM_015383 /// NM_017940 /// NM_032264 /// NM_173638 /// NM_183372 /// XM_001717398 /// XM_001717802 /// XM_001721345 /// XM_001721349 /// XM_001722184 /// XM_001723523 /// XM_001726946																				
2.38	2.61	0.23	2.56E-01	6.30E-01	WDR78	WD repeat domain 78	chr1p31.3	1554141_s_at	NM_024763 /// NM_207014																				
4.42	4.59	0.18	2.56E-01	6.30E-01	DLL1	delta-like 1 (Drosophila)	chr6q27	227938_s_at	NM_005618																				
2.50	2.66	0.15	2.56E-01	6.30E-01	TUSC3	tumor suppressor candidate 3	chr8p22	232770_at	NM_006765 /// NM_178234																				
2.01	2.25	0.24	2.56E-01	6.30E-01	MAB21L2	mab-21-like 2 (C. elegans)	chr4q31	210303_at	NM_006439																				
5.99	6.46	0.47	2.56E-01	6.30E-01	QKI	Quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	241938_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855																				

1.93	2.09	0.16	2.57E-01	6.30E-01	LOC255411	hypothetical LOC255411	chr12q13.12	1560619_at	XM_001719771 /// XM_001719772 /// XM_170708 /// XM_932014 /// XM_937994 /// XM_943509
2.74	3.01	0.27	2.57E-01	6.30E-01	---	---	---	1564381_s_at	---
5.50	5.96	0.46	2.57E-01	6.30E-01	TFAM	transcription factor A, mitochondrial	chr10q21	203176_s_at	NM_003201
2.46	2.66	0.20	2.57E-01	6.31E-01	---	---	---	243503_at	---
6.52	6.85	0.33	2.57E-01	6.31E-01	GOLGA4	golgi autoantigen, golgin subfamily a, 4	chr3p22-p21.3	201567_s_at	NM_002078
8.08	8.42	0.34	2.57E-01	6.31E-01	VPS26A	vacuolar protein sorting 26 homolog A (S. pombe)	chr10q21.1	201807_at	NM_001035260 /// NM_004896
2.55	2.80	0.24	2.57E-01	6.31E-01	---	---	---	233367_at	---
2.79	2.97	0.19	2.57E-01	6.31E-01	---	---	---	216932_at	---
4.24	4.68	0.44	2.57E-01	6.31E-01	---	---	---	231207_at	---
7.55	7.83	0.28	2.57E-01	6.31E-01	TTC1	tetratricopeptide repeat domain 1	chr5q33.3	201434_at	NM_003314 /// XM_001717166 /// XM_001722976 /// XM_001725128
3.77	3.94	0.17	2.57E-01	6.31E-01	---	---	---	239248_at	---
5.08	5.24	0.15	2.57E-01	6.31E-01	LONP2	lon peptidase 2, peroxisomal	chr16q12.1	229663_at	NM_031490
3.53	3.68	0.15	2.57E-01	6.31E-01	---	---	---	238255_at	---
3.73	3.97	0.24	2.57E-01	6.31E-01	LRRC46	leucine rich repeat containing 46	chr17q21.32	230600_at	NM_033413
4.21	4.77	0.56	2.57E-01	6.31E-01	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	chr9q21	227987_at	NM_001018037 /// NM_001018038 /// NM_015186 /// NM_033305
2.23	2.37	0.15	2.57E-01	6.31E-01	ZFP42	zinc finger protein 42 homolog (mouse)	chr4q35.2	1554777_at	NM_174900
2.45	2.67	0.22	2.57E-01	6.31E-01	---	---	---	1568887_at	---
1.85	2.01	0.17	2.57E-01	6.31E-01	AGK	acylglycerol kinase	chr7q34	1555610_at	NM_018238
3.23	3.48	0.25	2.57E-01	6.31E-01	KLRG1	killer cell lectin-like receptor subfamily G, member 1	chr12p12-p13	210288_at	NM_005810
6.13	6.33	0.20	2.57E-01	6.31E-01	EPS8L1	EPS8-like 1	chr19q13.42	218778_x_at	NM_017729 /// NM_133180
2.42	2.60	0.18	2.57E-01	6.31E-01	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	chr2q37.3	243152_at	NM_006710 /// NM_198189
2.73	2.97	0.24	2.57E-01	6.31E-01	ODF3	outer dense fiber of sperm tails 3	chr11p15.5	233795_at	NM_053280
2.25	2.47	0.22	2.57E-01	6.31E-01	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	chr3p14	239835_at	NM_032505
1.75	1.91	0.15	2.57E-01	6.31E-01	---	---	---	237962_x_at	---
2.28	2.43	0.15	2.57E-01	6.31E-01	---	---	---	1570592_a_at	---
2.03	2.17	0.14	2.57E-01	6.31E-01	---	---	---	240536_at	---
2.47	2.66	0.19	2.57E-01	6.31E-01	---	---	---	232714_at	---
2.23	2.47	0.25	2.57E-01	6.32E-01	CYSLTR1	cysteinyl leukotriene receptor 1	chrXq13.2-q21.1	230866_at	NM_006639
2.31	2.53	0.22	2.57E-01	6.32E-01	SPAG16	sperm associated antigen 16	chr2q34	240898_at	NM_001025436 /// NM_024532
2.61	2.77	0.16	2.58E-01	6.32E-01	---	---	---	1558553_at	---
3.05	3.31	0.25	2.58E-01	6.32E-01	CACNG2	calcium channel, voltage-dependent, gamma subunit 2	chr22q13.1	214495_at	NM_006078
3.07	3.33	0.26	2.58E-01	6.32E-01	LOC400568	hypothetical LOC400568	chr17p13.2	1560513_at	---
4.21	4.49	0.27	2.58E-01	6.32E-01	WASF2	WAS protein family, member 2	chr1p36.11-p34.3	224563_at	NM_006990
3.01	3.25	0.24	2.58E-01	6.32E-01	ZNF557	zinc finger protein 557	chr19p13.2	220444_at	NM_001044387 /// NM_001044388 /// NM_024341
2.39	2.57	0.18	2.58E-01	6.32E-01	CNGB1	cyclic nucleotide gated channel beta 1	chr16q13	207342_at	NM_001297
2.42	2.59	0.18	2.58E-01	6.32E-01	---	---	---	242351_at	---
2.96	3.14	0.18	2.58E-01	6.32E-01	---	---	---	237372_at	---
2.34	2.52	0.18	2.58E-01	6.32E-01	---	---	---	234153_at	---
2.12	2.28	0.16	2.58E-01	6.32E-01	TREML3	triggering receptor expressed on myeloid cells-like 3	chr6p21.1	1557446_x_at	XM_001717580 /// XM_929970 /// XM_941488
5.06	5.25	0.19	2.58E-01	6.32E-01	KHK	ketohexokinase (fructokinase)	chr2p23.3	211028_s_at	NM_000221 /// NM_006488
2.32	2.49	0.17	2.58E-01	6.32E-01	SMOC1	SPARC related modular calcium binding 1	chr14q24.2	222783_s_at	NM_001034852 /// NM_022137
2.99	3.21	0.21	2.58E-01	6.32E-01	ARL15	ADP-ribosylation factor-like 15	chr5p15.2	219842_at	NM_019087

3.65	3.82	0.17	2.58E-01	6.32E-01	---	---	---	234960_at	---
2.67	2.84	0.17	2.58E-01	6.32E-01	CDGAP	Cdc42 GTPase-activating protein	chr3q13.32-q13.33	226057_at	NM_020754
2.07	2.20	0.13	2.58E-01	6.32E-01	C18orf54	chromosome 18 open reading frame 54	chr18q21.2	244324_at	NM_173529
4.88	5.24	0.37	2.58E-01	6.32E-01	RBBP5	retinoblastoma binding protein 5	chr1q32	205169_at	NM_005057
4.54	4.74	0.20	2.58E-01	6.32E-01	MUC4	Mucin 4, cell surface associated	chr3q29	235055_x_at	NM_004532 /// NM_018406 /// NM_138297
3.75	3.97	0.22	2.58E-01	6.32E-01	CHD1L	Chromodomain helicase DNA binding protein 1-like	chr1q12	238070_at	NM_004284
2.75	3.34	0.59	2.58E-01	6.32E-01	---	---	---	241929_at	---
2.53	2.77	0.24	2.58E-01	6.32E-01	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	chr14q23.1	210407_at	NM_021003 /// NM_177951 /// NM_177952
2.01	2.16	0.15	2.58E-01	6.32E-01	HERC6	hect domain and RLD 6	chr4q22.1	1563659_at	NM_017912
6.14	6.46	0.32	2.58E-01	6.32E-01	MTMR6	myotubularin related protein 6	chr13q12	214429_at	NM_004685
2.50	2.68	0.18	2.58E-01	6.32E-01	---	---	---	233253_at	---
3.90	4.50	0.60	2.58E-01	6.33E-01	---	---	---	235613_at	---
2.42	2.71	0.29	2.59E-01	6.33E-01	---	---	---	240733_at	---
2.67	2.95	0.28	2.58E-01	6.33E-01	---	---	---	239751_at	---
2.97	3.15	0.18	2.58E-01	6.33E-01	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	chr20q13.33	244488_at	NM_144703
5.48	5.64	0.16	2.58E-01	6.33E-01	---	---	---	231212_x_at	---
4.94	5.41	0.47	2.59E-01	6.33E-01	LZIC	leucine zipper and CTNNBIP1 domain containing	chr1p36.22	226087_at	NM_032368
2.78	2.99	0.21	2.59E-01	6.33E-01	SHANK2	SH3 and multiple ankyrin repeat domains 2	chr11q13.3	215830_at	NM_012309 /// NM_133266
3.17	3.41	0.24	2.59E-01	6.33E-01	---	---	---	1557456_a_at	---
5.10	5.29	0.18	2.59E-01	6.33E-01	LRP6	low density lipoprotein receptor-related protein 6	chr12p11-p13	205606_at	NM_002336
4.69	5.28	0.59	2.59E-01	6.33E-01	LAMP2	lysosomal-associated membrane protein 2	chrXq24	226671_at	NM_001122606 /// NM_002294 /// NM_013995
3.14	3.72	0.58	2.59E-01	6.33E-01	CCDC76	coiled-coil domain containing 76	chr1pter-q31.3	232489_at	NM_019083
3.58	3.81	0.23	2.59E-01	6.33E-01	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	chr8q11.2	1557586_s_at	NM_015941 /// NM_213619 /// NM_213620
3.65	3.85	0.20	2.59E-01	6.33E-01	---	---	---	243291_at	---
3.26	3.44	0.19	2.59E-01	6.33E-01	---	---	---	239353_at	---
5.26	5.57	0.31	2.59E-01	6.33E-01	---	---	---	222282_at	---
2.43	2.64	0.21	2.59E-01	6.33E-01	FOXI1	forkhead box I1	chr5q34	208006_at	NM_012188 /// NM_144769
2.07	2.23	0.16	2.59E-01	6.33E-01	CD40	CD40 molecule, TNF receptor superfamily member 5	chr20q12-q13.2	222292_at	NM_001250 /// NM_152854
4.76	5.00	0.23	2.59E-01	6.33E-01	CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	chr16q22.3	223942_x_at	NM_024533
4.69	4.86	0.16	2.59E-01	6.33E-01	---	---	---	237851_at	---
1.95	2.09	0.15	2.59E-01	6.33E-01	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	chr1p13.3-p13.1	208011_at	NM_012411 /// NM_015967
2.12	2.34	0.22	2.59E-01	6.33E-01	STK32A	serine/threonine kinase 32A	chr5q32	1559624_at	NM_001112724 /// NM_145001
2.64	2.82	0.18	2.59E-01	6.33E-01	---	---	---	241037_at	---
2.25	2.47	0.22	2.59E-01	6.33E-01	C3orf25	chromosome 3 open reading frame 25	chr3q21.3	232639_at	NM_207307
2.13	2.33	0.20	2.59E-01	6.33E-01	---	---	---	1564014_at	---
5.71	6.04	0.32	2.59E-01	6.33E-01	CHP	calcium binding protein P22	chr15q13.3	207993_s_at	NM_007236
6.05	6.35	0.30	2.59E-01	6.33E-01	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	chr3p21.3	201906_s_at	NM_001008392 /// NM_005808
2.56	2.77	0.21	2.59E-01	6.33E-01	ACSL6	Acyl-CoA synthetase long-chain family member 6	chr5q31	216409_at	NM_001009185 /// NM_015256
4.36	4.73	0.37	2.59E-01	6.33E-01	---	---	---	229333_at	---
2.61	2.75	0.14	2.59E-01	6.34E-01	SMC4	structural maintenance of chromosomes 4	chr3q26.1	215623_x_at	NM_001002800 /// NM_005496
2.78	3.08	0.30	2.59E-01	6.34E-01	SLC39A2	solute carrier family 39 (zinc transporter), member 2	chr14q11.2	220413_at	NM_014579
5.55	5.79	0.25	2.60E-01	6.34E-01	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	chr1q32.1	210151_s_at	NM_001004023 /// NM_003582
2.74	2.95	0.21	2.60E-01	6.34E-01	SCGB3A2	secretoglobin, family 3A, member 2	chr5q32	228782_at	NM_054023
2.29	2.45	0.16	2.60E-01	6.34E-01	---	---	---	228215_at	---
4.34	4.69	0.35	2.60E-01	6.34E-01	SPATA21	spermatogenesis associated 21	chr1p36.13	1570241_at	NM_198546
8.13	8.38	0.25	2.60E-01	6.34E-01	GTF2H5	general transcription factor IIH, polypeptide 5	chr6q25.3	213357_at	NM_207118
3.38	3.62	0.25	2.60E-01	6.34E-01	KYNU	kynureninase (L-kynurenine hydrolase)	chr2q22.2	210663_s_at	NM_001032998 /// NM_003937
5.87	6.47	0.59	2.60E-01	6.34E-01	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	chr13q12.2-q13.3	202930_s_at	NM_003850
4.83	5.12	0.29	2.60E-01	6.34E-01	FLJ22662	hypothetical protein FLJ22662	chr12p13.1	218454_at	NM_024829
3.11	3.29	0.18	2.60E-01	6.34E-01	---	---	---	234451_at	---

1.74	1.90	0.15	2.60E-01	6.34E-01	DMP1	dentin matrix acidic phosphoprotein 1	chr4q21	208175_s_at	NM_001079911 /// NM_004407
1.91	2.06	0.15	2.60E-01	6.34E-01	---	---	---	233653_at	---
8.15	8.45	0.30	2.60E-01	6.34E-01	GRSF1	G-rich RNA sequence binding factor 1	chr4q13	201520_s_at	NM_001098477 /// NM_002092
2.43	2.66	0.23	2.60E-01	6.34E-01	---	---	---	1563073_at	---
2.63	2.76	0.13	2.60E-01	6.34E-01	---	---	---	244020_at	---
2.05	2.20	0.15	2.60E-01	6.34E-01	CXorf18	chromosome X open reading frame 18	chrXq27.2	1564491_at	XR_040312 /// XR_040313
2.21	2.34	0.13	2.60E-01	6.34E-01	LOC645961	similar to chromosome 9 open reading frame 36	chr9q22.1	215320_at	XR_040572 /// XR_040573 /// XR_040574
2.45	2.58	0.13	2.60E-01	6.34E-01	---	---	---	1559111_a_at	---
3.60	3.86	0.26	2.60E-01	6.34E-01	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	chr6q21	233089_at	NM_018292
2.11	2.28	0.17	2.60E-01	6.34E-01	SYTL4	synaptotagmin-like 4	chrXq21.33	1563513_at	NM_001129896 /// NM_080737
2.01	2.14	0.13	2.60E-01	6.34E-01	---	---	---	242947_at	---
3.99	4.20	0.21	2.60E-01	6.34E-01	---	---	---	242133_s_at	---
2.45	2.64	0.19	2.60E-01	6.34E-01	---	---	---	215386_at	---
2.38	2.55	0.17	2.60E-01	6.34E-01	C10orf140	chromosome 10 open reading frame 140	chr10p12.31	1559265_at	NM_207371
4.08	4.26	0.18	2.60E-01	6.35E-01	---	---	---	215875_at	---
3.64	3.81	0.17	2.60E-01	6.35E-01	OASL	2'-5'-oligoadenylate synthetase-like	chr12q24.2	210797_s_at	NM_003733 /// NM_198213
2.29	2.44	0.15	2.60E-01	6.35E-01	---	---	---	244492_at	---
3.99	4.22	0.24	2.60E-01	6.35E-01	SELENBP1	Selenium binding protein 1	chr1q21-q22	233267_at	NM_003944
2.74	2.95	0.21	2.60E-01	6.35E-01	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	chr21q22.3	222079_at	NM_004449 /// NM_182918
5.68	6.26	0.59	2.61E-01	6.35E-01	---	---	---	239296_at	---
5.50	5.93	0.42	2.61E-01	6.35E-01	LMBR1	limb region 1 homolog (mouse)	chr7q36	222505_at	NM_022458
7.72	8.09	0.37	2.61E-01	6.35E-01	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	chr2p23.2	211566_x_at	NM_004899 /// NM_199191 /// NM_199192 /// NM_199193 /// NM_199194
7.49	7.81	0.32	2.61E-01	6.35E-01	SNX6	sorting nexin 6	chr14q13.2	222410_s_at	NM_021249 /// NM_152233
4.14	4.44	0.31	2.60E-01	6.35E-01	LIN7B	lin-7 homolog B (C. elegans)	chr19q13.3	219760_at	NM_022165
3.47	3.65	0.18	2.61E-01	6.35E-01	---	---	---	1565701_at	---
1.94	2.09	0.16	2.60E-01	6.35E-01	NLGN1	Neuroligin 1	chr3q26.31	231361_at	NM_014932
2.01	2.15	0.15	2.61E-01	6.35E-01	DCLK3	doublecortin-like kinase 3	chr3p22.2	232399_at	NM_033403
1.88	2.02	0.14	2.60E-01	6.35E-01	---	---	---	1569948_at	---
2.23	2.36	0.13	2.61E-01	6.35E-01	---	---	---	AFFX-PheX-5_at	---
2.23	2.35	0.12	2.61E-01	6.35E-01	---	---	---	239669_at	---
1.97	2.09	0.11	2.60E-01	6.35E-01	---	---	---	1562310_at	---
4.37	4.83	0.46	2.61E-01	6.35E-01	PTPRC	protein tyrosine phosphatase, receptor type, C	chr1q31-q32	212587_s_at	NM_002838 /// NM_080921 /// NM_080922 /// NM_080923
8.03	8.38	0.35	2.61E-01	6.35E-01	MRPS22	mitochondrial ribosomal protein S22	chr3q23	226257_x_at	NM_020191
2.91	3.43	0.52	2.61E-01	6.35E-01	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	chr7q21-q22	215483_at	NM_005751 /// NM_147166 /// NM_147171 /// NM_147185
3.70	4.06	0.37	2.61E-01	6.35E-01	---	---	---	1559154_at	---
3.55	3.75	0.20	2.61E-01	6.35E-01	RAB35	RAB35, member RAS oncogene family	chr12q24.31	205461_at	NM_006861
2.44	2.62	0.18	2.61E-01	6.35E-01	ZCCHC13	zinc finger, CCHC domain containing 13	chrXq13.2	1554210_at	NM_203303
3.03	3.18	0.15	2.61E-01	6.35E-01	---	---	---	217662_x_at	---
4.27	4.56	0.29	2.61E-01	6.35E-01	GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide	chr9q21	224863_at	NM_002072
2.15	2.29	0.14	2.61E-01	6.35E-01	---	---	---	236197_at	---
5.20	5.95	0.75	2.61E-01	6.35E-01	SRP72	signal recognition particle 72kDa	chr4q11	208803_s_at	NM_006947
2.41	2.60	0.19	2.61E-01	6.35E-01	LOC646548	hypothetical LOC646548	chr14q24.2	242441_at	XR_017624 /// XR_019089 /// XR_038927
2.70	2.89	0.18	2.61E-01	6.35E-01	---	---	---	231150_at	---
3.94	4.11	0.17	2.61E-01	6.35E-01	ZNF75D	zinc finger protein 75D	chrXq26.3	214813_at	NM_007131
3.10	3.27	0.17	2.61E-01	6.35E-01	WFIKKN2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	chr17q21.33	1554773_at	NM_175575
3.25	3.42	0.17	2.61E-01	6.35E-01	LRRC37A3	leucine rich repeat containing 37, member A3	chr17q24.1	244478_at	NM_199340
2.03	2.19	0.15	2.61E-01	6.35E-01	ADAM7	ADAM metallopeptidase domain 7	chr8p21.2	211239_s_at	NM_003817
2.14	2.28	0.14	2.61E-01	6.35E-01	NPAS4	neuronal PAS domain protein 4	chr11q13	1554299_at	NM_178864

2.17	2.31	0.14	2.61E-01	6.35E-01	ZBP1	Z-DNA binding protein 1	chr20q13.31	242020_s_at	NM_030776
5.77	6.74	0.96	2.61E-01	6.35E-01	TMEM176B	transmembrane protein 176B	chr7q36.1	220532_s_at	NM_001101311 /// NM_001101312 /// NM_001101313 /// NM_001101314 /// NM_014020
5.77	6.57	0.80	2.61E-01	6.35E-01	ARHGAP18	Rho GTPase activating protein 18	chr6q22.33	225173_at	NM_033515
2.75	3.17	0.42	2.61E-01	6.35E-01	---	---	---	214803_at	---
4.49	4.81	0.32	2.61E-01	6.35E-01	---	---	---	242369_x_at	---
2.62	2.83	0.20	2.61E-01	6.35E-01	---	---	---	1568931_at	---
4.63	4.81	0.18	2.61E-01	6.35E-01	CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	chr8q24.23	201638_s_at	NM_013291
3.13	3.47	0.34	2.61E-01	6.35E-01	LOC654433	hypothetical LOC654433	chr2q13	228425_at	NR_015377 /// XR_041715 /// XR_041716 /// XR_041717
3.08	3.41	0.33	2.61E-01	6.35E-01	---	---	---	244075_at	---
2.48	2.78	0.30	2.61E-01	6.35E-01	---	---	---	231067_s_at	---
3.33	3.53	0.20	2.61E-01	6.35E-01	RIOK3	RIO kinase 3 (yeast)	chr18q11.2	240583_at	NM_003831
2.29	2.49	0.19	2.61E-01	6.35E-01	PDE11A	phosphodiesterase 11A	chr2q31.2	237248_at	NM_001077196 /// NM_001077197 /// NM_001077358 /// NM_016953
2.33	2.48	0.15	2.61E-01	6.35E-01	PIP3-E	phosphoinositide-binding protein PIP3-E	chr6q25.2	214735_at	NM_001130699 /// NM_001130700 /// NM_015553
2.45	2.98	0.53	2.62E-01	6.35E-01	IGHA1 /// IGHD /// IGHG1 /// IGHM /// IGHV4-31 /// IGHV@	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable group	chr14q32.33	216510_x_at	---
4.28	4.73	0.45	2.62E-01	6.35E-01	---	---	---	238918_at	---
2.21	2.40	0.19	2.62E-01	6.35E-01	GPR81	G protein-coupled receptor 81	chr12q24.31	224131_at	NM_032554
2.53	2.71	0.18	2.62E-01	6.35E-01	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	chr13q31.2-q32.3	215188_at	NM_001032296 /// NM_003576
2.12	2.28	0.16	2.62E-01	6.35E-01	---	---	---	1561253_at	---
2.25	2.44	0.19	2.62E-01	6.35E-01	---	---	---	216201_at	---
2.41	2.53	0.12	2.62E-01	6.35E-01	---	---	---	235826_at	---
3.52	3.90	0.38	2.62E-01	6.35E-01	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	chr9p21	236313_at	NM_004936 /// NM_078487
7.50	7.85	0.34	2.62E-01	6.35E-01	LOC100133724 /// VDAC1	similar to Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM) /// voltage-dependent anion channel 1	chr5q31	217140_s_at	NM_003374 /// XR_038734
2.77	3.00	0.24	2.62E-01	6.35E-01	HRH1	histamine receptor H1	chr3p25	205580_s_at	NM_000861 /// NM_001098211 /// NM_001098212 /// NM_001098213
3.64	3.86	0.22	2.62E-01	6.35E-01	HIST2H2AA3	histone cluster 2, H2aa3	chr1q21.2	218279_s_at	NM_003516
3.17	3.36	0.19	2.62E-01	6.35E-01	---	---	---	236829_at	---
1.88	2.05	0.18	2.62E-01	6.35E-01	LOC644231 /// LOC652637 /// WHDC1L1 /// WHDC1L2	similar to junction-mediating and regulatory protein p300 JMY-like hypothetical protein /// similar to junction-mediating and regulatory protein /// WAS protein homology region 2 domain containing 1-like 1 /// WAS protein homology region 2 domain containing 1-like 2	chr15q11.2 /// chr15q13.1 /// chr15q13.3	244105_at	NR_003521 /// XM_001723103 /// XM_001726978 /// XM_926785 /// XM_942188 /// XR_042166
2.41	2.58	0.17	2.62E-01	6.35E-01	---	---	---	241571_at	---
2.16	2.33	0.17	2.62E-01	6.35E-01	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	chr12q23.3	1556841_a_at	NM_001034173
2.53	2.69	0.15	2.62E-01	6.35E-01	KIAA1166	KIAA1166	chrXq11.1	234809_at	NM_018684
5.18	5.53	0.35	2.62E-01	6.35E-01	---	---	---	229835_s_at	---
3.46	3.66	0.21	2.62E-01	6.35E-01	CRYBB2P1	Crystallin, beta B2 pseudogene 1	chr22q11.2-q12.1	233556_at	---

7.18	7.51	0.33	2.62E-01	6.35E-01	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	chr16q23-q24	201705_at	NM_002811
3.02	3.24	0.22	2.62E-01	6.35E-01	FLJ14213	Protor-2	chr11p13-p12	233119_at	NM_024841
2.44	2.65	0.21	2.62E-01	6.35E-01	---	---	---	227545_at	---
2.20	2.37	0.17	2.62E-01	6.35E-01	OR12D3 /// OR5V1	olfactory receptor, family 12, subfamily D, member 3 /// olfactory receptor, family 5, subfamily V, member 1	chr6p22.1	234840_s_at	NM_030876 /// NM_030959
7.40	7.76	0.36	2.62E-01	6.36E-01	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	chr1p22-p21	202850_at	NM_001122674 /// NM_002858
2.67	2.92	0.25	2.62E-01	6.36E-01	ZFP1	Zinc finger protein 1 homolog (mouse)	chr16q23.1	234810_at	NM_153688
2.59	3.25	0.66	2.62E-01	6.36E-01	---	---	---	1566551_at	---
5.36	5.96	0.60	2.62E-01	6.36E-01	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	chr15q24	201879_at	NM_005744
2.44	2.61	0.17	2.62E-01	6.36E-01	TTTY4 /// TTTY4B /// TTTY4C	testis-specific transcript, Y-linked 4 /// testis-specific transcript, Y-linked 4B /// testis-specific transcript, Y-linked 4C	chrYq11.2 /// chrYq11.223	234913_at	NR_001525 /// NR_002177 /// NR_002178
4.48	5.13	0.65	2.62E-01	6.36E-01	LGALS8	lectin, galactoside-binding, soluble, 8	chr1q42-q43	208935_s_at	NM_006499 /// NM_201543 /// NM_201544 /// NM_201545
5.64	5.98	0.34	2.62E-01	6.36E-01	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	chr5q22.2	212919_at	NM_152624
3.37	3.64	0.27	2.62E-01	6.36E-01	SNORA28	small nucleolar RNA, H/ACA box 28	chr14q32.32	241843_at	NR_002964
3.30	3.54	0.24	2.62E-01	6.36E-01	ZNF626	zinc finger protein 626	chr19p12	1559616_x_at	NM_001076675 /// NM_145297
3.34	3.55	0.22	2.62E-01	6.36E-01	---	---	---	243454_at	---
2.44	2.63	0.20	2.62E-01	6.36E-01	---	---	---	237296_at	---
3.61	3.80	0.19	2.62E-01	6.36E-01	HS1BP3	HCLS1 binding protein 3	chr2p24.1	236530_at	NM_022460
2.26	2.42	0.16	2.62E-01	6.36E-01	---	---	---	236598_at	---
2.26	2.37	0.11	2.62E-01	6.36E-01	TLK2	tousled-like kinase 2	chr17q23	233349_at	NM_001112707 /// NM_006852
3.14	3.32	0.18	2.62E-01	6.36E-01	VENTXP1	VENT homeobox (Xenopus laevis) pseudogene 1	chrXp21.3	216726_at	NR_001559 /// XR_042160
5.68	6.79	1.11	2.62E-01	6.36E-01	C20orf74	Chromosome 20 open reading frame 74	chr20p11.22	234314_at	NM_020343
6.35	7.04	0.69	2.62E-01	6.36E-01	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	chr8q22.3	202874_s_at	NM_001695
3.24	3.89	0.66	2.62E-01	6.36E-01	---	---	---	1556989_at	---
5.38	5.94	0.56	2.62E-01	6.36E-01	RABEP1	rabaptin, RAB GTPase binding effector protein 1	chr17p13.2	225064_at	NM_001083585 /// NM_004703
3.96	4.18	0.22	2.63E-01	6.36E-01	RSU1	Ras suppressor protein 1	chr10p13	215618_at	NM_012425 /// NM_152724
3.11	3.28	0.17	2.63E-01	6.36E-01	---	---	---	241091_at	---
2.94	3.11	0.16	2.62E-01	6.36E-01	ZNF589	zinc finger protein 589	chr3p21	1569108_a_at	NM_016089
2.16	2.32	0.16	2.62E-01	6.36E-01	OLIG3	oligodendrocyte transcription factor 3	chr6q23.3	1556371_at	NM_175747
6.21	6.35	0.13	2.62E-01	6.36E-01	PECR	peroxisomal trans-2-enoyl-CoA reductase	chr2q35	223619_x_at	NM_018441
2.10	2.25	0.16	2.63E-01	6.36E-01	LRRN2	leucine rich repeat neuronal 2	chr1q32.1	216167_at	NM_006338 /// NM_201630
3.67	4.20	0.53	2.63E-01	6.36E-01	WDFY2	WD repeat and FYVE domain containing 2	chr13q14.3	1560112_at	NM_052950
2.01	2.17	0.17	2.63E-01	6.36E-01	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	chr1p34.3	233760_at	NM_016037
2.10	2.25	0.15	2.63E-01	6.36E-01	DST	Dystonin	chr6p12.1	215810_x_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380
6.34	6.65	0.30	2.63E-01	6.37E-01	BTN3A3	butyrophilin, subfamily 3, member A3	chr6p21.3	204821_at	NM_006994 /// NM_197974
4.75	5.28	0.53	2.63E-01	6.37E-01	PAPOLA	poly(A) polymerase alpha	chr14q32.31	212720_at	NM_032632
5.69	6.00	0.31	2.63E-01	6.37E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	210564_x_at	NM_001127183 /// NM_001127184 /// NM_003879
2.41	2.60	0.19	2.63E-01	6.37E-01	TEDDM1	transmembrane epididymal protein 1	chr1q25.3	1552940_at	NM_172000
5.97	6.33	0.35	2.63E-01	6.37E-01	SLFN5	schlafen family member 5	chr17q12	238430_x_at	NM_144975
2.71	2.91	0.20	2.63E-01	6.37E-01	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	chr18p11	232919_at	NM_006796
5.07	5.26	0.19	2.63E-01	6.37E-01	SLC22A6	solute carrier family 22 (organic anion transporter), member 6	chr11q13.1-q13.2	210343_s_at	NM_004790 /// NM_153276 /// NM_153277 /// NM_153278
2.09	2.25	0.16	2.63E-01	6.37E-01	F5	coagulation factor V (proaccelerin, labile factor)	chr1q23	231029_at	NM_000130
2.14	2.28	0.14	2.63E-01	6.37E-01	---	---	---	1566491_at	---
2.50	2.71	0.20	2.63E-01	6.37E-01	NOL10	nucleolar protein 10	chr2p25.1	218591_s_at	NM_024894
2.19	2.39	0.19	2.63E-01	6.37E-01	---	---	---	239410_at	---
2.67	2.85	0.18	2.63E-01	6.37E-01	---	---	---	1564784_at	---
2.28	2.41	0.13	2.63E-01	6.37E-01	---	---	---	239008_at	---
2.24	2.37	0.13	2.63E-01	6.37E-01	CCNB1	cyclin B1	chr5q12	228729_at	NM_031966

3.76	4.12	0.36	2.63E-01	6.37E-01	---	---	---	236663_at	---
2.50	2.80	0.30	2.63E-01	6.37E-01	MAP9	microtubule-associated protein 9	chr4q32.1	220145_at	NM_001039580
6.20	6.43	0.23	2.63E-01	6.37E-01	NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	chr16q23.1	228855_at	NM_001105663
4.39	4.62	0.23	2.64E-01	6.37E-01	PRINS	psoriasis associated RNA induced by stress (non-protein coding)	chr10p12.1	216051_x_at	NR_023388
3.02	3.25	0.22	2.64E-01	6.37E-01	---	---	---	1560618_at	---
4.59	4.80	0.21	2.63E-01	6.37E-01	C22orf36	chromosome 22 open reading frame 36	chr22q11.23	228064_at	NM_207644
3.79	3.99	0.20	2.63E-01	6.37E-01	KSR1	kinase suppressor of ras 1	chr17q11.1	213769_at	NM_014238
3.58	3.77	0.19	2.63E-01	6.37E-01	MAST1	microtubule associated serine/threonine kinase 1	chr19p13.2	217231_s_at	NM_014975
3.65	3.84	0.19	2.63E-01	6.37E-01	---	---	---	237308_at	---
2.25	2.42	0.17	2.63E-01	6.37E-01	---	---	---	237997_s_at	---
4.63	4.80	0.17	2.64E-01	6.37E-01	---	---	---	240988_x_at	---
2.10	2.24	0.15	2.64E-01	6.37E-01	FRMD4B	FERM domain containing 4B	chr3p14.1	216131_at	NM_015123
4.24	4.56	0.32	2.64E-01	6.37E-01	CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	chr22q13.1	215809_at	NM_000106 /// NM_001025161
2.42	2.77	0.36	2.64E-01	6.37E-01	MAP3K13	Mitogen-activated protein kinase kinase kinase 13	chr3q27	1562440_at	NM_004721
2.93	3.14	0.21	2.64E-01	6.37E-01	VWF	von Willebrand factor	chr12p13.3	233980_s_at	NM_000552
6.81	7.41	0.60	2.64E-01	6.37E-01	YME1L1	YME1-like 1 (S. cerevisiae)	chr10p14	201351_s_at	NM_014263 /// NM_139312
8.19	8.54	0.35	2.64E-01	6.37E-01	SET	SET nuclear oncogene	chr9q34	40189_at	NM_001122821 /// NM_003011
5.04	5.29	0.25	2.64E-01	6.37E-01	CSNK1G1	casein kinase 1, gamma 1	chr15q22.1-q22.31	226888_at	NM_022048
2.70	2.93	0.24	2.64E-01	6.37E-01	NRSN1	neurensin 1	chr6p22.2	239293_at	NM_080723
2.01	2.14	0.12	2.64E-01	6.37E-01	ZNF492	zinc finger protein 492	chr19p12	215532_x_at	NM_020855
4.69	5.21	0.52	2.64E-01	6.37E-01	---	---	---	230688_at	---
4.01	4.19	0.18	2.64E-01	6.38E-01	FLJ31222	hypothetical LOC388387	chr17q21.31	1556737_at	XR_041466 /// XR_041467 /// XR_041468
1.78	1.88	0.11	2.64E-01	6.38E-01	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	chr1p31	215671_at	NM_001037339 /// NM_001037340 /// NM_001037341 /// NM_002600
2.21	2.41	0.20	2.64E-01	6.38E-01	SQLE	squalene epoxidase	chr8q24.1	1557352_at	NM_003129
3.72	3.90	0.18	2.64E-01	6.38E-01	RNF212	ring finger protein 212	chr4p16.3	1557031_at	NM_001131034 /// NM_194439
2.74	2.95	0.22	2.64E-01	6.38E-01	FOXE1	forkhead box E1 (thyroid transcription factor 2)	chr9q22	208239_at	NM_004473
1.86	2.01	0.15	2.64E-01	6.38E-01	SLC5A12	solute carrier family 5 (sodium/glucose cotransporter), member 12	chr11p14.2	214389_at	NM_178498
1.89	2.03	0.14	2.64E-01	6.38E-01	---	---	---	241744_x_at	---
2.57	2.90	0.33	2.64E-01	6.38E-01	---	---	---	233518_at	---
2.82	3.07	0.25	2.64E-01	6.38E-01	---	---	---	240193_at	---
2.88	3.08	0.20	2.64E-01	6.38E-01	INSL3 /// JAK3	insulin-like 3 (Leydig cell) /// Janus kinase 3 (a protein tyrosine kinase, leukocyte)	chr19p13.1 /// chr19p13.2-p12	214400_at	NM_000215 /// NM_005543
2.67	2.84	0.17	2.64E-01	6.38E-01	---	---	---	234157_at	---
2.46	2.60	0.14	2.64E-01	6.38E-01	LOC152225	hypothetical LOC152225	chr3q12.3	1562048_at	XM_001720130 /// XM_001721196 /// XM_001722599
2.89	3.09	0.19	2.64E-01	6.38E-01	PPP1R9B	protein phosphatase 1, regulatory (inhibitor) subunit 9B	chr17q21.33	230455_at	NM_032595
3.30	3.47	0.17	2.64E-01	6.38E-01	SPAG4L	sperm associated antigen 4-like	chr20q11.21	233905_at	NM_080675
5.82	6.03	0.21	2.64E-01	6.38E-01	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	chr11q23.1-q23.2	223478_at	NM_012459
4.85	5.07	0.22	2.64E-01	6.38E-01	GPR137	G protein-coupled receptor 137	chr11cen-q22.3	221966_at	NM_020155
3.41	3.63	0.21	2.65E-01	6.38E-01	PGK2	phosphoglycerate kinase 2	chr6p12.3	217009_at	NM_138733
3.45	3.62	0.17	2.65E-01	6.38E-01	---	---	---	235446_at	---
3.68	4.08	0.39	2.65E-01	6.38E-01	CCT6B	chaperonin containing TCP1, subunit 6B (zeta 2)	chr17q12	206587_at	NM_006584
1.88	2.00	0.12	2.65E-01	6.38E-01	---	---	---	1567174_at	---
6.98	7.18	0.20	2.65E-01	6.38E-01	SNAPC2	small nuclear RNA activating complex, polypeptide 2, 45kDa	chr19p13.3-p13.2	204104_at	NM_003083
3.13	3.31	0.19	2.65E-01	6.38E-01	NPAT	nuclear protein, ataxia-telangiectasia locus	chr11q22-q23	211584_s_at	NM_002519
2.07	2.24	0.17	2.65E-01	6.38E-01	NHEDC1	Na+/H+ exchanger domain containing 1	chr4q24	1555141_a_at	NM_001100874 /// NM_139173
2.85	3.00	0.15	2.65E-01	6.38E-01	---	---	---	217361_at	---
2.17	2.30	0.13	2.65E-01	6.38E-01	---	---	---	1559735_at	---

4.86	5.09	0.23	2.65E-01	6.38E-01	GALNT9 /// LOC100133441	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (GalNAc-T9) /// similar to UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase	chr12q24.33	229451_at	NM_001122636 /// NM_021808 /// XM_001129598 /// XM_001713890 /// XM_001716058 /// XM_001719380																						
4.25	4.56	0.30	2.65E-01	6.38E-01	PML	promyelocytic leukemia	chr15q22	206503_x_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250																					
2.77	2.92	0.15	2.65E-01	6.38E-01	C4orf46	chromosome 4 open reading frame 46	chr4q32.1	235088_at	NM_001008393																					
4.26	4.46	0.20	2.65E-01	6.38E-01	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	chr4p16	205465_x_at	NM_005114																					
2.31	2.49	0.17	2.65E-01	6.38E-01	FAM53B	Family with sequence similarity 53, member B	chr10q26.13	237297_at	NM_014661																					
4.19	4.82	0.63	2.65E-01	6.38E-01	LPL	lipoprotein lipase	chr8p22	203548_s_at	NM_000237																					
4.94	5.43	0.49	2.65E-01	6.39E-01	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	chr11q23	209970_x_at	NM_001223 /// NM_033292 /// NM_033293 /// NM_033294 /// NM_033295																					
2.14	2.30	0.15	2.65E-01	6.39E-01	LOC285708	hypothetical protein LOC285708	chr5q21.2	1569923_s_at	---																					
3.82	3.99	0.17	2.65E-01	6.39E-01	OTOP2	otopetrin 2	chr17q25.1	234551_at	NM_178160																					
2.90	3.07	0.18	2.65E-01	6.39E-01	SOX6	SRY (sex determining region Y)-box 6	chr11p15.3	224178_s_at	NM_017508 /// NM_033326																					
6.90	7.47	0.57	2.65E-01	6.39E-01	JAZF1	JAZF zinc finger 1	chr7p15.2-p15.1	225798_at	NM_175061																					
2.32	2.49	0.17	2.65E-01	6.39E-01	FCRL5	Fc receptor-like 5	chr1q21	1555799_at	NM_031281																					
4.71	5.33	0.62	2.65E-01	6.39E-01	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	chr11q24.2	203562_at	NM_005103 /// NM_022549																					
4.78	5.36	0.58	2.65E-01	6.39E-01	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	chr4q26	231793_s_at	NM_001221 /// NM_172115 /// NM_172127 /// NM_172128																					
3.32	3.85	0.53	2.65E-01	6.39E-01	CPXM2	carboxypeptidase X (M14 family), member 2	chr10q26.13	226824_at	NM_198148																					
3.72	4.20	0.48	2.65E-01	6.39E-01	NPAS3	neuronal PAS domain protein 3	chr14q12-q13	220316_at	NM_022123 /// NM_173159																					
5.95	6.37	0.41	2.65E-01	6.39E-01	AZIN1	antizyme inhibitor 1	chr8q22.3	201772_at	NM_015878 /// NM_148174																					
3.54	3.91	0.37	2.65E-01	6.39E-01	LOC100131015	hypothetical LOC100131015	chr2q36.3	244659_at	XM_001726042 /// XM_001732817 /// XM_001732818																					
3.90	4.26	0.36	2.65E-01	6.39E-01	---	---	---	215062_at	---																					
3.46	3.82	0.36	2.65E-01	6.39E-01	HSPD1 /// LOC644745	heat shock 60kDa protein 1 (chaperonin) /// similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60)	chr12q13.2 /// chr2q33.1	243372_at	NM_002156 /// NM_199440 /// XR_016744 /// XR_018757 /// XR_038862																				
5.87	6.16	0.28	2.65E-01	6.39E-01	TCN2	transcobalamin II; macrocytic anemia	chr22q12.2	204043_at	NM_000355																					
5.98	6.23	0.26	2.65E-01	6.39E-01	OSGIN1	oxidative stress induced growth inhibitor 1	chr16q23.3	219475_at	NM_013370 /// NM_182980 /// NM_182981																					
3.11	3.33	0.22	2.65E-01	6.39E-01	---	---	---	216799_at	---																					
2.64	2.84	0.20	2.65E-01	6.39E-01	BAT2D1	BAT2 domain containing 1	chr1q23.3	214052_x_at	NM_015172																					
2.39	2.58	0.19	2.65E-01	6.39E-01	---	---	---	230968_at	---																					

2.87	3.05	0.18	2.65E-01	6.39E-01	LOC284648	hypothetical protein LOC284648	chr1q25.3	231427_at	XM_001715964 /// XM_001718570 /// XM_001719093
2.28	2.44	0.16	2.65E-01	6.39E-01	---	---	---	1558588_at	---
2.25	2.40	0.16	2.65E-01	6.39E-01	---	---	---	244651_at	---
2.62	2.85	0.23	2.66E-01	6.39E-01	---	---	---	240660_at	---
2.12	2.31	0.19	2.66E-01	6.39E-01	---	---	---	1566571_at	---
2.05	2.19	0.14	2.66E-01	6.39E-01	ARL6	ADP-ribosylation factor-like 6	chr3q11.2	223735_at	NM_032146 /// NM_177976
2.43	2.62	0.19	2.66E-01	6.39E-01	---	---	---	228893_at	---
2.41	2.60	0.19	2.66E-01	6.39E-01	CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9q34.3	220409_at	NM_015447
5.66	5.98	0.32	2.66E-01	6.39E-01	ZNF213	zinc finger protein 213	chr16p13.3	227207_x_at	NM_001134655 /// NM_004220
2.37	2.57	0.20	2.66E-01	6.39E-01	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	chr1q23.1	216502_at	NM_030980
1.93	2.06	0.13	2.66E-01	6.39E-01	SH3TC2	SH3 domain and tetratricopeptide repeats 2	chr5q32	240966_at	NM_024577
5.56	6.13	0.57	2.66E-01	6.39E-01	C14orf101	chromosome 14 open reading frame 101	chr14q23.1	219757_s_at	NM_017799
2.73	3.02	0.28	2.66E-01	6.39E-01	APC	adenomatous polyposis coli	chr5q21-q22	215310_at	NM_000038 /// NM_001127510 /// NM_001127511
4.81	4.99	0.18	2.66E-01	6.39E-01	C10orf41	chromosome 10 open reading frame 41	chr10q22.2	228048_at	XM_001716000 /// XM_001716275 /// XM_001716693
1.87	2.00	0.13	2.66E-01	6.39E-01	ARID4B	AT rich interactive domain 4B (RBP1-like)	chr1q42.1-q43	224322_at	NM_016374 /// NM_031371
1.98	2.10	0.12	2.66E-01	6.39E-01	TRBV25-1	T cell receptor beta variable 25-1	chr7q34	234865_at	---
2.11	2.28	0.17	2.66E-01	6.39E-01	---	---	---	237380_at	---
4.79	4.94	0.15	2.66E-01	6.39E-01	DTX2 /// LOC100134197	deltex homolog 2 (Drosophila) /// hypothetical protein LOC100134197	chr7q11.23	215732_s_at	NM_001102594 /// NM_001102595 /// NM_001102596 /// NM_020892 /// XM_001716399
2.09	2.24	0.14	2.66E-01	6.39E-01	NF1	neurofibromin 1	chr17q11.2	210631_at	NM_000267 /// NM_001042492 /// NM_001128147
4.27	4.49	0.22	2.66E-01	6.39E-01	---	---	---	217357_at	---
4.03	4.51	0.48	2.66E-01	6.39E-01	C20orf74	chromosome 20 open reading frame 74	chr20p11.22	232500_at	NM_020343
3.55	3.75	0.20	2.66E-01	6.39E-01	---	---	---	237754_at	---
7.82	8.23	0.41	2.66E-01	6.39E-01	USO1	USO1 homolog, vesicle docking protein (yeast)	chr4q21.1	201832_s_at	NM_003715
3.62	3.85	0.23	2.66E-01	6.39E-01	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1	chr3q21	242567_at	NM_032548 /// NM_172027 /// NM_172028
4.99	5.20	0.21	2.66E-01	6.39E-01	---	---	---	238388_x_at	---
2.57	2.75	0.18	2.66E-01	6.39E-01	LOC100131498	similar to hCG1778991	chr16p13.3	228085_at	XR_038627 /// XR_042319 /// XR_042455
1.82	1.96	0.14	2.66E-01	6.39E-01	C8orf49	chromosome 8 open reading frame 49	chr8p23.1	1564315_at	XR_040402 /// XR_040403 /// XR_040404
2.99	3.17	0.18	2.66E-01	6.39E-01	---	---	---	240996_at	---
2.61	2.79	0.17	2.66E-01	6.39E-01	TLE1	Transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	chr9q21.32	227130_s_at	NM_005077
5.52	6.17	0.66	2.66E-01	6.39E-01	ZNF277	zinc finger protein 277	chr7q31.1	218645_at	NM_021994
3.77	4.01	0.24	2.66E-01	6.39E-01	CPNE6	copine VI (neuronal)	chr14q11.2	215700_x_at	NM_006032
6.39	6.83	0.44	2.66E-01	6.40E-01	RNF20	ring finger protein 20	chr9q22	222683_at	NM_019592
2.28	2.45	0.17	2.66E-01	6.40E-01	CDH17	cadherin 17, LI cadherin (liver-intestine)	chr8q22.1	209847_at	NM_004063
3.34	3.55	0.20	2.66E-01	6.40E-01	FLJ14126	hypothetical protein FLJ14126	chr2p24.1	220531_at	XR_040917 /// XR_040918
2.77	2.92	0.15	2.66E-01	6.40E-01	MGAT5B	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	chr17q25.2	1563137_at	NM_144677 /// NM_198955
2.47	2.67	0.20	2.66E-01	6.40E-01	---	---	---	222378_at	---
3.34	3.56	0.22	2.66E-01	6.40E-01	---	---	---	234611_at	---

3.79	3.94	0.15	2.66E-01	6.40E-01	KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	chr1p36.3	211791_s_at	NM_003636 /// NM_172130
2.95	3.09	0.14	2.66E-01	6.40E-01	---	---	---	237975_at	---
3.08	3.34	0.26	2.67E-01	6.40E-01	---	---	---	231436_at	---
4.99	5.24	0.25	2.67E-01	6.40E-01	ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	chrXp22.1	208174_x_at	NM_005089
5.21	5.62	0.41	2.67E-01	6.40E-01	WDR36	WD repeat domain 36	chr5q22.1	226180_at	NM_139281
2.83	3.00	0.17	2.67E-01	6.40E-01	C15orf31	chromosome 15 open reading frame 31	chr15q21.3	208254_at	---
2.00	2.11	0.12	2.67E-01	6.40E-01	CORIN	corin, serine peptidase	chr4p13-p12	220356_at	NM_006587
6.17	6.72	0.55	2.67E-01	6.40E-01	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	chr20q13.13	222518_at	NM_006420
2.18	2.30	0.12	2.67E-01	6.40E-01	---	---	---	243559_at	---
8.64	9.05	0.41	2.67E-01	6.40E-01	TXNRD1	thioredoxin reductase 1	chr12q23-q24.1	201266_at	NM_001093771 /// NM_003330 /// NM_182729 /// NM_182742 /// NM_182743
2.36	2.50	0.14	2.67E-01	6.40E-01	---	---	---	244748_at	---
1.91	2.05	0.14	2.67E-01	6.40E-01	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	chr10q24	215103_at	NM_000772 /// NM_001128925
6.23	6.48	0.24	2.67E-01	6.40E-01	ABHD11	abhydrolase domain containing 11	chr7q11.23	221927_s_at	NM_148912
2.02	2.15	0.14	2.67E-01	6.40E-01	---	---	---	1569892_at	---
3.43	3.76	0.33	2.67E-01	6.40E-01	PPIG	peptidylprolyl isomerase G (cyclophilin G)	chr2q31.1	208995_s_at	NM_004792
2.25	2.38	0.14	2.67E-01	6.40E-01	---	---	---	240049_at	---
2.27	2.70	0.43	2.67E-01	6.40E-01	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	chr11q12	228592_at	NM_021950 /// NM_152866
2.26	2.63	0.37	2.67E-01	6.40E-01	PCDH21	protocadherin 21	chr10q22.1-q22.3	1555019_at	NM_033100
4.48	4.71	0.23	2.67E-01	6.40E-01	C20orf191 /// LOC100133918 /// NCOR1	chromosome 20 open reading frame 191 /// similar to nuclear receptor co-repressor 1 /// nuclear receptor co-repressor 1	chr17p11.2 /// chr20p11.1	200855_at	NM_006311 /// NR_003678 /// XM_001725872
1.95	2.11	0.16	2.67E-01	6.40E-01	C5orf48	chromosome 5 open reading frame 48	chr5q23.2	237428_at	NM_207408
7.94	8.34	0.40	2.67E-01	6.40E-01	GRAMD1B	GRAM domain containing 1B	chr11q24.1	212906_at	NM_020716
5.31	5.58	0.27	2.67E-01	6.40E-01	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	chr11q13.2	222566_at	NM_016028 /// NM_017635
2.51	2.73	0.22	2.67E-01	6.40E-01	CEP70	centrosomal protein 70kDa	chr3q22-q23	224150_s_at	NM_024491
2.34	2.55	0.21	2.67E-01	6.40E-01	IL17RD	interleukin 17 receptor D	chr3p14.3	227997_at	NM_001080973 /// NM_017563
4.31	4.51	0.21	2.67E-01	6.40E-01	LOC202051	hypothetical protein LOC202051	chr5q31.2	238027_at	XM_001721173 /// XM_114430 /// XM_940745
2.75	2.95	0.20	2.67E-01	6.40E-01	---	---	---	215939_at	---
2.12	2.26	0.14	2.67E-01	6.40E-01	---	---	---	235658_at	---
4.03	4.29	0.26	2.67E-01	6.40E-01	EXOC2	exocyst complex component 2	chr6p25.3	226270_at	NM_018303
3.15	3.34	0.20	2.67E-01	6.40E-01	MYO1A	myosin IA	chr12q13-q14	211916_s_at	NM_005379
1.90	2.04	0.14	2.67E-01	6.40E-01	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	chr2p25	214690_at	NM_005680
6.65	7.18	0.52	2.67E-01	6.40E-01	SLC30A7	solute carrier family 30 (zinc transporter), member 7	chr1p21.2	226217_at	NM_133496
4.09	4.28	0.19	2.67E-01	6.40E-01	NSFL1C	NSFL1 (p97) cofactor (p47)	chr20p13	236951_at	NM_016143 /// NM_018839 /// NM_182483
2.88	3.09	0.22	2.67E-01	6.40E-01	ANKRD37	ankyrin repeat domain 37	chr4q35.1	242548_x_at	NM_181726
2.43	2.58	0.15	2.67E-01	6.40E-01	LOC100130700	similar to hCG2038355	chr16p11.1	237730_at	XM_001721089 /// XM_001724770 /// XM_001725949
3.30	3.46	0.16	2.67E-01	6.40E-01	---	---	---	224091_at	---
1.83	1.96	0.12	2.67E-01	6.41E-01	SOX2OT	SOX2 overlapping transcript (non-protein coding)	chr3q26.3-q27	231898_x_at	NR_002810 /// NR_004053
11.45	11.58	0.14	2.67E-01	6.41E-01	GNAS	GNAS complex locus	chr20q13.3	212273_x_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259

6.11	6.45	0.34	2.67E-01	6.41E-01	MKKS	McKusick-Kaufman syndrome	chr20p12	218138_at	NM_018848 /// NM_170784
2.04	2.18	0.15	2.67E-01	6.41E-01	CAPN6	calpain 6	chrXq23	202965_s_at	NM_014289
4.44	4.67	0.23	2.68E-01	6.41E-01	KLK13	kallikrein-related peptidase 13	chr19q13.3-q13.4	216670_at	NM_015596
2.45	2.65	0.20	2.68E-01	6.41E-01	DHFRL1	dihydrofolate reductase-like 1	chr3q11.2	235675_at	NM_176815
2.39	2.55	0.16	2.68E-01	6.41E-01	---	---	---	237221_at	---
2.41	2.60	0.19	2.68E-01	6.41E-01	TMEM31	transmembrane protein 31	chrXq22.2	231569_at	NM_182541
2.69	2.88	0.19	2.68E-01	6.41E-01	KCNQ1OT1	KCNQ1 overlapping transcript 1 (non-protein coding)	chr11p15	237249_at	NR_002728
2.81	3.18	0.36	2.68E-01	6.41E-01	JUP /// KRT19	junction plakoglobin /// keratin 19	chr17q21 /// chr17q21.2	201650_at	NM_002230 /// NM_002276 /// NM_021991
2.13	2.26	0.13	2.68E-01	6.41E-01	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	chr1p31	240349_at	NM_006252
2.42	2.57	0.15	2.68E-01	6.41E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	234964_at	---
3.56	3.76	0.19	2.68E-01	6.41E-01	PDX1	pancreatic and duodenal homeobox 1	chr13q12.1	208559_at	NM_000209
3.74	4.15	0.41	2.68E-01	6.41E-01	GPR176	G protein-coupled receptor 176	chr15q14-q15.1	227846_at	NM_007223
4.43	4.94	0.51	2.68E-01	6.41E-01	SLU7	SLU7 splicing factor homolog (S. cerevisiae)	chr5q33.3	231718_at	NM_006425
4.99	5.34	0.35	2.68E-01	6.41E-01	CLN5	ceroid-lipofuscinosis, neuronal 5	chr13q21.1-q32	204085_s_at	NM_006493
1.98	2.13	0.15	2.68E-01	6.41E-01	---	---	---	235831_at	---
2.66	2.90	0.24	2.68E-01	6.41E-01	LOC554203	hypothetical LOC554203	chrXq13.2	1554447_at	XR_017716 /// XR_017797
2.80	2.97	0.17	2.68E-01	6.41E-01	MTHFSD	methenyltetrahydrofolate synthetase domain containing	chr16q24.1	230442_at	NM_022764
1.98	2.12	0.14	2.68E-01	6.41E-01	SNTG1	Syntrophin, gamma 1	chr8q11-q12	1562287_at	NM_018967
4.31	4.71	0.40	2.68E-01	6.41E-01	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	chr13q14.11	226479_at	NM_152903
6.41	6.79	0.37	2.68E-01	6.41E-01	SUB1	SUB1 homolog (S. cerevisiae)	chr5p13.3	224587_at	NM_006713
2.34	2.58	0.24	2.68E-01	6.41E-01	PTBP2	polypyrimidine tract binding protein 2	chr1p22.1-p21.3	1554614_a_at	NM_021190
2.27	2.46	0.18	2.68E-01	6.41E-01	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	chrXp22.13	242800_at	NM_198270
2.97	3.16	0.18	2.68E-01	6.41E-01	ZNF286A	zinc finger protein 286A	chr17p11.2	220250_at	NM_001130842 /// NM_020652
2.35	2.53	0.17	2.68E-01	6.41E-01	IGHM	immunoglobulin heavy constant mu	chr14q32.33	212827_at	---
2.61	2.75	0.15	2.68E-01	6.41E-01	AADAT	aminoadipate aminotransferase	chr4q33	223593_at	NM_016228 /// NM_182662
1.99	2.11	0.11	2.68E-01	6.41E-01	---	---	---	1556318_s_at	---
2.58	2.78	0.19	2.68E-01	6.42E-01	UPB1	ureidopropionase, beta	chr22q11.2	220507_s_at	NM_016327
1.97	2.13	0.16	2.68E-01	6.42E-01	---	---	---	241310_at	---
3.49	3.74	0.25	2.68E-01	6.42E-01	---	---	---	1562454_at	---
2.59	2.77	0.18	2.68E-01	6.42E-01	---	---	---	241164_at	---
6.36	6.87	0.51	2.68E-01	6.42E-01	STX17	syntaxin 17	chr9q31.1	222708_s_at	NM_017919
2.83	3.05	0.22	2.68E-01	6.42E-01	C19orf15	chromosome 19 open reading frame 15	chr19q13.1	234353_at	NM_021185
3.14	3.29	0.16	2.68E-01	6.42E-01	WDR38	WD repeat domain 38	chr9q33.3	243900_at	NM_001045476
3.15	3.32	0.18	2.69E-01	6.42E-01	PDE5A	phosphodiesterase 5A, cGMP-specific	chr4q25-q27	1562227_at	NM_001083 /// NM_033430 /// NM_033437
2.59	2.75	0.17	2.69E-01	6.42E-01	---	---	---	1554946_at	---
2.05	2.20	0.14	2.69E-01	6.42E-01	---	---	---	214282_at	---
4.59	5.00	0.42	2.69E-01	6.42E-01	---	---	---	236153_at	---
2.57	2.91	0.34	2.69E-01	6.42E-01	---	---	---	1570165_at	---
7.71	8.04	0.33	2.69E-01	6.42E-01	HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11	chr4q22.1	217989_at	NM_016245
4.73	4.98	0.26	2.69E-01	6.42E-01	ZZZ3	zinc finger, ZZ-type containing 3	chr1p31.1	229325_at	NM_015534
5.65	5.88	0.23	2.69E-01	6.42E-01	LTBR	Lymphotoxin beta receptor (TNFR superfamily, member 3)	chr12p13	232819_s_at	NM_002342
2.77	2.96	0.19	2.69E-01	6.42E-01	PGLS	6-phosphogluconolactonase	chr19p13.2	230699_at	NM_012088
6.22	6.42	0.19	2.69E-01	6.42E-01	ST14	suppression of tumorigenicity 14 (colon carcinoma)	chr11q24-q25	202005_at	NM_021978
2.12	2.31	0.19	2.69E-01	6.42E-01	---	---	---	1563460_at	---
3.41	3.58	0.17	2.69E-01	6.42E-01	RUNX1 /// SH3D19	runt-related transcription factor 1 /// SH3 domain containing 19	chr21q22.3 /// chr4q31.3	211620_x_at	NM_001001890 /// NM_001009555 /// NM_001122607 /// NM_001128923 /// NM_001128924 /// NM_001754
1.97	2.14	0.16	2.69E-01	6.42E-01	---	---	---	216007_at	---
2.34	2.49	0.15	2.69E-01	6.42E-01	ANXA9	annexin A9	chr1q21	211712_s_at	NM_003568
2.09	2.22	0.13	2.69E-01	6.42E-01	C10orf12	chromosome 10 open reading frame 12	chr10q24.1	219601_s_at	NM_015652
5.61	6.25	0.64	2.69E-01	6.42E-01	RIOK2	RIO kinase 2 (yeast)	chr5q15	218535_s_at	NM_018343
2.56	2.71	0.16	2.69E-01	6.42E-01	---	---	---	243025_at	---
2.45	2.62	0.16	2.69E-01	6.42E-01	TCTN2	tectonic family member 2	chr12q24.31	239928_at	NM_024809
2.07	2.21	0.14	2.69E-01	6.42E-01	---	---	---	242681_at	---

6.29	6.81	0.52	2.69E-01	6.42E-01	FAS	Fas (TNF receptor superfamily, member 6)	chr10q24.1	204781_s_at	NM_000043 /// NM_152871 /// NM_152872 /// NM_152873 /// NM_152874 /// NM_152875 /// NM_152876 /// NM_152877																			
4.40	4.72	0.32	2.69E-01	6.42E-01	PML	promyelocytic leukemia	chr15q22	211013_x_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250																			
2.72	2.94	0.21	2.69E-01	6.42E-01	---	---	---	234417_at	---																			
2.60	2.80	0.21	2.69E-01	6.42E-01	RAP2B	RAP2B, member of RAS oncogene family	chr3q25.2	238622_at	NM_002886																			
1.83	1.97	0.14	2.69E-01	6.42E-01	---	---	---	243281_at	---																			
2.52	2.72	0.21	2.69E-01	6.42E-01	OR2F1	olfactory receptor, family 2, subfamily F, member 1	chr7q35	208526_at	NM_012369																			
5.24	5.72	0.48	2.69E-01	6.42E-01	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	chr6p25-p24|18q21	210154_at	NM_002396																			
4.07	4.42	0.34	2.69E-01	6.42E-01	ANKHD1 /// ANKHD1-EIF4EBP3 /// EIF4EBP3	ankyrin repeat and KH domain containing 1 /// ANKHD1-EIF4EBP3 /// eukaryotic translation initiation factor 4E binding protein 3	chr5q31.3	233292_s_at	NM_003732 /// NM_017747 /// NM_017978 /// NM_020690 /// NM_024668																			
2.73	3.09	0.36	2.69E-01	6.42E-01	XCL1	chemokine (C motif) ligand 1	chr1q23	206366_x_at	NM_002995																			
4.17	4.51	0.34	2.69E-01	6.42E-01	---	---	---	216472_at	---																			
3.94	4.17	0.23	2.69E-01	6.42E-01	---	---	---	238892_at	---																			
1.98	2.17	0.19	2.69E-01	6.42E-01	---	---	---	1570632_at	---																			
4.81	5.00	0.19	2.69E-01	6.42E-01	---	---	---	232347_x_at	---																			
2.45	2.63	0.19	2.69E-01	6.42E-01	CACNG5	calcium channel, voltage-dependent, gamma subunit 5	chr17q24	221401_at	NM_014404 /// NM_145811																			
3.13	3.43	0.31	2.70E-01	6.43E-01	ARMC8	armadillo repeat containing 8	chr3q22.3	236966_at	NM_014154 /// NM_015396 /// NM_213654																			
2.34	2.52	0.19	2.70E-01	6.43E-01	---	---	---	234618_at	---																			
2.83	3.02	0.19	2.70E-01	6.43E-01	HS3ST5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	chr6q22.31	240479_at	NM_153612																			
2.11	2.29	0.18	2.70E-01	6.43E-01	---	---	---	243577_at	---																			
2.21	2.37	0.16	2.70E-01	6.43E-01	---	---	---	242150_at	---																			
1.99	2.13	0.14	2.70E-01	6.43E-01	---	---	---	234467_at	---																			
4.64	4.79	0.15	2.70E-01	6.43E-01	RP5-886K2.1	neuronal thread protein AD7c-NTP	chr1p36	207953_at	---																			
1.83	1.96	0.13	2.70E-01	6.43E-01	---	---	---	242198_at	---																			
2.74	2.92	0.17	2.70E-01	6.43E-01	HDC	histidine decarboxylase	chr15q21-q22	207067_s_at	NM_002112																			
2.02	2.17	0.15	2.70E-01	6.43E-01	FLJ25770	hypothetical protein FLJ25770	chr4q21.1	243875_at	NM_001042784																			
4.52	4.92	0.40	2.70E-01	6.43E-01	BACE2	beta-site APP-cleaving enzyme 2	chr21q22.3	217867_x_at	NM_012105 /// NM_138991 /// NM_138992																			
2.04	2.18	0.14	2.70E-01	6.43E-01	IQCH	IQ motif containing H	chr15q23	220361_at	NM_001031715 /// NM_022784																			
2.37	2.51	0.14	2.70E-01	6.43E-01	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	242854_x_at	NR_002612																			
2.15	2.27	0.12	2.70E-01	6.43E-01	---	---	---	239244_at	---																			
7.03	7.39	0.36	2.70E-01	6.43E-01	CALU	calumenin	chr7q32.1	200755_s_at	NM_001130674 /// NM_001219																			
7.59	7.87	0.28	2.70E-01	6.43E-01	CLPTM1	cleft lip and palate associated transmembrane protein 1	chr19q13.2-q13.3	211136_s_at	NM_001294																			
3.72	3.91	0.19	2.70E-01	6.43E-01	LAMB2L	laminin, beta 2-like	chr3p21.3-p21.2	230616_at	NR_004405																			
2.15	2.30	0.15	2.70E-01	6.43E-01	TRIM14	tripartite motif-containing 14	chr9q22.33	211044_at	NM_014788 /// NM_033219 /// NM_033220 /// NM_033221																			

2.41	2.57	0.15	2.70E-01	6.43E-01	NOX1	NADPH oxidase 1	chrXq22	207217_s_at	NM_007052 /// NM_013955
3.07	3.28	0.21	2.70E-01	6.43E-01	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	chr7p14-p13	1554152_a_at	NM_001003941 /// NM_002541
2.21	2.35	0.13	2.70E-01	6.43E-01	PDE10A	phosphodiesterase 10A	chr6q26	205501_at	NM_001130690 /// NM_006661
2.10	2.22	0.12	2.70E-01	6.43E-01	---	---	---	237692_at	---
5.10	5.96	0.86	2.70E-01	6.43E-01	---	---	---	240188_at	---
6.69	6.93	0.24	2.70E-01	6.43E-01	EXOC4	exocyst complex component 4	chr7q31	224926_at	NM_001037126 /// NM_021807
1.85	2.07	0.22	2.70E-01	6.43E-01	FLJ35409	FLJ35409 protein	chr1p21.3	1559504_at	XR_017838 /// XR_017942 /// XR_040284
2.51	2.67	0.16	2.70E-01	6.43E-01	---	---	---	217195_at	---
4.97	5.85	0.88	2.70E-01	6.43E-01	C9orf33	chromosome 9 open reading frame 33	chr9q22.1	217130_at	---
2.05	2.17	0.12	2.70E-01	6.43E-01	ATP1A4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	chr1q21-q23	1565346_a_at	NM_001001734 /// NM_144699
2.42	2.60	0.18	2.70E-01	6.43E-01	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	chr16q13	215912_at	NM_020988 /// NM_138736
3.90	4.68	0.78	2.70E-01	6.43E-01	IGK@ /// IGKV3-20 /// IGKV3D-11 /// IGKV3D-15	immunoglobulin kappa locus /// immunoglobulin kappa variable 3-20 /// immunoglobulin kappa variable 3D-11 /// immunoglobulin kappa variable 3D-15	chr2p12	211643_x_at	---
4.76	5.30	0.54	2.70E-01	6.43E-01	APLNR	apelin receptor	chr11q12	213592_at	NM_005161
4.70	5.17	0.48	2.70E-01	6.43E-01	ALG6	asparagine-linked glycosylation 6 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)	chr1p31.3	219649_at	NM_013339
5.73	6.14	0.41	2.70E-01	6.43E-01	---	---	---	235705_at	---
2.52	2.86	0.34	2.70E-01	6.43E-01	PLXDC1	plexin domain containing 1	chr17q21.1	219700_at	NM_020405
2.15	2.33	0.18	2.70E-01	6.43E-01	---	---	---	241579_at	---
2.30	2.47	0.17	2.70E-01	6.43E-01	---	---	---	1569808_at	---
2.32	2.45	0.13	2.70E-01	6.43E-01	---	---	---	234144_at	---
4.90	5.09	0.19	2.70E-01	6.43E-01	STK38L	serine/threonine kinase 38 like	chr12p11.23	212565_at	NM_015000
5.93	6.44	0.51	2.70E-01	6.43E-01	ZNF462	zinc finger protein 462	chr9q31.2	226575_at	NM_021224
3.80	4.10	0.29	2.70E-01	6.43E-01	STK38	serine/threonine kinase 38	chr6p21	1553117_a_at	NM_007271
4.20	4.35	0.15	2.70E-01	6.43E-01	BRI3BP	BRI3 binding protein	chr12q24.31	231810_at	NM_080626
2.24	2.40	0.16	2.70E-01	6.43E-01	GYPA	glycophorin A (MNS blood group)	chr4q28.2-q31.1	211820_x_at	NM_002099
2.51	2.75	0.24	2.70E-01	6.43E-01	---	---	---	238243_at	---
3.76	3.97	0.20	2.70E-01	6.43E-01	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	chr11q13	213919_at	NM_005528
2.09	2.27	0.18	2.70E-01	6.43E-01	---	---	---	1561217_at	---
4.39	4.64	0.25	2.70E-01	6.43E-01	---	---	---	1570197_at	---
2.23	2.42	0.19	2.70E-01	6.43E-01	KIAA1853	KIAA1853	chr12q24.23	237828_at	NM_194286
2.68	2.94	0.25	2.71E-01	6.43E-01	PHTF2	putative homeodomain transcription factor 2	chr7q11.23-q21	217097_s_at	NM_001127357 /// NM_001127358 /// NM_001127359 /// NM_001127360 /// NM_020432
1.82	1.99	0.17	2.71E-01	6.43E-01	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	chr7p12.1	244163_at	NM_006080
2.20	2.35	0.15	2.71E-01	6.43E-01	LOC146513	hypothetical protein LOC146513	chr16q24.1	1562623_at	---
4.47	4.98	0.51	2.71E-01	6.43E-01	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	chr18p11.22	228480_at	NM_003574 /// NM_194434
4.71	5.06	0.36	2.71E-01	6.43E-01	TDRD3	tudor domain containing 3	chr13q21.2	208089_s_at	NM_030794
3.15	3.48	0.33	2.71E-01	6.43E-01	DLG1	discs, large homolog 1 (Drosophila)	chr3q29	202516_s_at	NM_001098424 /// NM_004087
2.60	2.84	0.24	2.71E-01	6.43E-01	WNT7B	wingless-type MMTV integration site family, member 7B	chr22q13	217681_at	NM_058238 /// XM_001718758
2.98	3.21	0.23	2.71E-01	6.43E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	214362_at	NM_002926 /// NM_198227 /// NM_198229
3.39	3.61	0.22	2.71E-01	6.43E-01	---	---	---	239939_at	---
2.72	2.92	0.20	2.71E-01	6.43E-01	WDR61	WD repeat domain 61	chr15q25.1	237208_at	NM_025234
3.24	3.42	0.18	2.71E-01	6.43E-01	NTSR1	neurotensin receptor 1 (high affinity)	chr20q13	207360_s_at	NM_002531
2.30	2.48	0.18	2.71E-01	6.43E-01	MSR1	macrophage scavenger receptor 1	chr8p22	208422_at	NM_002445 /// NM_138715 /// NM_138716
3.21	3.38	0.17	2.71E-01	6.43E-01	---	---	---	1555157_at	---
2.27	2.42	0.15	2.71E-01	6.43E-01	---	---	---	216753_at	---

4.06	4.33	0.27	2.71E-01	6.43E-01	TRIO	Triple functional domain (PTPRF interacting)	chr5p15.2	231403_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929																				
2.96	3.18	0.22	2.71E-01	6.43E-01	IPO9	importin 9	chr1q32.1	242561_at	NM_018085																				
5.68	5.86	0.19	2.71E-01	6.43E-01	DGCR14	DiGeorge syndrome critical region gene 14	chr22q11.21|22q11.2	241748_x_at	NM_022719																				
2.36	2.55	0.19	2.71E-01	6.43E-01	HBP1	HMG-box transcription factor 1	chr7q22-q31	236645_at	NM_012257																				
2.32	2.50	0.18	2.71E-01	6.43E-01	PRDM13	PR domain containing 13	chr6q16-q21	221168_at	NM_021620																				
3.51	3.78	0.27	2.71E-01	6.43E-01	---	---	---	240064_at	---																				
4.13	4.36	0.23	2.71E-01	6.43E-01	LCORL	ligand dependent nuclear receptor corepressor-like	chr4p15.32	240592_at	NM_153686																				
2.41	2.58	0.16	2.71E-01	6.44E-01	AGR2	anterior gradient homolog 2 (Xenopus laevis)	chr7p21.3	228969_at	NM_006408																				
4.12	4.30	0.18	2.71E-01	6.44E-01	MUC13	mucin 13, cell surface associated	chr3q21.2	218687_s_at	NM_033049																				
1.94	2.07	0.13	2.71E-01	6.44E-01	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	chr18q21.3	1555551_at	NM_002639																				
3.70	4.03	0.33	2.71E-01	6.44E-01	PAPLN	papilin, proteoglycan-like sulfated glycoprotein	chr14q24.2	226435_at	NM_173462																				
3.71	4.25	0.55	2.71E-01	6.44E-01	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	chr5q13.3	223465_at	NM_001130105 /// NM_005713 /// NM_031361																				
4.45	4.87	0.42	2.71E-01	6.44E-01	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	chr3p22	207334_s_at	NM_001024847 /// NM_003242																				
5.89	6.12	0.23	2.71E-01	6.44E-01	AGTRAP	angiotensin II receptor-associated protein	chr1p36.22	225059_at	NM_001040194 /// NM_001040195 /// NM_001040196 /// NM_001040197 /// NM_020350																				
2.40	2.55	0.15	2.71E-01	6.44E-01	---	---	---	239686_at	---																				
3.23	3.42	0.20	2.71E-01	6.44E-01	BDKRB1	bradykinin receptor B1	chr14q32.1-q32.2	207510_at	NM_000710																				
2.47	2.59	0.13	2.71E-01	6.44E-01	L2HGDH	L-2-hydroxyglutarate dehydrogenase	chr14q22.1	220089_at	NM_024884																				
3.89	4.28	0.40	2.72E-01	6.44E-01	STK17A	serine/threonine kinase 17a	chr7p12-p14	202695_s_at	NM_004760																				
2.47	2.65	0.18	2.72E-01	6.44E-01	GK5	glycerol kinase 5 (putative)	chr3q23	238121_at	NM_001039547																				
3.85	4.01	0.17	2.72E-01	6.44E-01	SORBS1	sorbin and SH3 domain containing 1	chr10q23.3-q24.1	211705_s_at	NM_001034954 /// NM_001034955 /// NM_001034956 /// NM_001034957 /// NM_006434 /// NM_015385 /// NM_024991																				
1.97	2.10	0.13	2.72E-01	6.44E-01	---	---	---	1560552_a_at	---																				
6.37	6.92	0.54	2.72E-01	6.44E-01	---	---	---	237310_at	---																				
4.47	4.68	0.21	2.72E-01	6.44E-01	AFTPH	aftiphilin	chr2p14	222472_at	NM_001002243 /// NM_017657 /// NM_203437																				
4.09	4.29	0.20	2.72E-01	6.44E-01	CLDN11	claudin 11	chr3q26.2-q26.3	206908_s_at	NM_005602																				
2.57	2.83	0.26	2.72E-01	6.45E-01	KRT4	keratin 4	chr12q12-q13	213240_s_at	NM_002272																				
2.53	2.71	0.18	2.72E-01	6.45E-01	DBF4B	DBF4 homolog B (S. cerevisiae)	chr17q21.31|17q21	238508_at	NM_025104 /// NM_145663																				
2.09	2.23	0.14	2.72E-01	6.45E-01	LOC100128641	similar to hCG1641533	chr10p12.33-p12.32	242660_at	XM_001715990 /// XM_001716836 /// XM_001718667																				
2.06	2.20	0.14	2.72E-01	6.45E-01	---	---	---	235351_at	---																				
5.22	5.91	0.69	2.72E-01	6.45E-01	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	chr13q14.1	227808_at	NM_013238																				

5.02	5.58	0.56	2.72E-01	6.45E-01	PHLDB2 /// PLCXD2	pleckstrin homology-like domain, family B, member 2 /// phosphatidylinositol-specific phospholipase C, X domain containing 2	chr3q13.2	225688_s_at	NM_001134437 /// NM_001134438 /// NM_001134439 /// NM_001134478 /// NM_145753 /// NM_153268
2.41	2.83	0.42	2.72E-01	6.45E-01	---	---	---	244181_at	---
3.28	3.67	0.40	2.72E-01	6.45E-01	TRAM1L1	translocation associated membrane protein 1-like 1	chr4q26	244334_at	NM_152402
8.11	8.43	0.32	2.72E-01	6.45E-01	PDIA6	protein disulfide isomerase family A, member 6	chr2p25.1	216640_s_at	NM_005742
5.36	5.60	0.24	2.72E-01	6.45E-01	C17orf59	chromosome 17 open reading frame 59	chr17p13.1	222882_s_at	NM_017622
4.12	4.35	0.23	2.72E-01	6.45E-01	TRIM66	tripartite motif-containing 66	chr11p15.4	213748_at	XM_001716253 /// XM_001716830 /// XM_001717903
3.46	3.68	0.23	2.72E-01	6.45E-01	---	---	---	1561386_at	---
4.12	4.31	0.19	2.72E-01	6.45E-01	HTRA3	HtrA serine peptidase 3	chr4p16.1	228580_at	NM_053044
2.13	2.31	0.18	2.72E-01	6.45E-01	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	chr9p13-p12	216156_at	NM_021111
2.03	2.21	0.18	2.72E-01	6.45E-01	MIB1	mindbomb homolog 1 (Drosophila)	chr18q11.2	1558645_at	NM_020774
2.10	2.28	0.17	2.72E-01	6.45E-01	SLC12A5	solute carrier family 12 (potassium-chloride transporter), member 5	chr20q13.12	210040_at	NM_020708
3.01	3.18	0.17	2.72E-01	6.45E-01	CASZ1	castor zinc finger 1	chr1p36.22	233863_at	NM_001079843 /// NM_017766
3.63	3.79	0.16	2.72E-01	6.45E-01	---	---	---	216324_at	---
2.53	2.68	0.16	2.72E-01	6.45E-01	INF2	inverted formin, FH2 and WH2 domain containing	chr14q32.33	222534_s_at	NM_001031714 /// NM_022489 /// NM_032714
2.14	2.29	0.15	2.72E-01	6.45E-01	---	---	---	AFFX-r2-Bs-phe-M_at	---
2.33	2.48	0.15	2.72E-01	6.45E-01	---	---	---	243855_at	---
1.91	2.05	0.14	2.72E-01	6.45E-01	---	---	---	241369_at	---
1.86	1.98	0.12	2.72E-01	6.45E-01	SYCP2	Synaptonemal complex protein 2	chr20q13.33	237920_at	NM_014258
5.07	5.33	0.26	2.72E-01	6.45E-01	JSRP1	junctional sarcoplasmic reticulum protein 1	chr19p13.3	235863_at	NM_144616
3.30	3.46	0.16	2.72E-01	6.45E-01	PSKH2	protein serine kinase H2	chr8q21.2	1553060_at	NM_033126
2.13	2.28	0.15	2.72E-01	6.45E-01	---	---	---	237361_at	---
2.55	2.74	0.19	2.72E-01	6.45E-01	---	---	---	243497_at	---
2.71	2.90	0.19	2.72E-01	6.45E-01	PDE1A	phosphodiesterase 1A, calmodulin-dependent	chr2q32.1	231213_at	NM_001003683 /// NM_005019
6.89	7.43	0.53	2.72E-01	6.45E-01	FYTTD1	forty-two-three domain containing 1	chr3q29	224641_at	NM_001011537 /// NM_032288
1.85	1.98	0.13	2.72E-01	6.45E-01	KLHL32	kelch-like 32 (Drosophila)	chr6q16.1	1553765_a_at	NM_052904
2.16	2.29	0.12	2.73E-01	6.45E-01	---	---	---	1560596_at	---
2.48	2.64	0.17	2.73E-01	6.45E-01	---	---	---	230302_at	---
6.11	6.39	0.28	2.73E-01	6.45E-01	---	---	---	217549_at	---
5.81	6.19	0.38	2.73E-01	6.45E-01	ZMYM4	zinc finger, MYM-type 4	chr1p32-p34	202049_s_at	NM_005095
8.59	8.97	0.38	2.73E-01	6.45E-01	PECI	peroxisomal D3,D2-enoyl-CoA isomerase	chr6p24.3	218025_s_at	NM_006117 /// NM_206836
1.97	2.23	0.26	2.73E-01	6.45E-01	PCSK2	proprotein convertase subtilisin/kexin type 2	chr20p11.2	204869_at	NM_002594
3.28	3.50	0.22	2.73E-01	6.45E-01	TP53I13	Tumor protein p53 inducible protein 13	chr17q11.2	229056_at	NM_138349
3.56	3.78	0.22	2.73E-01	6.45E-01	BTNL9	Butyrophilin-like 9	chr5q35.3	241496_at	NM_152547
3.86	4.06	0.21	2.73E-01	6.45E-01	DRD2	dopamine receptor D2	chr11q23	206590_x_at	NM_000795 /// NM_016574
2.43	2.57	0.15	2.73E-01	6.45E-01	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	chr12q12-q14	216382_s_at	NM_003482
3.97	4.21	0.24	2.73E-01	6.45E-01	---	---	---	243260_x_at	---
2.51	2.71	0.20	2.73E-01	6.45E-01	---	---	---	239165_at	---
1.95	2.09	0.14	2.73E-01	6.45E-01	CCNYL2	cyclin Y-like 2	chr10q11.21	1569878_at	XM_001714283 /// XM_374787 /// XM_936368
1.84	1.96	0.12	2.73E-01	6.45E-01	CLDN23	claudin 23	chr8p23.1	228706_s_at	NM_194284
4.50	5.10	0.61	2.73E-01	6.45E-01	IFI16	interferon, gamma-inducible protein 16	chr1q22	208965_s_at	NM_005531
3.84	4.20	0.36	2.73E-01	6.45E-01	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	chrXp22.1-p21.3	204835_at	NM_016937
5.84	6.06	0.22	2.73E-01	6.45E-01	HDAC6	histone deacetylase 6	chrXp11.23	216224_s_at	NM_006044
1.93	2.09	0.15	2.73E-01	6.45E-01	---	---	---	1560187_at	---
2.78	2.93	0.14	2.73E-01	6.45E-01	---	---	---	232818_at	---
2.11	2.23	0.12	2.73E-01	6.45E-01	---	---	---	241663_at	---
5.05	5.23	0.17	2.73E-01	6.46E-01	ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	chr7q36	206317_s_at	NM_007188

7.57	8.55	0.98	2.73E-01	6.46E-01	RGS5	regulator of G-protein signaling 5	chr1q23.1	209070_s_at	NM_003617
5.99	6.38	0.39	2.73E-01	6.46E-01	MRPS10	mitochondrial ribosomal protein S10	chr6p21.1	222522_x_at	NM_018141
5.76	6.55	0.78	2.73E-01	6.46E-01	JAK1	Janus kinase 1 (a protein tyrosine kinase)	chr1p32.3-p31.3	1552610_a_at	NM_002227
8.03	8.41	0.38	2.73E-01	6.46E-01	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	chr2q33	208761_s_at	NM_001005781 /// NM_001005782 /// NM_003352
4.11	4.29	0.18	2.73E-01	6.46E-01	---	---	---	238247_at	---
3.80	3.96	0.16	2.73E-01	6.46E-01	---	---	---	228896_at	---
5.66	6.15	0.49	2.73E-01	6.46E-01	---	---	---	AFFX-HUMRGE/M10098_M_at	---
2.70	2.89	0.19	2.73E-01	6.46E-01	NSMAF	Neutral sphingomyelinase (N-SMase) activation associated factor	chr8q12-q13	232148_at	NM_003580
3.83	4.00	0.17	2.73E-01	6.46E-01	LOC402665	hCG1651476	chr19q13.33	244694_at	NM_001101372
2.29	2.52	0.23	2.73E-01	6.46E-01	FABP4	fatty acid binding protein 4, adipocyte	chr8q21	235978_at	NM_001442
1.84	1.95	0.11	2.73E-01	6.46E-01	SLC26A7	solute carrier family 26, member 7	chr8q23	1552826_at	NM_052832 /// NM_134266
4.88	5.29	0.41	2.74E-01	6.46E-01	TULP4	Tubby like protein 4	chr6q25-q26	239742_at	NM_001007466 /// NM_020245
2.04	2.20	0.16	2.74E-01	6.46E-01	C7orf44	chromosome 7 open reading frame 44	chr7p13	206497_at	NM_018224
2.39	2.52	0.13	2.74E-01	6.46E-01	CRYBA2	crystallin, beta A2	chr2q34-q36	220136_s_at	NM_005209 /// NM_057093 /// NM_057094
2.27	2.51	0.24	2.74E-01	6.46E-01	C16orf81	chromosome 16 open reading frame 81	chr16q24.3	1553450_s_at	XM_001126835 /// XM_001134340 /// XM_001719860
2.63	2.81	0.17	2.74E-01	6.46E-01	---	---	---	216514_at	---
2.18	2.35	0.17	2.74E-01	6.46E-01	TMEM144	transmembrane protein 144	chr4q32.1	217613_at	NM_018342
2.65	2.82	0.17	2.74E-01	6.46E-01	ITSN1	intersectin 1 (SH3 domain protein)	chr21q22.1-q22.2	210713_at	NM_001001132 /// NM_003024
11.46	11.59	0.13	2.74E-01	6.46E-01	GNAS	GNAS complex locus	chr20q13.3	200780_x_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259
4.83	5.42	0.59	2.74E-01	6.46E-01	---	---	---	244414_at	---
2.49	2.73	0.24	2.74E-01	6.46E-01	ZNF563	zinc finger protein 563	chr19p13.2	1552770_s_at	NM_145276
1.98	2.12	0.14	2.74E-01	6.46E-01	LOC100130703	similar to hCG2042168	chr5q21.1	207596_at	XM_001714375 /// XM_001715488 /// XM_001724520
1.91	2.02	0.11	2.74E-01	6.46E-01	LOC100128180	PRO2116	chr4q24	223966_at	XM_001723577 /// XM_001723629 /// XM_001724820
5.74	6.22	0.48	2.74E-01	6.46E-01	KPNA1	karyopherin alpha 1 (importin alpha 5)	chr3q21	202056_at	NM_002264
8.45	8.89	0.43	2.74E-01	6.46E-01	PAIP2	poly(A) binding protein interacting protein 2	chr5q31.2	222984_at	NM_001033112 /// NM_016480
5.40	5.80	0.40	2.74E-01	6.46E-01	FXYD1	FXYD domain containing ion transport regulator 1	chr19q13.1	205384_at	NM_005031 /// NM_021902
8.80	9.11	0.31	2.74E-01	6.46E-01	SUB1	SUB1 homolog (S. cerevisiae)	chr5p13.3	224586_x_at	NM_006713
3.61	3.86	0.25	2.74E-01	6.46E-01	LOC100129175	hypothetical protein LOC100129175	chr2q35	1557879_at	XM_001714355 /// XM_001715986 /// XM_001717896
3.04	3.25	0.21	2.74E-01	6.46E-01	CD84	CD84 molecule	chr1q24	211190_x_at	NM_003874

3.06	3.38	0.33	2.74E-01	6.46E-01	FLJ32255	hypothetical protein LOC643977	chr5p12	235292_at	XM_001720829 /// XM_001722479 /// XM_001723787
2.81	2.99	0.18	2.74E-01	6.46E-01	ATOH1	atonal homolog 1 (Drosophila)	chr4q22	221336_at	NM_005172
2.87	3.01	0.14	2.74E-01	6.46E-01	PPP4R1L	protein phosphatase 4, regulatory subunit 1-like	chr20q13.32	233069_at	NR_003505
2.01	2.16	0.15	2.74E-01	6.46E-01	PEX5L	peroxisomal biogenesis factor 5-like	chr3q26.33	219642_s_at	NM_016559
2.53	2.73	0.21	2.74E-01	6.46E-01	---	---	---	236437_at	---
2.41	2.55	0.14	2.74E-01	6.46E-01	LOC643503	similar to hCG39525	chr20p12.3	216420_at	XM_001723751 /// XM_001725260 /// XM_001725280
3.96	4.19	0.23	2.74E-01	6.46E-01	TMEM30B	transmembrane protein 30B	chr14q23.1	230471_at	NM_001017970
3.58	3.87	0.29	2.74E-01	6.46E-01	---	---	---	1556205_at	---
2.18	2.33	0.15	2.74E-01	6.46E-01	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	chr2q33.3-q34	233494_at	NM_001042599 /// NM_005235
4.21	4.77	0.56	2.75E-01	6.47E-01	GTPBP10	GTP-binding protein 10 (putative)	chr7q21.13	234311_s_at	NM_001042717 /// NM_033107
2.70	2.92	0.21	2.74E-01	6.47E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31 /// LOC100126583 /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant gamma 4 (G4m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical LOC100126583 /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	217217_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001724554 /// XM_941465
3.09	3.29	0.20	2.75E-01	6.47E-01	TPRXL	tetra-peptide repeat homeobox-like	chr3p25.1	239061_at	NR_002223
4.52	4.72	0.20	2.74E-01	6.47E-01	NUMA1	nuclear mitotic apparatus protein 1	chr11q13	214251_s_at	NM_006185
4.13	4.32	0.19	2.75E-01	6.47E-01	---	---	---	231537_at	---
2.53	2.68	0.15	2.75E-01	6.47E-01	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	chr20q13.2-q13.3	231801_at	NM_012340 /// NM_173091
2.06	2.21	0.14	2.75E-01	6.47E-01	---	---	---	237269_at	---
6.00	6.89	0.89	2.75E-01	6.47E-01	PTPN11	protein tyrosine phosphatase, non-receptor type 11	chr12q24	209896_s_at	NM_002834
5.69	6.46	0.77	2.75E-01	6.47E-01	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	chr9q21	227988_s_at	NM_001018037 /// NM_001018038 /// NM_015186 /// NM_033305
8.35	9.04	0.69	2.75E-01	6.47E-01	MAP3K5	mitogen-activated protein kinase kinase kinase 5	chr6q22.33	203836_s_at	NM_005923
3.56	3.81	0.25	2.75E-01	6.47E-01	LAMA4	laminin, alpha 4	chr6q21	210089_s_at	NM_001105206 /// NM_001105207 /// NM_001105208 /// NM_001105209 /// NM_002290
3.15	3.39	0.25	2.75E-01	6.47E-01	---	---	---	1569930_at	---
2.96	3.17	0.21	2.75E-01	6.47E-01	---	---	---	1566500_at	---
2.29	2.48	0.19	2.75E-01	6.47E-01	FBXO39	F-box protein 39	chr17p13.2	1552830_at	NM_153230
3.42	3.61	0.19	2.75E-01	6.47E-01	C19orf26	chromosome 19 open reading frame 26	chr19p13.3	1552355_s_at	NM_152769
3.04	3.23	0.19	2.75E-01	6.47E-01	CA1	carbonic anhydrase I	chr8q13-q22.1	205950_s_at	NM_001128829 /// NM_001128830 /// NM_001128831 /// NM_001738
2.44	2.62	0.18	2.75E-01	6.47E-01	LOC284009	hypothetical protein LOC284009	chr17p13.3	1557399_at	NM_001025459
2.04	2.22	0.18	2.75E-01	6.47E-01	LOC169834	hypothetical protein LOC169834	chr9q32	230876_at	NM_001101338
2.51	2.69	0.18	2.75E-01	6.47E-01	SLC22A1	solute carrier family 22 (organic cation transporter), member 1	chr6q26	207201_s_at	NM_003057 /// NM_153187
2.82	3.00	0.18	2.75E-01	6.47E-01	C1orf177	chromosome 1 open reading frame 177	chr1p32.3	1557016_a_at	NM_001110533 /// NM_152607
2.21	2.34	0.13	2.75E-01	6.47E-01	---	---	---	1570206_at	---
2.12	2.24	0.12	2.75E-01	6.47E-01	---	---	---	236304_at	---
3.98	4.36	0.37	2.75E-01	6.47E-01	---	---	---	230503_at	---

4.17	4.54	0.37	2.75E-01	6.47E-01	---	---	---	232601_at	---
2.16	2.29	0.13	2.75E-01	6.47E-01	FLJ36665	hypothetical protein FLJ36665	chr3p21.33	1556558_s_at	---
2.09	2.26	0.17	2.75E-01	6.47E-01	---	---	---	226777_at	---
5.38	5.69	0.30	2.75E-01	6.47E-01	LSAMP	limbic system-associated membrane protein	chr3q13.2-q21	214460_at	NM_002338
1.96	2.09	0.13	2.75E-01	6.47E-01	---	---	---	1561672_at	---
6.89	7.10	0.21	2.75E-01	6.47E-01	MAPK3	mitogen-activated protein kinase 3	chr16p11.2	212046_x_at	NM_001040056 /// NM_001109891 /// NM_002746
2.02	2.25	0.23	2.75E-01	6.47E-01	---	---	---	243368_at	---
2.53	2.65	0.12	2.75E-01	6.47E-01	ZNF493	zinc finger protein 493	chr19p12	235604_x_at	NM_001076678 /// NM_175910
3.75	4.02	0.27	2.75E-01	6.47E-01	---	---	---	239744_at	---
2.22	2.41	0.19	2.75E-01	6.47E-01	FLJ34503	hypothetical FLJ34503	chr6q22.1	1553448_at	XR_040042 /// XR_040043 /// XR_040044
2.74	2.87	0.14	2.75E-01	6.47E-01	CHML	choroideremia-like (Rab escort protein 2)	chr1q42-qter	206079_at	NM_001821
5.23	5.81	0.58	2.75E-01	6.47E-01	ERBB2IP	erbb2 interacting protein	chr5q12.3	222473_s_at	NM_001006600 /// NM_018695
4.57	4.77	0.20	2.75E-01	6.47E-01	SPDEF	SAM pointed domain containing ets transcription factor	chr6p21.3	220192_x_at	NM_012391
2.06	2.22	0.16	2.76E-01	6.47E-01	---	---	---	240745_at	---
4.57	4.93	0.36	2.76E-01	6.47E-01	PTCD2	pentatricopeptide repeat domain 2	chr5q13.2	1555910_at	NM_024754
3.30	3.56	0.26	2.76E-01	6.47E-01	---	---	---	1563045_at	---
2.94	3.11	0.17	2.76E-01	6.47E-01	---	---	---	1562078_at	---
2.18	2.34	0.16	2.76E-01	6.47E-01	DTWD1	DTW domain containing 1	chr15q21.2	244146_at	NM_020234
2.12	2.29	0.18	2.76E-01	6.48E-01	---	---	---	1561339_at	---
4.88	5.16	0.28	2.76E-01	6.48E-01	PICALM	phosphatidylinositol binding clathrin assembly protein	chr11q14	203134_at	NM_001008660 /// NM_007166
4.12	4.37	0.26	2.76E-01	6.48E-01	NUP210	nucleoporin 210kDa	chr3p25.1	212315_s_at	NM_024923
2.00	2.16	0.16	2.76E-01	6.48E-01	ANKRD20A1 /// ANKRD20A2 /// ANKRD20A3 /// ANKRD20A4 /// CCDC29	ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family, member A2 /// ankyrin repeat domain 20 family, member A3 /// ankyrin repeat domain 20 family, member A4 /// coiled-coil domain containing 29	chr9p11.2 /// chr9p12-p11.2 /// chr9q12	224012_at	NM_001012419 /// NM_001012421 /// NM_001098805 /// NM_001098806 /// NM_032250
3.69	3.89	0.20	2.76E-01	6.48E-01	MASP2	mannan-binding lectin serine peptidase 2	chr1p36.3-p36.2	216968_at	NM_006610 /// NM_139208
2.35	2.50	0.15	2.76E-01	6.48E-01	C22orf33	chromosome 22 open reading frame 33	chr22q12-q13	231617_at	NM_178552
6.48	7.18	0.70	2.76E-01	6.48E-01	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	chr12q24.2-q24.3	216449_x_at	NM_003299
4.14	4.55	0.42	2.76E-01	6.48E-01	---	---	---	243524_at	---
2.65	2.85	0.20	2.76E-01	6.48E-01	STK4	serine/threonine kinase 4	chr20q11.2-q13.2	243981_at	NM_006282
7.58	7.74	0.16	2.76E-01	6.48E-01	MYO1C	myosin IC	chr17p13	214656_x_at	NM_001080779 /// NM_001080950 /// NM_033375
2.46	2.61	0.16	2.76E-01	6.48E-01	---	---	---	242527_at	---
3.38	3.77	0.39	2.76E-01	6.48E-01	---	---	---	240498_at	---
7.82	8.34	0.52	2.76E-01	6.48E-01	ZMYND11	zinc finger, MYND domain containing 11	chr10p14	202136_at	NM_006624 /// NM_212479
3.60	3.76	0.16	2.76E-01	6.48E-01	LOC387895	Hypothetical gene supported by BC040060	chr12q24.32	1560818_at	XM_373553 /// XM_945559
3.15	3.29	0.14	2.76E-01	6.48E-01	MGC12488	hypothetical protein MGC12488	---	211386_at	---
2.98	3.10	0.12	2.76E-01	6.48E-01	---	---	---	233526_at	---
5.02	5.40	0.38	2.76E-01	6.48E-01	TDRD7	tudor domain containing 7	chr9q22.33	213361_at	NM_014290
6.38	6.74	0.35	2.76E-01	6.48E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	208485_x_at	NM_001127183 /// NM_001127184 /// NM_003879
2.10	2.25	0.15	2.76E-01	6.48E-01	ADAM2	ADAM metallopeptidase domain 2	chr8p11.2	207664_at	NM_001464
2.31	2.45	0.14	2.76E-01	6.48E-01	41528	Septin 11	chr4q21.1	214293_at	NM_018243
2.30	2.69	0.39	2.76E-01	6.48E-01	PCLO	piccolo (presynaptic cytomatrix protein)	chr7q11.23-q21.3	210650_s_at	NM_014510 /// NM_033026
4.29	4.49	0.20	2.76E-01	6.48E-01	LOC199800	hypothetical protein LOC199800	chr19q13.33	232154_at	NM_001101340
2.92	3.05	0.13	2.76E-01	6.48E-01	DOCK1	Dedicator of cytokinesis 1	chr10q26.13-q26.3	232930_at	NM_001380
2.22	2.35	0.12	2.76E-01	6.48E-01	---	---	---	243217_at	---

5.80	6.35	0.55	2.77E-01	6.48E-01	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	chr9p22	204917_s_at	NM_004529																					
10.87	11.24	0.37	2.77E-01	6.48E-01	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	chr10p15.1	205711_x_at	NM_001001973 /// NM_005174																					
3.88	4.14	0.27	2.77E-01	6.48E-01	---	---	---	241166_at	---																					
4.04	4.26	0.22	2.77E-01	6.48E-01	ZNF565	zinc finger protein 565	chr19q13.12	228305_at	NM_001042474 /// NM_152477																					
4.93	5.15	0.22	2.77E-01	6.48E-01	---	---	---	1569604_at	---																					
5.28	5.48	0.20	2.77E-01	6.48E-01	LOC339984	Hypothetical protein LOC339984	chr4p16.3	228880_at	---																					
2.57	2.77	0.20	2.77E-01	6.48E-01	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	chr7q34	240391_at	NM_004546																					
4.13	4.30	0.17	2.77E-01	6.48E-01	SBF1	SET binding factor 1	chr22q13.33	212389_at	NM_002972																					
1.89	2.03	0.14	2.77E-01	6.48E-01	---	---	---	240542_at	---																					
3.96	4.31	0.34	2.77E-01	6.48E-01	---	---	---	230241_at	---																					
3.52	3.74	0.22	2.77E-01	6.48E-01	---	---	---	236435_at	---																					
3.54	3.73	0.19	2.77E-01	6.48E-01	CCDC85B	Coiled-coil domain containing 85B	chr11q12.1	213250_at	NM_006848																					
4.90	5.07	0.17	2.77E-01	6.48E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	216412_x_at	---																					
1.94	2.10	0.16	2.77E-01	6.48E-01	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	chr5q31.1-q33.1	1568612_at	NM_000816 /// NM_198903 /// NM_198904																					
2.14	2.32	0.18	2.77E-01	6.48E-01	PRLR	prolactin receptor	chr5p14-p13	206346_at	NM_000949																					
2.09	2.23	0.14	2.77E-01	6.48E-01	PLA2R1	phospholipase A2 receptor 1, 180kDa	chr2q23-q24	207415_at	NM_001007267 /// NM_007366																					
2.54	2.75	0.21	2.77E-01	6.48E-01	RBL1	retinoblastoma-like 1 (p107)	chr20q11.2	1555004_a_at	NM_002895 /// NM_183404																					
2.31	2.47	0.16	2.77E-01	6.48E-01	P2RY4	pyrimidinergic receptor P2Y, G-protein coupled, 4	chrXq13	221466_at	NM_002565																					
2.30	2.46	0.16	2.77E-01	6.48E-01	ZNF557	zinc finger protein 557	chr19p13.2	239259_at	NM_001044387 /// NM_001044388 /// NM_024341																					
9.36	9.60	0.25	2.77E-01	6.49E-01	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	chr4q24	200668_s_at	NM_003340 /// NM_181886 /// NM_181887 /// NM_181888 /// NM_181889 /// NM_181890 /// NM_181891 /// NM_181892 /// NM_181893																					
3.07	3.26	0.20	2.77E-01	6.49E-01	CT47.7 /// CT47.8 /// RP6-166C19.1 /// RP6-166C19.10 /// RP6-166C19.11 /// RP6-166C19.2 /// RP6-166C19.3 /// RP6-166C19.4 /// RP6-166C19.5 /// RP6-166C19.6 /// RP6-166C19.9	cancer/testis CT47 family, member 7 /// cancer/testis CT47 family, member 8 /// cancer/testis CT47 family, member 1 /// cancer/testis CT47 family, member 10 /// cancer/testis CT47 family, member 11 /// cancer/testis CT47 family, member 2 /// cancer/testis CT47 family, member 3 /// cancer/testis CT47 family, member 4 /// cancer/testis CT47 family, member 5 /// cancer/testis CT47 family, member 6 /// cancer/testis CT47 family, member 9	chrXq24	231568_at	NM_001080137 /// NM_001080138 /// NM_001080139 /// NM_001080140 /// NM_001080141 /// NM_001080142 /// NM_001080143 /// NM_001080144 /// NM_001080145 /// NM_001080146 /// NM_173571																					
5.96	6.39	0.43	2.77E-01	6.49E-01	DYM	dymeclin	chr18q12-q21.1	223171_at	NM_017653																					
2.26	2.44	0.19	2.77E-01	6.49E-01	---	---	---	217288_at	---																					
4.61	4.78	0.17	2.77E-01	6.49E-01	RUFY1	RUN and FYVE domain containing 1	chr5q35.3	233381_at	NM_001040451 /// NM_001040452 /// NM_025158																					
1.89	2.01	0.12	2.77E-01	6.49E-01	---	---	---	244567_at	---																					
3.94	4.20	0.26	2.77E-01	6.49E-01	ZNF274	zinc finger protein 274	chr19qter	232436_at	NM_016324 /// NM_016325 /// NM_133502																					

2.37	2.58	0.21	2.77E-01	6.49E-01	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	chr1p34	205282_at	NM_001018054 /// NM_004631 /// NM_017522 /// NM_033300
6.07	6.31	0.24	2.77E-01	6.49E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	214543_x_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855
2.18	2.32	0.14	2.77E-01	6.49E-01	---	---	---	235642_at	---
2.22	2.41	0.19	2.77E-01	6.49E-01	PLCL1	phospholipase C-like 1	chr2q33	241859_at	NM_001114661 /// NM_006226
5.89	6.29	0.41	2.77E-01	6.49E-01	UBL3	ubiquitin-like 3	chr13q12-q13	201534_s_at	NM_007106
2.33	2.44	0.11	2.77E-01	6.49E-01	SFRS8	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	chr12q24.33	240078_at	NM_004592
3.63	3.89	0.26	2.78E-01	6.49E-01	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	chrXp22.2	203299_s_at	NM_003916
2.51	2.72	0.21	2.78E-01	6.49E-01	---	---	---	1560753_at	---
2.49	2.67	0.18	2.78E-01	6.49E-01	---	---	---	233501_at	---
2.80	2.97	0.17	2.78E-01	6.49E-01	NAT8	N-acetyltransferase 8	chr2p13.1-p12	210289_at	NM_003960
3.14	3.40	0.26	2.78E-01	6.49E-01	---	---	---	230300_at	---
3.92	4.18	0.26	2.78E-01	6.49E-01	SLC22A25	solute carrier family 22, member 25	chr11q12.3	1561093_at	NM_199352
8.42	8.67	0.26	2.78E-01	6.49E-01	BTN3A2 /// BTN3A3	butyrophilin, subfamily 3, member A2 /// butyrophilin, subfamily 3, member A3	chr6p21.3 /// chr6p22.1	204820_s_at	NM_006994 /// NM_007047 /// NM_197974
2.45	2.70	0.25	2.78E-01	6.49E-01	---	---	---	240121_x_at	---
4.47	4.67	0.20	2.78E-01	6.49E-01	---	---	---	243004_at	---
2.16	2.34	0.18	2.78E-01	6.49E-01	LOC729589	hypothetical LOC729589	chr18p11.21	241308_at	XM_001130715 /// XM_001130851 /// XM_001720858
2.97	3.14	0.17	2.78E-01	6.49E-01	TMPRSS4	transmembrane protease, serine 4	chr11q23.3	218960_at	NM_001083947 /// NM_019894
2.47	2.62	0.16	2.78E-01	6.49E-01	---	---	---	237542_at	---
2.08	2.23	0.15	2.78E-01	6.49E-01	MST1 /// MSTP9	macrophage stimulating 1 (hepatocyte growth factor-like) /// macrophage stimulating, pseudogene 9	chr1p36.13 /// chr3p21	213382_at	NM_020998 /// NR_002729
2.08	2.23	0.15	2.78E-01	6.49E-01	RBM26	RNA binding motif protein 26	chr13q31.1	220509_at	NM_022118
3.90	4.39	0.49	2.78E-01	6.49E-01	EXOC5	exocyst complex component 5	chr14q23.1	222726_s_at	NM_006544
6.64	6.99	0.35	2.78E-01	6.49E-01	STX12	syntaxin 12	chr1p35-p34.1	212111_at	NM_177424
1.99	2.14	0.14	2.78E-01	6.49E-01	IQCK	IQ motif containing K	chr16p12.3	216135_at	NM_153208
2.85	3.04	0.19	2.78E-01	6.49E-01	---	---	---	222189_at	---
4.68	4.89	0.21	2.78E-01	6.49E-01	CHST8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	chr19q13.1	221065_s_at	NM_001127895 /// NM_001127896 /// NM_022467
2.22	2.35	0.14	2.78E-01	6.49E-01	C15orf50	chromosome 15 open reading frame 50	---	1554716_s_at	---
2.62	2.97	0.35	2.78E-01	6.50E-01	---	---	---	237778_at	---
5.52	5.75	0.23	2.78E-01	6.50E-01	MMP19	matrix metallopeptidase 19	chr12q14	204574_s_at	NM_002429
5.80	6.34	0.53	2.78E-01	6.50E-01	TSHZ2	teashirt zinc finger homeobox 2	chr20q13.2	235616_at	NM_173485
2.25	2.38	0.13	2.78E-01	6.50E-01	HERC4	hect domain and RLD 4	chr10q21.3	233509_at	NM_015601 /// NM_022079
4.85	5.04	0.19	2.78E-01	6.50E-01	SCUBE3	Signal peptide, CUB domain, EGF-like 3	chr6p21.3	230253_at	NM_152753
6.01	6.29	0.27	2.78E-01	6.50E-01	TNPO1	transportin 1	chr5q13.2	225765_at	NM_002270 /// NM_153188
2.58	2.75	0.18	2.78E-01	6.50E-01	---	---	---	234443_at	---
2.68	2.84	0.16	2.78E-01	6.50E-01	---	---	---	1559877_at	---
4.38	4.62	0.23	2.79E-01	6.50E-01	---	---	---	236460_at	---
3.23	3.43	0.21	2.79E-01	6.50E-01	MMP2	Matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	chr16q13-q21	1566678_at	NM_001127891 /// NM_004530
4.61	4.80	0.19	2.78E-01	6.50E-01	APOA4	apolipoprotein A-IV	chr11q23	206894_at	NM_000482
2.93	3.12	0.18	2.79E-01	6.50E-01	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	chr11cen-q22.3	231295_at	NM_001014811 /// NM_006680
2.32	2.47	0.16	2.79E-01	6.50E-01	SPANXB1 /// SPANXB2 /// SPANXF1	SPANX family, member B1 /// SPANX family, member B2 /// SPANX family, member F1	chrXq27.1	220921_at	NM_032461 /// NM_139019 /// NM_145664 /// XM_001713741
3.91	4.19	0.28	2.79E-01	6.50E-01	PLXNC1	Plexin C1	chr12q23.3	235328_at	NM_005761

2.11	2.34	0.24	2.79E-01	6.50E-01	IGK@ /// IGKC /// IGKV1-5 /// LOC647506 /// LOC652694	immunoglobulin kappa locus /// immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5 /// similar to Ig kappa chain V-I region HK101 precursor /// similar to Ig kappa chain V-I region HK102 precursor	chr2p12	216829_at	XM_001713938 /// XM_942302
2.30	2.49	0.19	2.79E-01	6.50E-01	SNCAIP	synuclein, alpha interacting protein	chr5q23.1-q23.3	237834_at	NM_005460
2.84	3.10	0.26	2.79E-01	6.50E-01	CD22	CD22 molecule	chr19q13.1	217422_s_at	NM_001771
5.15	5.56	0.41	2.79E-01	6.50E-01	TMEM33	transmembrane protein 33	chr4p13	218465_at	NM_018126
2.05	2.20	0.14	2.79E-01	6.50E-01	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	chr11q14.3	1560490_at	NM_001008781
6.69	7.49	0.81	2.79E-01	6.50E-01	PSD3	pleckstrin and Sec7 domain containing 3	chr8pter-p23.3	203354_s_at	NM_015310 /// NM_206909
2.56	2.77	0.20	2.79E-01	6.51E-01	---	---	---	1557491_at	---
5.77	6.36	0.59	2.79E-01	6.51E-01	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	chr4q32.1	203096_s_at	NM_014247
3.28	3.55	0.27	2.79E-01	6.51E-01	LOC100131117	similar to hCG2045385	chr3q13.31	231497_at	XM_001715581 /// XM_001717009 /// XM_001717365
2.62	2.84	0.22	2.79E-01	6.51E-01	KIAA0241	KIAA0241	chr7p14.3	244355_at	NM_015060
5.84	6.14	0.31	2.79E-01	6.51E-01	HNMT	histamine N-methyltransferase	chr2q22.1	204112_s_at	NM_001024074 /// NM_001024075 /// NM_006895
5.46	5.65	0.19	2.79E-01	6.51E-01	TUT1	terminal uridylyl transferase 1, U6 snRNA-specific	chr11q12.2	218965_s_at	NM_022830
6.16	6.40	0.24	2.79E-01	6.51E-01	TRPV2	transient receptor potential cation channel, subfamily V, member 2	chr17p11.2	219282_s_at	NM_016113
2.08	2.21	0.13	2.79E-01	6.51E-01	ZFP42	zinc finger protein 42 homolog (mouse)	chr4q35.2	243161_x_at	NM_174900
4.71	5.09	0.38	2.79E-01	6.51E-01	KPNA4	karyopherin alpha 4 (importin alpha 3)	chr3q25.33	225267_at	NM_002268
2.01	2.15	0.14	2.79E-01	6.51E-01	---	---	---	1562857_at	---
2.93	3.19	0.27	2.79E-01	6.51E-01	ZNF253	zinc finger protein 253	chr19p13.11	206900_x_at	NM_021047
2.18	2.41	0.23	2.79E-01	6.51E-01	LRGUK	leucine-rich repeats and guanylate kinase domain containing	chr7q33	244710_at	NM_144648
5.42	5.89	0.47	2.79E-01	6.51E-01	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	chr5q23-q31	205032_at	NM_002203
2.22	2.39	0.17	2.79E-01	6.51E-01	LOC147804 /// TPM3	tropomyosin 3 pseudogene /// tropomyosin 3	chr19q13.41 /// chr1q21.2	234620_at	NM_001043351 /// NM_001043352 /// NM_001043353 /// NM_152263 /// NM_153649 /// NR_003148
2.35	2.51	0.16	2.79E-01	6.51E-01	NANOG	Nanog homeobox	chr12p13.31	220184_at	NM_024865
2.11	2.26	0.15	2.79E-01	6.51E-01	TBC1D7	TBC1 domain family, member 7	chr6p24.1	1563839_at	NM_016495
2.30	2.45	0.14	2.79E-01	6.51E-01	EIF5A2	eukaryotic translation initiation factor 5A2	chr3q26.2	220198_s_at	NM_020390
2.04	2.17	0.14	2.79E-01	6.51E-01	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	chr16q12	1561146_at	NM_018206
2.81	2.97	0.17	2.80E-01	6.51E-01	---	---	---	233761_at	---
2.74	2.94	0.20	2.80E-01	6.51E-01	TRIM4	tripartite motif-containing 4	chr7q22-q31.1	1554287_at	NM_033017 /// NM_033091
3.24	3.41	0.17	2.80E-01	6.51E-01	---	---	---	1556107_at	---
5.47	5.62	0.14	2.80E-01	6.51E-01	RSBN1L	round spermatid basic protein 1-like	chr7q11.23	232221_x_at	NM_198467
4.39	4.56	0.17	2.80E-01	6.51E-01	NXNL1	nucleoredoxin-like 1	chr19p13.11	1553755_at	NM_138454
2.13	2.28	0.15	2.80E-01	6.51E-01	---	---	---	1561262_at	---
2.44	2.58	0.14	2.80E-01	6.51E-01	LOC374491	TPTE and PTEN homologous inositol lipid phosphatase pseudogene	chr13q12.12	233879_at	NR_002815
6.29	6.50	0.21	2.80E-01	6.51E-01	SAMD14	Sterile alpha motif domain containing 14	chr17q21.33	1559995_at	NM_174920
2.65	2.85	0.20	2.80E-01	6.51E-01	CCDC85B	coiled-coil domain containing 85B	chr11q12.1	204609_at	NM_006848
3.49	3.66	0.16	2.80E-01	6.51E-01	KIAA0182	KIAA0182	chr16q24.1	232988_at	NM_001134473 /// NM_014615
1.87	2.05	0.18	2.80E-01	6.52E-01	SCN1A	sodium channel, voltage-gated, type I, alpha subunit	chr2q24.3	210383_at	NM_006920
5.84	6.01	0.17	2.80E-01	6.52E-01	FLJ12355	hypothetical protein FLJ12355	chr19q13.11	220465_at	XR_040980 /// XR_040981 /// XR_040982
2.16	2.33	0.17	2.80E-01	6.52E-01	---	---	---	234862_at	---
6.28	6.44	0.16	2.80E-01	6.52E-01	C21orf2	chromosome 21 open reading frame 2	chr21q22.3	203996_s_at	NM_004928
6.11	6.41	0.30	2.80E-01	6.52E-01	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	chrXq28	205142_x_at	NM_000033
2.39	2.57	0.18	2.80E-01	6.52E-01	---	---	---	1561911_at	---
4.48	4.65	0.17	2.80E-01	6.52E-01	VSIG2	V-set and immunoglobulin domain containing 2	chr11q24	229369_at	NM_014312
3.89	4.13	0.24	2.80E-01	6.52E-01	CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1	chr14q32.1	220331_at	NM_006668
2.96	3.19	0.23	2.80E-01	6.52E-01	WBSCR22	Williams Beuren syndrome chromosome region 22	---	231415_at	NM_017528
2.53	2.73	0.20	2.80E-01	6.52E-01	---	---	---	1556619_at	---
2.07	2.20	0.14	2.80E-01	6.52E-01	---	---	---	234824_at	---
2.23	2.65	0.42	2.80E-01	6.52E-01	---	---	---	233139_at	---
2.05	2.16	0.11	2.80E-01	6.52E-01	OR1Q1	olfactory receptor, family 1, subfamily Q, member 1	chr9q33.2	1567064_at	NM_012364

5.75	5.93	0.18	2.80E-01	6.52E-01	RANBP1	RAN binding protein 1	chr22q11.21	202482_x_at	NM_002882
2.05	2.23	0.17	2.81E-01	6.52E-01	THADA	Thyroid adenoma associated	chr2p21	1566888_at	NM_001083953 /// NM_022065
5.01	5.25	0.24	2.81E-01	6.52E-01	MCM3AP	minichromosome maintenance complex component 3 associated protein	chr21q22.3	215582_x_at	NM_003906
3.44	3.63	0.19	2.81E-01	6.52E-01	MYH6 /// MYH7	myosin, heavy chain 6, cardiac muscle, alpha /// myosin, heavy chain 7, cardiac muscle, beta	chr14q12	204737_s_at	NM_000257 /// NM_002471
4.19	4.50	0.31	2.81E-01	6.52E-01	C16orf89	chromosome 16 open reading frame 89	chr16p13.3	229177_at	NM_001098514 /// NM_152459
1.82	1.96	0.14	2.81E-01	6.52E-01	---	---	---	237717_x_at	---
5.22	5.71	0.48	2.81E-01	6.53E-01	STAG2	stromal antigen 2	chrXq25	209023_s_at	NM_001042749 /// NM_001042750 /// NM_001042751 /// NM_006603
5.04	5.43	0.39	2.81E-01	6.53E-01	DPYSL3	dihydropyrimidinase-like 3	chr5q32	201431_s_at	NM_001387
6.96	7.34	0.38	2.81E-01	6.53E-01	USP48	ubiquitin specific peptidase 48	chr1p36.12	220079_s_at	NM_001032730 /// NM_032236
2.30	2.47	0.17	2.81E-01	6.53E-01	---	---	---	232614_at	---
7.08	7.36	0.29	2.81E-01	6.53E-01	CEPT1	choline/ethanolamine phosphotransferase 1	chr1p13.3	219375_at	NM_001007794 /// NM_006090
7.41	7.98	0.57	2.81E-01	6.53E-01	NDRG2	NDRG family member 2	chr14q11.2	214279_s_at	NM_016250 /// NM_201535 /// NM_201536 /// NM_201537 /// NM_201538 /// NM_201539 /// NM_201540 /// NM_201541
3.28	3.45	0.17	2.81E-01	6.53E-01	HOXA6	homeobox A6	chr7p15-p14	208557_at	NM_024014
1.95	2.09	0.13	2.81E-01	6.53E-01	---	---	---	237987_x_at	---
1.95	2.07	0.12	2.81E-01	6.53E-01	PCDHB6	protocadherin beta 6	chr5q31	239443_at	NM_018939
1.88	1.98	0.11	2.81E-01	6.53E-01	---	---	---	1564610_at	---
2.45	2.62	0.16	2.81E-01	6.53E-01	---	---	---	234229_at	---
2.19	2.31	0.12	2.81E-01	6.53E-01	---	---	---	237672_at	---
8.03	8.24	0.21	2.81E-01	6.53E-01	---	---	---	AFFX-r2-Ec-bioC-3_at	---
3.94	4.11	0.17	2.81E-01	6.53E-01	CA12	carbonic anhydrase XII	chr15q22	204509_at	NM_001218 /// NM_206925
2.01	2.15	0.14	2.81E-01	6.53E-01	---	---	---	1562053_at	---
2.78	3.47	0.68	2.81E-01	6.53E-01	FNDC1	fibronectin type III domain containing 1	chr6q25	226930_at	NM_032532
6.35	6.78	0.43	2.81E-01	6.53E-01	FLJ35390	hypothetical LOC255031	chr7p13	1564207_at	---
2.84	3.06	0.22	2.81E-01	6.53E-01	---	---	---	1560763_at	---
2.45	2.61	0.16	2.81E-01	6.53E-01	---	---	---	244361_at	---
3.48	3.62	0.14	2.81E-01	6.53E-01	RBP2	retinol binding protein 2, cellular	chr3q23	231734_at	NM_004164
4.26	4.39	0.13	2.81E-01	6.53E-01	RABIF	RAB interacting factor	chr1q32-q41	204477_at	NM_002871
2.01	2.16	0.15	2.81E-01	6.53E-01	---	---	---	216728_at	---
2.11	2.25	0.13	2.81E-01	6.53E-01	---	---	---	236462_at	---
5.62	6.21	0.60	2.81E-01	6.53E-01	WDR75	WD repeat domain 75	chr2q32.2	224721_at	NM_032168
4.25	4.61	0.36	2.81E-01	6.53E-01	TTC17	tetratricopeptide repeat domain 17	chr11p12-p11.2	224852_at	NM_018259
2.87	3.10	0.23	2.81E-01	6.53E-01	PKNOX2	PBX/knotted 1 homeobox 2	---	63305_at	NM_022062
5.13	5.34	0.21	2.81E-01	6.53E-01	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	chr16p11.2	213475_s_at	NM_001114380 /// NM_002209
3.22	3.42	0.20	2.81E-01	6.53E-01	---	---	---	243054_at	---
4.13	4.32	0.19	2.81E-01	6.53E-01	ENDOGL1	endonuclease G-like 1	chr3p21.3	206903_at	NM_005107
4.25	4.44	0.19	2.81E-01	6.53E-01	LOC100134295 /// SLCO4A1	similar to Solute carrier organic anion transporter family, member 4A1 /// solute carrier organic anion transporter family, member 4A1	chr20q13.33	219911_s_at	NM_016354 /// XM_001720240
2.60	2.77	0.17	2.81E-01	6.53E-01	HSD17B7P2	hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2	chr10p11.21	224058_s_at	NR_003086 /// XR_042142
2.02	2.17	0.15	2.81E-01	6.53E-01	FAM9B	family with sequence similarity 9, member B	chrXp22.32	1553461_at	NM_205849
2.15	2.29	0.15	2.81E-01	6.53E-01	STK17B	serine/threonine kinase 17b	chr2q32.3	243797_at	NM_004226
2.01	2.14	0.13	2.81E-01	6.53E-01	LOC202451	hypothetical protein LOC202451	chr6q23.3	242098_at	XM_928403 /// XM_941101
1.95	2.07	0.13	2.81E-01	6.53E-01	---	---	---	1569168_at	---
2.51	2.69	0.18	2.81E-01	6.53E-01	---	---	---	240730_at	---
2.19	2.48	0.28	2.82E-01	6.53E-01	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	chr6p21.1-p11.2	237054_at	NM_021572
2.85	3.03	0.18	2.82E-01	6.53E-01	---	---	---	1566874_at	---

4.93	5.46	0.53	2.82E-01	6.53E-01	RAD50	RAD50 homolog (S. cerevisiae)	chr5q31	208393_s_at	NM_005732 /// NM_133482
8.42	8.86	0.44	2.82E-01	6.53E-01	ITFG1	integrin alpha FG-GAP repeat containing 1	chr16q12.1	221449_s_at	NM_030790
8.29	8.72	0.43	2.82E-01	6.53E-01	HSDL2	hydroxysteroid dehydrogenase like 2	chr9q32	209513_s_at	NM_032303
4.75	4.97	0.22	2.82E-01	6.53E-01	C21orf58	chromosome 21 open reading frame 58	chr21q22.3	238541_at	NM_058180
1.95	2.15	0.20	2.82E-01	6.53E-01	---	---	---	1563080_at	---
2.41	2.60	0.18	2.82E-01	6.53E-01	CYP2C9	Cytochrome P450, family 2, subfamily C, polypeptide 9	chr10q24	214420_s_at	NM_000771
3.74	3.91	0.17	2.82E-01	6.53E-01	---	---	---	244476_at	---
2.09	2.25	0.17	2.82E-01	6.53E-01	---	---	---	1556347_at	---
2.93	3.09	0.17	2.82E-01	6.53E-01	WNT5B	wingless-type MMTV integration site family, member 5B	chr12p13.3	223537_s_at	NM_030775 /// NM_032642
2.34	2.50	0.16	2.82E-01	6.53E-01	HMGA2	high mobility group AT-hook 2	chr12q15	1558683_a_at	NM_003483 /// NM_003484
2.32	2.46	0.14	2.82E-01	6.53E-01	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	chr2p14	234210_x_at	NM_001005386 /// NM_005722
2.41	2.54	0.13	2.82E-01	6.53E-01	---	---	---	237245_at	---
2.35	2.48	0.13	2.82E-01	6.53E-01	LOC641518	hypothetical protein LOC641518	chr4q23-q25	243363_at	XR_017788 /// XR_017912 /// XR_040484
1.92	2.05	0.13	2.82E-01	6.53E-01	DEFB129	defensin, beta 129	chr20p13	233160_at	NM_080831
4.43	4.93	0.51	2.82E-01	6.53E-01	VPS13C	Vacuolar protein sorting 13 homolog C (S. cerevisiae)	chr15q22.2	235023_at	NM_001018088 /// NM_017684 /// NM_018080 /// NM_020821
2.70	2.87	0.17	2.82E-01	6.53E-01	---	---	---	1563225_a_at	---
2.09	2.24	0.15	2.82E-01	6.53E-01	---	---	---	1557802_at	---
2.56	2.68	0.13	2.82E-01	6.53E-01	ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	chrXp22	222257_s_at	NM_021804
4.28	4.62	0.34	2.82E-01	6.53E-01	DAB2IP	DAB2 interacting protein	chr9q33.1-q33.3	225020_at	NM_032552 /// NM_138709
2.24	2.40	0.16	2.82E-01	6.53E-01	FBXO28	F-box protein 28	chr1q42.11	1555972_s_at	NM_015176
5.38	5.54	0.16	2.82E-01	6.53E-01	C1QTNF5 /// MFRP	C1q and tumor necrosis factor related protein 5 /// membrane frizzled-related protein	chr11q23 /// chr11q23.3	224286_at	NM_015645 /// NM_031433
3.65	4.13	0.48	2.82E-01	6.53E-01	MAST4	Microtubule associated serine/threonine kinase family member 4	chr5q12.3	222348_at	NM_015183 /// NM_198828
4.67	5.07	0.40	2.82E-01	6.53E-01	LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr15q21.2	235096_at	NM_138792
5.16	5.44	0.28	2.82E-01	6.53E-01	AQP2	aquaporin 2 (collecting duct)	chr12q12-q13	236630_at	NM_000486
3.77	4.01	0.24	2.82E-01	6.53E-01	PELI1	Pellino homolog 1 (Drosophila)	chr2p13.3	232213_at	NM_020651
3.20	3.38	0.18	2.82E-01	6.53E-01	INSRR	insulin receptor-related receptor	chr1q21-q23	215776_at	NM_014215
2.58	2.75	0.17	2.82E-01	6.53E-01	THAP11	THAP domain containing 11	chr16q22.1	226788_at	NM_020457
2.50	2.66	0.17	2.82E-01	6.53E-01	---	---	---	244150_at	---
7.17	7.43	0.26	2.82E-01	6.53E-01	LITAF	lipopolysaccharide-induced TNF factor	chr16p13.13	200704_at	NM_004862
2.24	3.39	1.15	2.82E-01	6.53E-01	NTS	neurotensin	chr12q21	206291_at	NM_006183
3.55	3.88	0.33	2.82E-01	6.53E-01	CCDC88A	coiled-coil domain containing 88A	chr2p16.1	221078_s_at	NM_018084
2.37	2.55	0.18	2.82E-01	6.53E-01	---	---	---	216569_at	---
2.24	2.42	0.19	2.82E-01	6.53E-01	PDE1A	phosphodiesterase 1A, calmodulin-dependent	chr2q32.1	233549_at	NM_001003683 /// NM_005019
12.29	12.66	0.37	2.82E-01	6.53E-01	RPS3A	ribosomal protein S3A	chr4q31.2-q31.3	201257_x_at	NM_001006
4.88	5.10	0.22	2.83E-01	6.53E-01	---	---	---	221071_at	---
2.20	2.40	0.20	2.82E-01	6.53E-01	---	---	---	1561468_at	---
2.24	2.42	0.18	2.83E-01	6.53E-01	MYF5	myogenic factor 5	chr12q21	207424_at	NM_005593
4.30	4.48	0.18	2.83E-01	6.53E-01	---	---	---	239658_at	---
3.64	3.80	0.15	2.83E-01	6.53E-01	LOC401351	hypothetical gene supported by BC040831	chr7q11.21	243083_at	XM_379843 /// XM_926596 /// XM_935479 /// XM_935792 /// XM_938438 /// XM_943672
2.09	2.22	0.13	2.83E-01	6.53E-01	---	---	---	1557778_at	---
2.13	2.28	0.14	2.83E-01	6.53E-01	LOC283693	Actin, gamma pseudogene	chr15q25.2	1565912_at	---
2.02	2.16	0.13	2.83E-01	6.54E-01	FHL5	four and a half LIM domains 5	chr6q16.1-q16.3	1570517_at	NM_020482
3.40	3.58	0.18	2.83E-01	6.54E-01	---	---	---	234890_at	---
9.36	9.58	0.22	2.83E-01	6.54E-01	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	chr6q27	200876_s_at	NM_002793
2.49	2.66	0.17	2.83E-01	6.54E-01	---	---	---	214996_at	---

11.14	11.51	0.36	2.83E-01	6.54E-01	RPS27A /// UBA52 /// UBB /// UBC	ribosomal protein S27a /// ubiquitin A-52 residue ribosomal protein fusion product 1 /// ubiquitin B /// ubiquitin C	chr12q24.3 /// chr17p12-p11.2 /// chr19p13.1-p12 /// chr2p16	208980_s_at	NM_001033930 /// NM_002954 /// NM_003333 /// NM_018955 /// NM_021009																					
4.70	5.19	0.49	2.83E-01	6.54E-01	ZRANB1	zinc finger, RAN-binding domain containing 1	chr10q26.13	225130_at	NM_017580																				
3.26	3.68	0.43	2.83E-01	6.54E-01	LTF	lactotransferrin	chr3p21.31	202018_s_at	NM_002343																				
6.63	6.95	0.33	2.83E-01	6.54E-01	GIMAP4	GTPase, IMAP family member 4	chr7q36.1	219243_at	NM_018326																				
3.54	3.86	0.32	2.83E-01	6.54E-01	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	1569519_at	NM_001037675 /// NM_001039703 /// NM_001101663 /// NM_001102663 /// NM_015383 /// NM_017940 /// NM_173638 /// NM_183372 /// XM_001717398 /// XM_001717802 /// XM_001721345 /// XM_001721349 /// XM_001722184 /// XM_001723523 /// XM_001726946																				
2.47	2.69	0.23	2.83E-01	6.54E-01	CLMN	calmin (calponin-like, transmembrane)	chr14q32.13	221042_s_at	NM_024734																				
3.48	3.66	0.17	2.83E-01	6.54E-01	---	---	---	1555196_at	---																				
3.29	3.46	0.17	2.83E-01	6.54E-01	LOC151300	hypothetical LOC151300	chr2q35	239507_at	XR_040352 /// XR_040353 /// XR_040354																				
2.43	2.57	0.13	2.83E-01	6.54E-01	C3orf58	Chromosome 3 open reading frame 58	chr3q24	235853_at	NM_001134470 /// NM_173552																				
3.17	3.35	0.17	2.83E-01	6.54E-01	---	---	---	240127_at	---																				
4.20	4.39	0.19	2.83E-01	6.54E-01	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	chr1q21.2	210459_at	NM_002810																				
5.17	5.76	0.59	2.83E-01	6.54E-01	APOOL	Apolipoprotein O-like	chrXq21.1	244187_at	NM_198450																				
3.27	3.47	0.20	2.83E-01	6.54E-01	ZNF230	zinc finger protein 230	chr19q13.31	205791_x_at	NM_006300																				
2.98	3.52	0.54	2.83E-01	6.54E-01	LRRC17	leucine rich repeat containing 17	chr7q22.1	205381_at	NM_001031692 /// NM_005824																				
5.71	5.98	0.26	2.83E-01	6.54E-01	GAMT	guanidinoacetate N-methyltransferase	chr19p13.3	1552473_at	NM_000156 /// NM_138924																				
2.34	2.50	0.17	2.83E-01	6.54E-01	---	---	---	243512_x_at	---																				
2.47	2.66	0.19	2.83E-01	6.54E-01	---	---	---	243474_at	---																				
4.31	4.55	0.24	2.83E-01	6.54E-01	DES	desmin	chr2q35	202222_s_at	NM_001927																				
3.35	3.53	0.17	2.84E-01	6.54E-01	---	---	---	217706_at	---																				
3.32	3.87	0.54	2.84E-01	6.54E-01	RGS18	regulator of G-protein signaling 18	chr1q31.2	223809_at	NM_130782																				
3.83	4.00	0.17	2.84E-01	6.54E-01	MUC5B	mucin 5B, oligomeric mucus/gel-forming	chr11p15.5	213432_at	NM_002458 /// XM_001719349																				
3.18	3.57	0.39	2.84E-01	6.55E-01	CP /// LOC100132553	ceruloplasmin (ferroxidase) /// similar to Ceruloplasmin precursor (Ferroxidase)	chr3q23-q25 /// chr8q21.3	228143_at	NM_000096 /// XR_038870 /// XR_038875 /// XR_038881																				
8.77	9.47	0.70	2.84E-01	6.55E-01	QPCT	glutaminyl-peptide cyclotransferase	chr2p22.2	205174_s_at	NM_012413																				
5.98	6.51	0.52	2.84E-01	6.55E-01	NUP133	nucleoporin 133kDa	chr1q42.13	202184_s_at	NM_018230																				
2.20	2.33	0.13	2.84E-01	6.55E-01	PYGO1	pygopus homolog 1 (Drosophila)	chr15q21.1	215520_at	NM_015617																				
2.03	2.16	0.13	2.84E-01	6.55E-01	C17orf66	chromosome 17 open reading frame 66	chr17q12	1553378_a_at	NM_152781																				
1.93	2.07	0.14	2.84E-01	6.55E-01	MIRHG1	microRNA host gene 1 (non-protein coding)	chr13q31.3	233636_at	XR_042147 /// XR_042176 /// XR_042177																				
5.30	5.54	0.24	2.84E-01	6.55E-01	LOC202181	hypothetical protein LOC202181	chr5q35.3	232309_at	XR_015120 /// XR_015544 /// XR_040243																				

2.28	2.46	0.18	2.84E-01	6.55E-01	COL28A1	collagen, type XXVIII, alpha 1	chr7p21.3	242345_at	NM_001037763																				
2.20	2.37	0.17	2.84E-01	6.55E-01	---	---	---	238956_at	---																				
5.37	5.67	0.30	2.84E-01	6.55E-01	SLC29A3	solute carrier family 29 (nucleoside transporters), member 3	chr10q22.1	219344_at	NM_018344																				
4.26	4.46	0.19	2.84E-01	6.55E-01	---	---	---	235861_at	---																				
2.13	2.29	0.16	2.84E-01	6.55E-01	LOC151300	hypothetical LOC151300	chr2q35	239506_s_at	XR_040352 /// XR_040353 /// XR_040354																				
1.97	2.12	0.14	2.84E-01	6.55E-01	IFT74	intraflagellar transport 74 homolog (Chlamydomonas)	chr9p21.2	61732_r_at	NM_001099222 /// NM_001099223 /// NM_001099224 /// NM_025103																				
7.59	8.15	0.56	2.84E-01	6.55E-01	CAST	calpastatin	chr5q15	212586_at	NM_001042440 /// NM_001042441 /// NM_001042442 /// NM_001042443 /// NM_001042444 /// NM_001042445 /// NM_001042446 /// NM_001750 /// NM_173060 /// NM_173061 /// NM_173063																				
2.53	2.99	0.46	2.84E-01	6.55E-01	HHIP	hedgehog interacting protein	chr4q28-q32	223775_at	NM_022475																				
3.16	3.35	0.19	2.84E-01	6.55E-01	ZFP28	zinc finger protein 28 homolog (mouse)	---	234300_s_at	NM_020828																				
2.65	2.83	0.18	2.84E-01	6.55E-01	PRND	prion protein 2 (dublet)	chr20pter-p12	223813_at	NM_012409																				
2.49	2.62	0.14	2.84E-01	6.55E-01	---	---	---	1566596_at	---																				
4.58	4.75	0.17	2.84E-01	6.55E-01	---	---	---	234293_x_at	---																				
2.03	2.16	0.13	2.84E-01	6.55E-01	ZDHHC14	zinc finger, DHHC-type containing 14	chr6q25.3	1556967_at	NM_024630 /// NM_153746																				
8.62	8.85	0.24	2.84E-01	6.55E-01	ARPP-19	cyclic AMP phosphoprotein, 19 kD	chr15q21.2	221483_s_at	NM_006628																				
5.60	6.35	0.75	2.84E-01	6.55E-01	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	chr3q26.32	221428_s_at	NM_024665																				
2.71	2.93	0.23	2.84E-01	6.55E-01	---	---	---	240493_at	---																				
2.70	2.85	0.15	2.84E-01	6.55E-01	TRERF1	transcriptional regulating factor 1	chr6p21.1-p12.1	233324_at	NM_033502																				
2.78	3.00	0.21	2.84E-01	6.55E-01	---	---	---	1566042_at	---																				
4.37	4.61	0.24	2.84E-01	6.55E-01	CLEC16A	C-type lectin domain family 16, member A	chr16p13.13	231221_at	NM_015226																				
3.74	3.95	0.21	2.84E-01	6.55E-01	---	---	---	227661_at	---																				
2.05	2.20	0.15	2.85E-01	6.55E-01	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	chr12q21.3	239352_at	NM_018057 /// NM_182767																				
2.19	2.33	0.14	2.85E-01	6.55E-01	---	---	---	1560755_at	---																				
4.82	5.37	0.54	2.85E-01	6.55E-01	CCDC50	coiled-coil domain containing 50	chr3q28	228693_at	NM_174908 /// NM_178335																				
4.77	5.26	0.48	2.85E-01	6.55E-01	---	---	---	232882_at	---																				
3.54	4.10	0.56	2.85E-01	6.55E-01	EXOC5	exocyst complex component 5	chr14q23.1	218748_s_at	NM_006544																				
2.99	3.19	0.20	2.85E-01	6.55E-01	---	---	---	236916_at	---																				
8.12	8.31	0.19	2.85E-01	6.55E-01	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	chr2p23	208630_at	NM_000182																				
6.02	6.34	0.32	2.85E-01	6.55E-01	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	chr3p26-p25	203710_at	NM_001099952 /// NM_002222																				
11.82	12.27	0.45	2.85E-01	6.55E-01	LOC439992 /// RPS3A	similar to v-fos transformation effector protein /// ribosomal protein S3A	chr10q23.1 /// chr4q31.2-q31.3	200099_s_at	NM_001006 /// XM_001723347 /// XM_001723350 /// XM_495839 /// XM_926528 /// XM_937069 /// XM_943171																				

6.88	7.26	0.38	2.85E-01	6.55E-01	CAST	calpastatin	chr5q15	207467_x_at	NM_001042440 /// NM_001042441 /// NM_001042442 /// NM_001042443 /// NM_001042444 /// NM_001042445 /// NM_001042446 /// NM_001750 /// NM_173060 /// NM_173061 /// NM_173063
3.65	3.89	0.23	2.85E-01	6.55E-01	---	---	---	217337_at	---
3.46	3.95	0.49	2.85E-01	6.56E-01	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	chr1p31.1	230482_at	NM_030965
2.75	2.94	0.19	2.85E-01	6.56E-01	---	---	---	240827_at	---
3.79	3.97	0.18	2.85E-01	6.56E-01	---	---	---	215556_at	---
2.80	3.01	0.20	2.85E-01	6.56E-01	VGLL1	vestigial like 1 (Drosophila)	chrXq26.3	215730_at	NM_016267
6.57	6.79	0.22	2.85E-01	6.56E-01	GOSR2	golgi SNAP receptor complex member 2	chr17q21	235041_at	NM_001012511 /// NM_004287 /// NM_054022
3.39	3.60	0.20	2.85E-01	6.56E-01	TSPAN18	tetraspanin 18	chr11p11.2	1561449_at	NM_001031730 /// NM_130783
3.00	3.20	0.20	2.85E-01	6.56E-01	---	---	---	220533_at	---
1.92	2.06	0.14	2.85E-01	6.56E-01	CPNE4	copine IV	chr3q22.1	231336_at	NM_130808
2.09	2.32	0.23	2.85E-01	6.56E-01	---	---	---	238297_at	---
2.04	2.16	0.12	2.85E-01	6.56E-01	---	---	---	1568848_at	---
2.76	2.98	0.22	2.85E-01	6.56E-01	HLA-DOB	major histocompatibility complex, class II, DO beta	chr6p21.3	205671_s_at	NM_002120
2.70	2.88	0.18	2.85E-01	6.56E-01	---	---	---	1561597_x_at	---
2.01	2.16	0.15	2.85E-01	6.56E-01	LOC100128175	similar to PRO2591	chr3q13.31	224095_at	XM_001721475 /// XM_001721518 /// XM_001722339
2.76	2.90	0.14	2.85E-01	6.56E-01	LOC154092	hypothetical protein LOC154092	chr6q23.2	237731_at	---
5.44	5.67	0.23	2.85E-01	6.56E-01	TMEM33	transmembrane protein 33	chr4p13	222642_s_at	NM_018126
2.00	2.14	0.14	2.85E-01	6.56E-01	KIAA1429	KIAA1429	chr8q22.1	243927_x_at	NM_015496 /// NM_183009
3.57	3.85	0.28	2.85E-01	6.56E-01	LOC100129195	hypothetical protein LOC100129195	chr6p22.1	236777_at	XM_001715702 /// XM_001719301 /// XM_001722758
3.69	4.04	0.35	2.85E-01	6.56E-01	---	---	---	233214_at	---
3.59	3.80	0.22	2.85E-01	6.56E-01	LIME1	Lck interacting transmembrane adaptor 1	chr20q13.3	219541_at	NM_017806
2.05	2.19	0.14	2.85E-01	6.56E-01	---	---	---	231315_at	---
2.55	2.71	0.16	2.85E-01	6.56E-01	PDHA2	pyruvate dehydrogenase (lipoamide) alpha 2	chr4q22-q23	214518_at	NM_005390
4.63	4.95	0.32	2.86E-01	6.56E-01	DAAM1	dishevelled associated activator of morphogenesis 1	chr14q23.1	226666_at	NM_014992
6.36	6.64	0.28	2.86E-01	6.56E-01	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	chr11p12-p11.2	213013_at	NM_005456
2.80	2.98	0.18	2.86E-01	6.56E-01	TBX1	T-box 1	chr22q11.21	211274_at	NM_005992 /// NM_080646 /// NM_080647
7.33	7.87	0.55	2.86E-01	6.56E-01	IPO7	importin 7	chr11p15.4	200992_at	NM_006391
4.84	5.26	0.42	2.86E-01	6.56E-01	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	chr7q21.3-q22	1568765_at	NM_000602
2.64	2.87	0.23	2.86E-01	6.56E-01	---	---	---	230856_at	---
6.66	6.82	0.16	2.86E-01	6.56E-01	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	chr1q41	202372_at	NM_012414
2.18	2.33	0.15	2.86E-01	6.56E-01	---	---	---	234057_at	---
2.03	2.17	0.14	2.86E-01	6.56E-01	---	---	---	239423_at	---
2.11	2.24	0.13	2.86E-01	6.56E-01	---	---	---	237932_at	---
1.90	2.03	0.13	2.86E-01	6.56E-01	LIPI	lipase, member I	chr21q11.2	242178_at	NM_198996
2.61	2.74	0.13	2.86E-01	6.56E-01	PRSS1	protease, serine, 1 (trypsin 1)	chr7q32-qter|7q34	205869_at	NM_002769
2.07	2.20	0.14	2.86E-01	6.56E-01	---	---	---	215679_at	---

4.42	5.01	0.59	2.86E-01	6.56E-01	CREB1	cAMP responsive element binding protein 1	chr2q34	204312_x_at	NM_004379 /// NM_134442
3.48	3.75	0.27	2.86E-01	6.56E-01	---	---	---	240328_at	---
2.15	2.42	0.27	2.86E-01	6.56E-01	NLGN4Y	neuroligin 4, Y-linked	chrYq11.221	207703_at	NM_014893
2.32	2.53	0.21	2.86E-01	6.56E-01	---	---	---	244608_at	---
2.92	3.12	0.20	2.86E-01	6.56E-01	ISLR2	immunoglobulin superfamily containing leucine-rich repeat 2	chr15q24.1	232208_at	NM_001130136 /// NM_001130137 /// NM_001130138 /// NM_020851
2.86	3.03	0.16	2.86E-01	6.56E-01	GTPBP1	GTP binding protein 1	chr22q13.1	205275_at	NM_004286
2.80	2.96	0.16	2.86E-01	6.56E-01	---	---	---	233217_at	---
1.93	2.09	0.15	2.86E-01	6.56E-01	CLCA4	chloride channel, calcium activated, family member 4	chr1p31-p22	220026_at	NM_012128
2.39	2.54	0.15	2.86E-01	6.56E-01	LOC100129112	Hypothetical protein LOC100129112	chr17q23.2	241180_at	XM_001724999 /// XM_001726257 /// XM_001726808
1.96	2.11	0.15	2.86E-01	6.56E-01	---	---	---	1566201_at	---
1.98	2.13	0.14	2.86E-01	6.56E-01	C2orf14	chromosome 2 open reading frame 14	chr2q21.1	224278_at	NR_023391 /// XM_001723977
1.93	2.06	0.13	2.86E-01	6.56E-01	SPATA22	Spermatogenesis associated 22	chr17p13.3	1558667_at	NM_032598
2.42	2.55	0.13	2.86E-01	6.56E-01	---	---	---	244440_at	---
3.42	3.74	0.32	2.86E-01	6.56E-01	---	---	---	240824_at	---
2.02	2.15	0.13	2.86E-01	6.56E-01	---	---	---	1556504_at	---
6.24	6.36	0.13	2.86E-01	6.56E-01	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	chr19p13.12	216272_x_at	NM_033025
3.73	4.17	0.44	2.86E-01	6.57E-01	RWDD2B	RWD domain containing 2B	chr21q22.11	222614_at	NM_016940
2.37	2.55	0.19	2.86E-01	6.57E-01	IGHA1	immunoglobulin heavy constant alpha 1	chr14q32.33	217169_at	---
2.22	2.39	0.17	2.86E-01	6.57E-01	---	---	---	233034_at	---
1.87	1.99	0.12	2.87E-01	6.57E-01	SMC5	structural maintenance of chromosomes 5	chr9q21.11	237725_x_at	NM_015110
3.36	3.93	0.57	2.87E-01	6.57E-01	---	---	---	244022_at	---
3.16	3.32	0.16	2.87E-01	6.57E-01	PDE7B	phosphodiesterase 7B	chr6q23-q24	220343_at	NM_018945
3.70	3.84	0.14	2.87E-01	6.57E-01	EPS8L1	EPS8-like 1	chr19q13.42	91826_at	NM_017729 /// NM_133180
3.09	3.28	0.19	2.87E-01	6.57E-01	TRBV7-3	T cell receptor beta variable 7-3	chr7q34	234883_x_at	---
2.30	2.48	0.18	2.87E-01	6.57E-01	---	---	---	1566598_at	---
2.98	3.44	0.47	2.87E-01	6.57E-01	PCDH7	protocadherin 7	chr4p15	228640_at	NM_002589 /// NM_032456 /// NM_032457
8.28	8.58	0.30	2.87E-01	6.57E-01	NSFL1C	NSFL1 (p97) cofactor (p47)	chr20p13	232520_s_at	NM_016143 /// NM_018839 /// NM_182483
2.18	2.32	0.15	2.87E-01	6.57E-01	PCDHGB6	protocadherin gamma subfamily B, 6	chr5q31	221682_s_at	NM_018926 /// NM_032100
5.42	5.78	0.36	2.87E-01	6.57E-01	---	---	---	226399_at	---
2.08	2.30	0.22	2.87E-01	6.57E-01	LOC284033	hypothetical LOC284033	chr17p12	229266_at	---
3.81	4.02	0.20	2.87E-01	6.57E-01	---	---	---	1557302_at	---
2.10	2.28	0.19	2.87E-01	6.57E-01	---	---	---	1570430_at	---
4.80	4.96	0.16	2.87E-01	6.57E-01	MGC34796	SPR pseudogene	chr1p32	240692_at	---
1.89	2.02	0.13	2.87E-01	6.57E-01	---	---	---	215831_at	---
2.42	2.72	0.29	2.87E-01	6.57E-01	CHRM3	cholinergic receptor, muscarinic 3	chr1q43	1553705_a_at	NM_000740
5.75	6.00	0.26	2.87E-01	6.57E-01	PPP1R12C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	chr19q13.42	223152_at	NM_017607
4.64	4.82	0.18	2.87E-01	6.57E-01	---	---	---	217352_at	---
5.80	6.09	0.29	2.87E-01	6.57E-01	COL6A1	collagen, type VI, alpha 1	chr21q22.3	212091_s_at	NM_001848
2.14	2.25	0.11	2.87E-01	6.57E-01	MARK3	MAP/microtubule affinity-regulating kinase 3	chr14q32.3	232537_x_at	NM_001128918 /// NM_001128919 /// NM_001128920 /// NM_001128921 /// NM_002376
2.38	2.61	0.23	2.87E-01	6.57E-01	---	---	---	207960_at	---
7.74	8.26	0.52	2.87E-01	6.57E-01	EBP	emopamil binding protein (sterol isomerase)	chrXp11.23-p11.22	202735_at	NM_006579
4.67	5.12	0.45	2.87E-01	6.57E-01	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	chr8q11.23	235507_at	NM_052937
2.58	2.78	0.20	2.87E-01	6.57E-01	---	---	---	242359_at	---
3.36	3.54	0.17	2.87E-01	6.57E-01	LRRC28	leucine rich repeat containing 28	chr15q26.3	1553940_a_at	NM_144598
6.27	6.43	0.16	2.87E-01	6.57E-01	---	---	---	231552_at	---

2.25	2.40	0.15	2.87E-01	6.57E-01	KRTAP1-1 /// LOC728946	keratin associated protein 1-1 /// hypothetical LOC728946	chr17q12|17q12-q21	220976_s_at	NM_030967 /// XM_001128870
2.10	2.21	0.12	2.87E-01	6.57E-01	---	---	---	240186_at	---
5.65	6.03	0.37	2.87E-01	6.57E-01	ZMYM4	zinc finger, MYM-type 4	chr1p32-p34	202050_s_at	NM_005095
3.76	4.02	0.27	2.87E-01	6.57E-01	SLIT1	slit homolog 1 (Drosophila)	chr10q23.3-q24	208221_s_at	NM_003061
2.48	2.72	0.24	2.87E-01	6.57E-01	---	---	---	242051_at	---
3.46	3.67	0.22	2.87E-01	6.57E-01	---	---	---	230823_at	---
2.53	2.73	0.20	2.87E-01	6.57E-01	INADL	InaD-like (Drosophila)	chr1p31.3	239173_at	NM_176877
2.61	2.76	0.16	2.87E-01	6.57E-01	---	---	---	238240_at	---
2.62	2.75	0.12	2.88E-01	6.57E-01	DSE	Dermatan sulfate epimerase	chr6q22	1558868_a_at	NM_001080976 /// NM_013352
7.39	7.61	0.22	2.88E-01	6.57E-01	RPL38	ribosomal protein L38	chr17q23-q25	202028_s_at	NM_000999 /// NM_001035258
5.09	5.59	0.50	2.88E-01	6.57E-01	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	chr4q24	240383_at	NM_003340 /// NM_181886 /// NM_181887 /// NM_181888 /// NM_181889 /// NM_181890 /// NM_181891 /// NM_181892 /// NM_181893
4.87	5.37	0.49	2.88E-01	6.57E-01	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	chr8q13	202955_s_at	NM_006421
4.94	5.42	0.49	2.88E-01	6.57E-01	CUL4B	cullin 4B	chrXq23	202213_s_at	NM_001079872 /// NM_003588
5.87	6.33	0.45	2.88E-01	6.57E-01	---	---	---	239251_at	---
2.22	2.37	0.15	2.88E-01	6.57E-01	PRO1483	hypothetical LOC55448	chr11p13	1553475_at	---
2.27	2.39	0.12	2.88E-01	6.57E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	216190_x_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376
2.12	2.72	0.60	2.88E-01	6.57E-01	PLN	phospholamban	chr6q22.1	204938_s_at	NM_002667
3.46	3.99	0.53	2.88E-01	6.57E-01	CHRFAM7A /// CHRNA7 /// LOC732445	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) fusion /// cholinergic receptor, nicotinic, alpha 7 /// similar to CHRNA7-FAM7A fusion isoform 1	chr15q13.1 /// chr15q14	210123_s_at	NM_000746 /// NM_139320 /// NM_148911 /// XM_001717875
2.91	3.12	0.21	2.88E-01	6.57E-01	NFASC	neurofascin homolog (chicken)	chr1q32.1	214799_at	NM_015090
2.35	2.53	0.18	2.88E-01	6.57E-01	CRCT1	cysteine-rich C-terminal 1	chr1q21	220620_at	NM_019060
2.62	2.79	0.17	2.88E-01	6.57E-01	FAM181B	family with sequence similarity 181, member B	chr11q14.1	231430_at	NM_175885
3.23	3.39	0.16	2.88E-01	6.57E-01	---	---	---	238646_at	---
1.84	1.99	0.15	2.88E-01	6.57E-01	LRRN1	leucine rich repeat neuronal 1	chr3p26.2	226884_at	NM_020873
2.45	2.60	0.15	2.88E-01	6.57E-01	SLC29A2	Solute carrier family 29 (nucleoside transporters), member 2	chr11q13	1560062_at	NM_001532
1.91	2.06	0.15	2.88E-01	6.57E-01	---	---	---	1557341_x_at	---
2.11	2.25	0.15	2.88E-01	6.57E-01	---	---	---	241023_at	---
1.97	2.10	0.13	2.88E-01	6.57E-01	C20orf19	chromosome 20 open reading frame 19	chr20pter-q11.23	233241_at	NM_018474
3.81	4.04	0.23	2.88E-01	6.57E-01	NFX1	nuclear transcription factor, X-box binding 1	chr9p13.3	202585_s_at	NM_002504 /// NM_147133 /// NM_147134
2.44	2.65	0.21	2.88E-01	6.58E-01	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	chr6p21.3	210747_at	NM_002123 /// XM_001722253 /// XM_001723447
2.88	3.11	0.23	2.88E-01	6.58E-01	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	chr8q12-q13	1558775_s_at	NM_003580
2.32	2.47	0.15	2.88E-01	6.58E-01	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	chr14q22.1	1555286_at	NM_004196
1.87	1.99	0.12	2.88E-01	6.58E-01	TEX9	testis expressed 9	chr15q21.3	1562259_at	NM_198524
5.53	6.11	0.59	2.88E-01	6.58E-01	YIPF5	Yip1 domain family, member 5	chr5q32	221423_s_at	NM_001024947 /// NM_030799
3.83	3.97	0.14	2.88E-01	6.58E-01	---	---	---	1561539_at	---

6.02	6.28	0.25	2.88E-01	6.58E-01	FAF1	Fas (TNFRSF6) associated factor 1	chr1p33	224217_s_at	NM_007051
2.99	3.19	0.20	2.88E-01	6.58E-01	---	---	---	228914_at	---
3.12	3.31	0.19	2.88E-01	6.58E-01	PLCE1	phospholipase C, epsilon 1	chr10q23	205112_at	NM_016341
6.04	6.39	0.34	2.88E-01	6.58E-01	VTA1	Vps20-associated 1 homolog (S. cerevisiae)	chr6q24.1	223022_s_at	NM_016485
2.13	2.27	0.14	2.89E-01	6.58E-01	---	---	---	241554_at	---
3.14	3.38	0.24	2.89E-01	6.58E-01	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	chr11p12-p11.2	213014_at	NM_005456
3.52	3.73	0.21	2.89E-01	6.58E-01	FBXO17	F-box protein 17	chr19q13.2	220233_at	NM_024907 /// NM_148169
2.58	2.76	0.18	2.89E-01	6.58E-01	MFAP3L	microfibrillar-associated protein 3-like	chr4q32.3	205442_at	NM_001009554 /// NM_021647
3.24	3.42	0.18	2.89E-01	6.58E-01	---	---	---	236041_at	---
3.81	3.98	0.17	2.89E-01	6.58E-01	hCG_20426	hCG20426	chr1p36.33	1556181_at	XR_040433 /// XR_040434 /// XR_040435
2.11	2.26	0.15	2.89E-01	6.58E-01	---	---	---	215456_at	---
2.13	2.27	0.14	2.89E-01	6.58E-01	---	---	---	238252_at	---
2.26	2.44	0.18	2.89E-01	6.58E-01	KCNC1	potassium voltage-gated channel, Shaw-related subfamily, member 1	chr11p15	208477_at	NM_001112741 /// NM_004976
5.10	5.28	0.18	2.89E-01	6.58E-01	---	---	---	239125_at	---
9.66	10.25	0.59	2.89E-01	6.58E-01	LEPROT	leptin receptor overlapping transcript	chr1p31.3	202378_s_at	NM_017526
5.79	6.17	0.38	2.89E-01	6.58E-01	---	---	---	1559156_at	---
4.31	4.56	0.24	2.89E-01	6.58E-01	LOC151174	hypothetical protein LOC151174	chr2q37.3	231135_at	XR_041817 /// XR_041818 /// XR_041819
5.84	6.28	0.44	2.89E-01	6.58E-01	ZC3H13	zinc finger CCCH-type containing 13	chr13q14.12	212402_at	NM_015070
2.66	2.85	0.19	2.89E-01	6.58E-01	CDX4	caudal type homeobox 4	chrXq13.2	221340_at	NM_005193
2.12	2.30	0.18	2.89E-01	6.58E-01	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	chr10q24	1557166_at	NM_014456 /// NM_145341
2.48	2.62	0.14	2.89E-01	6.58E-01	---	---	---	241144_at	---
2.07	2.22	0.14	2.89E-01	6.58E-01	LRRIQ1	leucine-rich repeats and IQ motif containing 1	chr12q21.31	223817_at	NM_001079910 /// NM_032165
6.93	7.20	0.27	2.89E-01	6.58E-01	XPR1	xenotropic and polytropic retrovirus receptor	chr1q25.1	222581_at	NM_004736
2.04	2.15	0.11	2.89E-01	6.58E-01	---	---	---	237148_at	---
2.86	3.12	0.26	2.89E-01	6.58E-01	---	---	---	231322_at	---
4.01	4.26	0.25	2.89E-01	6.58E-01	---	---	---	240527_at	---
3.03	3.19	0.17	2.89E-01	6.58E-01	BCL2L2	BCL2-like 2	chr14q11.2-q12	1555140_a_at	NM_004050
3.18	3.33	0.15	2.89E-01	6.58E-01	C12orf25	chromosome 12 open reading frame 25	chr12q13.12	224039_at	NM_032130
2.46	2.61	0.15	2.89E-01	6.58E-01	AMOT	angiomotin	chrXq23	209521_s_at	NM_001113490 /// NM_133265
4.28	4.59	0.31	2.89E-01	6.58E-01	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	chr19p13.2	204735_at	NM_001111307 /// NM_001111308 /// NM_001111309 /// NM_006202
2.44	2.68	0.23	2.89E-01	6.58E-01	CREM	cAMP responsive element modulator	chr10p11.21	210171_s_at	NM_001881 /// NM_181571 /// NM_182717 /// NM_182718 /// NM_182719 /// NM_182720 /// NM_182721 /// NM_182722 /// NM_182723 /// NM_182724 /// NM_182725 /// NM_182769 /// NM_182770 /// NM_182771 /// NM_182772 /// NM_182850 /// NM_182853 /// NM_183011 /// NM_183012 /// NM_183013 /// NM_183060
3.57	3.77	0.20	2.89E-01	6.58E-01	MRPS12	mitochondrial ribosomal protein S12	chr19q13.1-q13.2	204330_s_at	NM_021107 /// NM_033362 /// NM_033363
3.70	3.84	0.14	2.89E-01	6.58E-01	SEZ6	seizure related 6 homolog (mouse)	chr17q11.2	243430_at	NM_001098635 /// NM_178860

5.61	6.18	0.57	2.89E-01	6.59E-01	C14orf108	chromosome 14 open reading frame 108	chr14q23.1	222531_s_at	NM_018229
5.08	5.56	0.48	2.89E-01	6.59E-01	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	235077_at	NR_002766 /// NR_003530 /// NR_003531
5.51	5.86	0.35	2.89E-01	6.59E-01	WDR26	WD repeat domain 26	chr1q42.11	224905_at	NM_001115113 /// NM_025160
5.28	5.59	0.30	2.89E-01	6.59E-01	---	---	---	222275_at	---
3.22	3.47	0.25	2.90E-01	6.59E-01	TPD52L3	tumor protein D52-like 3	chr9p24.1	231554_at	NM_001001874 /// NM_001001875 /// NM_033516
3.04	3.27	0.23	2.90E-01	6.59E-01	LOC440956	hypothetical LOC440956	chr3p21.1	236661_at	XM_001723383 /// XM_496643 /// XM_941417
2.90	3.13	0.22	2.90E-01	6.59E-01	---	---	---	241697_at	---
4.09	4.28	0.19	2.89E-01	6.59E-01	DIO2	deiodinase, iodothyronine, type II	chr14q24.2-q24.3	211215_x_at	NM_000793 /// NM_001007023 /// NM_013989
2.37	2.54	0.16	2.89E-01	6.59E-01	---	---	---	241299_at	---
4.34	4.50	0.16	2.89E-01	6.59E-01	---	---	---	237532_at	---
2.38	2.53	0.15	2.90E-01	6.59E-01	CADM3	cell adhesion molecule 3	chr1q21.2-q22	213948_x_at	NM_001127173 /// NM_021189
1.87	2.02	0.15	2.89E-01	6.59E-01	LOC645158	hypothetical protein LOC645158	chr18p11.32	1557488_at	XM_932692 /// XM_943932
2.17	2.31	0.13	2.89E-01	6.59E-01	NUMB	Numb homolog (Drosophila)	chr14q24.3	236930_at	NM_001005743 /// NM_001005744 /// NM_001005745 /// NM_003744
4.43	5.48	1.04	2.90E-01	6.59E-01	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	chr12p13	203453_at	NM_001038
8.85	9.51	0.67	2.90E-01	6.59E-01	RGS5	regulator of G-protein signaling 5	chr1q23.1	209071_s_at	NM_003617
3.71	3.96	0.25	2.90E-01	6.59E-01	---	---	---	215802_at	---
2.40	2.57	0.17	2.90E-01	6.59E-01	LOC92482	UPF0604 protein	chr10q25.2	232910_at	XM_001716109 /// XM_001725802 /// XM_001725803 /// XM_001725804 /// XM_001726022 /// XM_001726023 /// XM_001726024
1.87	1.99	0.12	2.90E-01	6.59E-01	---	---	---	216169_at	---
2.45	2.62	0.17	2.90E-01	6.59E-01	---	---	---	239541_at	---
2.64	2.94	0.29	2.90E-01	6.59E-01	---	---	---	236350_at	---
7.95	8.21	0.26	2.90E-01	6.59E-01	GLUD1	glutamate dehydrogenase 1	chr10q23.3	200947_s_at	NM_005271
4.22	4.51	0.28	2.90E-01	6.59E-01	---	---	---	226795_at	---
1.94	2.06	0.13	2.90E-01	6.59E-01	TAAR1	trace amine associated receptor 1	chr6q23.2	1553930_at	NM_138327
9.58	9.88	0.30	2.90E-01	6.59E-01	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	chr22q13.2	207040_s_at	NM_003932
2.82	3.04	0.22	2.90E-01	6.59E-01	---	---	---	234965_at	---
2.52	2.72	0.20	2.90E-01	6.59E-01	CLEC4A	C-type lectin domain family 4, member A	chr12p13	219947_at	NM_016184 /// NM_194447 /// NM_194448 /// NM_194450
2.72	2.91	0.18	2.90E-01	6.59E-01	GAS5	Growth arrest-specific 5 (non-protein coding)	chr1q25.1	235712_at	NR_002578
5.83	6.00	0.17	2.90E-01	6.59E-01	GLUL	glutamate-ammonia ligase (glutamine synthetase)	chr1q31	217203_at	NM_001033044 /// NM_001033056 /// NM_002065
2.78	2.94	0.17	2.90E-01	6.59E-01	RIMS1	regulating synaptic membrane exocytosis 1	chr6q12-q13	231986_at	NM_014989
2.33	2.47	0.14	2.90E-01	6.59E-01	FABP7	fatty acid binding protein 7, brain	chr6q22-q23	216192_at	NM_001446

2.37	2.50	0.13	2.90E-01	6.59E-01	GABRA1	gamma-aminobutyric acid (GABA) A receptor, alpha 1	chr5q34-q35	206678_at	NM_000806 /// NM_001127643 /// NM_001127644 /// NM_001127645 /// NM_001127646 /// NM_001127647 /// NM_001127648
1.78	1.91	0.13	2.90E-01	6.59E-01	RAB3IP	RAB3A interacting protein (rabin3)	chr12q14.3	1565800_x_at	NM_001024647 /// NM_022456 /// NM_175623 /// NM_175624 /// NM_175625
1.94	2.06	0.11	2.90E-01	6.59E-01	---	---	---	238203_at	---
2.16	2.30	0.14	2.90E-01	6.59E-01	---	---	---	235681_at	---
2.22	2.33	0.11	2.90E-01	6.59E-01	---	---	---	240149_at	---
4.81	5.09	0.28	2.90E-01	6.59E-01	FLJ10213	hypothetical protein FLJ10213	chr3p13	219906_at	NM_018029
2.47	2.65	0.18	2.90E-01	6.59E-01	---	---	---	243782_at	---
3.70	4.04	0.34	2.90E-01	6.59E-01	---	---	---	232744_x_at	---
2.88	3.08	0.19	2.90E-01	6.59E-01	CD300A	CD300a molecule	chr17q25.1	217072_at	NM_007261
7.97	8.81	0.84	2.90E-01	6.59E-01	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	chr17p13.1	202283_at	NM_002615
2.63	3.33	0.70	2.90E-01	6.59E-01	SLC13A5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	chr17p13.2	228844_at	NM_177550
4.86	5.37	0.51	2.90E-01	6.59E-01	---	---	---	235196_at	---
6.04	6.26	0.22	2.90E-01	6.59E-01	IFT52	intraflagellar transport 52 homolog (Chlamydomonas)	---	218709_s_at	NM_016004
5.23	5.42	0.19	2.90E-01	6.59E-01	DNAL1	dynein, axonemal, light chain 1	chr14q24.3	226309_at	NM_031427
2.97	3.15	0.18	2.90E-01	6.59E-01	---	---	---	232331_at	---
2.62	2.79	0.17	2.90E-01	6.59E-01	---	---	---	239705_at	---
2.50	2.67	0.16	2.90E-01	6.59E-01	---	---	---	240888_at	---
2.09	2.24	0.15	2.90E-01	6.59E-01	GPR98	G protein-coupled receptor 98	chr5q13	240631_at	NM_032119 /// NR_003149
2.22	2.37	0.15	2.90E-01	6.59E-01	LOC285740	hypothetical protein LOC285740	chr6q24.2	1556859_a_at	---
1.90	2.02	0.12	2.90E-01	6.59E-01	IFNA1 /// IFNA13	interferon, alpha 1 /// interferon, alpha 13	chr9p22	208375_at	NM_006900 /// NM_024013
5.10	5.25	0.15	2.91E-01	6.59E-01	C17orf72	chromosome 17 open reading frame 72	chr17q23.3	232972_at	NR_015354 /// XM_001724631 /// XM_001724632 /// XM_001726065 /// XM_001726066 /// XM_001726842 /// XM_001726843
4.45	5.07	0.62	2.91E-01	6.59E-01	OLFML2A	olfactomedin-like 2A	chr9q33.3	213075_at	NM_182487
2.21	2.34	0.14	2.91E-01	6.59E-01	BPIL3	bactericidal/permeability-increasing protein-like 3	chr20q11.21	1555535_at	NM_174897
4.55	4.75	0.20	2.91E-01	6.59E-01	LOC100134685	hypothetical protein LOC100134685	---	240624_x_at	XM_001718383
3.61	3.76	0.15	2.91E-01	6.59E-01	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	chr14q23.3	212821_at	NM_015549
3.63	3.77	0.14	2.91E-01	6.59E-01	TRPV3	transient receptor potential cation channel, subfamily V, member 3	chr17p13.3	1552586_at	NM_145068
2.23	2.35	0.12	2.91E-01	6.59E-01	---	---	---	238457_at	---
5.72	6.26	0.54	2.91E-01	6.59E-01	---	---	---	232333_at	---
3.84	3.99	0.16	2.91E-01	6.59E-01	---	---	---	1568907_at	---
2.24	2.44	0.20	2.91E-01	6.60E-01	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	chr2q12	219797_at	NM_012214
2.39	2.56	0.18	2.91E-01	6.60E-01	---	---	---	233670_at	---
2.20	2.37	0.18	2.91E-01	6.60E-01	LOC100129856	similar to hCG2040214	chr7q34	240932_at	XM_001723586 /// XM_001726712
2.30	2.45	0.15	2.91E-01	6.60E-01	---	---	---	239698_at	---
5.07	5.60	0.54	2.91E-01	6.60E-01	---	---	---	236907_at	---
3.24	3.54	0.29	2.91E-01	6.60E-01	C19orf33	chromosome 19 open reading frame 33	chr19q13.2	223631_s_at	NM_033520
4.59	4.82	0.23	2.91E-01	6.60E-01	FLJ20444	hypothetical protein FLJ20444	chr9q21	232897_at	XM_933028
2.90	3.12	0.23	2.91E-01	6.60E-01	---	---	---	1568876_a_at	---

2.34	2.52	0.18	2.91E-01	6.60E-01	TUBB2B	tubulin, beta 2B	chr6p25	214023_x_at	NM_178012
8.17	8.49	0.32	2.91E-01	6.60E-01	CNOT7	CCR4-NOT transcription complex, subunit 7	chr8p22-p21.3	225053_at	NM_013354 /// NM_054026
5.85	7.35	1.49	2.91E-01	6.60E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	209138_x_at	---
6.92	7.38	0.46	2.91E-01	6.60E-01	ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	chr15q24	201880_at	NM_005744
3.59	3.81	0.22	2.91E-01	6.60E-01	N-PAC	cytokine-like nuclear factor n-pac	chr16p13.3	221628_s_at	NM_032569
2.45	2.66	0.21	2.91E-01	6.60E-01	---	---	---	1566947_at	---
3.11	3.28	0.17	2.91E-01	6.60E-01	GRIK5	glutamate receptor, ionotropic, kainate 5	chr19q13.2	214966_at	NM_002088
2.73	2.89	0.16	2.91E-01	6.60E-01	XYLB	xylulokinase homolog (H. influenzae)	chr3p22-p21.3	1569683_at	NM_005108
3.24	3.39	0.16	2.91E-01	6.60E-01	---	---	---	241263_at	---
8.36	8.66	0.30	2.91E-01	6.60E-01	SCARB2	scavenger receptor class B, member 2	chr4q21.1	224983_at	NM_005506
4.25	4.59	0.34	2.91E-01	6.60E-01	OSTM1	osteopetrosis associated transmembrane protein 1	chr6q21	235198_at	NM_014028
4.55	4.78	0.23	2.91E-01	6.60E-01	MUC20	mucin 20, cell surface associated	chr3q29	243774_at	NM_001098516 /// NM_152673 /// XM_001726694
2.18	2.29	0.11	2.91E-01	6.60E-01	MURC	muscle-restricted coiled-coil protein	chr9q31.1	241749_at	NM_001018116
2.02	2.14	0.13	2.91E-01	6.60E-01	ZNF682	zinc finger protein 682	chr19p12	216468_s_at	NM_001077349 /// NM_033196
2.46	2.59	0.13	2.92E-01	6.60E-01	CAD	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	chr2p22-p21	1564084_at	NM_004341
2.78	3.02	0.24	2.92E-01	6.60E-01	UHRF1BP1L	UHRF1 binding protein 1-like	chr12q23.1	213120_at	NM_001006947 /// NM_015054
3.93	4.12	0.18	2.92E-01	6.60E-01	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	chr2p23	217156_at	NM_000182
2.62	2.77	0.15	2.92E-01	6.60E-01	---	---	---	217459_at	---
7.91	8.30	0.39	2.92E-01	6.60E-01	TCEA1	transcription elongation factor A (SII), 1	chr8q11.2	216241_s_at	NM_006756 /// NM_201437
2.92	3.14	0.22	2.92E-01	6.60E-01	---	---	---	234494_x_at	---
5.31	5.53	0.22	2.92E-01	6.60E-01	TTLL5	tubulin tyrosine ligase-like family, member 5	chr14q24.3	214672_at	NM_015072
2.57	2.78	0.21	2.92E-01	6.60E-01	---	---	---	241115_at	---
2.22	2.38	0.16	2.92E-01	6.60E-01	---	---	---	234835_at	---
3.47	3.63	0.15	2.92E-01	6.60E-01	TCEA1	transcription elongation factor A (SII), 1	chr8q11.2	1566207_at	NM_006756 /// NM_201437
7.11	7.59	0.47	2.92E-01	6.60E-01	EZR	ezrin	chr6q25.2-q26	217234_s_at	NM_001111077 /// NM_003379
7.72	7.90	0.18	2.92E-01	6.60E-01	UBE2K	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	chr4p14	202347_s_at	NM_001111112 /// NM_001111113 /// NM_005339
2.00	2.18	0.18	2.92E-01	6.60E-01	MCM3AP	minichromosome maintenance complex component 3 associated protein	chr21q22.3	214514_at	NM_003906
6.82	7.37	0.54	2.92E-01	6.60E-01	CCDC6	coiled-coil domain containing 6	chr10q21	225010_at	NM_005436
3.56	3.70	0.14	2.92E-01	6.60E-01	---	---	---	1561526_at	---
2.26	2.49	0.23	2.92E-01	6.60E-01	---	---	---	244731_at	---
5.85	6.10	0.25	2.92E-01	6.60E-01	ACSS1	acyl-CoA synthetase short-chain family member 1	chr20p11.23-p11.21	224882_at	NM_032501
2.80	2.94	0.14	2.92E-01	6.60E-01	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	chr19q13.2	211848_s_at	NM_006890
8.83	9.24	0.41	2.92E-01	6.60E-01	SET	SET nuclear oncogene	chr9q34	200631_s_at	NM_001122821 /// NM_003011
1.99	2.12	0.13	2.92E-01	6.61E-01	---	---	---	244762_at	---
2.49	2.62	0.14	2.92E-01	6.61E-01	STK35	serine/threonine kinase 35	chr20p13	1553673_at	NM_080836
4.14	4.39	0.25	2.92E-01	6.61E-01	TRA@	T cell receptor alpha locus	chr14q11.2	211902_x_at	---
4.72	5.22	0.50	2.92E-01	6.61E-01	XPO1	exportin 1 (CRM1 homolog, yeast)	chr2p16	235927_at	NM_003400
5.08	5.33	0.24	2.92E-01	6.61E-01	---	---	---	239532_at	---
3.18	3.35	0.17	2.92E-01	6.61E-01	DAAM1	dishevelled associated activator of morphogenesis 1	chr14q23.1	244062_at	NM_014992
6.88	7.22	0.34	2.92E-01	6.61E-01	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	chr1p13.2	200848_at	NM_006621
3.04	3.22	0.18	2.92E-01	6.61E-01	PASK	PAS domain containing serine/threonine kinase	chr2q37.3	213534_s_at	NM_015148
4.28	4.43	0.15	2.93E-01	6.61E-01	PTEN	Phosphatase and tensin homolog	chr10q23.3	227469_at	NM_000314
3.08	3.38	0.30	2.93E-01	6.61E-01	---	---	---	216094_at	---
4.76	5.05	0.29	2.93E-01	6.61E-01	---	---	---	239311_at	---
3.71	3.90	0.19	2.93E-01	6.61E-01	KLKB1	kallikrein B, plasma (Fletcher factor) 1	chr4q34-q35	206541_at	NM_000892
2.32	2.50	0.19	2.93E-01	6.61E-01	AP4B1	Adaptor-related protein complex 4, beta 1 subunit	chr1p13.2	236221_at	NM_006594
1.83	1.96	0.13	2.93E-01	6.61E-01	ZNF763	zinc finger protein 763	chr19p13.2	1558754_at	NM_001012753
2.04	2.23	0.19	2.93E-01	6.61E-01	---	---	---	215853_at	---

3.89	4.25	0.36	2.93E-01	6.61E-01	DKFZp547E087	hypothetical gene LOC283846	chr18p11.21	235167_at	XM_496136 /// XM_931802 /// XM_931808 /// XM_931814 /// XM_931818 /// XM_931827 /// XM_931837 /// XM_931840																				
2.67	2.85	0.18	2.93E-01	6.61E-01	RBMY1A1 /// RBMY1B /// RBMY1D /// RBMY1E /// RBMY1F /// RBMY1H /// RBMY1J /// RBMY3AP	RNA binding motif protein, Y-linked, family 1, member A1 /// RNA binding motif protein, Y-linked, family 1, member B /// RNA binding motif protein, Y-linked, family 1, member D /// RNA binding motif protein, Y-linked, family 1, member E /// RNA binding motif protein, Y-linked, family 1, member F /// RNA binding motif protein, Y-linked, family 1, member H /// RNA binding motif protein, Y-linked, family 1, member J /// RNA binding motif protein, Y-linked, family 3, member A pseudogene	chrYp11.2 /// chrYq11.223 /// chrYq11.23	208307_at	NM_001006117 /// NM_001006118 /// NM_001006120 /// NM_001006121 /// NM_001007526 /// NM_005058 /// NM_152585 /// NR_001573																		
3.12	3.72	0.60	2.93E-01	6.61E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	216560_x_at	---																				
4.86	5.25	0.39	2.93E-01	6.61E-01	LOC145758	hypothetical protein LOC145758	chr15q26.3	226513_at	---																				
5.24	5.62	0.38	2.93E-01	6.61E-01	NUP205	nucleoporin 205kDa	chr7q33	212247_at	NM_015135																				
3.14	3.34	0.20	2.93E-01	6.61E-01	ZNF428	zinc finger protein 428	chr19q13.31	1565848_at	NM_182498																				
2.65	2.82	0.17	2.93E-01	6.61E-01	---	---	---	242465_at	---																				
4.02	4.18	0.15	2.93E-01	6.61E-01	---	---	---	1566452_at	---																				
2.60	2.75	0.15	2.93E-01	6.61E-01	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	chr1p34.1	1555678_at	NM_006279 /// NM_174963 /// NM_174964 /// NM_174965 /// NM_174966 /// NM_174967 /// NM_174968 /// NM_174969 /// NM_174970 /// NM_174971																				
2.23	2.37	0.15	2.93E-01	6.61E-01	---	---	---	234745_at	---																				
3.70	3.86	0.17	2.93E-01	6.61E-01	TUBGCP5	tubulin, gamma complex associated protein 5	chr15q11.2	227967_at	NM_001102610 /// NM_052903																				
2.72	2.87	0.15	2.93E-01	6.61E-01	LELP1	late cornified envelope-like proline-rich 1	chr1q21.3	231363_at	NM_001010857																				
6.09	6.50	0.41	2.93E-01	6.61E-01	FASTKD1	FAST kinase domains 1	chr2q31	219002_at	NM_024622																				
4.42	4.80	0.37	2.93E-01	6.61E-01	C16orf72	chromosome 16 open reading frame 72	chr16p13.2	1568954_s_at	NM_014117																				
3.80	4.17	0.36	2.93E-01	6.61E-01	XPO7	exportin 7	chr8p21	240168_at	NM_001100161 /// NM_001100162 /// NM_015024																				
8.49	8.81	0.31	2.93E-01	6.61E-01	PDIA6	protein disulfide isomerase family A, member 6	chr2p25.1	208638_at	NM_005742																				
4.57	4.83	0.26	2.93E-01	6.61E-01	DNAJC30	DnaJ (Hsp40) homolog, subfamily C, member 30	chr7q11.23	239018_at	NM_032317																				
4.99	5.24	0.25	2.93E-01	6.61E-01	PPP1R12C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	chr19q13.42	234286_at	NM_017607																				
2.29	2.49	0.20	2.93E-01	6.61E-01	---	---	---	243898_at	---																				
2.68	2.85	0.17	2.93E-01	6.61E-01	---	---	---	242593_at	---																				
2.23	2.39	0.16	2.93E-01	6.61E-01	TACSTD2	tumor-associated calcium signal transducer 2	chr1p32-p31	202287_s_at	NM_002353																				
1.93	2.08	0.15	2.93E-01	6.61E-01	---	---	---	217532_x_at	---																				
1.96	2.09	0.13	2.93E-01	6.61E-01	ANGPT1	angiopoietin 1	chr8q22.3-q23	1552939_at	NM_001146																				
2.33	2.50	0.17	2.93E-01	6.61E-01	ZNF496	Zinc finger protein 496	chr1q44	238145_at	NM_032752																				
5.50	5.86	0.36	2.93E-01	6.62E-01	FBXL3	F-box and leucine-rich repeat protein 3	chr13q22	242829_x_at	NM_012158																				
4.73	4.94	0.20	2.94E-01	6.62E-01	---	---	---	239633_at	---																				
4.39	4.70	0.30	2.94E-01	6.62E-01	TMEM63C	transmembrane protein 63C	chr14q24.3	227733_at	NM_020431																				
7.12	7.68	0.56	2.94E-01	6.62E-01	SF3B1	splicing factor 3b, subunit 1, 155kDa	chr2q33.1	214305_s_at	NM_001005526 /// NM_012433																				
4.38	4.57	0.18	2.94E-01	6.62E-01	---	---	---	1554650_a_at	---																				
2.13	2.26	0.13	2.94E-01	6.62E-01	HTR3B	5-hydroxytryptamine (serotonin) receptor 3B	chr11q23.1	221084_at	NM_006028																				
5.92	6.14	0.22	2.94E-01	6.62E-01	PRX	periaxin	chr19q13.13- q13.2	220024_s_at	NM_020956 /// NM_181882																				
4.09	4.32	0.22	2.94E-01	6.62E-01	LOC644450	hypothetical protein LOC644450	chr1q12	1564544_x_at	XM_927590																				
1.98	2.10	0.12	2.94E-01	6.62E-01	WBP2NL	WBP2 N-terminal like	chr22q13.2	1552514_at	NM_152613																				
3.20	3.63	0.43	2.94E-01	6.62E-01	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	chr11q23.3	1555355_a_at	NM_005238																				
2.14	2.28	0.14	2.94E-01	6.62E-01	DEFB106A /// DEFB106B	defensin, beta 106A /// defensin, beta 106B	chr8p23.1	1552412_a_at	NM_001040704 /// NM_152251																				
3.79	4.00	0.21	2.94E-01	6.62E-01	---	---	---	215370_at	---																				
6.93	7.36	0.43	2.94E-01	6.62E-01	CENTA2	centaurin, alpha 2	chr17q11.2	222876_s_at	NM_018404																				
7.66	7.96	0.30	2.94E-01	6.62E-01	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	chr1p13.2	200849_s_at	NM_006621																				

2.86	3.11	0.25	2.94E-01	6.62E-01	LARP7	La ribonucleoprotein domain family, member 7	chr4q25	241385_at	NM_015454 /// NM_016648
2.37	2.59	0.21	2.94E-01	6.62E-01	---	---	---	1565889_at	---
2.18	2.38	0.20	2.94E-01	6.62E-01	CTLA4	cytotoxic T-lymphocyte-associated protein 4	chr2q33	236341_at	NM_001037631 /// NM_005214
2.29	2.48	0.19	2.94E-01	6.62E-01	---	---	---	240670_at	---
2.71	2.88	0.17	2.94E-01	6.62E-01	---	---	---	215996_at	---
2.49	2.65	0.16	2.94E-01	6.62E-01	---	---	---	234207_at	---
2.74	2.90	0.16	2.94E-01	6.62E-01	---	---	---	233508_at	---
4.14	4.31	0.18	2.94E-01	6.62E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	238340_at	NM_015726
1.83	1.97	0.14	2.94E-01	6.62E-01	ZNF675	zinc finger protein 675	chr19p12	217547_x_at	NM_138330
3.49	3.69	0.20	2.94E-01	6.62E-01	MGC5566	hypothetical protein MGC5566	chr20q13.12	220449_at	XM_926767 /// XM_938022
5.65	5.96	0.31	2.95E-01	6.63E-01	SLC27A4	solute carrier family 27 (fatty acid transporter), member 4	chr9q34.11	225779_at	NM_005094
2.62	2.80	0.18	2.95E-01	6.63E-01	---	---	---	1553083_at	---
4.99	5.56	0.56	2.95E-01	6.63E-01	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	chr3p22.3	235099_at	NM_178868
6.37	6.82	0.45	2.95E-01	6.63E-01	RNF6	ring finger protein (C3H2C3 type) 6	chr13q12.2	203403_s_at	NM_005977 /// NM_183043 /// NM_183044
2.03	2.16	0.13	2.95E-01	6.63E-01	RAB5A	RAB5A, member RAS oncogene family	chr3p24-p22	240990_at	NM_004162
3.08	3.26	0.17	2.95E-01	6.63E-01	CTLA4	cytotoxic T-lymphocyte-associated protein 4	chr2q33	231794_at	NM_001037631 /// NM_005214
8.19	8.45	0.25	2.95E-01	6.63E-01	---	---	---	224601_at	---
2.09	2.25	0.16	2.95E-01	6.63E-01	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	chr8p23.1	1569391_at	NM_003747
4.47	4.99	0.52	2.95E-01	6.63E-01	EPAS1	endothelial PAS domain protein 1	chr2p21-p16	200879_s_at	NM_001430
4.32	4.56	0.24	2.95E-01	6.63E-01	SDCCAG8	serologically defined colon cancer antigen 8	chr1q43-q44	243772_at	NM_006642
4.44	4.63	0.18	2.95E-01	6.63E-01	---	---	---	244450_at	---
2.21	2.35	0.14	2.95E-01	6.63E-01	ACSS1	acyl-CoA synthetase short-chain family member 1	chr20p11.23-p11.21	234483_at	NM_032501
2.07	2.19	0.12	2.95E-01	6.63E-01	LOC339751	hypothetical protein LOC339751	chr2q31.1	1558653_at	---
2.68	2.86	0.17	2.95E-01	6.63E-01	DCTN2	Dynactin 2 (p50)	chr12q13.2-q13.3	214384_s_at	NM_006400
6.71	7.31	0.60	2.95E-01	6.63E-01	TGFBR3	transforming growth factor, beta receptor III	chr1p33-p32	204731_at	NM_003243
5.41	5.63	0.22	2.95E-01	6.63E-01	ZNF207	zinc finger protein 207	chr17q11.2	229765_at	NM_001032293 /// NM_001098507 /// NM_003457
2.79	2.92	0.14	2.95E-01	6.63E-01	LOC100129014	hypothetical protein LOC100129014	chrXq11.1	233749_at	XM_001715068 /// XM_001715396 /// XM_001716283
2.26	2.40	0.14	2.95E-01	6.63E-01	---	---	---	1566825_at	---
2.62	2.82	0.20	2.95E-01	6.63E-01	ATP10B	ATPase, class V, type 10B	chr5q34	220920_at	NM_025153
9.76	9.89	0.13	2.95E-01	6.63E-01	COX7B	cytochrome c oxidase subunit VIIb	chrXq21.1	202110_at	NM_001866
2.15	2.28	0.13	2.95E-01	6.63E-01	---	---	---	1556272_a_at	---
2.43	2.65	0.23	2.95E-01	6.63E-01	LOC730057	Hypothetical LOC730057	chr3p14.1	1562295_at	XM_001132251 /// XM_001132871 /// XM_001716450
5.36	5.56	0.20	2.95E-01	6.63E-01	RAB40B	RAB40B, member RAS oncogene family	chr17q25.3	217597_x_at	NM_006822
2.64	2.80	0.16	2.95E-01	6.63E-01	CCDC62	coiled-coil domain containing 62	chr12q24.31	231567_s_at	NM_032573 /// NM_201435
6.67	7.17	0.50	2.95E-01	6.63E-01	TMEM123	transmembrane protein 123	chr11q22.1	211967_at	NM_052932
3.12	3.32	0.20	2.95E-01	6.63E-01	---	---	---	241610_x_at	---
6.33	6.66	0.33	2.95E-01	6.63E-01	STXBP1	syntaxin binding protein 1	chr9q34.1	202260_s_at	NM_001032221 /// NM_003165
2.97	3.16	0.19	2.95E-01	6.63E-01	---	---	---	240978_at	---
2.79	2.95	0.17	2.95E-01	6.63E-01	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	chr1p36.21	1560097_at	NM_052929 /// XM_001714211 /// XM_934889 /// XM_946265
2.01	2.17	0.16	2.95E-01	6.63E-01	CCDC65	coiled-coil domain containing 65	chr12q13.12	1561523_at	NM_033124
3.94	4.16	0.21	2.96E-01	6.64E-01	GP1BB /// SEPT5	glycoprotein Ib (platelet), beta polypeptide /// septin 5	chr22q11.21 /// chr22q11.21-q11.23|22q11.21	209768_s_at	NM_000407 /// NM_002688

5.20	5.59	0.40	2.96E-01	6.64E-01	LAMA2	laminin, alpha 2	chr6q22-q23	213519_s_at	NM_000426 /// NM_001079823																				
5.00	5.26	0.26	2.96E-01	6.64E-01	FOLR2	Folate receptor 2 (fetal)	chr11q13.3-q13.5	229619_at	NM_000803 /// NM_001113534 /// NM_001113535 /// NM_001113536																				
2.44	2.56	0.12	2.96E-01	6.64E-01	---	---	---	1566726_at	---																				
2.33	2.72	0.39	2.96E-01	6.64E-01	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	chr13q14.11	1553111_a_at	NM_152903																				
9.41	9.76	0.35	2.96E-01	6.64E-01	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	chr3p14	200761_s_at	NM_006407																				
6.35	6.57	0.22	2.96E-01	6.64E-01	IFIT5	interferon-induced protein with tetratricopeptide repeats 5	chr10q23.31	203596_s_at	NM_012420																				
9.01	9.22	0.21	2.96E-01	6.64E-01	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	chr2p25.1	200693_at	NM_006826																				
2.75	2.93	0.18	2.96E-01	6.64E-01	---	---	---	231232_at	---																				
2.65	2.81	0.16	2.96E-01	6.64E-01	MUC12	mucin 12, cell surface associated	chr7q22	1557907_x_at	XM_001714400 /// XM_001724943 /// XM_379904 /// XM_936315																				
3.64	3.77	0.13	2.96E-01	6.64E-01	OBP2A /// OBP2B	odorant binding protein 2A /// odorant binding protein 2B	chr9q34	220959_s_at	NM_014581 /// NM_014582																				
2.31	2.44	0.13	2.96E-01	6.64E-01	---	---	---	242929_at	---																				
2.68	2.80	0.12	2.96E-01	6.64E-01	---	---	---	215868_x_at	---																				
2.00	2.12	0.11	2.96E-01	6.64E-01	---	---	---	244328_x_at	---																				
7.10	7.49	0.40	2.96E-01	6.64E-01	ATAD1	ATPase family, AAA domain containing 1	chr10q23.2	224850_at	NM_032810																				
2.40	2.62	0.23	2.96E-01	6.64E-01	LOC100125871	hypothetical protein LOC100125871	---	243056_at	---																				
3.94	4.28	0.34	2.96E-01	6.64E-01	---	---	---	238902_at	---																				
2.85	3.02	0.17	2.96E-01	6.64E-01	---	---	---	234439_at	---																				
1.80	1.91	0.11	2.96E-01	6.64E-01	ZNF226	zinc finger protein 226	chr19q13.2	231717_s_at	NM_001032372 /// NM_001032373 /// NM_001032374 /// NM_001032375 /// NM_015919																				
1.89	2.05	0.16	2.96E-01	6.64E-01	---	---	---	243257_at	---																				
2.78	2.97	0.19	2.96E-01	6.64E-01	---	---	---	244375_at	---																				
1.98	2.14	0.16	2.96E-01	6.64E-01	ANO1	anoctamin 1, calcium activated chloride channel	chr11q13.3	218804_at	NM_018043																				
4.76	4.92	0.16	2.96E-01	6.64E-01	OTUD7B	OTU domain containing 7B	chr1q21.2	238994_at	NM_020205																				
2.14	2.29	0.16	2.96E-01	6.64E-01	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	chr19q13.2	207913_at	NM_000774																				
1.87	2.01	0.14	2.96E-01	6.64E-01	PLK4	polo-like kinase 4 (Drosophila)	chr4q28	204886_at	NM_014264																				
2.62	2.76	0.14	2.96E-01	6.64E-01	GPRIN1	G protein regulated inducer of neurite outgrowth 1	chr5q35.2	229922_at	NM_052899																				
3.85	4.06	0.22	2.96E-01	6.64E-01	TRBC1 /// TRBC2 /// TRBV19 /// TRBV7-4 /// TRBV7-6 /// TRBV7-7 /// TRBV7-8	T cell receptor beta constant 1 /// T cell receptor beta constant 2 /// T cell receptor beta variable 19 /// T cell receptor beta variable 7-4 /// T cell receptor beta variable 7-6 /// T cell receptor beta variable 7-7 /// T cell receptor beta variable 7-8	chr7q34	217326_x_at	---																				
2.92	3.12	0.19	2.96E-01	6.64E-01	UBE2J1	Ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	chr6q15	228924_s_at	NM_016021																				
4.31	4.49	0.19	2.96E-01	6.64E-01	CAMKV	CaM kinase-like vesicle-associated	chr3p21.31	219365_s_at	NM_024046																				
4.64	4.80	0.16	2.96E-01	6.64E-01	---	---	---	213930_at	---																				
6.67	7.10	0.44	2.96E-01	6.64E-01	ERMP1	endoplasmic reticulum metallopeptidase 1	chr9p24	222603_at	NM_024896																				
2.29	2.44	0.15	2.96E-01	6.64E-01	---	---	---	234848_at	---																				
4.81	4.95	0.14	2.96E-01	6.64E-01	C21orf2	Chromosome 21 open reading frame 2	chr21q22.3	221975_s_at	NM_004928																				
1.98	2.10	0.12	2.96E-01	6.64E-01	---	---	---	241652_x_at	---																				
2.05	2.22	0.17	2.97E-01	6.64E-01	---	---	---	1563189_at	---																				
3.31	3.76	0.45	2.97E-01	6.64E-01	C21orf66	chromosome 21 open reading frame 66	chr21q21.3	1555125_at	NM_013329 /// NM_016631 /// NM_058191																				
2.19	2.63	0.44	2.97E-01	6.64E-01	PLN	Phospholamban	chr6q22.1	228202_at	NM_002667																				
3.25	3.69	0.43	2.97E-01	6.64E-01	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	chr9q22.33	222773_s_at	NM_024642																				
2.35	2.66	0.30	2.97E-01	6.64E-01	LOC100128311	PRO1495	chr4q13.3	224115_at	XM_001720162 /// XM_001720222 /// XM_001721934																				

5.46	5.74	0.29	2.97E-01	6.64E-01	---	---	---	213573_at	---
3.34	3.59	0.25	2.97E-01	6.64E-01	FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	chrXp22.31	206742_at	NM_004469
3.82	4.05	0.23	2.97E-01	6.64E-01	---	---	---	239396_at	---
2.78	2.99	0.21	2.97E-01	6.64E-01	AKAP3	A kinase (PRKA) anchor protein 3	chr12p13.3	207344_at	NM_006422
2.73	2.93	0.20	2.97E-01	6.64E-01	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	chr9q32	224618_at	NM_005156
2.69	2.89	0.20	2.97E-01	6.64E-01	C20orf152	chromosome 20 open reading frame 152	chr20q11.23	1552686_at	NM_080834
4.82	5.01	0.19	2.97E-01	6.64E-01	POU6F1	POU class 6 homeobox 1	chr12q13.13	205878_at	NM_002702
2.84	3.01	0.18	2.97E-01	6.64E-01	ULK4	unc-51-like kinase 4 (C. elegans)	chr3p22.1	231149_s_at	NM_017886
2.22	2.39	0.18	2.97E-01	6.64E-01	---	---	---	235656_s_at	---
2.75	2.91	0.16	2.97E-01	6.64E-01	IGFN1	Immunoglobulin-like and fibronectin type III domain containing 1	chr1q32.1	1563098_at	NM_178275
3.22	3.38	0.15	2.97E-01	6.64E-01	FLJ34208	hypothetical gene supported by AK091527	chr3q29	1566761_a_at	XM_001713883 /// XM_001715353 /// XM_001719177
2.28	2.43	0.15	2.97E-01	6.64E-01	SPTBN1	spectrin, beta, non-erythrocytic 1	chr2p21	242220_at	NM_003128 /// NM_178313
2.09	2.23	0.14	2.97E-01	6.64E-01	ZMAT1	zinc finger, matrin type 1	chrXq21	241328_at	NM_001011657 /// NM_032441
2.98	3.11	0.13	2.97E-01	6.64E-01	LOC283711	hypothetical protein LOC283711	chr15q13.3	1564463_at	XR_040656
2.06	2.18	0.13	2.97E-01	6.64E-01	DENND5B	DENN/MADD domain containing 5B	chr12p11.21	243613_at	NM_144973
5.54	5.89	0.35	2.97E-01	6.64E-01	RABL3	RAB, member of RAS oncogene family-like 3	chr3q13.33	226090_x_at	NM_173825
3.57	3.75	0.18	2.97E-01	6.64E-01	MUC13	mucin 13, cell surface associated	chr3q21.2	222712_s_at	NM_033049
2.14	2.27	0.13	2.97E-01	6.64E-01	---	---	---	237552_at	---
4.17	4.63	0.46	2.97E-01	6.64E-01	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	chr14q31.1	233208_x_at	NM_017437
3.86	4.13	0.27	2.97E-01	6.64E-01	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	chr19p12	232915_at	NM_019070
2.00	2.16	0.16	2.97E-01	6.64E-01	ENY2	enhancer of yellow 2 homolog (Drosophila)	chr8q23.1	226776_at	NM_020189
8.60	9.26	0.66	2.97E-01	6.64E-01	TncRNA	trophoblast-derived noncoding RNA	chr11q13.1	227062_at	NR_002802
3.55	3.68	0.13	2.97E-01	6.64E-01	TEX13B	testis expressed 13B	chrXq22.3	221034_s_at	NM_031273
2.39	2.60	0.22	2.97E-01	6.64E-01	---	---	---	238261_at	---
2.55	2.72	0.16	2.97E-01	6.64E-01	ACSM1	acyl-CoA synthetase medium-chain family member 1	chr16p12.2	215432_at	NM_052956
2.73	2.88	0.15	2.97E-01	6.64E-01	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	chr13q12.11-q12.3	224090_s_at	NM_018647 /// NM_148957
2.05	2.18	0.13	2.97E-01	6.64E-01	HTR4	5-hydroxytryptamine (serotonin) receptor 4	chr5q31-q33	216939_s_at	NM_000870 /// NM_001040169 /// NM_001040171 /// NM_001040172 /// NM_001040173 /// NM_001040174 /// NM_199453
1.82	1.93	0.11	2.97E-01	6.64E-01	ASZ1	ankyrin repeat, SAM and basic leucine zipper domain containing 1	chr7q31.2	1569729_a_at	NM_130768 /// NR_023315
1.92	2.08	0.16	2.97E-01	6.64E-01	---	---	---	1562260_at	---
6.97	7.40	0.43	2.97E-01	6.64E-01	PWP1	PWP1 homolog (S. cerevisiae)	chr12q23.3	201606_s_at	NM_007062
2.63	2.81	0.18	2.97E-01	6.64E-01	TBX2	T-box 2	chr17q23	221977_at	NM_005994
6.69	6.96	0.27	2.97E-01	6.64E-01	RSPRY1	ring finger and SPRY domain containing 1	chr16q13	225770_at	NM_133368
6.00	6.66	0.66	2.97E-01	6.65E-01	COL4A2	collagen, type IV, alpha 2	chr13q34	211966_at	NM_001846
3.50	3.68	0.18	2.97E-01	6.65E-01	---	---	---	237042_at	---
3.24	3.41	0.17	2.97E-01	6.65E-01	C14orf113	chromosome 14 open reading frame 113	chr14q32.13	221101_at	XR_041392 /// XR_041393 /// XR_041394
1.86	2.02	0.16	2.97E-01	6.65E-01	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	chr8p21.1	241252_at	NM_001017420
2.13	2.25	0.12	2.97E-01	6.65E-01	---	---	---	1556659_at	---
2.06	2.19	0.13	2.97E-01	6.65E-01	---	---	---	AFFX-r2-Bs-lys-3_at	---
2.22	2.42	0.19	2.97E-01	6.65E-01	S100A8	S100 calcium binding protein A8	chr1q21	214370_at	NM_002964
3.59	4.17	0.59	2.98E-01	6.65E-01	RSRC1	arginine/serine-rich coiled-coil 1	chr3q25.32	219507_at	NM_016625
8.63	9.20	0.57	2.98E-01	6.65E-01	LIPA	lipase A, lysosomal acid, cholesterol esterase	chr10q23.2-q23.3	201847_at	NM_000235 /// NM_001127605
5.35	5.84	0.49	2.98E-01	6.65E-01	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	chr8p22-p21.3	225516_at	NM_001008539 /// NM_003046
5.18	5.63	0.44	2.98E-01	6.65E-01	WDR41	WD repeat domain 41	chr5q14.1	222503_s_at	NM_018268
7.09	7.47	0.38	2.98E-01	6.65E-01	RBMS1	RNA binding motif, single stranded interacting protein 1	chr2q24.2	207266_x_at	NM_002897 /// NM_016836 /// NM_016839
3.27	3.53	0.25	2.98E-01	6.65E-01	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	238534_at	NM_004735

2.93	3.18	0.24	2.98E-01	6.65E-01	NF1	neurofibromin 1	chr17q11.2	211094_s_at	NM_000267 /// NM_001042492 /// NM_001128147																				
4.59	4.81	0.23	2.98E-01	6.65E-01	PHGDH	phosphoglycerate dehydrogenase	chr1p12	201397_at	NM_006623																				
9.34	9.55	0.21	2.98E-01	6.65E-01	RPN2	ribophorin II	chr20q12-q13.1	208689_s_at	NM_002951																				
3.51	3.71	0.20	2.98E-01	6.65E-01	NRXN2	neurexin 2	chr11q13	209982_s_at	NM_015080 /// NM_138732 /// NM_138734																				
1.92	2.11	0.19	2.98E-01	6.65E-01	SLC6A11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	chr3p25.3	1554724_at	NM_014229																				
3.48	3.67	0.19	2.98E-01	6.65E-01	ZDHHC4	zinc finger, DHHC-type containing 4	chr7p22.1	223137_at	NM_001134387 /// NM_001134388 /// NM_001134389 /// NM_018106																				
7.80	7.96	0.16	2.98E-01	6.65E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	200622_x_at	NM_001743 /// NM_005184 /// NM_006888																				
2.06	2.21	0.16	2.98E-01	6.65E-01	IL10	interleukin 10	chr1q31-q32	207433_at	NM_000572																				
2.08	2.23	0.15	2.98E-01	6.65E-01	INSC	inscuteable homolog (Drosophila)	chr11p15.2	237056_at	NM_001031853 /// NM_001042536																				
3.81	3.95	0.14	2.98E-01	6.65E-01	---	---	---	239859_x_at	---																				
2.04	2.18	0.14	2.98E-01	6.65E-01	FMN2	formin 2	chr1q43	1555471_a_at	NM_020066																				
2.07	2.20	0.13	2.98E-01	6.65E-01	BMP2K	BMP2 inducible kinase	chr4q21.21	214716_at	NM_017593 /// NM_198892																				
2.70	2.88	0.19	2.98E-01	6.65E-01	C19orf18	chromosome 19 open reading frame 18	chr19q13.43	236847_at	NM_152474																				
2.59	2.76	0.18	2.98E-01	6.65E-01	VIPR2	vasoactive intestinal peptide receptor 2	chr7q36.3	205947_s_at	NM_003382																				
2.59	2.73	0.13	2.98E-01	6.65E-01	---	---	---	1569668_at	---																				
4.22	4.49	0.27	2.98E-01	6.65E-01	---	---	---	226107_at	---																				
5.67	5.90	0.22	2.98E-01	6.65E-01	SLC43A2	solute carrier family 43, member 2	chr17p13.3	226629_at	NM_152346																				
2.90	3.08	0.19	2.98E-01	6.65E-01	PCDHGA12 /// PCDHGC3	protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily C, 3	chr5q31	214564_s_at	NM_002588 /// NM_003735 /// NM_032094 /// NM_032402 /// NM_032403																				
2.69	2.87	0.18	2.98E-01	6.65E-01	---	---	---	234790_at	---																				
2.64	2.81	0.18	2.98E-01	6.65E-01	---	---	---	230392_at	---																				
2.48	2.64	0.16	2.98E-01	6.65E-01	---	---	---	233678_at	---																				
2.02	2.18	0.16	2.98E-01	6.65E-01	MYO3A	myosin IIIA	chr10p11.1	244364_at	NM_017433																				
6.97	7.35	0.38	2.98E-01	6.65E-01	LOC401504	hypothetical gene supported by AK091718	chr9p13.2	225640_at	---																				
2.31	2.49	0.18	2.98E-01	6.65E-01	LGALS4	lectin, galactoside-binding, soluble, 4	chr19q13.2	204272_at	NM_006149																				
3.58	3.77	0.19	2.98E-01	6.65E-01	SOHLH1	spermatogenesis and oogenesis specific basic helix-loop-helix 1	chr9q34.3	1561403_at	NM_001012415 /// NM_001101677																				
3.67	3.86	0.20	2.99E-01	6.65E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	232509_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359																				
4.44	4.66	0.22	2.99E-01	6.65E-01	ZNF397OS	zinc finger protein 397 opposite strand	chr18q12.2	228130_at	NM_001112734 /// XM_001720071 /// XM_001722380 /// XM_001723235																				
2.54	2.68	0.14	2.99E-01	6.65E-01	---	---	---	1565733_at	---																				
2.50	2.65	0.14	2.99E-01	6.66E-01	BMP3	bone morphogenetic protein 3	chr4q21	208244_at	NM_001201																				
6.28	6.57	0.28	2.99E-01	6.66E-01	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	chr7q32	225526_at	NM_013255																				
4.58	4.79	0.21	2.99E-01	6.66E-01	---	---	---	238129_s_at	---																				
2.96	3.15	0.19	2.99E-01	6.66E-01	MYO7B	myosin VIIB	chr2q21.1	216662_at	NM_001080527																				

2.15	2.31	0.16	2.99E-01	6.66E-01	PLAG1	pleiomorphic adenoma gene 1	chr8q12	205372_at	NM_001114634 /// NM_001114635 /// NM_002655																				
2.99	3.25	0.26	2.99E-01	6.66E-01	---	---	---	234148_at	---																				
2.44	2.60	0.16	2.99E-01	6.66E-01	---	---	---	1561224_at	---																				
4.29	4.45	0.15	2.99E-01	6.66E-01	MEGF11	multiple EGF-like-domains 11	chr15q22.31	1569879_a_at	NM_032445																				
6.24	6.41	0.17	2.99E-01	6.66E-01	REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	chr19p13.3	233939_at	NM_020695																				
7.70	8.01	0.31	2.99E-01	6.66E-01	PPAP2A	phosphatidic acid phosphatase type 2A	chr5q11	209147_s_at	NM_003711 /// NM_176895																				
8.56	8.79	0.23	2.99E-01	6.66E-01	TACC1	transforming, acidic coiled-coil containing protein 1	chr8p11	200911_s_at	NM_001122824 /// NM_006283																				
3.22	3.45	0.22	2.99E-01	6.66E-01	---	---	---	229155_at	---																				
2.70	2.91	0.22	2.99E-01	6.66E-01	LOC400581	GRB2-related adaptor protein-like	chr17p11.2	1560524_at	NM_001129778 /// XM_001720657 /// XM_001723190																				
1.85	2.02	0.16	2.99E-01	6.66E-01	---	---	---	241858_at	---																				
2.56	2.73	0.17	2.99E-01	6.66E-01	RP11-589B3.4 /// SFTPA2B	surfactant, pulmonary-associated protein A2 /// surfactant protein A2B	chr10q22.3	218835_at	NM_001098668 /// NM_006926																				
4.36	4.56	0.20	2.99E-01	6.66E-01	ZDHHC1	Zinc finger, DHHC-type containing 1	chr16q22.1	237228_at	NM_013304																				
2.64	2.80	0.16	2.99E-01	6.66E-01	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	chr2q31.3	228646_at	NM_001080545																				
2.54	2.70	0.16	2.99E-01	6.66E-01	LOC400748	hypothetical gene supported by BC040627	chr1p35.2	1564401_at	---																				
2.09	2.23	0.15	2.99E-01	6.66E-01	ABI1	abl-interactor 1	chr10p11.2	1559890_a_at	NM_001012750 /// NM_001012751 /// NM_001012752 /// NM_005470																				
2.47	2.62	0.15	2.99E-01	6.66E-01	FGF1	fibroblast growth factor 1 (acidic)	chr5q31	208240_s_at	NM_000800 /// NM_033136 /// NM_033137																				
2.01	2.13	0.12	2.99E-01	6.66E-01	NAALADL2	N-acetylated alpha-linked acidic dipeptidase-like 2	chr3q26.31	1557998_at	NM_207015																				
4.96	5.48	0.52	3.00E-01	6.66E-01	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	chr18p11.31-p11.21	202932_at	NM_005433																				
2.78	2.92	0.14	3.00E-01	6.66E-01	---	---	---	240981_at	---																				
1.99	2.12	0.13	3.00E-01	6.66E-01	GRIA4	glutamate receptor, ionotrophic, AMPA 4	chr11q22	238663_x_at	NM_000829 /// NM_001077243 /// NM_001077244 /// NM_001112812																				
4.86	5.01	0.15	3.00E-01	6.67E-01	ICA1	islet cell autoantigen 1, 69kDa	chr7p22	230639_at	NM_004968 /// NM_022307																				
3.78	4.01	0.22	3.00E-01	6.67E-01	ZCCHC3	zinc finger, CCHC domain containing 3	chr20p13-p12.2	225072_at	NM_033089																				
2.27	2.40	0.12	3.00E-01	6.67E-01	---	---	---	215406_at	---																				
6.51	6.89	0.38	3.00E-01	6.67E-01	API5	apoptosis inhibitor 5	chr11p11.2	201687_s_at	NM_006595																				
3.54	3.85	0.31	3.00E-01	6.67E-01	AHCYL2	S-adenosylhomocysteine hydrolase-like 2	chr7q32.1	215672_s_at	NM_001130720 /// NM_001130722 /// NM_001130723 /// NM_015328																				
2.04	2.18	0.14	3.00E-01	6.67E-01	---	---	---	237164_at	---																				
1.95	2.13	0.17	3.00E-01	6.67E-01	CDKL3	cyclin-dependent kinase-like 3	chr5q31	241911_at	NM_001113575 /// NM_016508																				
2.71	2.88	0.17	3.00E-01	6.67E-01	---	---	---	230859_at	---																				
2.02	2.13	0.12	3.00E-01	6.67E-01	FBXO4	F-box protein 4	chr5p12	233366_at	NM_012176 /// NM_033484																				
4.53	5.06	0.54	3.00E-01	6.67E-01	---	---	---	243037_at	---																				
5.75	6.08	0.33	3.00E-01	6.67E-01	AKAP12	A kinase (PRKA) anchor protein 12	chr6q24-q25	210517_s_at	NM_005100 /// NM_144497																				
2.77	2.93	0.16	3.00E-01	6.67E-01	TCL6	T-cell leukemia/lymphoma 6	chr14q32.1	219839_x_at	NM_012468 /// NM_014418 /// NM_020550 /// NM_020552 /// NM_020553 /// NM_020554																				

1.93	2.05	0.13	3.00E-01	6.67E-01	SUNC1	Sad1 and UNC84 domain containing 1	chr7p12.3	231618_s_at	NM_001030019 /// NM_152782
4.65	5.40	0.75	3.00E-01	6.67E-01	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	chr5p13	232898_at	NM_001343
2.92	3.21	0.28	3.00E-01	6.67E-01	AQP9	aquaporin 9	chr15q22.1-q22.2	205568_at	NM_020980
7.05	7.28	0.23	3.00E-01	6.67E-01	SREBF2	sterol regulatory element binding transcription factor 2	chr22q13	201248_s_at	NM_004599
2.03	2.19	0.15	3.00E-01	6.67E-01	LOC283392	hypothetical protein LOC283392	chr12q21.1	1560698_a_at	XR_039893 /// XR_039894 /// XR_039895
2.88	3.03	0.15	3.00E-01	6.67E-01	---	---	---	231707_at	---
2.00	2.13	0.13	3.00E-01	6.67E-01	---	---	---	238175_at	---
6.55	7.04	0.49	3.00E-01	6.67E-01	MRPL42	mitochondrial ribosomal protein L42	chr12q22	217919_s_at	NM_014050 /// NM_172177 /// NM_172178
5.67	6.02	0.35	3.00E-01	6.67E-01	C12orf35	chromosome 12 open reading frame 35	chr12p11.21	218614_at	NM_018169
4.48	4.77	0.29	3.00E-01	6.67E-01	IFNAR1	interferon (alpha, beta and omega) receptor 1	chr21q22.1|21q22.11	225661_at	NM_000629
4.56	4.74	0.18	3.00E-01	6.67E-01	NPAL2	NIPA-like domain containing 2	chr8q22.2	220128_s_at	NM_024759
2.32	2.48	0.16	3.00E-01	6.67E-01	ZBTB26	zinc finger and BTB domain containing 26	chr9q33.2	1554973_a_at	NM_020924
1.79	1.90	0.12	3.00E-01	6.67E-01	THSD7A	Thrombospondin, type I, domain containing 7A	chr7p21.3	229159_at	NM_015204
1.92	2.03	0.12	3.00E-01	6.67E-01	C10orf81	chromosome 10 open reading frame 81	chr10q25.3	219857_at	NM_024889
5.32	5.53	0.21	3.00E-01	6.67E-01	MGC31957 /// TNFRSF10C	hypothetical protein MGC31957 /// tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	chr8p21.2 /// chr8p22-p21	210483_at	NM_003841
2.82	3.01	0.19	3.00E-01	6.67E-01	---	---	---	238836_at	---
5.79	5.97	0.18	3.00E-01	6.67E-01	FOXP3	forkhead box P3	chrXp11.23	221333_at	NM_001114377 /// NM_014009
1.81	1.93	0.12	3.00E-01	6.67E-01	---	---	---	1562607_at	---
2.63	2.79	0.16	3.01E-01	6.67E-01	---	---	---	234060_at	---
9.08	9.25	0.17	3.01E-01	6.67E-01	TXNL1	thioredoxin-like 1	chr18q21.31	201588_at	NM_004786
4.26	4.67	0.41	3.01E-01	6.67E-01	SLC39A8	solute carrier family 39 (zinc transporter), member 8	chr4q22-q24	219869_s_at	NM_022154
3.82	4.03	0.20	3.01E-01	6.67E-01	---	---	---	244863_at	---
2.11	2.28	0.17	3.01E-01	6.67E-01	---	---	---	240949_x_at	---
3.54	3.96	0.42	3.01E-01	6.67E-01	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	chr14q23.3	219321_at	NM_022474
6.16	6.30	0.14	3.01E-01	6.67E-01	LOC493754	Hypothetical LOC441245	chr7q11.21	231992_x_at	NR_002933
2.46	2.59	0.13	3.01E-01	6.67E-01	LRRC69	leucine rich repeat containing 69	chr8q21.3	238214_at	NM_001129890 /// XM_001716998 /// XM_001717028 /// XM_001717145
3.12	3.41	0.29	3.01E-01	6.67E-01	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	chr14q22.1	235512_at	NM_004196
2.96	3.15	0.19	3.01E-01	6.67E-01	R3HDML	R3H domain containing-like	chr20q13.12	234774_at	NM_178491
4.52	4.90	0.38	3.01E-01	6.67E-01	SFRS15	splicing factor, arginine/serine-rich 15	chr21q22.1	222311_s_at	NM_020706
5.88	6.14	0.26	3.01E-01	6.67E-01	SDAD1	SDA1 domain containing 1	chr4q21.1	218607_s_at	NM_018115
3.61	3.79	0.18	3.01E-01	6.67E-01	GJC2	Gap junction protein, gamma 2, 47kDa	chr1q42.13	214302_x_at	NM_020435
2.13	2.31	0.17	3.01E-01	6.67E-01	---	---	---	243422_at	---
2.33	2.50	0.16	3.01E-01	6.67E-01	---	---	---	231507_at	---
2.77	2.92	0.15	3.01E-01	6.68E-01	---	---	---	1566001_at	---
2.36	2.55	0.19	3.01E-01	6.68E-01	ITGB1BP2	integrin beta 1 binding protein (melusin) 2	chrXq12-q13.1	219829_at	NM_012278
3.58	3.85	0.26	3.01E-01	6.68E-01	SVIP	small VCP/p97-interacting protein	chr11p14.2	230006_s_at	NM_148893
2.71	2.94	0.23	3.01E-01	6.68E-01	---	---	---	234371_at	---
4.62	4.83	0.21	3.01E-01	6.68E-01	SIX4	SIX homeobox 4	chr14q23	229796_at	NM_017420
4.21	4.40	0.19	3.01E-01	6.68E-01	---	---	---	241054_at	---
2.18	2.35	0.17	3.01E-01	6.68E-01	---	---	---	216757_at	---
1.95	2.11	0.16	3.01E-01	6.68E-01	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	chr2q33.3	239192_at	NM_057177 /// NM_152526 /// NM_205863
2.43	2.56	0.13	3.01E-01	6.68E-01	C8orf79	chromosome 8 open reading frame 79	chr8p22	239297_at	NM_001099677 /// NM_020844
2.12	2.24	0.12	3.01E-01	6.68E-01	---	---	---	240731_at	---
2.63	2.78	0.15	3.01E-01	6.68E-01	MTL5	metallothionein-like 5, testis-specific (tesmin)	chr11q13.2-q13.3	219786_at	NM_001039656 /// NM_004923
8.89	9.16	0.26	3.01E-01	6.68E-01	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	chr1p34.2	200625_s_at	NM_001105530 /// NM_006367
2.60	2.74	0.14	3.01E-01	6.68E-01	---	---	---	232782_at	---
3.64	3.82	0.18	3.01E-01	6.68E-01	---	---	---	244713_at	---
3.72	4.28	0.56	3.01E-01	6.68E-01	---	---	---	234032_at	---
8.25	8.58	0.33	3.01E-01	6.68E-01	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	chr5p15.2	208696_at	NM_012073
3.60	3.85	0.25	3.01E-01	6.68E-01	CCDC113	coiled-coil domain containing 113	chr16q21	222890_at	NM_014157

2.41	2.54	0.13	3.01E-01	6.68E-01	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	chr13q13.3	233503_at	NM_017826
2.48	2.64	0.16	3.02E-01	6.68E-01	---	---	---	1566599_at	---
4.62	5.00	0.38	3.02E-01	6.68E-01	GCOM1 /// GRINL1A	GRINL1A complex locus /// glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	chr15q21.3 /// chr15q22.1	212241_at	NM_001018090 /// NM_001018091 /// NM_001018100 /// NM_001018102 /// NM_001018103 /// NM_015532 /// NM_152451
2.48	2.75	0.27	3.02E-01	6.68E-01	---	---	---	242715_at	---
2.31	2.48	0.17	3.02E-01	6.68E-01	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	chr10q24	208126_s_at	NM_000772 /// NM_001128925
2.09	2.22	0.14	3.02E-01	6.68E-01	LOC100131613	PRO1454	chr12q15	210928_at	XM_001723128 /// XM_001724337 /// XM_001726579
2.26	2.38	0.12	3.02E-01	6.68E-01	---	---	---	231139_at	---
4.45	4.92	0.47	3.02E-01	6.68E-01	SEC63	SEC63 homolog (S. cerevisiae)	chr6q21	201915_at	NM_007214
6.70	7.05	0.34	3.02E-01	6.68E-01	ZBTB33	zinc finger and BTB domain containing 33	chrXq23	226255_at	NM_006777
3.48	3.81	0.34	3.02E-01	6.68E-01	---	---	---	1560137_at	---
7.03	7.30	0.26	3.02E-01	6.68E-01	---	---	---	226883_at	---
3.57	3.74	0.17	3.02E-01	6.68E-01	---	---	---	1566803_at	---
8.20	8.48	0.29	3.02E-01	6.68E-01	KARS	lysyl-tRNA synthetase	chr16q23-q24	200079_s_at	NM_001130089 /// NM_005548
2.91	3.12	0.21	3.02E-01	6.68E-01	C20orf186	chromosome 20 open reading frame 186	chr20q11.21	233523_at	NM_182519
2.54	3.13	0.59	3.02E-01	6.69E-01	---	---	---	236300_at	---
2.81	3.29	0.48	3.02E-01	6.69E-01	SELL	selectin L	chr1q23-q25	204563_at	NM_000655
1.95	2.18	0.23	3.02E-01	6.69E-01	POU2F3	POU class 2 homeobox 3	chr11q23.3	207109_at	NM_014352
7.36	7.89	0.53	3.02E-01	6.69E-01	C15orf15	chromosome 15 open reading frame 15	chr15q21	217915_s_at	NM_016304
4.39	4.58	0.20	3.02E-01	6.69E-01	---	---	---	236346_at	---
2.75	2.92	0.17	3.02E-01	6.69E-01	LOC643837	Hypothetical LOC643837	chr1p36.33	236624_at	NR_015368 /// XM_927114
3.82	3.98	0.16	3.02E-01	6.69E-01	CCIN	calicin	chr9p13.3	210642_at	NM_005893
1.95	2.07	0.12	3.02E-01	6.69E-01	MLLT10	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	238257_at	NM_001009569 /// NM_004641
7.64	7.94	0.30	3.02E-01	6.69E-01	---	---	---	224691_at	---
4.21	4.42	0.21	3.02E-01	6.69E-01	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	chr16q24.3	235325_at	NM_003119 /// NM_199367
2.86	3.05	0.19	3.02E-01	6.69E-01	LOC400794	hypothetical gene supported by BC030596	chr1q23.2	1556801_at	---
3.25	3.44	0.19	3.02E-01	6.69E-01	SYNE1	spectrin repeat containing, nuclear envelope 1	chr6q25	244144_at	NM_015293 /// NM_033071 /// NM_133650 /// NM_182961
3.37	3.54	0.17	3.02E-01	6.69E-01	---	---	---	241540_at	---
2.33	2.50	0.17	3.02E-01	6.69E-01	CTAG1A /// CTAG1B	cancer/testis antigen 1A /// cancer/testis antigen 1B	chrXq28	210546_x_at	NM_001327 /// NM_139250 /// XM_001719185
2.38	2.54	0.16	3.02E-01	6.69E-01	SFRS12	splicing factor, arginine/serine-rich 12	chr5q12.3	1568783_at	NM_001077199 /// NM_139168
2.01	2.12	0.11	3.02E-01	6.69E-01	C6orf190	chromosome 6 open reading frame 190	chr6q22.33	1558971_at	NM_001010923
2.02	2.18	0.16	3.02E-01	6.69E-01	---	---	---	239708_at	---
2.42	2.57	0.15	3.02E-01	6.69E-01	---	---	---	242717_at	---
3.32	3.59	0.27	3.02E-01	6.69E-01	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	chr7p14.2	225630_at	NM_030636
2.68	2.83	0.15	3.02E-01	6.69E-01	---	---	---	1561451_a_at	---
5.59	5.91	0.32	3.02E-01	6.69E-01	---	---	---	232685_at	---
2.90	3.07	0.17	3.02E-01	6.69E-01	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	chr17q21.32	204625_s_at	NM_000212
2.08	2.22	0.14	3.03E-01	6.69E-01	C4orf23	chromosome 4 open reading frame 23	chr4p16.1	220891_at	NM_152544
3.50	3.87	0.37	3.03E-01	6.69E-01	RSF1	remodeling and spacing factor 1	chr11q14.1	218166_s_at	NM_016578
5.89	6.17	0.28	3.03E-01	6.69E-01	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	chr4p14	212140_at	NM_001100399 /// NM_001100400 /// NM_015200

4.56	4.78	0.22	3.03E-01	6.69E-01	LOC729822 /// PITPNC1	similar to phosphatidylinositol transfer protein, cytoplasmic 1 /// phosphatidylinositol transfer protein, cytoplasmic 1	chr17q24.2	1568949_at	NM_012417 /// NM_181671 /// XR_040859 /// XR_040860 /// XR_040861
4.71	4.84	0.14	3.03E-01	6.69E-01	PKD2L1	polycystic kidney disease 2-like 1	chr10q24	221061_at	NM_016112
2.04	2.18	0.14	3.03E-01	6.69E-01	---	---	---	236120_at	---
2.44	2.60	0.16	3.03E-01	6.69E-01	CDCP1	CUB domain containing protein 1	chr3p21.31	1554110_at	NM_022842 /// NM_178181
3.00	3.15	0.16	3.03E-01	6.69E-01	JMJD2C	jumonji domain containing 2C	chr9p24.1	214861_at	NM_015061
4.37	4.91	0.55	3.03E-01	6.69E-01	POLK	polymerase (DNA directed) kappa	chr5q13	223260_s_at	NM_016218
3.18	3.42	0.24	3.03E-01	6.69E-01	---	---	---	216496_s_at	---
5.82	6.04	0.22	3.03E-01	6.69E-01	KPNA6	karyopherin alpha 6 (importin alpha 7)	chr1p35.1-p34.3	212103_at	NM_012316
7.38	7.60	0.22	3.03E-01	6.69E-01	ADRM1	adhesion regulating molecule 1	chr20q13.33	201281_at	NM_007002 /// NM_175573
5.95	6.13	0.18	3.03E-01	6.69E-01	ZFYVE9	zinc finger, FYVE domain containing 9	chr1p32.3	204893_s_at	NM_004799 /// NM_007323 /// NM_007324
2.00	2.14	0.14	3.03E-01	6.69E-01	---	---	---	237351_at	---
3.96	4.13	0.18	3.03E-01	6.69E-01	---	---	---	241788_x_at	---
2.48	2.64	0.16	3.03E-01	6.69E-01	---	---	---	1570296_at	---
1.98	2.13	0.15	3.03E-01	6.69E-01	---	---	---	221117_at	---
5.13	5.51	0.38	3.03E-01	6.69E-01	FAM45A /// FAM45B	family with sequence similarity 45, member A /// family with sequence similarity 45, member B	chr10q25 /// chrXq25	222955_s_at	NM_018472 /// NM_207009
2.89	3.05	0.15	3.03E-01	6.70E-01	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	212079_s_at	NM_005933
4.05	4.27	0.22	3.03E-01	6.70E-01	---	---	---	243616_at	---
3.44	3.65	0.21	3.03E-01	6.70E-01	TMEM174	transmembrane protein 174	chr5q13.2	240114_s_at	NM_153217
8.13	8.69	0.56	3.03E-01	6.70E-01	PHACTR2	phosphatase and actin regulator 2	chr6q24.2	204049_s_at	NM_001100164 /// NM_001100165 /// NM_001100166 /// NM_014721
4.10	4.41	0.31	3.03E-01	6.70E-01	CBR3	carbonyl reductase 3	chr21q22.2	205379_at	NM_001236
3.32	3.54	0.23	3.03E-01	6.70E-01	---	---	---	234208_at	---
5.24	5.64	0.40	3.03E-01	6.70E-01	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	chr11q22-q23	204977_at	NM_004398
2.72	2.84	0.12	3.03E-01	6.70E-01	---	---	---	243642_x_at	---
4.99	5.15	0.16	3.03E-01	6.70E-01	ACTN1	Actinin, alpha 1	chr14q24.1-q24.2|14q24|14q22-q24	237401_at	NM_001102 /// NM_001130004 /// NM_001130005
2.07	2.28	0.20	3.03E-01	6.70E-01	---	---	---	208061_at	---
4.84	5.02	0.18	3.03E-01	6.70E-01	MYLK2	myosin light chain kinase 2	chr20q13.31	231792_at	NM_033118
3.99	4.27	0.28	3.04E-01	6.70E-01	---	---	---	1555742_at	---
4.54	4.78	0.24	3.04E-01	6.70E-01	ANGPTL2	angiopoietin-like 2	chr9q34	213004_at	NM_012098
6.91	7.27	0.36	3.04E-01	6.70E-01	RHOT1	ras homolog gene family, member T1	chr17q11.2	222148_s_at	NM_001033566 /// NM_001033568 /// NM_018307
2.62	2.78	0.16	3.04E-01	6.70E-01	---	---	---	216628_at	---
2.18	2.33	0.15	3.04E-01	6.70E-01	MYCNOS	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) opposite strand	chr2p24.1	216188_at	XR_039828 /// XR_039829 /// XR_039830
5.36	5.85	0.49	3.04E-01	6.70E-01	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	chr3q12.2	201512_s_at	NM_014820
5.24	5.63	0.39	3.04E-01	6.70E-01	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	chr18q11.1	214578_s_at	NM_005406 /// XM_001713904 /// XM_001722015 /// XM_001723570
2.77	3.03	0.26	3.04E-01	6.70E-01	hCG_2009921	hypothetical locus LOC441204	chr7p15.2	240424_s_at	NR_015364 /// XM_001722132 /// XM_001723644 /// XM_001723694 /// XM_499061 /// XM_943507

6.55	6.79	0.24	3.04E-01	6.70E-01	RCOR2	REST corepressor 2	chr11q13.1	236030_at	NM_173587
3.24	3.41	0.17	3.04E-01	6.70E-01	TRIM26	Tripartite motif-containing 26	chr6p21.3	242812_at	NM_003449
2.20	2.36	0.17	3.04E-01	6.70E-01	LOC100126784	hypothetical LOC100126784	chr11p15.1	240407_at	XR_040478 /// XR_040479 /// XR_040480
3.22	3.38	0.16	3.04E-01	6.70E-01	---	---	---	237916_at	---
2.76	2.91	0.15	3.04E-01	6.70E-01	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	chr2q11.2	208364_at	NM_001134224 /// NM_001134225 /// NM_001566 /// NM_004027
6.65	6.80	0.15	3.04E-01	6.70E-01	ARMC5	armadillo repeat containing 5	chr16p11.2	227738_s_at	NM_001105247 /// NM_024742
2.19	2.36	0.17	3.04E-01	6.70E-01	RAP2B	RAP2B, member of RAS oncogene family	chr3q25.2	214488_at	NM_002886
2.75	2.91	0.15	3.04E-01	6.70E-01	---	---	---	1559201_a_at	---
5.56	5.94	0.38	3.04E-01	6.70E-01	FNDC3B	fibronectin type III domain containing 3B	chr3q26.31	222692_s_at	NM_022763
5.22	5.42	0.20	3.04E-01	6.70E-01	RECQL4	RecQ protein-like 4	chr8q24.3	213520_at	NM_004260
3.90	4.29	0.39	3.04E-01	6.70E-01	BCLAF1	BCL2-associated transcription factor 1	chr6q22-q23	201083_s_at	NM_001077440 /// NM_001077441 /// NM_014739
3.01	3.16	0.15	3.04E-01	6.70E-01	BICD2	bicaudal D homolog 2 (Drosophila)	chr9q22.31	1553021_s_at	NM_001003800 /// NM_015250
2.28	2.43	0.15	3.04E-01	6.70E-01	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	chr1p31	207709_at	NM_006252
5.48	6.10	0.62	3.04E-01	6.70E-01	DDR2	Discoidin domain receptor tyrosine kinase 2	chr1q23.3	235631_at	NM_001014796 /// NM_006182
4.83	5.30	0.47	3.04E-01	6.70E-01	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	chr1q41	202374_s_at	NM_012414
7.79	8.16	0.37	3.04E-01	6.70E-01	JAK1	Janus kinase 1 (a protein tyrosine kinase)	chr1p32.3-p31.3	201648_at	NM_002227
4.99	5.31	0.32	3.04E-01	6.70E-01	DHRS13	dehydrogenase/reductase (SDR family) member 13	chr17q11.2	226121_at	NM_144683
5.18	5.49	0.31	3.04E-01	6.70E-01	SART3	squamous cell carcinoma antigen recognized by T cells 3	chr12q24.1	209127_s_at	NM_014706
3.73	3.98	0.25	3.04E-01	6.70E-01	LOC728485	hypothetical protein LOC728485	chr19q13.12	235358_at	XR_041661 /// XR_041662 /// XR_041663
2.25	2.47	0.22	3.04E-01	6.70E-01	---	---	---	241190_at	---
2.19	2.36	0.17	3.04E-01	6.70E-01	HGD /// LOC100132552 /// LOC727722	homogentisate 1,2-dioxygenase (homogentisate oxidase) /// similar to homogentisate 1,2-dioxygenase /// homogentisate 1,2-dioxygenase like	chr3q13.33	214307_at	NM_000187 /// XM_001713606 /// XM_001719739
2.81	2.95	0.14	3.04E-01	6.70E-01	---	---	---	236990_at	---
3.68	3.81	0.14	3.04E-01	6.70E-01	---	---	---	243853_at	---
2.13	2.27	0.13	3.04E-01	6.70E-01	---	---	---	1561148_at	---
1.88	1.99	0.11	3.04E-01	6.70E-01	---	---	---	1561154_at	---
6.63	7.26	0.63	3.04E-01	6.70E-01	---	---	---	AFFX-HUMRGE/M10098_3_at	---
3.35	3.73	0.38	3.04E-01	6.70E-01	TRIM23	tripartite motif-containing 23	chr5q12.3	204732_s_at	NM_001656 /// NM_033227 /// NM_033228
2.58	2.78	0.20	3.04E-01	6.70E-01	XPR1	Xenotropic and polytropic retrovirus receptor	chr1q25.1	244755_at	NM_004736
2.73	2.89	0.17	3.04E-01	6.70E-01	CCDC136	coiled-coil domain containing 136	chr7q33	226972_s_at	NM_022742
2.03	2.16	0.13	3.04E-01	6.70E-01	---	---	---	1559542_a_at	---
3.18	3.42	0.25	3.04E-01	6.70E-01	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	chr1q43-q44	224229_s_at	NM_005465 /// NM_181690
1.99	2.11	0.12	3.04E-01	6.70E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	1556583_a_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
1.98	2.09	0.11	3.04E-01	6.70E-01	---	---	---	234523_at	---
6.20	6.83	0.63	3.05E-01	6.71E-01	MYH11	myosin, heavy chain 11, smooth muscle	chr16p13.11	201497_x_at	NM_001040113 /// NM_001040114 /// NM_002474 /// NM_022844
2.12	2.27	0.15	3.05E-01	6.71E-01	ZNF80	Zinc finger protein 80	chr3q13.3	1556467_at	NM_007136
6.41	6.73	0.31	3.05E-01	6.71E-01	SAP18	Sin3A-associated protein, 18kDa	chr13q12.11	208741_at	NM_005870
2.80	2.98	0.18	3.05E-01	6.71E-01	---	---	---	1559745_at	---

2.44	2.61	0.17	3.05E-01	6.71E-01	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	chr4p16.1	228025_s_at	NM_020416 /// NM_181876
3.01	3.15	0.14	3.05E-01	6.71E-01	C9orf9	chromosome 9 open reading frame 9	chr9q34	239222_at	NM_018956
3.34	3.66	0.32	3.05E-01	6.71E-01	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	chr20q11.2	210052_s_at	NM_012112
4.93	5.13	0.21	3.05E-01	6.71E-01	41338	membrane-associated ring finger (C3HC4) 5	chr10q23.32	226394_at	NM_017824
2.68	2.86	0.18	3.05E-01	6.71E-01	STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	chr15q24.1	1569335_a_at	NM_022369
2.27	2.44	0.17	3.05E-01	6.71E-01	GARNL3	GTPase activating Rap/RanGAP domain-like 3	chr9q33.3	1563907_at	NM_032293
5.38	5.58	0.19	3.05E-01	6.71E-01	MED13L	mediator complex subunit 13-like	chr12q24.21	212208_at	NM_015335
3.00	3.15	0.15	3.05E-01	6.71E-01	ZNF19	zinc finger protein 19	chr16q22	228958_at	NM_006961
3.46	3.58	0.13	3.05E-01	6.71E-01	---	---	---	243638_at	---
5.75	6.09	0.34	3.05E-01	6.71E-01	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	chr3q26.32-q26.33	225710_at	NM_021629
2.37	2.53	0.16	3.05E-01	6.71E-01	FLJ35379	similar to Alu subfamily J sequence contamination warning entry	chr13q22.2	239553_at	XM_001127400 /// XM_001133227 /// XM_001722271
2.23	2.40	0.17	3.05E-01	6.71E-01	CD200R1	CD200 receptor 1	chr3q13.2	1552875_a_at	NM_138806 /// NM_138939 /// NM_138940 /// NM_170780
4.00	4.28	0.28	3.05E-01	6.71E-01	SIPA1L2	signal-induced proliferation-associated 1 like 2	chr1q42.2	233587_s_at	NM_020808
2.76	2.95	0.20	3.05E-01	6.71E-01	---	---	---	207756_at	---
2.12	2.24	0.12	3.05E-01	6.71E-01	---	---	---	239514_at	---
4.46	4.74	0.28	3.05E-01	6.71E-01	EPHB2	EPH receptor B2	chr1p36.1-p35	209588_at	NM_004442 /// NM_017449
2.55	2.74	0.19	3.05E-01	6.71E-01	CYS1	cystin 1	chr2p25.1	228739_at	NM_001037160
2.86	3.05	0.19	3.05E-01	6.71E-01	FLJ35024	hypothetical LOC401491	chr9p24.2	1558212_at	NR_015375 /// XR_040306 /// XR_040307 /// XR_040308
2.30	2.47	0.17	3.05E-01	6.71E-01	BTN1A1	butyrophilin, subfamily 1, member A1	chr6p22.1	207395_at	NM_001732
2.11	2.26	0.16	3.05E-01	6.71E-01	CD96	CD96 molecule	chr3q13.13-q13.2	206761_at	NM_005816 /// NM_198196
2.20	2.32	0.12	3.05E-01	6.71E-01	LOC727924	hypothetical LOC727924	chr15q11.2	1564855_at	XR_039952
2.08	2.19	0.11	3.05E-01	6.71E-01	KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	chr17q23.3	211046_at	NM_030779 /// NM_173092
4.42	4.63	0.21	3.05E-01	6.71E-01	---	---	---	234175_at	---
7.12	7.30	0.18	3.05E-01	6.71E-01	ZNF428	zinc finger protein 428	chr19q13.31	215429_s_at	NM_182498
7.07	7.25	0.18	3.05E-01	6.71E-01	PRR11	proline rich 11	chr17q22	232215_x_at	NM_018304
2.92	3.06	0.14	3.05E-01	6.71E-01	---	---	---	219912_s_at	---
2.09	2.23	0.14	3.05E-01	6.71E-01	RP11-218C14.6	cystatin pseudogene	chr20p11.21	1558493_at	NR_001279
2.33	2.46	0.14	3.05E-01	6.71E-01	EN2	engrailed homeobox 2	chr7q36	207060_at	NM_001427
4.30	4.81	0.51	3.06E-01	6.71E-01	---	---	---	240297_at	---
4.87	5.03	0.15	3.06E-01	6.71E-01	---	---	---	217713_x_at	---
2.01	2.16	0.15	3.06E-01	6.71E-01	---	---	---	240485_at	---
3.38	3.58	0.20	3.06E-01	6.71E-01	TNNT3	troponin T type 3 (skeletal, fast)	chr11p15.5	205693_at	NM_001042780 /// NM_001042781 /// NM_001042782 /// NM_006757
6.47	6.81	0.35	3.06E-01	6.71E-01	MRVI1	murine retrovirus integration site 1 homolog	chr11p15	226047_at	NM_001098579 /// NM_001100163 /// NM_001100167 /// NM_130385
6.79	7.25	0.46	3.06E-01	6.71E-01	SLC44A1	solute carrier family 44, member 1	chr9q31.2	224596_at	NM_080546
3.32	3.48	0.16	3.06E-01	6.71E-01	---	---	---	214050_at	---
2.07	2.21	0.15	3.06E-01	6.71E-01	MLL	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	229935_s_at	NM_005933
4.30	4.51	0.21	3.06E-01	6.71E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	216892_at	---
4.09	4.49	0.40	3.06E-01	6.71E-01	---	---	---	236472_at	---
6.75	7.30	0.55	3.06E-01	6.71E-01	COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	chr4q21.22	218042_at	NM_016129
2.18	2.35	0.17	3.06E-01	6.72E-01	LOC283089	hypothetical protein LOC283089	chr10q26.13	1562831_a_at	---
3.91	4.18	0.27	3.06E-01	6.72E-01	CTSW	cathepsin W	chr11q13.1	214450_at	NM_001335
2.11	2.27	0.17	3.06E-01	6.72E-01	---	---	---	1557811_a_at	---
1.93	2.09	0.16	3.06E-01	6.72E-01	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1	chr4p12	1552943_at	NM_173536
2.68	2.83	0.15	3.06E-01	6.72E-01	LMBRD2	LMBR1 domain containing 2	chr5p13.2	232893_at	NM_001007527
1.98	2.10	0.12	3.06E-01	6.72E-01	CYP27C1	cytochrome P450, family 27, subfamily C, polypeptide 1	chr2q14.3	1568868_at	NM_001001665
5.37	5.59	0.22	3.06E-01	6.72E-01	SAMD1	Sterile alpha motif domain containing 1	chr19p13.12	228276_at	NM_138352

2.37	2.50	0.13	3.06E-01	6.72E-01	SKIV2L2	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	chr5q11.2	1562142_at	NM_015360
5.04	5.23	0.19	3.06E-01	6.72E-01	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	chr16p13.3	211008_s_at	NM_003345 /// NM_194259 /// NM_194260 /// NM_194261
2.34	2.46	0.12	3.06E-01	6.72E-01	LOC286083	hypothetical protein LOC286083	chr8p23.3	1561257_at	---
2.52	2.74	0.22	3.06E-01	6.72E-01	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	chr5q13	1556128_a_at	NM_006909
2.21	2.43	0.22	3.06E-01	6.72E-01	---	---	---	1568920_at	---
2.85	2.99	0.13	3.06E-01	6.72E-01	EPHA1	EPH receptor A1	chr7q34	205977_s_at	NM_005232
4.18	4.37	0.19	3.06E-01	6.72E-01	ZSCAN18	zinc finger and SCAN domain containing 18	chr19q13.43	217593_at	NM_023926
2.26	2.40	0.15	3.06E-01	6.72E-01	SPIRE2	Spire homolog 2 (Drosophila)	chr16q24	1568916_at	NM_032451
3.51	3.67	0.15	3.07E-01	6.72E-01	C1orf14	chromosome 1 open reading frame 14	chr1q25.3	220996_s_at	NM_030933
3.89	4.11	0.21	3.07E-01	6.72E-01	C11orf49	chromosome 11 open reading frame 49	chr11p11.2	239789_at	NM_001003676 /// NM_001003677 /// NM_001003678 /// NM_024113
2.13	2.29	0.16	3.07E-01	6.72E-01	---	---	---	233700_at	---
7.30	7.56	0.26	3.07E-01	6.72E-01	SH3GLB1	SH3-domain GRB2-like endophilin B1	chr1p22	210101_x_at	NM_016009
2.64	2.84	0.20	3.07E-01	6.72E-01	C13orf31	chromosome 13 open reading frame 31	chr13q14.11	1553141_at	NM_001128303 /// NM_153218
2.72	2.88	0.17	3.07E-01	6.72E-01	C21orf104	chromosome 21 open reading frame 104	---	1566926_at	---
2.63	2.80	0.17	3.07E-01	6.72E-01	CYP2A7P1	cytochrome P450, family 2, subfamily A, polypeptide 7 pseudogene 1	chr19q13.2	216340_s_at	---
2.15	2.28	0.13	3.07E-01	6.72E-01	FMO6P	flavin containing monooxygenase 6 pseudogene	chr1q24.3	215174_at	NR_002601
7.53	8.02	0.48	3.07E-01	6.72E-01	---	---	---	227121_at	---
4.75	5.03	0.28	3.07E-01	6.72E-01	NIPBL	Nipped-B homolog (Drosophila)	chr5p13.2	212483_at	NM_015384 /// NM_133433
2.48	2.61	0.14	3.07E-01	6.72E-01	---	---	---	238301_at	---
2.00	2.10	0.10	3.07E-01	6.72E-01	LRRC37A4	leucine rich repeat containing 37, member A4 (pseudogene)	chr17q21.31	220220_at	NR_002940
2.49	2.68	0.18	3.07E-01	6.72E-01	---	---	---	234122_at	---
6.86	7.33	0.48	3.07E-01	6.73E-01	EPM2AIP1	EPM2A (laforin) interacting protein 1	chr3p22.1	202909_at	NM_014805
5.90	6.20	0.30	3.07E-01	6.73E-01	ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	chr16p13.3	204343_at	NM_001089
5.77	6.32	0.55	3.07E-01	6.73E-01	C19orf2	Chromosome 19 open reading frame 2	chr19q12	222266_at	NM_003796 /// NM_134447
6.26	6.42	0.16	3.07E-01	6.73E-01	SKI	V-ski sarcoma viral oncogene homolog (avian)	chr1q22-q24	213755_s_at	NM_003036
2.21	2.35	0.14	3.07E-01	6.73E-01	HES2	hairy and enhancer of split 2 (Drosophila)	chr1p36.31-p36.11	216674_at	NM_019089
3.48	3.86	0.38	3.07E-01	6.73E-01	MTRF1	mitochondrial translational release factor 1	chr13q14.1-q14.3	219822_at	NM_004294
10.08	10.33	0.25	3.07E-01	6.73E-01	EIF3H	eukaryotic translation initiation factor 3, subunit H	chr8q24.11	201592_at	NM_003756
3.95	4.16	0.22	3.07E-01	6.73E-01	C11orf85	chromosome 11 open reading frame 85	chr11q13.1	231210_at	NM_001037225
3.79	4.00	0.21	3.07E-01	6.73E-01	---	---	---	215128_at	---
3.33	3.51	0.18	3.07E-01	6.73E-01	LCN2	lipocalin 2	chr9q34	212531_at	NM_005564
2.14	2.29	0.15	3.07E-01	6.73E-01	---	---	---	243607_at	---
2.31	2.46	0.15	3.07E-01	6.73E-01	METT5D1	Methyltransferase 5 domain containing 1	chr11p14.1	1562830_at	NM_001113528 /// NM_152636
2.07	2.21	0.14	3.07E-01	6.73E-01	EML5	echinoderm microtubule associated protein like 5	chr14q31.3	1570393_at	NM_183387
2.86	2.99	0.13	3.07E-01	6.73E-01	PFN4	profilin family, member 4	chr2p23.3	235627_at	NM_199346
4.17	4.40	0.23	3.07E-01	6.73E-01	---	---	---	235793_at	---
3.42	3.57	0.15	3.07E-01	6.73E-01	AQP6	aquaporin 6, kidney specific	chr12q13	208435_s_at	NM_001652
2.06	2.17	0.11	3.07E-01	6.73E-01	---	---	---	239589_at	---
2.20	2.34	0.14	3.07E-01	6.73E-01	---	---	---	1563002_at	---
2.04	2.16	0.12	3.07E-01	6.73E-01	LOC152024	hypothetical protein LOC152024	chr3p24.2	1561059_a_at	XR_015855
10.18	10.35	0.17	3.07E-01	6.73E-01	CCNI	cyclin I	chr4q21.1	208656_s_at	NM_006835
8.75	9.00	0.25	3.08E-01	6.73E-01	FKBP5	FK506 binding protein 5	chr6p21.3-p21.2	224840_at	NM_004117
2.31	2.43	0.12	3.08E-01	6.73E-01	---	---	---	238284_at	---
2.15	2.27	0.12	3.08E-01	6.73E-01	CCDC88C	coiled-coil domain containing 88C	chr14q32.12	215343_at	NM_001080414
3.61	3.86	0.25	3.08E-01	6.73E-01	---	---	---	220396_at	---
6.56	6.83	0.27	3.08E-01	6.73E-01	MTF1	metal-regulatory transcription factor 1	chr1p33	227150_at	NM_005955
2.19	2.36	0.17	3.08E-01	6.73E-01	GLUD2	glutamate dehydrogenase 2	chrXq24-q25	210447_at	NM_012084
2.37	2.52	0.16	3.08E-01	6.73E-01	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	chr12q13-q14	1569042_at	NM_002332
6.69	6.90	0.21	3.08E-01	6.73E-01	PPAN	peter pan homolog (Drosophila)	chr19p13	221649_s_at	NM_020230
1.97	2.12	0.15	3.08E-01	6.73E-01	LZTS1	leucine zipper, putative tumor suppressor 1	chr8p22	1569159_at	NM_021020
2.49	2.68	0.19	3.08E-01	6.73E-01	TTLL7	tubulin tyrosine ligase-like family, member 7	chr1p31.1	219882_at	NM_024686
2.76	2.98	0.22	3.08E-01	6.73E-01	SOCS6	suppressor of cytokine signaling 6	chr18q22.2	214462_at	NM_004232
1.86	2.05	0.18	3.08E-01	6.73E-01	---	---	---	235268_at	---
2.41	2.57	0.16	3.08E-01	6.73E-01	---	---	---	224235_at	---
2.48	2.63	0.15	3.08E-01	6.73E-01	---	---	---	239900_x_at	---

5.28	5.57	0.29	3.08E-01	6.73E-01	NET1	neuroepithelial cell transforming gene 1	chr10p15	201829_at	NM_001047160 /// NM_005863
1.88	1.99	0.11	3.08E-01	6.74E-01	---	---	---	1566632_at	---
2.78	3.11	0.33	3.08E-01	6.74E-01	---	---	---	231640_at	---
3.79	3.99	0.20	3.08E-01	6.74E-01	---	---	---	243906_at	---
2.84	3.02	0.18	3.08E-01	6.74E-01	F7	coagulation factor VII (serum prothrombin conversion accelerator)	chr13q34	207300_s_at	NM_000131 /// NM_019616
2.31	2.48	0.17	3.08E-01	6.74E-01	---	---	---	240653_at	---
3.21	3.44	0.23	3.08E-01	6.74E-01	LOC650392	Hypothetical protein LOC650392	---	1558463_s_at	XM_944170
5.02	5.22	0.20	3.08E-01	6.74E-01	ZNF397OS	zinc finger protein 397 opposite strand	chr18q12.2	228125_at	NM_001112734 /// XM_001720071 /// XM_001722380 /// XM_001723235
4.30	4.56	0.25	3.08E-01	6.74E-01	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	chr2q21	206997_s_at	NM_004807
5.08	5.33	0.25	3.08E-01	6.74E-01	TRIM62	tripartite motif-containing 62	chr1p35.1	58308_at	NM_018207
2.50	2.66	0.16	3.08E-01	6.74E-01	---	---	---	241555_at	---
2.52	2.71	0.19	3.09E-01	6.74E-01	---	---	---	242833_at	---
6.74	6.96	0.22	3.09E-01	6.74E-01	USP34	ubiquitin specific peptidase 34	chr2p15	207365_x_at	NM_014709
6.77	6.97	0.20	3.09E-01	6.74E-01	SPRYD3	SPRY domain containing 3	chr12q13.13	225134_at	NM_032840
5.21	5.43	0.21	3.09E-01	6.74E-01	TBXA2R	thromboxane A2 receptor	chr19p13.3	207555_s_at	NM_001060 /// NM_201636
2.86	3.06	0.20	3.09E-01	6.74E-01	---	---	---	234326_at	---
2.82	2.96	0.14	3.09E-01	6.74E-01	ZNF668	zinc finger protein 668	chr16p11.2	222813_at	NM_024706
2.20	2.32	0.11	3.09E-01	6.74E-01	---	---	---	1562300_at	---
3.94	4.19	0.24	3.09E-01	6.74E-01	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1	chr19q13.1	223385_at	NM_030622
2.89	3.07	0.19	3.09E-01	6.74E-01	GRM1	glutamate receptor, metabotropic 1	chr6q24	210940_s_at	NM_000838 /// NM_001114329
2.36	2.48	0.12	3.09E-01	6.74E-01	LOC730217	Hypothetical LOC730217	chr14q32.2	1563007_at	XM_001132986 /// XM_001717021 /// XM_001717536
1.70	1.79	0.10	3.09E-01	6.75E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	233620_at	NM_015313
2.36	2.51	0.15	3.09E-01	6.75E-01	---	---	---	236642_at	---
2.32	2.48	0.16	3.09E-01	6.75E-01	RNASEH2B	ribonuclease H2, subunit B	chr13q14.3	219056_at	NM_024570
1.73	1.83	0.11	3.09E-01	6.75E-01	---	---	---	244048_x_at	---
2.78	2.92	0.14	3.09E-01	6.75E-01	---	---	---	231344_at	---
4.64	4.82	0.18	3.09E-01	6.75E-01	MGC33556	Hypothetical LOC339541	chr1p34.1	239844_x_at	XR_039961 /// XR_039962 /// XR_039963
1.78	1.91	0.13	3.09E-01	6.75E-01	---	---	---	240781_x_at	---
3.34	3.47	0.13	3.09E-01	6.75E-01	TMEM108	transmembrane protein 108	chr3q21	234813_at	NM_023943
3.95	4.08	0.13	3.09E-01	6.75E-01	---	---	---	243255_at	---
2.47	2.59	0.12	3.09E-01	6.75E-01	UPK1B	uroplakin 1B	chr3q13.3-q21	210065_s_at	NM_006952
1.91	2.01	0.11	3.09E-01	6.75E-01	---	---	---	234758_at	---
4.33	4.48	0.15	3.09E-01	6.75E-01	SLC5A2	solute carrier family 5 (sodium/glucose cotransporter), member 2	chr16p12-p11	207771_at	NM_003041
2.95	3.19	0.24	3.09E-01	6.75E-01	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	chr3q25	211812_s_at	NM_001038628 /// NM_003781 /// NM_033167 /// NM_033168 /// NM_033169
5.38	5.58	0.21	3.09E-01	6.75E-01	ACSF3	acyl-CoA synthetase family member 3	chr16q24.3	227464_at	NM_001127214 /// NM_174917 /// NR_023316
2.05	2.25	0.20	3.09E-01	6.75E-01	---	---	---	222325_at	---
6.02	6.20	0.18	3.09E-01	6.75E-01	---	---	---	41856_at	---
3.10	3.27	0.17	3.09E-01	6.75E-01	TRPC4	transient receptor potential cation channel, subfamily C, member 4	chr13q13.1-q13.2	224220_x_at	NM_016179
2.63	2.77	0.14	3.09E-01	6.75E-01	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	chr5p13.2	235001_at	NM_001012339 /// NM_194283
3.20	3.33	0.13	3.09E-01	6.75E-01	---	---	---	241768_at	---
1.85	1.98	0.12	3.09E-01	6.75E-01	TNKS2	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	chr10q23.3	241909_at	NM_025235
2.24	2.36	0.12	3.09E-01	6.75E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	1562278_at	NM_015512
2.88	2.99	0.11	3.09E-01	6.75E-01	---	---	---	1565746_at	---
4.02	4.23	0.21	3.09E-01	6.75E-01	---	---	---	216621_at	---
1.81	1.92	0.12	3.10E-01	6.75E-01	FAM135A	family with sequence similarity 135, member A	chr6q12-q13	221233_s_at	NM_001105531 /// NM_020819

2.03	2.19	0.16	3.10E-01	6.75E-01	---	---	---	1562923_at	---
2.89	3.07	0.18	3.10E-01	6.75E-01	---	---	---	244154_at	---
1.90	2.02	0.12	3.10E-01	6.75E-01	GUCA1C	guanylate cyclase activator 1C	chr3q13.1	233953_at	NM_005459
4.99	5.51	0.52	3.10E-01	6.75E-01	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	chr1q24	219553_at	NM_013330 /// NM_197972
7.34	7.81	0.47	3.10E-01	6.75E-01	SMAD2	SMAD family member 2	chr18q21.1	203076_s_at	NM_001003652 /// NM_005901
7.86	8.31	0.45	3.10E-01	6.75E-01	CAPRIN1	cell cycle associated protein 1	chr11p13	200723_s_at	NM_005898 /// NM_203364
2.90	3.06	0.16	3.10E-01	6.75E-01	---	---	---	232491_at	---
2.85	2.99	0.14	3.10E-01	6.75E-01	---	---	---	244823_at	---
3.51	3.92	0.41	3.10E-01	6.75E-01	ANKRD36B	ankyrin repeat domain 36B	chr2q11.2	220940_at	NM_025190
1.85	1.96	0.12	3.10E-01	6.75E-01	MGC27382	hypothetical protein MGC27382	chr1p31.1	1570235_at	XM_373850 /// XM_945645
3.41	3.56	0.14	3.10E-01	6.75E-01	---	---	---	223957_at	---
2.36	2.55	0.19	3.10E-01	6.75E-01	MS4A5	membrane-spanning 4-domains, subfamily A, member 5	chr11q12	220790_s_at	NM_023945
2.20	2.34	0.14	3.10E-01	6.75E-01	C18orf16	chromosome 18 open reading frame 16	chr18q11.2	1560751_at	XR_040524 /// XR_040525 /// XR_040526
2.00	2.13	0.12	3.10E-01	6.75E-01	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	chr5q12-q13	1560033_at	NM_022132
2.97	3.21	0.24	3.10E-01	6.75E-01	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	chr7q21.1	208367_x_at	NM_017460
3.01	3.23	0.22	3.10E-01	6.75E-01	---	---	---	236484_at	---
2.58	2.74	0.16	3.10E-01	6.75E-01	TRPM3	transient receptor potential cation channel, subfamily M, member 3	chr9q21.11-q21.12	1555252_a_at	NM_001007470 /// NM_001007471 /// NM_020952 /// NM_024971 /// NM_206944 /// NM_206945 /// NM_206946 /// NM_206947 /// NM_206948
1.73	1.84	0.11	3.10E-01	6.75E-01	---	---	---	1563187_at	---
3.51	3.94	0.43	3.10E-01	6.75E-01	---	---	---	1566166_at	---
4.58	4.86	0.28	3.10E-01	6.75E-01	PWWP2A	PWWP domain containing 2A	chr5q33.3	228336_at	NM_001130864 /// NM_052927
2.36	2.50	0.14	3.10E-01	6.75E-01	---	---	---	236521_at	---
5.02	5.31	0.29	3.10E-01	6.75E-01	SMC3	structural maintenance of chromosomes 3	chr10q25	209259_s_at	NM_005445
5.03	5.25	0.23	3.10E-01	6.75E-01	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	chr9q34	220937_s_at	NM_175039 /// NM_175040
3.40	3.62	0.22	3.10E-01	6.75E-01	PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha isoform	chr1q32.2-q32.3	202186_x_at	NM_006243
5.38	5.59	0.21	3.10E-01	6.76E-01	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	chr10q24	209346_s_at	NM_018425
4.66	4.81	0.15	3.10E-01	6.76E-01	---	---	---	233017_x_at	---
7.01	7.71	0.70	3.10E-01	6.76E-01	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	chr21q22.12	213164_at	NM_006933
2.95	3.10	0.16	3.10E-01	6.76E-01	CXorf51	chromosome X open reading frame 51	chrXq27.3	231159_at	XM_001720768 /// XM_001721645
1.95	2.14	0.19	3.10E-01	6.76E-01	---	---	---	237240_at	---
1.97	2.08	0.10	3.10E-01	6.76E-01	---	---	---	1562715_at	---
3.02	3.21	0.19	3.11E-01	6.76E-01	---	---	---	1560787_at	---
2.68	2.87	0.19	3.11E-01	6.76E-01	---	---	---	234654_at	---
3.64	3.82	0.17	3.11E-01	6.76E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	216318_at	---
2.47	2.64	0.16	3.11E-01	6.76E-01	---	---	---	240488_at	---
3.47	3.63	0.16	3.11E-01	6.76E-01	---	---	---	240291_at	---
1.91	2.06	0.15	3.10E-01	6.76E-01	---	---	---	244337_at	---
2.14	2.27	0.13	3.11E-01	6.76E-01	CD226	CD226 molecule	chr18q22.3	207315_at	NM_006566
2.08	2.21	0.13	3.11E-01	6.76E-01	HAR1A	highly accelerated region 1A (non-protein coding)	chr20q13.33	1557098_s_at	NR_003244
4.14	4.30	0.16	3.11E-01	6.76E-01	ITGB7	integrin, beta 7	chr12q13.13	205718_at	NM_000889
1.82	1.95	0.13	3.11E-01	6.76E-01	---	---	---	1568872_at	---
2.48	2.61	0.12	3.11E-01	6.76E-01	SIRPD	signal-regulatory protein delta	chr20p13	232891_at	NM_178460
2.21	2.32	0.11	3.11E-01	6.76E-01	---	---	---	241309_at	---
1.91	2.05	0.14	3.11E-01	6.76E-01	PDE5A	phosphodiesterase 5A, cGMP-specific	chr4q25-q27	240088_at	NM_001083 /// NM_033430 /// NM_033437

3.13	3.27	0.13	3.11E-01	6.76E-01	LOC100128416	Similar to RB28	chrXq26.3	229999_at	XR_037268 /// XR_037418																				
7.04	7.55	0.50	3.11E-01	6.76E-01	CAB39	calcium binding protein 39	chr2q37.1	217873_at	NM_001130849 /// NM_001130850 /// NM_016289																				
4.31	4.74	0.43	3.11E-01	6.76E-01	CDC14B /// CDC14C	CDC14 cell division cycle 14 homolog B (S. cerevisiae) /// CDC14 cell division cycle 14 homolog C (S. cerevisiae)	chr7p12.3 /// chr9q22.33	221555_x_at	NM_001077181 /// NM_003671 /// NM_033331 /// NR_003595																				
4.46	4.73	0.28	3.11E-01	6.76E-01	PRB1 /// PRB2 /// PRB4 /// PRH1 /// PRH2	proline-rich protein BstNI subfamily 1 /// proline-rich protein BstNI subfamily 2 /// proline-rich protein BstNI subfamily 4 /// proline-rich protein HaeIII subfamily 1 /// proline-rich protein HaeIII subfamily 2	chr12p13.2	211531_x_at	NM_001110213 /// NM_002723 /// NM_005039 /// NM_005042 /// NM_006248 /// NM_006250 /// NM_199353 /// NM_199354																				
2.98	3.12	0.14	3.11E-01	6.76E-01	PLXNA4	plexin A4	chr7q32.3	232317_at	NM_001105543 /// NM_020911 /// NM_181775																				
6.31	6.73	0.43	3.11E-01	6.76E-01	KIFAP3	kinesin-associated protein 3	chr1q24.2	203333_at	NM_014970																				
3.94	4.21	0.27	3.11E-01	6.76E-01	CFP	complement factor properdin	chrXp11.3-p11.23	206380_s_at	NM_002621																				
3.38	3.73	0.36	3.11E-01	6.76E-01	C6	complement component 6	chr5p13	210168_at	NM_000065 /// NM_001115131																				
2.83	3.08	0.26	3.11E-01	6.76E-01	---	---	---	1563597_at	---																				
4.70	4.88	0.18	3.11E-01	6.76E-01	HFE	hemochromatosis	chr6p21.3	210864_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011																				
8.73	9.35	0.62	3.11E-01	6.76E-01	UGP2	UDP-glucose pyrophosphorylase 2	chr2p14-p13	205480_s_at	NM_001001521 /// NM_006759																				
6.70	7.14	0.44	3.11E-01	6.76E-01	TTRAP	TRAF and TNF receptor associated protein	chr6p22.3-p22.1	202266_at	NM_016614																				
3.25	3.56	0.31	3.11E-01	6.76E-01	---	---	---	215316_at	---																				
2.89	3.05	0.15	3.11E-01	6.76E-01	FGA	fibrinogen alpha chain	chr4q28	205650_s_at	NM_000508 /// NM_021871																				
3.08	3.33	0.25	3.11E-01	6.76E-01	AZI2	5-azacytidine induced 2	chr3p24.1	218043_s_at	NM_001134432 /// NM_001134433 /// NM_022461																				
4.12	4.33	0.21	3.11E-01	6.76E-01	SFXN5	sideroflexin 5	---	241999_at	NM_144579																				
4.31	4.64	0.32	3.11E-01	6.76E-01	TPK1	thiamin pyrophosphokinase 1	chr7q34-q35	221218_s_at	NM_001042482 /// NM_022445																				
3.70	3.85	0.15	3.11E-01	6.76E-01	LOC400960	hypothetical gene supported by BC040598	chr2p14	227969_at	XM_934552 /// XM_945536																				
2.03	2.17	0.14	3.11E-01	6.76E-01	COL20A1	collagen, type XX, alpha 1	chr20q13.33	232638_at	NM_020882																				
3.02	3.19	0.17	3.12E-01	6.76E-01	KIAA0317	KIAA0317	chr14q24.3	1554989_at	NM_001039479																				
2.01	2.16	0.16	3.12E-01	6.76E-01	---	---	---	236414_at	---																				
2.38	2.54	0.16	3.12E-01	6.77E-01	---	---	---	214424_s_at	---																				
2.29	2.43	0.14	3.12E-01	6.77E-01	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	chr6p21.2-p21.1	231398_at	NM_006672 /// NM_153320																				
7.20	7.80	0.60	3.12E-01	6.77E-01	GBP2	guanylate binding protein 2, interferon-inducible	chr1p22.2	202748_at	NM_004120																				
4.87	5.44	0.57	3.12E-01	6.77E-01	MRVI1	murine retrovirus integration site 1 homolog	chr11p15	230214_at	NM_001098579 /// NM_001100163 /// NM_001100167 /// NM_130385																				

6.17	6.70	0.54	3.12E-01	6.77E-01	CAPRIN1	cell cycle associated protein 1	chr11p13	200722_s_at	NM_005898 /// NM_203364
5.57	5.98	0.40	3.12E-01	6.77E-01	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	chr2p13.3	212885_at	NM_005791
3.27	3.54	0.27	3.12E-01	6.77E-01	KIAA1715	KIAA1715	chr2q31	229173_at	NM_030650
3.12	3.34	0.21	3.12E-01	6.77E-01	TCL6	T-cell leukemia/lymphoma 6	chr14q32.1	239964_at	NM_012468 /// NM_014418 /// NM_020550 /// NM_020552 /// NM_020553 /// NM_020554
2.50	2.69	0.19	3.12E-01	6.77E-01	CTXN3	cortexin 3	chr5q23.2	236374_at	NM_001048252 /// NM_001127385
2.83	3.02	0.19	3.12E-01	6.77E-01	ZNF488	zinc finger protein 488	chr10q11.22	229901_at	NM_153034
2.79	2.97	0.18	3.12E-01	6.77E-01	CCDC40	coiled-coil domain containing 40	chr17q25.3	1563563_at	NM_017950
2.49	2.67	0.18	3.12E-01	6.77E-01	CALY	calcyon neuron-specific vesicular protein	chr10q26.3	219896_at	NM_015722
2.58	2.75	0.16	3.12E-01	6.77E-01	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	chr1q32	217484_at	NM_000573 /// NM_000651
3.93	4.09	0.16	3.12E-01	6.77E-01	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	chr11q25	1553427_at	NM_139055
3.55	3.70	0.15	3.12E-01	6.77E-01	PTK6	PTK6 protein tyrosine kinase 6	chr20q13.3	1553114_a_at	NM_005975
7.30	7.45	0.15	3.12E-01	6.77E-01	SOX4	SRY (sex determining region Y)-box 4	chr6p22.3	201418_s_at	NM_003107
1.99	2.13	0.14	3.12E-01	6.77E-01	---	---	---	1568941_a_at	---
1.93	2.05	0.13	3.12E-01	6.77E-01	C1orf161	chromosome 1 open reading frame 161	chr1p13.1	1553333_at	NM_152367
3.11	3.23	0.12	3.12E-01	6.77E-01	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1	chr2p25.1-p24.1	241757_x_at	NM_001012665 /// NM_015522 /// NM_016008
1.73	1.85	0.11	3.12E-01	6.77E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1565026_a_at	NM_153003
2.51	2.62	0.11	3.12E-01	6.77E-01	MC3R	melanocortin 3 receptor	chr20q13.2-q13.3	221442_at	NM_019888
1.99	2.10	0.11	3.12E-01	6.77E-01	FOXP2	forkhead box P2	chr7q31	1555648_at	NM_014491 /// NM_148898 /// NM_148899
4.55	5.00	0.45	3.12E-01	6.77E-01	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	chr12q21.3	209281_s_at	NM_001001323 /// NM_001682
7.31	7.78	0.47	3.12E-01	6.77E-01	ASPH	aspartate beta-hydroxylase	chr8q12.1	210896_s_at	NM_004318 /// NM_020164 /// NM_032466 /// NM_032467 /// NM_032468
5.35	5.61	0.26	3.12E-01	6.77E-01	POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	chr1q21.1	209382_at	NM_006468
5.99	6.22	0.23	3.12E-01	6.77E-01	---	---	---	AFFX-r2-Ec-bioB-M_at	---
2.32	2.51	0.19	3.12E-01	6.77E-01	LOC100129386	Hypothetical protein LOC100129386	chr11p15.4	1557177_at	XM_001715291 /// XM_001716175 /// XM_001716751
2.92	3.07	0.15	3.12E-01	6.77E-01	CSNK1E /// LOC400927	casein kinase 1, epsilon /// TPTE and PTEN homologous inositol lipid phosphatase pseudogene	chr22q13.1	234943_at	NM_001894 /// NM_152221 /// NR_002821
2.69	2.83	0.14	3.12E-01	6.77E-01	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	chr12q24.2	232666_at	NM_006187
2.41	2.53	0.12	3.12E-01	6.77E-01	STRN	striatin, calmodulin binding protein	chr2p22-p21	205520_at	NM_003162
2.49	2.68	0.19	3.12E-01	6.77E-01	TSKS	testis-specific kinase substrate	chr19q13.3	220545_s_at	NM_021733
2.22	2.38	0.16	3.12E-01	6.77E-01	OR51E2	olfactory receptor, family 51, subfamily E, member 2	chr11p15	236121_at	NM_030774
6.96	7.15	0.20	3.12E-01	6.77E-01	TMEM129	transmembrane protein 129	chr4p16.3	225587_at	NM_001127266 /// NM_138385
6.06	6.25	0.19	3.12E-01	6.77E-01	---	---	---	228971_at	---
5.70	5.88	0.18	3.12E-01	6.77E-01	ADRA2C	adrenergic, alpha-2C-, receptor	chr4p16	206128_at	NM_000683
2.01	2.15	0.13	3.12E-01	6.77E-01	LOC387790	hypothetical LOC387790	chr11q13.5	1561198_at	NM_001013634
4.27	4.66	0.40	3.12E-01	6.77E-01	FOXO3	forkhead box O3	chr6q21	210655_s_at	NM_001455 /// NM_201559
6.26	6.46	0.20	3.13E-01	6.77E-01	C17orf59	chromosome 17 open reading frame 59	chr17p13.1	219417_s_at	NM_017622
2.48	2.68	0.20	3.13E-01	6.77E-01	NKAIN3	Na+/K+ transporting ATPase interacting 3	chr8q12.3	1553241_at	NM_173688
2.43	2.58	0.15	3.13E-01	6.77E-01	WDR60	WD repeat domain 60	chr7q36.3	1562516_at	NM_018051

4.71	5.25	0.54	3.13E-01	6.77E-01	USP16	ubiquitin specific peptidase 16	chr21q22.11	222616_s_at	NM_001001992 /// NM_001032410 /// NM_006447																				
4.19	4.43	0.23	3.13E-01	6.77E-01	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	chr1q42.13	220427_at	NM_001098623 /// NM_052843																				
2.74	2.95	0.21	3.13E-01	6.77E-01	SEC14L1	SEC14-like 1 (S. cerevisiae)	chr17q25.1-q25.2	240036_at	NM_001039573 /// NM_003003																				
2.58	2.76	0.18	3.13E-01	6.77E-01	CLDN18	claudin 18	chr3q22.3	221133_s_at	NM_001002026 /// NM_016369																				
2.92	3.07	0.16	3.13E-01	6.77E-01	CAMTA1	calmodulin binding transcription activator 1	chr1p36.31-p36.23	1555370_a_at	NM_015215																				
2.06	2.20	0.13	3.13E-01	6.77E-01	MAL2	mal, T-cell differentiation protein 2	chr8q23	224650_at	NM_052886																				
2.40	2.52	0.12	3.13E-01	6.77E-01	GJA10	gap junction protein, alpha 10, 62kDa	chr6q15-q16	1553044_at	NM_032602																				
3.17	3.34	0.17	3.13E-01	6.77E-01	FAM122C	family with sequence similarity 122C	chrXq26.3	1562641_at	NM_138819																				
2.07	2.18	0.11	3.13E-01	6.77E-01	---	---	---	243655_x_at	---																				
2.35	2.46	0.11	3.13E-01	6.77E-01	---	---	---	242238_at	---																				
2.35	2.50	0.15	3.13E-01	6.77E-01	LSM11	LSM11, U7 small nuclear RNA associated	chr5q33.3	242112_at	NM_173491																				
4.20	4.35	0.15	3.13E-01	6.77E-01	POLD3	Polymerase (DNA-directed), delta 3, accessory subunit	chr11q14	239816_at	NM_006591																				
2.29	2.43	0.14	3.13E-01	6.77E-01	---	---	---	244226_s_at	---																				
2.30	2.47	0.18	3.13E-01	6.77E-01	---	---	---	1559837_at	---																				
2.50	2.66	0.17	3.13E-01	6.77E-01	L1TD1	LINE-1 type transposase domain containing 1	chr1p31.3	219955_at	NM_019079																				
6.09	6.23	0.14	3.13E-01	6.77E-01	NUMBL	numb homolog (Drosophila)-like	chr19q13.13-q13.2	242195_x_at	NM_004756																				
3.05	3.34	0.29	3.13E-01	6.77E-01	---	---	---	230970_at	---																				
3.12	3.33	0.21	3.13E-01	6.77E-01	---	---	---	240769_at	---																				
2.10	2.24	0.14	3.13E-01	6.77E-01	---	---	---	234646_at	---																				
2.38	2.51	0.12	3.13E-01	6.77E-01	---	---	---	240083_at	---																				
3.94	4.37	0.43	3.13E-01	6.77E-01	DLG1	discs, large homolog 1 (Drosophila)	chr3q29	217208_s_at	NM_001098424 /// NM_004087																				
6.02	6.58	0.56	3.13E-01	6.77E-01	CAND1	cullin-associated and neddylation-dissociated 1	chr12q14	207483_s_at	NM_018448																				
5.29	5.72	0.43	3.13E-01	6.77E-01	---	---	---	240458_at	---																				
2.89	3.15	0.27	3.13E-01	6.77E-01	---	---	---	236763_at	---																				
7.20	7.70	0.50	3.13E-01	6.77E-01	PJA2	praja 2, RING-H2 motif containing	chr5q21.3	201133_s_at	NM_014819																				
2.38	2.54	0.16	3.13E-01	6.78E-01	LECT1	leukocyte cell derived chemotaxin 1	chr13q14-q21	206309_at	NM_001011705 /// NM_007015																				
2.72	2.95	0.22	3.13E-01	6.78E-01	HOXC12	homeobox C12	chr12q12-q13	1553512_at	NM_173860																				
5.00	5.46	0.46	3.14E-01	6.78E-01	NR3C2	nuclear receptor subfamily 3, group C, member 2	chr4q31.1	205259_at	NM_000901																				
2.01	2.16	0.15	3.14E-01	6.78E-01	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	chr10q21.3-q23.1	243335_at	NM_000917 /// NM_001017962																				
3.49	3.65	0.17	3.14E-01	6.78E-01	USF1	upstream transcription factor 1	chr1q22-q23	231768_at	NM_007122 /// NM_207005																				
2.65	2.83	0.18	3.14E-01	6.78E-01	FAM115C	family with sequence similarity 115, member C	chr7q35	1564028_s_at	NM_001130025 /// NM_001130026 /// NM_173678																				
3.05	3.22	0.17	3.14E-01	6.78E-01	LRRC68	leucine rich repeat containing 68	chr19q13.32	213751_at	XM_001722969 /// XM_001723010 /// XM_001724714																				
2.09	2.24	0.14	3.14E-01	6.78E-01	TRIM9	tripartite motif-containing 9	chr14q22.1	230280_at	NM_015163 /// NM_052978																				
1.88	2.01	0.13	3.14E-01	6.78E-01	C10orf81	chromosome 10 open reading frame 81	chr10q25.3	1554190_s_at	NM_024889																				
2.06	2.19	0.12	3.14E-01	6.78E-01	RXFP2	relaxin/insulin-like family peptide receptor 2	chr13q13.1	1553326_at	NM_130806																				
4.59	4.78	0.19	3.14E-01	6.78E-01	COL11A2	collagen, type XI, alpha 2	chr6p21.3	216993_s_at	NM_080679 /// NM_080680 /// NM_080681																				
3.04	3.22	0.17	3.14E-01	6.78E-01	FLJ40125	hypothetical protein FLJ40125	chr19q13.32	229559_at	NM_001080401																				
4.58	5.28	0.70	3.14E-01	6.78E-01	SORBS2	Sorbin and SH3 domain containing 2	chr4q35.1	233720_at	NM_003603 /// NM_021069																				
1.91	2.07	0.15	3.14E-01	6.78E-01	---	---	---	1559665_at	---																				
7.83	8.02	0.18	3.14E-01	6.78E-01	---	---	---	213642_at	---																				
3.11	3.25	0.14	3.14E-01	6.78E-01	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	chr2q23.3	208194_s_at	NM_005843																				

3.75	4.04	0.28	3.14E-01	6.78E-01	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	chrXp22.32 and Yp11.3	211286_x_at	NM_006140 /// NM_172245 /// NM_172246 /// NM_172247 /// NM_172249
2.74	2.92	0.18	3.14E-01	6.78E-01	---	---	---	234061_at	---
2.52	2.66	0.14	3.14E-01	6.78E-01	IL1A	interleukin 1, alpha	chr2q14	210118_s_at	NM_000575
2.87	2.99	0.12	3.14E-01	6.78E-01	ZNF594	Zinc finger protein 594	chr17p13	243980_at	NM_032530
1.99	2.09	0.10	3.14E-01	6.78E-01	FOXE1	forkhead box E1 (thyroid transcription factor 2)	chr9q22	206912_at	NM_004473
2.56	2.80	0.24	3.14E-01	6.78E-01	---	---	---	236944_at	---
4.74	4.91	0.17	3.14E-01	6.78E-01	VPS8	vacuolar protein sorting 8 homolog (S. cerevisiae)	chr3q27.2	209553_at	NM_001009921 /// NM_015303
2.12	2.25	0.13	3.14E-01	6.78E-01	---	---	---	231033_at	---
1.95	2.08	0.13	3.14E-01	6.78E-01	LOC196415	hypothetical protein LOC196415	chr12p12.1	239691_at	NM_001101339
4.11	4.36	0.25	3.14E-01	6.78E-01	MAP7	microtubule-associated protein 7	chr6q23.3	202889_x_at	NM_003980
3.18	3.31	0.13	3.14E-01	6.78E-01	---	---	---	233121_at	---
7.30	7.68	0.38	3.14E-01	6.78E-01	MAP1B	microtubule-associated protein 1B	chr5q13	212233_at	NM_005909
9.85	10.08	0.23	3.14E-01	6.78E-01	UQCRB	ubiquinol-cytochrome c reductase binding protein	chr8q22	205849_s_at	NM_006294
2.34	2.48	0.14	3.14E-01	6.78E-01	---	---	---	1562942_at	---
2.02	2.17	0.15	3.15E-01	6.78E-01	VPS13D	Vacuolar protein sorting 13 homolog D (S. cerevisiae)	chr1p36.22	1557571_at	NM_015378 /// NM_018156
2.11	2.24	0.13	3.15E-01	6.78E-01	hCG_2015956 /// LOC100127893 /// LOC100130892 /// LOC100131085 /// LOC388401 /// LOC441896 /// LOC641900 /// LOC646346 /// LOC728380 /// LOC728843 /// RPL7	hCG2015956 /// similar to ribosomal protein L7 /// hypothetical protein LOC100130892 /// hypothetical LOC100131085 /// similar to ribosomal protein L7 /// similar to ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// similar to ribosomal protein L7 /// hypothetical LOC728380 /// hypothetical LOC728843 /// ribosomal protein L7	chr17q21.33 /// chr1p13.3 /// chr2p22.2 /// chr5q14.1 /// chr5q34 /// chr6p22.3 /// chr7q31.1 /// chr8q21.11 /// chrXp21.3	216580_at	NM_000971 /// XM_001719048 /// XM_001720172 /// XM_001722435 /// XM_001722574 /// XM_001725978 /// XM_943842 /// XR_015391 /// XR_015500 /// XR_015600 /// XR_015705 /// XR_016234 /// XR_016879 /// XR_017105 /// XR_018042 /// XR_018794 /// XR_019544 /// XR_038286 /// XR_038691 /// XR_038779 /// XR_038885 /// XR_038901 /// XR_038947 /// XR_039043 /// XR_039090 /// XR_039345 /// XR_039473 /// XR_039795
2.68	2.85	0.16	3.15E-01	6.79E-01	---	---	---	240273_at	---
2.46	2.59	0.13	3.15E-01	6.79E-01	---	---	---	239573_at	---
4.30	4.67	0.37	3.15E-01	6.79E-01	---	---	---	229460_at	---
4.68	4.84	0.17	3.15E-01	6.79E-01	FTCD	formiminotransferase cyclodeaminase	chr21q22.3	223702_x_at	NM_006657 /// NM_206965
1.89	2.01	0.12	3.15E-01	6.79E-01	COL29A1	collagen, type XXIX, alpha 1	chr3q22.1	1553834_at	NM_153264 /// NR_022012
2.92	3.10	0.19	3.15E-01	6.79E-01	HINT3	histidine triad nucleotide binding protein 3	chr6q22.32	226533_at	NM_138571
1.79	1.90	0.11	3.15E-01	6.79E-01	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	chr2p13	1554889_at	NM_022037 /// NM_022173
3.57	3.94	0.36	3.15E-01	6.79E-01	---	---	---	243887_at	---
6.90	7.21	0.31	3.15E-01	6.79E-01	SGK269	NKF3 kinase family member	chr15q24.3	225913_at	NM_024776
1.95	2.12	0.17	3.15E-01	6.79E-01	RIMBP2	RIMS binding protein 2	chr12q24.33	237995_at	NM_015347
1.76	1.86	0.10	3.15E-01	6.79E-01	---	---	---	1561177_at	---
2.41	2.55	0.14	3.15E-01	6.79E-01	FOXE3	forkhead box E3	chr1p32	220621_at	NM_012186
2.01	2.14	0.13	3.15E-01	6.79E-01	---	---	---	234629_at	---
4.89	5.34	0.45	3.15E-01	6.79E-01	ETV6	ets variant gene 6 (TEL oncogene)	chr12p13	239740_at	NM_001987
5.88	6.06	0.18	3.15E-01	6.79E-01	LRRC28	leucine rich repeat containing 28	chr15q26.3	227423_at	NM_144598
2.03	2.18	0.15	3.15E-01	6.79E-01	PROM2	prominin 2	chr2q11.1	1552797_s_at	NM_144707
5.41	5.77	0.35	3.15E-01	6.79E-01	C10orf10	chromosome 10 open reading frame 10	chr10q11.21	209182_s_at	NM_007021
4.86	5.11	0.26	3.15E-01	6.79E-01	SDS	serine dehydratase	chr12q24.13	205695_at	NM_006843
2.88	3.14	0.25	3.15E-01	6.79E-01	---	---	---	215534_at	---

2.70	2.91	0.21	3.15E-01	6.79E-01	FANCI	Fanconi anemia, complementation group I	chr15q26.1	223785_at	NM_001113378 /// NM_018193																			
2.50	2.67	0.17	3.15E-01	6.79E-01	C11orf63	chromosome 11 open reading frame 63	chr11q24.1	1555787_at	NM_024806 /// NM_199124																			
2.22	2.39	0.17	3.15E-01	6.79E-01	GPR126	G protein-coupled receptor 126	chr6q24.1	1553025_at	NM_001032394 /// NM_001032395 /// NM_020455 /// NM_198569																			
2.16	2.32	0.16	3.15E-01	6.79E-01	---	---	---	217481_x_at	---																			
2.01	2.16	0.15	3.15E-01	6.79E-01	ALDH1L2	Aldehyde dehydrogenase 1 family, member L2	chr12q23.3	231202_at	NM_001034173																			
1.97	2.10	0.13	3.15E-01	6.79E-01	CNTN5	Contactin 5	chr11q21-q22.2	244632_at	NM_014361 /// NM_175566																			
1.74	1.86	0.13	3.15E-01	6.79E-01	---	---	---	217698_at	---																			
2.09	2.20	0.11	3.15E-01	6.79E-01	LOC92482	UPF0604 protein	chr10q25.2	232885_at	XM_001716109 /// XM_001725802 /// XM_001725803 /// XM_001725804 /// XM_001726022 /// XM_001726023 /// XM_001726024																			
3.15	3.35	0.20	3.15E-01	6.79E-01	SDS	serine dehydratase	chr12q24.13	1555539_at	NM_006843																			
2.63	2.82	0.19	3.15E-01	6.79E-01	C21orf41	Chromosome 21 open reading frame 41	chr21q22.11	1560378_at	NR_002214 /// NR_002215 /// XM_001720046 /// XM_001724646 /// XM_001725376																			
2.07	2.19	0.11	3.15E-01	6.79E-01	---	---	---	243488_at	---																			
2.32	2.43	0.11	3.15E-01	6.79E-01	SLC23A1	solute carrier family 23 (nucleobase transporters), member 1	chr5q31.2-q31.3	223732_at	NM_005847 /// NM_152685																			
3.35	3.57	0.22	3.15E-01	6.79E-01	---	---	---	234143_at	---																			
4.01	4.18	0.17	3.15E-01	6.79E-01	ANKRD44	ankyrin repeat domain 44	chr2q33.1	233361_at	NM_153697																			
3.44	3.66	0.22	3.15E-01	6.79E-01	---	---	---	1559478_at	---																			
3.71	4.46	0.75	3.16E-01	6.79E-01	---	---	---	215571_at	---																			
3.46	3.73	0.28	3.16E-01	6.79E-01	ICA1	islet cell autoantigen 1, 69kDa	chr7p22	210547_x_at	NM_004968 /// NM_022307																			
5.92	6.17	0.25	3.16E-01	6.79E-01	FLJ35390	hypothetical LOC255031	chr7p13	1564208_x_at	---																			
4.38	4.60	0.21	3.16E-01	6.79E-01	BCAT2	branched chain aminotransferase 2, mitochondrial	chr19q13	215654_at	NM_001190																			
7.17	7.36	0.20	3.16E-01	6.79E-01	FLJ35220	hypothetical protein FLJ35220	chr17q25.3	238402_s_at	NM_173627																			
3.42	3.60	0.18	3.16E-01	6.79E-01	---	---	---	237091_at	---																			
2.39	2.56	0.17	3.16E-01	6.79E-01	LOC643733	hypothetical LOC643733	chr11q22.3	240890_at	XM_001718789 /// XM_001718827 /// XM_001718847																			
2.72	2.89	0.17	3.16E-01	6.79E-01	---	---	---	236993_at	---																			
2.23	2.38	0.15	3.16E-01	6.79E-01	---	---	---	233497_at	---																			
2.68	2.80	0.12	3.16E-01	6.79E-01	---	---	---	1560642_at	---																			
5.23	5.39	0.16	3.16E-01	6.79E-01	MYO9A	myosin IXA	chr15q22-q23	219027_s_at	NM_006901																			
4.36	5.09	0.73	3.16E-01	6.79E-01	PTER	phosphotriesterase related	chr10p12	218967_s_at	NM_001001484 /// NM_030664																			
4.82	5.09	0.27	3.16E-01	6.79E-01	KIAA1919	KIAA1919	chr6q22	242851_at	NM_153369																			
2.99	3.19	0.19	3.16E-01	6.79E-01	ALPK2	alpha-kinase 2	chr18q21.31-q21.32	228367_at	NM_052947																			
2.77	2.92	0.15	3.16E-01	6.79E-01	LOC254100	hypothetical protein LOC254100	chr11q13.1	1557131_at	---																			
2.76	2.91	0.15	3.16E-01	6.79E-01	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	chr9q32	236927_at	NM_153366																			
1.84	1.96	0.12	3.16E-01	6.79E-01	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1	chr2p25.1-p24.1	1554324_s_at	NM_001012665 /// NM_015522 /// NM_016008																			

2.57	2.69	0.12	3.16E-01	6.79E-01	PAX3	paired box 3	chr2q35-q37|2q35	216059_at	NM_000438 /// NM_001127366 /// NM_013942 /// NM_181457 /// NM_181458 /// NM_181459 /// NM_181460 /// NM_181461
4.98	5.38	0.40	3.16E-01	6.79E-01	GRK5	G protein-coupled receptor kinase 5	chr10q24-qter	204395_s_at	NM_005308
5.33	5.71	0.38	3.16E-01	6.79E-01	EFTUD1	elongation factor Tu GTP binding domain containing 1	chr15q25.2	218973_at	NM_001040610 /// NM_024580
4.31	4.54	0.23	3.16E-01	6.79E-01	EHD1	EH-domain containing 1	chr11q13	209038_s_at	NM_006795
2.53	2.74	0.21	3.16E-01	6.79E-01	SPAG11B	sperm associated antigen 11B	chr8p23-p22	211381_x_at	NM_016512 /// NM_058200 /// NM_058201 /// NM_058202 /// NM_058203 /// NM_058206 /// NM_058207
3.47	3.68	0.21	3.16E-01	6.79E-01	ENOX2	ecto-NOX disulfide-thiol exchanger 2	chrXq25-q26.2	204644_at	NM_006375 /// NM_182314
2.46	2.65	0.19	3.16E-01	6.79E-01	---	---	---	236293_at	---
6.49	6.65	0.16	3.16E-01	6.79E-01	GTSE1	G-2 and S-phase expressed 1	chr22q13.2-q13.3	211040_x_at	NM_016426
2.82	2.96	0.14	3.16E-01	6.79E-01	HNRNPM	heterogeneous nuclear ribonucleoprotein M	chr19p13.3-p13.2	233605_x_at	NM_005968 /// NM_031203
2.61	2.73	0.12	3.16E-01	6.79E-01	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	chr13q34	242999_at	NM_001113511 /// NM_001113512 /// NM_001113513 /// NM_003899 /// NM_145735
2.47	2.58	0.12	3.16E-01	6.79E-01	USP43	ubiquitin specific peptidase 43	chr17p13.1	237439_at	NM_153210
2.30	2.43	0.12	3.16E-01	6.79E-01	---	---	---	236323_at	---
4.63	5.24	0.61	3.16E-01	6.79E-01	---	---	---	229026_at	---
2.97	3.36	0.40	3.16E-01	6.79E-01	---	---	---	232125_at	---
2.92	3.09	0.16	3.16E-01	6.79E-01	C21orf77	chromosome 21 open reading frame 77	chr21q22.11	220826_at	XR_017737 /// XR_017792 /// XR_040362
1.86	2.02	0.15	3.16E-01	6.79E-01	---	---	---	241156_at	---
2.24	2.39	0.15	3.16E-01	6.79E-01	---	---	---	1561418_at	---
2.28	2.40	0.12	3.16E-01	6.79E-01	FLJ37644 /// LOC727973	hypothetical gene supported by AK094963 /// hypothetical protein LOC727973	chr17q24.3	230419_at	XM_001126807 /// XM_001134151 /// XM_001725777 /// XR_039996 /// XR_039997 /// XR_039998
2.02	2.13	0.12	3.16E-01	6.79E-01	KIAA0562	KIAA0562	chr1p36.32	243696_at	NM_014704
2.06	2.17	0.11	3.16E-01	6.79E-01	SFRS11	Splicing factor, arginine/serine-rich 11	chr1p31	236948_x_at	NM_004768
2.51	2.74	0.23	3.16E-01	6.79E-01	---	---	---	243859_at	---
2.44	2.56	0.13	3.16E-01	6.80E-01	DPF3	D4, zinc and double PHD fingers, family 3	chr14q24.3-q31.1	235357_at	NM_012074
1.83	1.95	0.12	3.16E-01	6.80E-01	---	---	---	234432_at	---
3.59	4.11	0.52	3.16E-01	6.80E-01	WSCD1	WSC domain containing 1	chr17p13.2	213155_at	NM_015253
2.88	3.06	0.18	3.16E-01	6.80E-01	PRLR	prolactin receptor	chr5p14-p13	216638_s_at	NM_000949
2.57	2.71	0.14	3.17E-01	6.80E-01	---	---	---	231483_at	---
3.76	3.93	0.17	3.17E-01	6.80E-01	---	---	---	240023_at	---
3.74	3.91	0.17	3.17E-01	6.80E-01	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	chr4q31.21	212960_at	NM_015130
1.99	2.11	0.12	3.17E-01	6.80E-01	---	---	---	231432_at	---
3.61	3.87	0.26	3.17E-01	6.80E-01	CLDN3	claudin 3	chr7q11.23	203954_x_at	NM_001306
5.43	5.76	0.34	3.17E-01	6.80E-01	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	chr3q22.3	212688_at	NM_006219
3.41	3.64	0.23	3.17E-01	6.80E-01	SCFD2	sec1 family domain containing 2	chr4q12	236834_at	NM_152540
9.00	9.42	0.42	3.17E-01	6.80E-01	S100A6	S100 calcium binding protein A6	chr1q21	217728_at	NM_014624
3.54	3.81	0.27	3.17E-01	6.80E-01	---	---	---	231259_s_at	---
3.25	3.47	0.22	3.17E-01	6.80E-01	CDH26	cadherin-like 26	chr20q13.2-q13.33	233391_at	NM_021810 /// NM_177980

6.05	6.26	0.21	3.17E-01	6.80E-01	PTRH1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	chr9q34.11	228014_at	NM_001002913
4.37	4.56	0.19	3.17E-01	6.80E-01	LASS1	LAG1 homolog, ceramide synthase 1	chr19p12	229448_at	NM_021267 /// NM_198207
2.03	2.21	0.18	3.17E-01	6.80E-01	---	---	---	239494_at	---
2.91	3.07	0.16	3.17E-01	6.80E-01	---	---	---	240521_at	---
5.52	5.68	0.16	3.17E-01	6.80E-01	HOXB8	Homeobox B8	chr17q21.3	230114_at	NM_024016
2.05	2.20	0.15	3.17E-01	6.80E-01	RP13-36C9.6	cancer/testis antigen CT45-5	chrXq26.3	235700_at	NM_001007551
2.69	2.84	0.15	3.17E-01	6.80E-01	H2AFY	H2A histone family, member Y	chr5q31.3-q32	1558780_a_at	NM_001040158 /// NM_004893 /// NM_138609 /// NM_138610
2.46	2.61	0.15	3.17E-01	6.80E-01	---	---	---	1566697_at	---
1.95	2.09	0.14	3.17E-01	6.80E-01	---	---	---	224033_at	---
2.17	2.32	0.14	3.17E-01	6.80E-01	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	chr18q21.3	209719_x_at	NM_006919
1.97	2.09	0.12	3.17E-01	6.80E-01	---	---	---	239317_at	---
2.41	2.64	0.23	3.17E-01	6.80E-01	MYL2	myosin, light chain 2, regulatory, cardiac, slow	chr12q24.11	209742_s_at	NM_000432
3.39	3.61	0.23	3.17E-01	6.80E-01	HRB	HIV-1 Rev binding protein	chr2q36.3	213928_s_at	NM_004504
2.20	2.37	0.17	3.17E-01	6.80E-01	---	---	---	238769_at	---
2.37	2.66	0.29	3.17E-01	6.80E-01	MGC29506	hypothetical protein MGC29506	chr5q23-q31	223565_at	NM_016459
3.31	3.51	0.20	3.17E-01	6.80E-01	---	---	---	230606_at	---
3.33	3.53	0.20	3.17E-01	6.80E-01	MIAT	Myocardial infarction associated transcript (non-protein coding)	chr22q12.1	240607_at	NR_003491
2.94	3.14	0.20	3.17E-01	6.80E-01	MCM4	minichromosome maintenance complex component 4	chr8q11.2	212142_at	NM_005914 /// NM_182746
3.66	3.84	0.18	3.17E-01	6.80E-01	IGLV1-44	immunoglobulin lambda variable 1-44	chr22q11.2	234707_x_at	---
2.17	2.30	0.13	3.17E-01	6.80E-01	KCNH8	potassium voltage-gated channel, subfamily H (eag-related), member 8	chr3p24.3	1552742_at	NM_144633
1.76	1.88	0.12	3.17E-01	6.80E-01	F11	coagulation factor XI	chr4q35	1569591_at	NM_000128
5.03	5.67	0.64	3.17E-01	6.80E-01	C21orf56	chromosome 21 open reading frame 56	chr21q22.3	223360_at	NM_032261
2.66	2.99	0.33	3.17E-01	6.80E-01	COL21A1	collagen, type XXI, alpha 1	chr6p12.3-p11.2|6p12.3-p11.2	208096_s_at	NM_030820
4.30	4.55	0.25	3.17E-01	6.80E-01	MRGPRF	MAS-related GPR, member F	chr11q13.2	227727_at	NM_001098515 /// NM_145015
2.67	2.92	0.25	3.17E-01	6.80E-01	SLC4A5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	chr2p13	1555277_a_at	NM_021196 /// NM_133478
4.88	5.13	0.25	3.18E-01	6.80E-01	H2AFY2	H2A histone family, member Y2	chr10q22	218445_at	NM_018649
4.25	4.45	0.20	3.17E-01	6.80E-01	UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	chr2q14.3	222568_at	NM_001025777 /// NM_020120
3.61	3.80	0.18	3.18E-01	6.80E-01	FOXJ1	forkhead box J1	chr17q22-q25	205906_at	NM_001454
2.75	2.92	0.17	3.18E-01	6.80E-01	KCTD7	potassium channel tetramerisation domain containing 7	chr7q11.21	1555569_a_at	NM_153033
2.76	2.92	0.16	3.17E-01	6.80E-01	---	---	---	215906_at	---
2.14	2.28	0.15	3.17E-01	6.80E-01	---	---	---	216643_at	---
2.04	2.18	0.14	3.17E-01	6.80E-01	RAB39B	RAB39B, member RAS oncogene family	chrXq28	238695_s_at	NM_171998
1.81	1.94	0.13	3.17E-01	6.80E-01	GLRA3	glycine receptor, alpha 3	chr4q33-q34	207928_s_at	NM_001042543 /// NM_006529
3.00	3.12	0.12	3.18E-01	6.80E-01	---	---	---	1557452_at	---
4.99	5.55	0.57	3.18E-01	6.80E-01	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	201862_s_at	NM_004735
7.14	7.62	0.48	3.18E-01	6.80E-01	---	---	---	226331_at	---
3.62	3.81	0.19	3.18E-01	6.80E-01	TAPT1	transmembrane anterior posterior transformation 1	chr4p15.32	216507_at	NM_153365
2.07	2.22	0.16	3.18E-01	6.80E-01	---	---	---	1568812_at	---
2.33	2.51	0.18	3.18E-01	6.80E-01	RAB27B	RAB27B, member RAS oncogene family	chr18q21.2	228708_at	NM_004163
2.80	3.01	0.21	3.18E-01	6.80E-01	---	---	---	222278_at	---
3.99	4.17	0.18	3.18E-01	6.80E-01	LOC100129722	hypothetical protein LOC100129722	chr9q34.3	238093_at	XM_001720584 /// XM_001723078 /// XM_001723633
2.20	2.33	0.13	3.18E-01	6.80E-01	---	---	---	1556921_at	---
6.14	6.55	0.42	3.18E-01	6.80E-01	MRPL42	mitochondrial ribosomal protein L42	chr12q22	222466_s_at	NM_014050 /// NM_172177 /// NM_172178
4.24	4.48	0.24	3.18E-01	6.80E-01	ELAC1	elaC homolog 1 (E. coli)	chr18q21	222869_s_at	NM_018696
2.87	3.04	0.17	3.18E-01	6.80E-01	FA2H	fatty acid 2-hydroxylase	chr16q23	234963_s_at	NM_024306
2.07	2.21	0.15	3.18E-01	6.80E-01	GULP1	GULP, engulfment adaptor PTB domain containing 1	chr2q32.3-q33	215915_at	NM_016315
2.72	2.90	0.18	3.18E-01	6.80E-01	---	---	---	233522_at	---
2.14	2.27	0.13	3.18E-01	6.80E-01	---	---	---	237893_at	---
4.04	4.35	0.31	3.18E-01	6.80E-01	USP2	ubiquitin specific peptidase 2	chr11q23.3	229337_at	NM_004205 /// NM_171997
5.83	6.07	0.23	3.18E-01	6.80E-01	---	---	---	217055_x_at	---
3.69	3.89	0.20	3.18E-01	6.80E-01	AHNAK	AHNAK nucleoprotein	chr11q12.2	220016_at	NM_001620 /// NM_024060
2.01	2.14	0.13	3.18E-01	6.80E-01	---	---	---	242014_at	---

2.71	2.85	0.14	3.18E-01	6.81E-01	TRPV6	transient receptor potential cation channel, subfamily V, member 6	chr7q33-q34	1559405_a_at	NM_018646
3.54	3.67	0.12	3.18E-01	6.81E-01	PABPC1L2A /// PABPC1L2B	poly(A) binding protein, cytoplasmic 1-like 2A /// poly(A) binding protein, cytoplasmic 1-like 2B	chrXq13.1 /// chrXq13.2	1557203_at	NM_001012977 /// NM_001042506
7.55	7.97	0.42	3.18E-01	6.81E-01	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	chr9q31.1	203505_at	NM_005502
4.94	5.15	0.21	3.18E-01	6.81E-01	ZNF598	zinc finger protein 598	chr16p13.3	232367_x_at	NM_178167
3.21	3.38	0.16	3.18E-01	6.81E-01	TMEM194B	transmembrane protein 194B	chr2q32.2	238014_at	XM_001723469 /// XM_001723498 /// XM_001726342
2.68	2.89	0.21	3.18E-01	6.81E-01	LMCD1	LIM and cysteine-rich domains 1	chr3p26-p24	242767_at	NM_014583
3.21	3.41	0.20	3.18E-01	6.81E-01	LOC284749	hypothetical protein LOC284749	chr20q13.13	236854_at	XR_041612 /// XR_041613 /// XR_041614
2.44	2.61	0.18	3.18E-01	6.81E-01	GNRHR	gonadotropin-releasing hormone receptor	chr4q21.2	216341_s_at	NM_000406 /// NM_001012763
2.40	2.55	0.15	3.18E-01	6.81E-01	WNK4	WNK lysine deficient protein kinase 4	chr17q21-q22	229158_at	NM_032387
2.89	3.06	0.18	3.18E-01	6.81E-01	IL20RA	Interleukin 20 receptor, alpha	chr6q22.33-q23.1	240396_at	NM_014432
2.54	2.65	0.11	3.18E-01	6.81E-01	PTPRS	protein tyrosine phosphatase, receptor type, S	chr19p13.3	1555666_at	NM_002850 /// NM_130853 /// NM_130854 /// NM_130855
3.29	3.51	0.22	3.18E-01	6.81E-01	KLF5	Kruppel-like factor 5 (intestinal)	chr13q22.1	209212_s_at	NM_001730
3.42	3.84	0.42	3.19E-01	6.81E-01	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)	chrXq22.3	238067_at	NM_017752 /// NM_198881
4.64	4.83	0.18	3.19E-01	6.81E-01	FUT5	fucosyltransferase 5 (alpha (1,3) fucosyltransferase)	chr19p13.3	211225_at	NM_002034
2.23	2.41	0.17	3.19E-01	6.81E-01	OSGEP	O-sialoglycoprotein endopeptidase	chr14q11.2	242930_at	NM_017807
3.30	3.44	0.14	3.19E-01	6.81E-01	---	---	---	233348_at	---
2.47	2.61	0.15	3.19E-01	6.81E-01	LOC440944	hypothetical gene supported by AK128398	chr3p25.3	1557357_at	XR_017845 /// XR_017949 /// XR_041324
7.90	8.58	0.68	3.19E-01	6.81E-01	---	---	---	213872_at	---
2.71	2.85	0.14	3.19E-01	6.81E-01	IL1F6	interleukin 1 family, member 6 (epsilon)	chr2q12-q14.1	221404_at	NM_014440
2.65	2.83	0.18	3.19E-01	6.81E-01	SLC16A3	Solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	chr17q25	213522_s_at	NM_001042422 /// NM_001042423 /// NM_004207
2.69	2.89	0.21	3.19E-01	6.81E-01	RRM2	ribonucleotide reductase M2 polypeptide	chr2p25-p24	201890_at	NM_001034
5.60	5.78	0.18	3.19E-01	6.81E-01	TFAM	transcription factor A, mitochondrial	chr10q21	208541_x_at	NM_003201
1.91	2.03	0.12	3.19E-01	6.81E-01	FCRL4	Fc receptor-like 4	chr1q21	224401_s_at	NM_031282
2.19	2.33	0.14	3.19E-01	6.81E-01	KIAA1712	KIAA1712	chr4q34	241426_at	NM_001040157
2.33	2.46	0.13	3.19E-01	6.81E-01	SLC9A3R2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	chr16p13.3	209830_s_at	NM_001130012 /// NM_004785
1.92	2.05	0.13	3.19E-01	6.81E-01	LOC728723	hypothetical LOC728723	chr5q14.1	1570204_at	XR_042120 /// XR_042121 /// XR_042122
2.38	2.54	0.16	3.19E-01	6.81E-01	KIF6	kinesin family member 6	chr6p21.2	1552538_a_at	NM_145027
2.40	2.56	0.16	3.19E-01	6.81E-01	LOC100127971	hypothetical protein LOC100127971	chr12q13.13	237790_at	XM_001720872 /// XM_001720877 /// XM_001725504
2.38	2.50	0.11	3.19E-01	6.81E-01	ZNF480	zinc finger protein 480	chr19q13.33	222283_at	NM_144684
3.54	3.72	0.19	3.19E-01	6.81E-01	DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	chrXq13.1	212727_at	NM_020730 /// NM_021120
1.91	2.06	0.15	3.19E-01	6.81E-01	C11orf65	chromosome 11 open reading frame 65	chr11q22.3	1552988_at	NM_152587
5.23	5.83	0.59	3.19E-01	6.81E-01	SRP72	signal recognition particle 72kDa	chr4q11	208800_at	NM_006947
3.77	3.88	0.11	3.19E-01	6.81E-01	FLJ12986 /// ZNF778	hypothetical protein FLJ12986 /// zinc finger protein 778	chr16q24.3	220730_at	NM_182531 /// XR_016086
5.01	5.53	0.51	3.19E-01	6.81E-01	RFWD2	ring finger and WD repeat domain 2	chr1q25.1-q25.2	1552617_a_at	NM_001001740 /// NM_022457
2.13	2.34	0.20	3.19E-01	6.81E-01	C4orf7	chromosome 4 open reading frame 7	chr4q13|4q13	229152_at	NM_152997
2.23	2.39	0.16	3.19E-01	6.81E-01	PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	chr1q23-q25	215242_at	NM_002642 /// NM_153747
2.11	2.25	0.13	3.19E-01	6.81E-01	---	---	---	1563010_at	---
2.23	2.36	0.13	3.19E-01	6.81E-01	RBMXL2	RNA binding motif protein, X-linked-like 2	chr11p15	207208_at	NM_014469
2.08	2.22	0.13	3.19E-01	6.81E-01	---	---	---	1561737_at	---

3.70	3.93	0.22	3.19E-01	6.81E-01	GAS2L3	growth arrest-specific 2 like 3	chr12q23.1	235709_at	NM_174942
2.42	2.52	0.10	3.19E-01	6.81E-01	---	---	---	231048_at	---
2.49	2.65	0.16	3.19E-01	6.81E-01	ZNF709	zinc finger protein 709	chr19p13.2	1570366_x_at	NM_152601
2.63	2.78	0.15	3.19E-01	6.81E-01	---	---	---	216692_at	---
4.09	4.38	0.29	3.19E-01	6.81E-01	BACE1	beta-site APP-cleaving enzyme 1	chr11q23.2-q23.3	224335_s_at	NM_012104 /// NM_138971 /// NM_138972 /// NM_138973
2.21	2.36	0.15	3.19E-01	6.81E-01	SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	chr22q11.2|22q11.21	205576_at	NM_000185
2.82	2.95	0.13	3.19E-01	6.81E-01	---	---	---	243973_at	---
2.47	2.60	0.13	3.19E-01	6.81E-01	---	---	---	234065_at	---
4.74	5.16	0.42	3.20E-01	6.81E-01	---	---	---	221788_at	---
2.82	3.15	0.33	3.20E-01	6.81E-01	---	---	---	216130_at	---
4.82	5.03	0.21	3.20E-01	6.81E-01	C17orf56	chromosome 17 open reading frame 56	chr17q25.3	239681_at	NM_144679
2.66	2.85	0.19	3.20E-01	6.81E-01	ZC3H3	Zinc finger CCCH-type containing 3	chr8q24.3	241056_at	NM_015117
2.08	2.25	0.18	3.20E-01	6.81E-01	---	---	---	240489_at	---
2.23	2.40	0.17	3.19E-01	6.81E-01	---	---	---	215968_at	---
6.37	6.52	0.16	3.20E-01	6.81E-01	FKSG49	FKSG49	chr5q13.3	224284_x_at	XR_041698
2.80	2.95	0.15	3.20E-01	6.81E-01	PART1	prostate androgen-regulated transcript 1	chr5q12.1	205833_s_at	XR_040430 /// XR_040431 /// XR_040432
1.94	2.06	0.12	3.19E-01	6.81E-01	LRRC7	leucine rich repeat containing 7	chr1p31.1	1552666_a_at	NM_020794
2.61	2.73	0.12	3.19E-01	6.81E-01	EDA	ectodysplasin A	chrXq12-q13.1|Xq12	211129_x_at	NM_001005609 /// NM_001005610 /// NM_001005611 /// NM_001005612 /// NM_001005615 /// NM_001399
1.97	2.08	0.12	3.19E-01	6.81E-01	KIAA1257	KIAA1257	chr3q21.3	232250_at	NM_020741
4.31	4.43	0.11	3.20E-01	6.81E-01	HCG2P7	HLA complex group 2 pseudogene 7	chr6p21.3	216229_x_at	NR_001318
3.03	3.17	0.14	3.20E-01	6.81E-01	TRPC4	transient receptor potential cation channel, subfamily C, member 4	chr13q13.1-q13.2	220818_s_at	NM_016179
1.96	2.08	0.12	3.20E-01	6.81E-01	TMEM67	transmembrane protein 67	chr8q22.1	232023_at	NM_153704
2.12	2.27	0.15	3.20E-01	6.81E-01	GABRA4	gamma-aminobutyric acid (GABA) A receptor, alpha 4	chr4p12	233437_at	NM_000809
6.52	7.00	0.48	3.20E-01	6.81E-01	SF3B1	splicing factor 3b, subunit 1, 155kDa	chr2q33.1	201070_x_at	NM_001005526 /// NM_012433
7.39	7.79	0.40	3.20E-01	6.81E-01	SEC63	SEC63 homolog (S. cerevisiae)	chr6q21	201916_s_at	NM_007214
2.65	2.83	0.18	3.20E-01	6.81E-01	MBNL3	muscleblind-like 3 (Drosophila)	chrXq26.2	219814_at	NM_018388 /// NM_133486
4.36	4.51	0.15	3.20E-01	6.81E-01	C1orf203	Chromosome 1 open reading frame 203	chr1p12	236623_at	---
1.99	2.12	0.14	3.20E-01	6.82E-01	---	---	---	234628_at	---
2.01	2.13	0.12	3.20E-01	6.82E-01	---	---	---	1556817_a_at	---
5.88	6.21	0.33	3.20E-01	6.82E-01	GOLGA4	golgi autoantigen, golgin subfamily a, 4	chr3p22-p21.3	215203_at	NM_002078
2.72	2.89	0.18	3.20E-01	6.82E-01	CCDC142	coiled-coil domain containing 142	chr2p13.1	239922_at	NM_032779
6.00	6.18	0.18	3.20E-01	6.82E-01	CLCC1	chloride channel CLIC-like 1	chr1p13.3	213628_at	NM_001048210 /// NM_015127
4.97	5.26	0.29	3.20E-01	6.82E-01	ZNF532	zinc finger protein 532	chr18q21.32	220617_s_at	NM_018181
2.20	2.39	0.19	3.20E-01	6.82E-01	RHOJ	ras homolog gene family, member J	chr14q23.2	238906_s_at	NM_020663
2.63	2.79	0.15	3.20E-01	6.82E-01	---	---	---	243919_at	---
2.14	2.27	0.13	3.20E-01	6.82E-01	PSG3	pregnancy specific beta-1-glycoprotein 3	chr19q13.2	211741_x_at	NM_021016
4.22	4.61	0.39	3.20E-01	6.82E-01	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	chr4q31.1-q31.2	213859_x_at	NM_003601
2.29	2.40	0.11	3.20E-01	6.82E-01	---	---	---	232159_at	---
2.36	2.47	0.11	3.20E-01	6.82E-01	---	---	---	1556508_s_at	---
7.89	8.20	0.31	3.20E-01	6.82E-01	PMP22	peripheral myelin protein 22	chr17p12-p11.2	210139_s_at	NM_000304 /// NM_153321 /// NM_153322
2.14	2.26	0.12	3.20E-01	6.82E-01	LOC285758	hypothetical protein LOC285758	chr6q21	1557359_at	---
2.06	2.19	0.13	3.20E-01	6.82E-01	GPR111	G protein-coupled receptor 111	chr6p12.3	1553036_at	NM_153839
2.96	3.10	0.14	3.21E-01	6.82E-01	ZSCAN20	zinc finger and SCAN domain containing 20	chr1p34.3	1552498_at	NM_145238
9.41	9.63	0.22	3.21E-01	6.82E-01	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	chr6p12	214359_s_at	NM_007355
2.74	2.91	0.17	3.21E-01	6.82E-01	---	---	---	237565_at	---
2.74	2.88	0.14	3.21E-01	6.82E-01	ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	chr16q24.1	236171_at	NM_014861
5.03	5.33	0.30	3.21E-01	6.82E-01	UTP14A /// UTP14C	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast) /// UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	chr13q14.2 /// chrXq25	221513_s_at	NM_006649 /// NM_021645
7.45	7.72	0.26	3.21E-01	6.82E-01	TAGLN2	transgelin 2	chr1q21-q25	200916_at	NM_003564

2.86	3.00	0.15	3.21E-01	6.82E-01	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	chr3q26.1	208213_s_at	NM_003471 /// NM_172159 /// NM_172160																				
6.21	6.36	0.14	3.21E-01	6.82E-01	MKRN1	makorin ring finger protein 1	chr7q34	208082_x_at	NM_013446																				
1.93	2.07	0.14	3.21E-01	6.82E-01	---	---	---	234080_at	---																				
2.58	2.70	0.12	3.21E-01	6.83E-01	LOC554174	hypothetical LOC554174	chr22q13.31	1554949_at	---																				
6.44	6.83	0.39	3.21E-01	6.83E-01	MAPK1	mitogen-activated protein kinase 1	chr22q11.2|22q11.21	212271_at	NM_002745 /// NM_138957																				
2.38	2.54	0.16	3.21E-01	6.83E-01	SIRPG	signal-regulatory protein gamma	chr20p13	220485_s_at	NM_001039508 /// NM_018556 /// NM_080816																				
7.02	7.45	0.43	3.21E-01	6.83E-01	VDAC3	voltage-dependent anion channel 3	chr8p11.2	208846_s_at	NM_005662																				
8.61	8.83	0.22	3.21E-01	6.83E-01	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	chr19q13.2-q13.3	202120_x_at	NM_004069 /// NM_021575																				
2.70	2.87	0.17	3.21E-01	6.83E-01	---	---	---	1560285_at	---																				
6.21	6.58	0.36	3.21E-01	6.83E-01	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	chr17p13.3	210317_s_at	NM_006761 /// NR_024058																				
4.85	5.05	0.20	3.21E-01	6.83E-01	---	---	---	216427_at	---																				
4.14	4.34	0.20	3.21E-01	6.83E-01	PODXL2	podocalyxin-like 2	chr3q21.3	219152_at	NM_015720																				
1.93	2.11	0.18	3.21E-01	6.83E-01	GK5	glycerol kinase 5 (putative)	chr3q23	241384_x_at	NM_001039547																				
2.88	3.04	0.17	3.21E-01	6.83E-01	---	---	---	1560474_at	---																				
2.23	2.39	0.17	3.21E-01	6.83E-01	---	---	---	242692_at	---																				
3.62	3.81	0.19	3.21E-01	6.83E-01	GK /// GK3P	glycerol kinase /// glycerol kinase 3 pseudogene	chr4q32.1 /// chrXp21.3	216316_x_at	NM_000167 /// NM_001128127 /// NM_203391																				
2.84	3.01	0.17	3.21E-01	6.83E-01	SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	chr2p16.3	205799_s_at	NM_000341																				
2.61	2.78	0.17	3.21E-01	6.83E-01	---	---	---	1554615_at	---																				
6.15	6.31	0.16	3.21E-01	6.83E-01	NUP188	nucleoporin 188kDa	chr9q34.11	212691_at	NM_015354																				
6.80	6.96	0.16	3.21E-01	6.83E-01	SPN	sialophorin	chr16p11.2	206056_x_at	NM_001030288 /// NM_003123																				
2.07	2.23	0.16	3.21E-01	6.83E-01	---	---	---	1561554_at	---																				
2.86	3.02	0.16	3.21E-01	6.83E-01	PML	promyelocytic leukemia	chr15q22	209640_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250																				
4.47	4.62	0.15	3.21E-01	6.83E-01	---	---	---	81737_at	---																				
5.47	5.64	0.17	3.21E-01	6.83E-01	---	---	---	1567985_at	---																				
2.11	2.26	0.16	3.21E-01	6.83E-01	PTH2R	parathyroid hormone 2 receptor	chr2q33	206772_at	NM_005048																				
2.78	2.93	0.15	3.21E-01	6.83E-01	SLC25A42	solute carrier family 25, member 42	chr19p13.11	228921_at	NM_178526																				
2.41	2.56	0.15	3.21E-01	6.83E-01	---	---	---	234328_at	---																				
2.08	2.22	0.14	3.21E-01	6.83E-01	ZNF770	zinc finger protein 770	chr15q14	238687_x_at	NM_014106																				
2.47	2.68	0.22	3.22E-01	6.83E-01	KCNMB2	potassium large conductance calcium-activated channel, subfamily M, beta member 2	chr3q26.2-q27.1	221097_s_at	NM_005832 /// NM_181361																				
3.01	3.22	0.21	3.22E-01	6.83E-01	PCDHA3	protocadherin alpha 3	chr5q31	211870_s_at	NM_018906 /// NM_031497																				
3.04	3.17	0.13	3.22E-01	6.83E-01	LOC100129884	Hypothetical protein LOC100129884	chr13q22.1	236560_at	XM_001718836 /// XM_001722013 /// XM_001723940																				
5.24	5.45	0.22	3.22E-01	6.83E-01	---	---	---	232670_at	---																				
1.96	2.07	0.11	3.22E-01	6.83E-01	C18orf21	Chromosome 18 open reading frame 21	chr18q12.2	1558990_at	NM_031446																				
1.73	1.84	0.11	3.22E-01	6.83E-01	LOC642426	hypothetical LOC642426	chr14q11.1	1562223_at	XR_041385																				
2.05	2.24	0.19	3.22E-01	6.83E-01	LOC553137	Hypothetical LOC553137	chr6q21	237888_at	NR_015365 /// XR_001059 /// XR_001268																				

2.22	2.37	0.15	3.22E-01	6.83E-01	SF1	splicing factor 1	chr11q13	1555749_at	NM_004630 /// NM_201995 /// NM_201997 /// NM_201998
2.29	2.41	0.12	3.22E-01	6.83E-01	---	---	---	237017_s_at	---
1.92	2.02	0.10	3.22E-01	6.83E-01	FRRS1	ferric-chelate reductase 1	chr1p21.2	1570207_at	NM_001013660
2.35	2.56	0.22	3.22E-01	6.83E-01	---	---	---	1562059_at	---
4.29	4.46	0.17	3.22E-01	6.83E-01	ASB2	ankyrin repeat and SOCS box-containing 2	chr14q31-q32	227915_at	NM_016150
3.50	3.73	0.23	3.22E-01	6.83E-01	STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	chr15q24.1	221701_s_at	NM_022369
3.68	3.90	0.22	3.22E-01	6.83E-01	ARID4A	AT rich interactive domain 4A (RBP1-like)	chr14q23.1	205062_x_at	NM_002892 /// NM_023000 /// NM_023001
2.31	2.47	0.16	3.22E-01	6.83E-01	---	---	---	237757_at	---
2.47	2.65	0.18	3.22E-01	6.83E-01	NGDN	neuroguidin, EIF4E binding protein	chr14q11.2	216263_s_at	NM_001042635 /// NM_015514
4.30	4.79	0.49	3.22E-01	6.83E-01	---	---	---	229074_at	---
7.02	7.41	0.39	3.22E-01	6.83E-01	IPO5	importin 5	chr13q32.2	211955_at	NM_002271
2.33	2.53	0.20	3.22E-01	6.83E-01	---	---	---	235018_at	---
3.28	3.46	0.18	3.22E-01	6.83E-01	C11orf66	chromosome 11 open reading frame 66	chr11q12.2	235402_at	NM_145017
2.27	2.42	0.16	3.22E-01	6.83E-01	CASC2	cancer susceptibility candidate 2	chr10q26.11	239713_at	XR_041332 /// XR_041333 /// XR_041334
1.99	2.14	0.15	3.22E-01	6.83E-01	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	chr18q11-q12	205856_at	NM_001128588 /// NM_015865
2.28	2.41	0.14	3.22E-01	6.83E-01	LOC150577	hypothetical protein LOC150577	chr2q11.2	1563679_at	XR_041752 /// XR_041753 /// XR_041754
4.52	4.72	0.20	3.22E-01	6.83E-01	LOC729623 /// PRKAR1B	similar to protein kinase, cAMP-dependent, regulatory, type I, beta /// protein kinase, cAMP-dependent, regulatory, type I, beta	chr7p22	212559_at	NM_002735 /// XM_001716155
2.56	2.72	0.16	3.22E-01	6.83E-01	PRSS21	protease, serine, 21 (testisin)	chr16p13.3	220051_at	NM_006799 /// NM_144956 /// NM_144957
2.00	2.15	0.15	3.22E-01	6.83E-01	HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	chr1p34	233884_at	NM_001127714 /// NM_024503
7.08	7.48	0.40	3.22E-01	6.84E-01	AEBP1	AE binding protein 1	chr7p13	201792_at	NM_001129
4.55	4.85	0.29	3.22E-01	6.84E-01	---	---	---	235427_at	---
2.99	3.19	0.21	3.23E-01	6.84E-01	---	---	---	236946_at	---
3.35	3.54	0.20	3.22E-01	6.84E-01	NSMAF	Neutral sphingomyelinase (N-SMase) activation associated factor	chr8q12-q13	240056_at	NM_003580
3.56	3.76	0.20	3.23E-01	6.84E-01	---	---	---	233612_at	---
2.48	2.63	0.15	3.23E-01	6.84E-01	---	---	---	1561067_at	---
2.39	2.52	0.13	3.22E-01	6.84E-01	RTP3	receptor (chemosensory) transporter protein 3	chr3p21.3	1552569_a_at	NM_031440
2.40	2.53	0.13	3.23E-01	6.84E-01	HOMEZ	homeobox and leucine zipper encoding	chr14q11.2	231868_at	NM_020834
2.03	2.14	0.11	3.23E-01	6.84E-01	HBS1L	HBS1-like (S. cerevisiae)	chr6q23-q24	240602_at	NM_006620
2.80	3.04	0.24	3.23E-01	6.84E-01	HSDL2	hydroxysteroid dehydrogenase like 2	chr9q32	1559128_at	NM_032303
2.29	2.43	0.14	3.23E-01	6.84E-01	---	---	---	236394_at	---
1.93	2.04	0.11	3.23E-01	6.84E-01	---	---	---	207875_at	---
5.53	5.78	0.25	3.23E-01	6.84E-01	ATF7IP	activating transcription factor 7 interacting protein	chr12p13.1	218987_at	NM_018179
5.78	6.05	0.26	3.23E-01	6.84E-01	TBXA2R	thromboxane A2 receptor	chr19p13.3	207554_x_at	NM_001060 /// NM_201636
2.40	2.64	0.24	3.23E-01	6.84E-01	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	chr2q23.3-q24.1	234472_at	NM_052917
2.32	2.45	0.13	3.23E-01	6.84E-01	---	---	---	224545_at	---
6.03	6.41	0.39	3.23E-01	6.84E-01	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	chr1p31.1-p22.1	203285_s_at	NM_001134492 /// NM_012262
6.43	6.77	0.34	3.23E-01	6.84E-01	ABHD2	abhydrolase domain containing 2	chr15q26.1	221815_at	NM_007011 /// NM_152924
2.64	2.76	0.13	3.23E-01	6.84E-01	LOC100132861	Hypothetical protein LOC100132861	chr4p14	235943_at	XM_001714011 /// XM_001716443 /// XM_001717227
4.67	5.14	0.47	3.23E-01	6.84E-01	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	chr11q23	211368_s_at	NM_001223 /// NM_033292 /// NM_033293 /// NM_033294 /// NM_033295

2.13	2.32	0.19	3.23E-01	6.84E-01	---	---	---	234789_at	---
7.53	7.67	0.14	3.23E-01	6.84E-01	C14orf153	Chromosome 14 open reading frame 153	chr14q32.33	232814_x_at	NM_032374
2.29	2.43	0.14	3.23E-01	6.84E-01	GPR135	G protein-coupled receptor 135	chr14q23.1	214503_x_at	NM_022571
7.23	7.51	0.28	3.23E-01	6.84E-01	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	chr11q23.3	225549_at	NM_004397
3.75	3.89	0.14	3.23E-01	6.84E-01	---	---	---	236806_at	---
2.87	3.01	0.14	3.23E-01	6.84E-01	HBE1	hemoglobin, epsilon 1	chr11p15.5	205919_at	NM_005330
2.26	2.43	0.17	3.23E-01	6.84E-01	---	---	---	1568869_at	---
4.81	4.96	0.16	3.23E-01	6.84E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	238618_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833
2.55	2.69	0.14	3.23E-01	6.84E-01	CHRNA4	cholinergic receptor, nicotinic, alpha 4	chr20q13.2-q13.3	216900_s_at	NM_000744
3.18	3.38	0.20	3.23E-01	6.84E-01	SIGLEC10	sialic acid binding Ig-like lectin 10	chr19q13.3	1552806_a_at	NM_033130
3.44	3.59	0.16	3.23E-01	6.84E-01	TMEM196	transmembrane protein 196	chr7p15.3	1552293_at	NM_152774
4.31	4.56	0.25	3.23E-01	6.84E-01	CSRP2BP	CSRP2 binding protein	chr20p11.23	233396_s_at	NM_020536 /// NM_177926
2.96	3.17	0.21	3.23E-01	6.84E-01	---	---	---	238133_at	---
6.59	6.84	0.26	3.23E-01	6.84E-01	IPO13	importin 13	chr1p34.1	203546_at	NM_014652
4.84	5.35	0.51	3.23E-01	6.84E-01	NAT13	N-acetyltransferase 13	chr3q13.2	222393_s_at	NM_025146
2.44	2.59	0.15	3.23E-01	6.84E-01	NR2F6	Nuclear receptor subfamily 2, group F, member 6	chr19p13.1	213354_s_at	NM_005234
2.15	2.28	0.13	3.23E-01	6.84E-01	SCLT1	sodium channel and clathrin linker 1	chr4q28.2	1569495_at	NM_144643
2.73	2.84	0.11	3.23E-01	6.84E-01	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	chr13q34	231023_at	NM_024537
2.20	2.34	0.14	3.23E-01	6.84E-01	DLX4	distal-less homeobox 4	chr17q21.33	210259_s_at	NM_001934 /// NM_138281
3.69	3.92	0.23	3.23E-01	6.84E-01	TRIB3	tribbles homolog 3 (Drosophila)	chr20p13-p12.2	1555788_a_at	NM_021158
2.40	2.53	0.13	3.23E-01	6.84E-01	---	---	---	242454_at	---
3.18	3.40	0.21	3.24E-01	6.84E-01	ZNF347	zinc finger protein 347	chr19q13.41	238819_at	NM_032584
2.23	2.33	0.10	3.24E-01	6.84E-01	---	---	---	244387_at	---
2.43	2.58	0.15	3.24E-01	6.84E-01	RAB37	RAB37, member RAS oncogene family	chr17q25.1	228113_at	NM_001006638 /// NM_175738
2.24	2.36	0.12	3.24E-01	6.84E-01	RTKN2	rhotekin 2	chr10q21.2	242047_at	NM_145307
4.56	5.35	0.79	3.24E-01	6.85E-01	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	chr8p11.23	1555326_a_at	NM_001005845 /// NM_003816
7.22	7.65	0.43	3.24E-01	6.85E-01	UBE4A	ubiquitination factor E4A (UFD2 homolog, yeast)	chr11q23.3	202038_at	NM_004788
8.05	8.35	0.30	3.24E-01	6.85E-01	MRPS22	mitochondrial ribosomal protein S22	chr3q23	219220_x_at	NM_020191
5.62	5.91	0.29	3.24E-01	6.85E-01	FKBP8	FK506 binding protein 8, 38kDa	chr19p12	208255_s_at	NM_012181
5.58	5.84	0.26	3.24E-01	6.85E-01	SOCS5	suppressor of cytokine signaling 5	chr2p21	209648_x_at	NM_014011 /// NM_144949
3.03	3.28	0.25	3.24E-01	6.85E-01	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16q22-q23	227312_at	NM_006750
3.84	4.09	0.25	3.24E-01	6.85E-01	FBXW4P1	F-box and WD repeat domain containing 4 pseudogene 1	chr22q11	214623_at	---
3.20	3.34	0.14	3.24E-01	6.85E-01	FOXD3	Forkhead box D3	chr1p32-p31	241609_at	NM_012183
2.39	2.51	0.13	3.24E-01	6.85E-01	---	---	---	1566419_at	---
3.01	3.14	0.13	3.24E-01	6.85E-01	SLC45A3	solute carrier family 45, member 3	chr1q32.1	238499_at	NM_033102
2.72	2.88	0.16	3.24E-01	6.85E-01	FUT2	fucosyltransferase 2 (secretor status included)	chr19q13.3	210608_s_at	NM_000511 /// NM_001097638
2.14	2.27	0.13	3.24E-01	6.85E-01	---	---	---	233444_at	---
2.54	2.67	0.13	3.24E-01	6.85E-01	---	---	---	1562476_at	---
2.74	2.99	0.25	3.24E-01	6.85E-01	---	---	---	231471_at	---
2.20	2.37	0.17	3.24E-01	6.85E-01	NEDD1	neural precursor cell expressed, developmentally down-regulated 1	chr12q23.1	1552417_a_at	NM_152905
3.57	3.74	0.17	3.24E-01	6.85E-01	CCDC19	coiled-coil domain containing 19	chr1q22	220308_at	NM_012337
2.07	2.21	0.14	3.24E-01	6.85E-01	---	---	---	1566030_at	---
3.31	3.52	0.21	3.24E-01	6.85E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	211182_x_at	NM_001001890 /// NM_001122607 /// NM_001754
2.05	2.18	0.14	3.24E-01	6.85E-01	---	---	---	241312_at	---
5.29	5.75	0.45	3.24E-01	6.85E-01	FBLN2	fibulin 2	chr3p25.1	203886_s_at	NM_001004019 /// NM_001998
3.70	3.93	0.23	3.24E-01	6.85E-01	NKAIN4	Na+/K+ transporting ATPase interacting 4	chr20q13.33	230668_at	NM_152864
4.42	4.60	0.18	3.24E-01	6.85E-01	LOC374569	Similar to Lysophospholipase	chr14q32.33	1557226_a_at	NM_001080464
2.09	2.20	0.11	3.24E-01	6.85E-01	---	---	---	1565637_at	---

4.08	4.39	0.32	3.25E-01	6.85E-01	RBM47	RNA binding motif protein 47	chr4p13-p12	229440_at	NM_001098634 /// NM_019027
3.49	3.68	0.19	3.25E-01	6.85E-01	---	---	---	1564498_at	---
2.81	2.98	0.18	3.25E-01	6.85E-01	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	chr4q21.1	207073_at	NM_003948
4.06	4.21	0.15	3.25E-01	6.85E-01	---	---	---	222973_at	---
1.89	2.00	0.11	3.25E-01	6.85E-01	---	---	---	234138_at	---
4.36	4.65	0.28	3.25E-01	6.85E-01	NELF	nasal embryonic LHRH factor	chr9q34.3	221214_s_at	NM_001130969 /// NM_001130970 /// NM_001130971 /// NM_015537
2.51	2.67	0.16	3.25E-01	6.85E-01	MRPS31	mitochondrial ribosomal protein S31	chr13q14.11	243821_at	NM_005830
2.46	2.60	0.14	3.25E-01	6.85E-01	KCNG1	potassium voltage-gated channel, subfamily G, member 1	chr20q13	214595_at	NM_002237 /// NM_172318
2.26	2.39	0.13	3.25E-01	6.85E-01	---	---	---	234550_at	---
10.95	11.26	0.30	3.25E-01	6.86E-01	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	chr10p15.1	213366_x_at	NM_001001973 /// NM_005174
3.77	3.98	0.21	3.25E-01	6.86E-01	KRT82	keratin 82	chr12q13	233158_at	NM_033033
2.95	3.13	0.18	3.25E-01	6.86E-01	JAKMIP1	janus kinase and microtubule interacting protein 1	chr4p16.1	238600_at	NM_001099433 /// NM_144720
2.15	2.29	0.14	3.25E-01	6.86E-01	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	chr2q24.1	240390_at	NM_014568
2.01	2.14	0.14	3.25E-01	6.86E-01	RPESP	RPE-spondin	chr8q21.11	214725_at	NM_153225
2.76	2.89	0.13	3.25E-01	6.86E-01	FLJ39582	hypothetical LOC439931	chr22q11.21	236403_at	---
2.54	2.65	0.11	3.25E-01	6.86E-01	HKDC1	hexokinase domain containing 1	chr10q21.3	220585_at	NM_025130
2.01	2.11	0.11	3.25E-01	6.86E-01	VNN3	vanin 3	chr6q23-q24	1553513_at	NM_001024460 /// NM_018399 /// NM_078625
3.79	3.98	0.19	3.25E-01	6.86E-01	UBIAD1	UbiA prenyltransferase domain containing 1	chr1p36-p34.1	230474_at	NM_013319
4.62	4.78	0.16	3.25E-01	6.86E-01	ADRB3	adrenergic, beta-3-, receptor	chr8p12-p11.2	217303_s_at	NM_000025
4.04	4.18	0.14	3.25E-01	6.86E-01	---	---	---	241958_at	---
2.35	2.47	0.12	3.25E-01	6.86E-01	---	---	---	236789_at	---
2.86	3.06	0.19	3.25E-01	6.86E-01	PTPN13	Protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	chr4q21.3	243792_x_at	NM_006264 /// NM_080683 /// NM_080684 /// NM_080685
2.72	2.86	0.14	3.25E-01	6.86E-01	---	---	---	207572_at	---
2.10	2.24	0.13	3.25E-01	6.86E-01	---	---	---	1563312_at	---
1.83	1.94	0.11	3.25E-01	6.86E-01	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	chr5q12	210837_s_at	NM_001104631 /// NM_006203
3.82	3.97	0.15	3.25E-01	6.86E-01	OXT	oxytocin, prepropeptide	chr20p13	207576_x_at	NM_000915
7.82	8.24	0.42	3.26E-01	6.86E-01	TM9SF3	transmembrane 9 superfamily member 3	chr10q24.1	222399_s_at	NM_020123
2.15	2.29	0.14	3.26E-01	6.86E-01	NR1H4	nuclear receptor subfamily 1, group H, member 4	chr12q23.1	243800_at	NM_005123
3.14	3.31	0.17	3.26E-01	6.86E-01	MCPH1	microcephalin 1	chr8p23.1	232243_at	NM_024596
2.34	2.48	0.14	3.26E-01	6.86E-01	PBRM1	polybromo 1	chr3p21	223399_x_at	NM_018165 /// NM_018313 /// NM_181042
1.97	2.11	0.14	3.26E-01	6.86E-01	IQCF1	IQ motif containing F1	chr3p21.1	1555001_at	NM_152397
1.94	2.06	0.12	3.26E-01	6.86E-01	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	chr15q22	240702_at	NM_003922
3.05	3.51	0.47	3.26E-01	6.86E-01	CDC40	cell division cycle 40 homolog (S. cerevisiae)	chr6q21	203377_s_at	NM_015891
2.13	2.32	0.19	3.26E-01	6.86E-01	---	---	---	1556964_s_at	---
6.32	6.67	0.35	3.26E-01	6.86E-01	ZCCHC24	zinc finger, CCHC domain containing 24	chr10q22.3	212423_at	NM_153367
4.57	4.85	0.28	3.26E-01	6.86E-01	TMEM86A	transmembrane protein 86A	chr11p15.1	242103_at	NM_153347
3.45	3.71	0.26	3.26E-01	6.86E-01	NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	chr5q21.2	223535_at	NM_031438
3.73	3.97	0.24	3.26E-01	6.86E-01	PFTK2	PFTAIRE protein kinase 2	chr2q33.2	239201_at	NM_139158
4.21	4.37	0.16	3.26E-01	6.86E-01	---	---	---	1556937_at	---
2.03	2.17	0.14	3.26E-01	6.86E-01	UBASH3B	ubiquitin associated and SH3 domain containing, B	chr11q24.1	238462_at	NM_032873
8.40	8.59	0.19	3.26E-01	6.87E-01	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	chr22q11.23	224932_at	NM_213720
2.10	2.23	0.12	3.26E-01	6.87E-01	LOC100131860	hypothetical protein LOC100131860	chr15q25.2	1559180_at	XM_001716100 /// XM_001720646 /// XM_001720708
3.85	4.12	0.26	3.26E-01	6.87E-01	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	chr3q26.32-q26.33	223488_s_at	NM_021629

5.54	6.33	0.79	3.26E-01	6.87E-01	LOC730200	Hypothetical LOC730200	chr2p14	233249_at	XM_001132901 /// XM_001133006 /// XM_001719237																				
7.04	7.35	0.32	3.26E-01	6.87E-01	PCM1	pericentriolar material 1	chr8p22-p21.3	214937_x_at	NM_006197																				
10.51	10.71	0.20	3.26E-01	6.87E-01	MRFAP1	Mof4 family associated protein 1	chr4p16.1	226091_s_at	NM_033296																				
6.53	6.71	0.18	3.26E-01	6.87E-01	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	chr17q11.1-q11.2	202840_at	NM_003487 /// NM_139215																				
5.12	5.27	0.15	3.26E-01	6.87E-01	---	---	---	238812_at	---																				
2.49	2.64	0.14	3.26E-01	6.87E-01	LOC145757	hypothetical LOC145757	chr15q26.3	1558649_at	XR_040806 /// XR_040807 /// XR_040808																				
1.94	2.08	0.14	3.26E-01	6.87E-01	EIF4E3	eukaryotic translation initiation factor 4E family member 3	chr3p14	225939_at	NM_001134649 /// NM_001134650 /// NM_001134651 /// NM_173359																				
2.37	2.50	0.13	3.26E-01	6.87E-01	---	---	---	243658_at	---																				
2.91	3.06	0.14	3.26E-01	6.87E-01	---	---	---	219776_s_at	---																				
2.82	2.97	0.15	3.26E-01	6.87E-01	OR5L2	olfactory receptor, family 5, subfamily L, member 2	chr11q11	1567286_at	NM_001004739																				
2.35	2.50	0.15	3.26E-01	6.87E-01	---	---	---	234262_at	---																				
4.70	4.84	0.14	3.26E-01	6.87E-01	CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	chr16q22.3	221164_x_at	NM_024533																				
2.02	2.13	0.11	3.26E-01	6.87E-01	TRPC5	transient receptor potential cation channel, subfamily C, member 5	chrXq23	220552_at	NM_012471																				
5.96	6.36	0.39	3.26E-01	6.87E-01	---	---	---	242022_at	---																				
2.79	2.92	0.13	3.26E-01	6.87E-01	---	---	---	233352_at	---																				
2.09	2.23	0.14	3.26E-01	6.87E-01	DST	Dystonin	chr6p12.1	215814_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380																				
4.25	4.74	0.49	3.27E-01	6.87E-01	DNM3	dynamin 3	chr1q24.3	209839_at	NM_015569																				
2.13	2.23	0.10	3.27E-01	6.87E-01	---	---	---	1557598_at	---																				
2.19	2.35	0.15	3.27E-01	6.87E-01	SLITRK6	SLIT and NTRK-like family, member 6	chr13q31.1	232176_at	NM_032229																				
4.24	4.50	0.26	3.27E-01	6.87E-01	SMAD2	SMAD family member 2	chr18q21.1	235598_at	NM_001003652 /// NM_005901																				
4.06	4.31	0.25	3.27E-01	6.87E-01	SAMD10	sterile alpha motif domain containing 10	chr20q13.33	233001_at	NM_080621																				
6.22	6.43	0.21	3.27E-01	6.87E-01	TMEM63B	transmembrane protein 63B	chr6p21.1	225271_at	NM_018426																				
5.67	5.86	0.19	3.27E-01	6.87E-01	TOX4	TOX high mobility group box family member 4	chr14q11.2	232097_at	NM_014828																				
1.75	1.88	0.13	3.27E-01	6.87E-01	SCEL	sciellin	chr13q22	1554921_a_at	NM_003843 /// NM_144777																				
1.74	1.86	0.12	3.27E-01	6.87E-01	---	---	---	1561644_x_at	---																				
2.06	2.17	0.11	3.27E-01	6.87E-01	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	chr3q25.2	207455_at	NM_002563																				
5.70	6.00	0.30	3.27E-01	6.87E-01	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	chr17q11.2	224938_at	NM_020772																				
9.35	9.51	0.16	3.27E-01	6.87E-01	PGK1	phosphoglycerate kinase 1	chrXq13	217356_s_at	NM_000291																				
5.56	6.11	0.55	3.27E-01	6.87E-01	PPP2R3C	protein phosphatase 2 (formerly 2A), regulatory subunit B", gamma	chr14q13.2	218852_at	NM_017917																				
2.42	2.60	0.18	3.27E-01	6.87E-01	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	chr6p22-p21	229386_at	NM_001546																				
3.89	4.15	0.26	3.27E-01	6.87E-01	GPHN	gephyrin	chr14q23.3	223319_at	NM_001024218 /// NM_020806																				
1.94	2.12	0.18	3.27E-01	6.87E-01	---	---	---	1568935_at	---																				
2.24	2.41	0.17	3.27E-01	6.87E-01	ZNF624	zinc finger protein 624	chr17p11.2	232272_at	NM_020787																				
1.90	2.02	0.12	3.27E-01	6.87E-01	---	---	---	244705_at	---																				
2.14	2.26	0.12	3.27E-01	6.87E-01	ANGPTL3	angiopoietin-like 3	chr1p31.1-p22.3	219803_at	NM_014495																				
2.22	2.34	0.12	3.27E-01	6.88E-01	---	---	---	217648_at	---																				
5.08	5.22	0.14	3.27E-01	6.88E-01	HNF4A	hepatocyte nuclear factor 4, alpha	chr20q12-q13.1	216889_s_at	NM_000457 /// NM_001030003 /// NM_001030004 /// NM_175914 /// NM_178849 /// NM_178850																				
3.59	3.92	0.32	3.27E-01	6.88E-01	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	chr17q11.2	209924_at	NM_002988																				
3.31	3.53	0.22	3.27E-01	6.88E-01	HSF1	heat shock transcription factor 1	chr8q24.3	213756_s_at	NM_005526																				
2.38	2.56	0.19	3.27E-01	6.88E-01	---	---	---	234553_at	---																				
2.14	2.32	0.18	3.27E-01	6.88E-01	MUC15	mucin 15, cell surface associated	chr11p14.3	227238_at	NM_145650																				
2.44	2.60	0.16	3.27E-01	6.88E-01	---	---	---	234250_at	---																				

3.05	3.21	0.15	3.27E-01	6.88E-01	LOC100129951 /// LOC100134638	hypothetical protein LOC100129951 /// hypothetical protein LOC100134638	chr7q36.3	242035_at	XM_001714763 /// XM_001715187 /// XM_001715862 /// XM_001719382
2.44	2.64	0.20	3.27E-01	6.88E-01	---	---	---	1566923_at	---
2.58	2.77	0.19	3.27E-01	6.88E-01	---	---	---	241093_at	---
2.57	2.75	0.18	3.27E-01	6.88E-01	---	---	---	244573_at	---
2.05	2.18	0.13	3.27E-01	6.88E-01	KIAA0999	KIAA0999 protein	chr11q23.3	1554929_at	NM_025164
3.29	3.54	0.25	3.28E-01	6.88E-01	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	chr2p25.1-p24.1	205801_s_at	NM_170672
12.38	12.55	0.17	3.28E-01	6.88E-01	EEF1A1 /// EEF1AL7 /// LOC100130211 /// LOC100132804 /// LOC389223 /// LOC401717 /// LOC645693 /// LOC645715 /// LOC728672	eukaryotic translation elongation factor 1 alpha 1 /// eukaryotic translation elongation factor 1 alpha-like 7 /// similar to translation elongation factor 1 alpha 1-like 14 /// hypothetical LOC100132804 /// similar to eukaryotic translation elongation factor 1 alpha 1 /// hypothetical LOC401717 /// hypothetical LOC645693 /// similar to hCG2043493 /// similar to hCG2043493	chr12p12.3 /// chr12q12 /// chr15q21.2 /// chr3p22.1 /// chr4q24 /// chr4q28.3 /// chr6q14.1 /// chr7q35 /// chrXq21.2	213583_x_at	NM_001402 /// NR_003586 /// XM_001716082 /// XM_001716448 /// XM_001717632 /// XR_015580 /// XR_015858 /// XR_016218 /// XR_017484 /// XR_017498 /// XR_017535 /// XR_018189 /// XR_018499 /// XR_019434 /// XR_037010 /// XR_037093 /// XR_038193 /// XR_038221 /// XR_038883 /// XR_039223 /// XR_039272 /// XR_039454 /// XR_039672
3.36	3.52	0.17	3.28E-01	6.88E-01	SS18	synovial sarcoma translocation, chromosome 18	chr18q11.2	217051_s_at	NM_001007559 /// NM_005637
2.04	2.19	0.15	3.28E-01	6.88E-01	---	---	---	1559835_at	---
3.56	4.07	0.50	3.28E-01	6.88E-01	DPT	dermatopontin	chr1q12-q23	213068_at	NM_001937
6.31	6.46	0.16	3.28E-01	6.88E-01	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3	chr7q32.3-q33	217972_at	NM_017812
2.59	2.76	0.16	3.28E-01	6.88E-01	LOC100101117 /// TTTY2	testis-specific transcript, Y-linked 2-like /// testis-specific transcript, Y-linked 2	chrYp11.2	217261_at	NR_001536 /// NR_003590
1.97	2.14	0.16	3.28E-01	6.88E-01	RP1-127L4.6	hypothetical protein LOC150297	chr22q12.3	1555991_s_at	NM_001010859
2.03	2.15	0.12	3.28E-01	6.88E-01	LIPJ	lipase, family member J	chr10q23.31	1569874_s_at	NM_001010939
2.75	2.86	0.12	3.28E-01	6.88E-01	MACROD2	MACRO domain containing 2	chr20p12.1	1553564_at	NM_001033087 /// NM_080676
3.23	3.41	0.18	3.28E-01	6.88E-01	---	---	---	230710_at	---
2.46	2.61	0.15	3.28E-01	6.88E-01	CAT	Catalase	chr11p13	215573_at	NM_001752
2.54	2.76	0.22	3.28E-01	6.88E-01	---	---	---	1557077_a_at	---
2.20	2.34	0.15	3.28E-01	6.88E-01	ZNF254	zinc finger protein 254	chr19p12	206862_at	NM_203282
3.73	3.86	0.14	3.28E-01	6.88E-01	---	---	---	230423_at	---
7.01	7.65	0.63	3.28E-01	6.88E-01	DPP8	dipeptidyl-peptidase 8	chr15q22	220939_s_at	NM_017743 /// NM_130434 /// NM_197960 /// NM_197961
5.34	5.83	0.49	3.28E-01	6.88E-01	---	---	---	242853_at	---
3.57	3.85	0.28	3.28E-01	6.88E-01	ZNF281	zinc finger protein 281	chr1q32.1	218401_s_at	NM_012482
4.24	4.49	0.25	3.28E-01	6.88E-01	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	chr19p13.3	209414_at	NM_016263
2.36	2.55	0.19	3.28E-01	6.88E-01	---	---	---	231245_s_at	---
3.37	3.54	0.17	3.28E-01	6.88E-01	---	---	---	216668_at	---
2.39	2.54	0.15	3.28E-01	6.88E-01	PLA2G2F	phospholipase A2, group IIF	chr1p35	221416_at	NM_022819
2.20	2.34	0.14	3.28E-01	6.88E-01	---	---	---	243775_at	---
2.14	2.28	0.14	3.28E-01	6.88E-01	---	---	---	234041_at	---
3.82	4.49	0.67	3.28E-01	6.88E-01	PRRX1	paired related homeobox 1	chr1q24	205991_s_at	NM_006902 /// NM_022716
2.40	2.60	0.19	3.28E-01	6.88E-01	---	---	---	239851_at	---
2.67	2.86	0.19	3.28E-01	6.88E-01	SNRK	SNF related kinase	chr3p22.1	1564514_at	NM_001100594 /// NM_017719

2.44	2.57	0.13	3.28E-01	6.88E-01	DCUN1D3 /// EXOD1	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) /// exonuclease domain containing 1	chr16p12.2	240604_at	NM_080663 /// NM_173475																					
2.04	2.16	0.12	3.28E-01	6.88E-01	---	---	---	1560533_at	---																					
4.65	5.01	0.36	3.28E-01	6.88E-01	CNOT10	CCR4-NOT transcription complex, subunit 10	chr3p22.3	223219_s_at	NM_015442																					
3.61	3.81	0.20	3.28E-01	6.88E-01	CD99L2	CD99 molecule-like 2	chrXq28	233844_at	NM_031462 /// NM_134445 /// NM_134446																					
2.13	2.31	0.18	3.28E-01	6.88E-01	CASC5	cancer susceptibility candidate 5	chr15q14	220247_at	NM_144508 /// NM_170589																					
3.55	3.73	0.18	3.28E-01	6.88E-01	C9orf131	chromosome 9 open reading frame 131	chr9p13.3	230985_at	NM_001040410 /// NM_001040411 /// NM_001040412 /// NM_203299																					
2.58	2.72	0.14	3.28E-01	6.88E-01	---	---	---	233529_at	---																					
1.85	1.97	0.12	3.28E-01	6.88E-01	STXBP4	syntaxin binding protein 4	chr17q22	1554329_x_at	NM_178509																					
1.92	2.03	0.11	3.28E-01	6.88E-01	KCNRG	potassium channel regulator	chr13q14.3	240288_at	NM_173605 /// NM_199464																					
2.19	2.29	0.11	3.28E-01	6.88E-01	MAOB	Monoamine oxidase B	chrXp11.23	1561009_at	NM_000898																					
1.89	2.00	0.11	3.28E-01	6.88E-01	DENR	density-regulated protein	chr12q24.31	238982_at	NM_003677																					
6.94	7.13	0.19	3.28E-01	6.88E-01	FXR2	fragile X mental retardation, autosomal homolog 2	chr17p13.1	203172_at	NM_004860																					
2.09	2.20	0.11	3.28E-01	6.88E-01	---	---	---	1566938_at	---																					
5.94	6.32	0.39	3.29E-01	6.88E-01	MAP2K4	mitogen-activated protein kinase kinase 4	chr17p11.2	203266_s_at	NM_003010																					
5.89	6.56	0.67	3.29E-01	6.88E-01	---	---	---	235112_at	---																					
6.68	7.00	0.31	3.29E-01	6.88E-01	OSBPL8	oxysterol binding protein-like 8	chr12q14	212585_at	NM_001003712 /// NM_020841																					
4.88	5.10	0.22	3.29E-01	6.88E-01	---	---	---	221861_at	---																					
2.88	3.05	0.18	3.29E-01	6.88E-01	---	---	---	235608_at	---																					
2.50	2.68	0.18	3.29E-01	6.88E-01	VPS13A	Vacuolar protein sorting 13 homolog A (S. cerevisiae)	chr9q21	231585_at	NM_001018037 /// NM_001018038 /// NM_015186 /// NM_033305																					
2.20	2.31	0.11	3.29E-01	6.88E-01	RAB3C	RAB3C, member RAS oncogene family	chr5q13	242328_at	NM_138453																					
2.72	2.88	0.16	3.29E-01	6.88E-01	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	chr19p13.2-p13.1	210770_s_at	NM_000068 /// NM_001127221 /// NM_001127222 /// NM_023035																					
2.54	2.67	0.13	3.29E-01	6.88E-01	PIGR	polymeric immunoglobulin receptor	chr1q31-q41	226147_s_at	NM_002644																					
3.40	3.65	0.25	3.29E-01	6.88E-01	XIST	X (inactive)-specific transcript (non-protein coding)	chrXq13.2	243712_at	NR_001564																					
6.26	6.60	0.33	3.29E-01	6.89E-01	PARP9	poly (ADP-ribose) polymerase family, member 9	chr3q13-q21	223220_s_at	NM_031458																					
6.14	6.60	0.46	3.29E-01	6.89E-01	S100A8	S100 calcium binding protein A8	chr1q21	202917_s_at	NM_002964																					
2.65	2.85	0.20	3.29E-01	6.89E-01	CHD2	Chromodomain helicase DNA binding protein 2	chr15q26	244443_at	NM_001042572 /// NM_001271																					
3.92	4.04	0.12	3.29E-01	6.89E-01	---	---	---	240567_at	---																					
3.83	4.07	0.24	3.29E-01	6.89E-01	IDI1	isopentenyl-diphosphate delta isomerase 1	chr10p15.3	242065_x_at	NM_004508																					
2.18	2.31	0.12	3.29E-01	6.89E-01	CHRNA5	cholinergic receptor, nicotinic, alpha 5	chr15q24	206533_at	NM_000745																					
4.58	5.04	0.45	3.29E-01	6.89E-01	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	chr1p33	207043_s_at	NM_001024845 /// NM_006934 /// NM_201649																					
3.89	4.05	0.16	3.29E-01	6.89E-01	---	---	---	1563048_at	---																					
2.19	2.32	0.13	3.29E-01	6.89E-01	C9orf156	chromosome 9 open reading frame 156	chr9q22.33	222188_at	NM_016481																					
7.44	7.67	0.23	3.29E-01	6.89E-01	RXRA	retinoid X receptor, alpha	chr9q34.3	202449_s_at	NM_002957																					
2.27	2.42	0.15	3.29E-01	6.89E-01	ENAH	Enabled homolog (Drosophila)	chr1q42.12	228553_at	NM_001008493 /// NM_018212																					
6.10	6.29	0.19	3.29E-01	6.89E-01	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	chr2q23.3	214941_s_at	NM_017892																					
2.11	2.25	0.15	3.29E-01	6.89E-01	CCDC65	coiled-coil domain containing 65	chr12q13.12	1552321_a_at	NM_033124																					
5.14	5.53	0.38	3.29E-01	6.89E-01	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	chr9p24.1	219343_at	NM_017913																					
4.22	4.54	0.32	3.29E-01	6.89E-01	KRCC1	lysine-rich coiled-coil 1	chr2p11.2	233329_s_at	NM_016618																					
3.68	3.92	0.25	3.29E-01	6.89E-01	SDCBP2	syndecan binding protein (syntenin) 2	chr20p13	233565_s_at	NM_015685 /// NM_080489																					
2.94	3.16	0.22	3.29E-01	6.89E-01	ZNF260	zinc finger protein 260	chr19q13.12	1558700_s_at	NM_001012756																					
3.11	3.30	0.19	3.29E-01	6.89E-01	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	chr2p25	216941_s_at	NM_005680																					

3.97	4.16	0.19	3.29E-01	6.89E-01	ARSA	Arylsulfatase A	chr22q13.31-qter|22q13.33	236541_at	NM_000487 /// NM_001085425 /// NM_001085426 /// NM_001085427 /// NM_001085428
4.35	4.52	0.17	3.29E-01	6.89E-01	WFDC3	WAP four-disulfide core domain 3	chr20q13.12	232602_at	NM_080614
3.03	3.19	0.16	3.29E-01	6.89E-01	C18orf1	chromosome 18 open reading frame 1	chr18p11.2	233138_at	NM_001003674 /// NM_001003675 /// NM_004338 /// NM_181481 /// NM_181482 /// NM_181483
2.36	2.51	0.15	3.29E-01	6.89E-01	---	---	---	243897_at	---
1.99	2.11	0.11	3.29E-01	6.89E-01	---	---	---	243876_at	---
4.14	4.36	0.22	3.29E-01	6.89E-01	C9orf165	chromosome 9 open reading frame 165	chr9p13.3	228403_at	NM_198573
3.68	3.90	0.22	3.30E-01	6.89E-01	P2RX2	purinergic receptor P2X, ligand-gated ion channel, 2	chr12q24.33	221356_x_at	NM_012226 /// NM_016318 /// NM_170682 /// NM_170683 /// NM_174872 /// NM_174873
5.38	5.52	0.14	3.30E-01	6.89E-01	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	chr3p21.3-p21.2	204843_s_at	NM_004157
2.73	2.87	0.14	3.30E-01	6.89E-01	CECR7	cat eye syndrome chromosome region, candidate 7	chr22q11.1	243048_at	NR_015352 /// XM_001715805 /// XM_001718067 /// XM_001719280
2.36	2.55	0.19	3.30E-01	6.89E-01	GDF10	growth differentiation factor 10	chr10q11.22	206159_at	NM_004962
3.22	3.41	0.19	3.30E-01	6.89E-01	---	---	---	1570133_at	---
1.99	2.17	0.17	3.30E-01	6.89E-01	---	---	---	1566950_at	---
2.38	2.54	0.16	3.30E-01	6.89E-01	---	---	---	1561278_at	---
2.08	2.19	0.11	3.30E-01	6.89E-01	---	---	---	237716_at	---
2.47	2.63	0.16	3.30E-01	6.89E-01	RHOXF2 /// RHOXF2B	Rhox homeobox family, member 2 /// Rhox homeobox family, member 2B	chrXq24	236920_at	NM_001099685 /// NM_032498
2.09	2.25	0.16	3.30E-01	6.89E-01	---	---	---	1561199_at	---
1.90	2.01	0.11	3.30E-01	6.89E-01	---	---	---	238394_at	---
5.82	6.24	0.42	3.30E-01	6.89E-01	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	chr13q32.2	227996_at	NM_001001715 /// NM_005766
2.09	2.20	0.11	3.30E-01	6.89E-01	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	chr6p24.2	211020_at	NM_001491 /// NM_145649 /// NM_145655
2.99	3.27	0.28	3.30E-01	6.89E-01	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	chr13q22.1	218362_s_at	NM_001128226 /// NM_014953
3.01	3.18	0.17	3.30E-01	6.89E-01	---	---	---	229688_at	---
2.65	2.80	0.15	3.30E-01	6.89E-01	LOC100129129	Hypothetical protein LOC100129129	chr8p23.1	1559871_s_at	XM_001715395 /// XM_001716192 /// XM_001716441
2.15	2.31	0.15	3.30E-01	6.89E-01	---	---	---	1566265_at	---
2.51	2.64	0.12	3.30E-01	6.89E-01	EPR1	effector cell peptidase receptor 1 (non-protein coding)	chr17q25	1555826_at	NR_002219
2.23	2.35	0.13	3.30E-01	6.90E-01	DRP2	dystrophin related protein 2	chrXq22	1556627_at	NM_001939
2.79	2.95	0.16	3.30E-01	6.90E-01	---	---	---	1557287_at	---
2.97	3.12	0.15	3.30E-01	6.90E-01	---	---	---	230675_at	---
6.32	6.66	0.35	3.30E-01	6.90E-01	MCEE	methylmalonyl CoA epimerase	chr2p13.3	226238_at	NM_032601
2.14	2.28	0.14	3.30E-01	6.90E-01	---	---	---	221202_at	---
3.49	3.74	0.25	3.30E-01	6.90E-01	---	---	---	1561180_at	---
3.87	4.21	0.34	3.30E-01	6.90E-01	RAD50	RAD50 homolog (S. cerevisiae)	chr5q31	209349_at	NM_005732 /// NM_133482
2.52	2.68	0.16	3.30E-01	6.90E-01	KCTD16	potassium channel tetramerisation domain containing 16	chr5q32	233234_at	NM_020768
2.29	2.46	0.17	3.30E-01	6.90E-01	KCNA1	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	chr12p13.32	230849_at	NM_000217
3.94	4.08	0.14	3.30E-01	6.90E-01	hCG_20426	hCG20426	chr1p36.33	1556182_x_at	XR_040433 /// XR_040434 /// XR_040435

2.04	2.22	0.18	3.30E-01	6.90E-01	LOC100129656	hypothetical protein LOC100129656	chr1q44	216868_s_at	XM_001717015 /// XM_001717020
4.12	4.33	0.21	3.31E-01	6.90E-01	---	---	---	231225_at	---
6.89	7.54	0.65	3.31E-01	6.90E-01	BZW1 /// BZW1L1	basic leucine zipper and W2 domains 1 /// basic leucine zipper and W2 domains 1 like 1	chr2q33 /// chr3q13.31	200776_s_at	NM_014670 /// XM_001721170 /// XM_045290 /// XM_938633
1.89	2.00	0.12	3.31E-01	6.90E-01	SLCO4C1	solute carrier organic anion transporter family, member 4C1	chr5q21.2	222071_s_at	NM_180991
5.16	5.86	0.69	3.31E-01	6.90E-01	AMDHD1	amidohydrolase domain containing 1	chr12q23.1	229596_at	NM_152435
2.04	2.20	0.16	3.31E-01	6.90E-01	---	---	---	240184_at	---
2.63	2.79	0.16	3.31E-01	6.90E-01	ACCN1	amiloride-sensitive cation channel 1, neuronal	chr17q12	206690_at	NM_001094 /// NM_183377
1.99	2.12	0.13	3.31E-01	6.90E-01	GPR103	G protein-coupled receptor 103	chr4q27	1555533_at	NM_198179
3.07	3.36	0.29	3.31E-01	6.90E-01	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	chr2q33	225186_at	NM_203365 /// NM_213589
3.99	4.19	0.20	3.31E-01	6.90E-01	C20orf191 /// LOC100133918 /// NCOR1	chromosome 20 open reading frame 191 /// similar to nuclear receptor co-repressor 1 /// nuclear receptor co-repressor 1	chr17p11.2 /// chr20p11.1	200856_x_at	NM_006311 /// NR_003678 /// XM_001725872
3.97	4.25	0.28	3.31E-01	6.90E-01	TGS1	trimethylguanosine synthase homolog (S. cerevisiae)	chr8q11	238346_s_at	NM_024831
3.90	4.04	0.14	3.31E-01	6.90E-01	---	---	---	241800_x_at	---
6.03	6.40	0.37	3.31E-01	6.90E-01	RPE	ribulose-5-phosphate-3-epimerase	chr2q32-q33.3	225040_s_at	NM_006916 /// NM_199229
3.70	3.84	0.13	3.31E-01	6.90E-01	DKFZp451A211	DKFZp451A211 protein	chr13q34	1556114_a_at	XR_041296 /// XR_041297
2.23	2.41	0.18	3.31E-01	6.90E-01	---	---	---	244806_at	---
3.47	3.63	0.16	3.31E-01	6.90E-01	---	---	---	243035_at	---
3.58	3.72	0.14	3.31E-01	6.90E-01	DEAF1	Deformed epidermal autoregulatory factor 1 (Drosophila)	chr11p15.5	230059_at	NM_021008
4.98	5.13	0.15	3.31E-01	6.90E-01	C19orf64	chromosome 19 open reading frame 64	chr19p13.3	236730_at	XM_001722785 /// XM_001726165 /// XM_001726185
7.83	8.25	0.42	3.31E-01	6.90E-01	GLUD1	glutamate dehydrogenase 1	chr10q23.3	200946_x_at	NM_005271
2.49	2.73	0.23	3.31E-01	6.90E-01	---	---	---	236289_at	---
2.43	2.60	0.18	3.31E-01	6.91E-01	---	---	---	1563715_at	---
3.29	3.43	0.14	3.31E-01	6.91E-01	PHLDB3	pleckstrin homology-like domain, family B, member 3	chr19q13.31	236082_at	NM_198850
2.03	2.16	0.14	3.31E-01	6.91E-01	---	---	---	1561719_at	---
4.48	4.72	0.24	3.31E-01	6.91E-01	C6orf173	chromosome 6 open reading frame 173	chr6q22.32	226936_at	NM_001012507
2.43	2.56	0.14	3.31E-01	6.91E-01	---	---	---	239130_at	---
2.63	2.76	0.14	3.31E-01	6.91E-01	TYRO3P	TYRO3P protein tyrosine kinase pseudogene	chr15q24.2	1566935_at	---
4.75	4.98	0.23	3.31E-01	6.91E-01	PPP1R9B	protein phosphatase 1, regulatory (inhibitor) subunit 9B	chr17q21.33	225124_at	NM_032595
3.17	3.42	0.25	3.31E-01	6.91E-01	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)	chr9p21.2	1563521_at	NM_024761
3.26	3.48	0.22	3.31E-01	6.91E-01	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	chr11q23.3	211846_s_at	NM_002855 /// NM_203285 /// NM_203286
6.70	7.23	0.53	3.32E-01	6.91E-01	TMOD1	tropomodulin 1	chr9q22.3	203662_s_at	NM_003275
5.29	5.66	0.37	3.32E-01	6.91E-01	CPE	carboxypeptidase E	chr4q32.3	201117_s_at	NM_001873
5.11	5.40	0.29	3.32E-01	6.91E-01	EVI5L	ecotropic viral integration site 5-like	chr19p13.2	226411_at	NM_145245
2.56	2.79	0.22	3.32E-01	6.91E-01	---	---	---	231230_at	---
3.20	3.37	0.18	3.32E-01	6.91E-01	C9orf109	chromosome 9 open reading frame 109	chr9q32	229059_at	XM_001717200 /// XM_001717211 /// XM_001718432
2.10	2.19	0.10	3.32E-01	6.91E-01	NCALD	neurocalcin delta	chr8q22.2	1562790_at	NM_001040624 /// NM_001040625 /// NM_001040626 /// NM_001040627 /// NM_001040628 /// NM_001040629 /// NM_001040630 /// NM_032041
2.22	2.38	0.16	3.32E-01	6.91E-01	AGXT	alanine-glyoxylate aminotransferase	chr2q36-q37	206957_at	NM_000030

2.93	3.16	0.23	3.32E-01	6.91E-01	LOC100130797	PRO0566	chr20q11.22	224096_at	XM_001718618 /// XM_001718842 /// XM_001720041																				
2.86	3.01	0.15	3.32E-01	6.91E-01	S100A14	S100 calcium binding protein A14	chr1q21.3	218677_at	NM_020672																				
7.84	8.26	0.42	3.32E-01	6.91E-01	FKBP5	FK506 binding protein 5	chr6p21.3-p21.2	224856_at	NM_004117																				
1.99	2.14	0.15	3.32E-01	6.91E-01	BPESC1	blepharophimosis, epicanthus inversus and ptosis, candidate 1	chr3q23	220772_at	NM_021812																				
3.97	4.16	0.19	3.32E-01	6.91E-01	---	---	---	204322_at	---																				
3.92	4.34	0.42	3.32E-01	6.91E-01	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	chr2q32.3-q33.1	232080_at	NM_020760																				
3.47	3.63	0.16	3.32E-01	6.91E-01	---	---	---	241038_at	---																				
5.97	6.68	0.71	3.32E-01	6.91E-01	---	---	---	232355_at	---																				
7.54	8.01	0.47	3.32E-01	6.91E-01	LAP3	leucine aminopeptidase 3	chr4p15.32	217933_s_at	NM_015907																				
5.29	5.64	0.35	3.32E-01	6.91E-01	ZFPM1	zinc finger protein, multitype 1	chr16q24.2	242282_at	NM_153813																				
5.20	5.44	0.24	3.32E-01	6.91E-01	ZNF766	zinc finger protein 766	chr19q13.33	227284_at	NM_001010851																				
2.30	2.47	0.18	3.32E-01	6.91E-01	---	---	---	1556279_at	---																				
2.28	2.43	0.15	3.32E-01	6.91E-01	---	---	---	243637_at	---																				
2.40	2.52	0.12	3.32E-01	6.91E-01	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	chr10q24	214421_x_at	NM_000771																				
2.55	2.67	0.12	3.32E-01	6.91E-01	TMEM217	transmembrane protein 217	chr6p21.2	237016_at	NM_145316																				
2.15	2.27	0.12	3.32E-01	6.91E-01	---	---	---	233102_at	---																				
2.03	2.14	0.11	3.32E-01	6.91E-01	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	chr1p13.3-p13.1	208010_s_at	NM_012411 /// NM_015967																				
2.15	2.25	0.10	3.32E-01	6.91E-01	---	---	---	241225_at	---																				
2.23	2.33	0.10	3.32E-01	6.91E-01	---	---	---	240439_at	---																				
2.89	3.22	0.33	3.32E-01	6.92E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	235518_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097																				
4.65	4.92	0.27	3.32E-01	6.92E-01	---	---	---	215221_at	---																				
6.83	7.26	0.42	3.32E-01	6.92E-01	CTSS	cathepsin S	chr1q21	202902_s_at	NM_004079																				
2.65	2.84	0.19	3.32E-01	6.92E-01	KANK1	KN motif and ankyrin repeat domains 1	chr9p24.3	237162_at	NM_015158 /// NM_153186																				
3.08	3.22	0.14	3.33E-01	6.92E-01	ZAN	zonadhesin	chr7q22	224264_x_at	NM_003386 /// NM_173059																				
2.35	2.47	0.12	3.32E-01	6.92E-01	---	---	---	237906_at	---																				
5.62	6.34	0.72	3.33E-01	6.92E-01	MTUS1	mitochondrial tumor suppressor 1	chr8p22	212093_s_at	NM_001001924 /// NM_001001925 /// NM_001001931 /// NM_020749																				
3.06	3.23	0.17	3.33E-01	6.92E-01	FAM181A	family with sequence similarity 181, member A	chr14q32.13	231117_at	NM_138344																				
2.35	2.48	0.14	3.33E-01	6.92E-01	---	---	---	241449_at	---																				
6.19	6.40	0.22	3.33E-01	6.92E-01	AGTRAP	angiotensin II receptor-associated protein	chr1p36.22	1555736_a_at	NM_001040194 /// NM_001040195 /// NM_001040196 /// NM_001040197 /// NM_020350																				
3.47	3.66	0.19	3.33E-01	6.92E-01	RETN	resistin	chr19p13.2	220570_at	NM_020415																				
4.92	5.09	0.16	3.33E-01	6.92E-01	FBXO44	F-box protein 44	chr1p36.22	223517_at	NM_001014765 /// NM_033182 /// NM_183412 /// NM_183413																				
2.14	2.28	0.14	3.33E-01	6.92E-01	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	chr11q13	204942_s_at	NM_000695 /// NM_001031615																				
2.27	2.41	0.14	3.33E-01	6.92E-01	DCLK1	doublecortin-like kinase 1	chr13q13	205399_at	NM_004734																				
2.11	2.23	0.12	3.33E-01	6.92E-01	C10orf90	chromosome 10 open reading frame 90	chr10q26.2	1556200_a_at	NM_001004298																				
3.89	4.03	0.14	3.33E-01	6.92E-01	GPBAR1	G protein-coupled bile acid receptor 1	chr2q35	1552501_a_at	NM_001077191 /// NM_001077194 /// NM_170699																				
3.77	4.18	0.41	3.33E-01	6.92E-01	COP1	caspase-1 dominant-negative inhibitor pseudo-ICE	---	1552701_a_at	NM_001017534 /// NM_052889																				

5.29	5.69	0.40	3.33E-01	6.92E-01	MTO1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	chr6q13	224430_s_at	NM_001123226 /// NM_012123 /// NM_133645
1.93	2.05	0.12	3.33E-01	6.92E-01	EPHA6	EPH receptor A6	chr3q11.2	1561396_at	NM_001080448 /// NM_173655
3.23	3.41	0.19	3.33E-01	6.92E-01	HRSP12	Heat-responsive protein 12	chr8q22	231705_at	NM_005836
6.03	7.23	1.21	3.33E-01	6.92E-01	IGL@ /// IGLC2 /// IGLV2-14	immunoglobulin lambda locus /// immunoglobulin lambda constant 2 (Kern-Oz- marker) /// immunoglobulin lambda variable 2-14	chr22q11.1-q11.2 /// chr22q11.2	215121_x_at	---
2.32	2.43	0.11	3.33E-01	6.92E-01	---	---	---	239745_at	---
5.45	6.03	0.58	3.33E-01	6.92E-01	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	chr11p15.1-p14	202453_s_at	NM_005316
3.12	3.38	0.26	3.33E-01	6.92E-01	---	---	---	238266_at	---
4.50	4.73	0.23	3.33E-01	6.92E-01	---	---	---	243088_at	---
3.73	3.92	0.19	3.33E-01	6.92E-01	LOC642891	hypothetical LOC642891	chr3p26.3	243432_at	XM_001714956 /// XM_931148 /// XM_943602
3.69	3.85	0.16	3.33E-01	6.92E-01	BAHCC1	BAH domain and coiled-coil containing 1	chr17q25.3	236604_at	NM_001080519
3.19	3.34	0.16	3.33E-01	6.92E-01	NT5C1A	5'-nucleotidase, cytosolic IA	chr1p34.3-p33	224529_s_at	NM_032526
3.54	3.70	0.16	3.33E-01	6.92E-01	GPR39	G protein-coupled receptor 39	chr2q21-q22	229104_s_at	NM_001508
2.22	2.36	0.15	3.33E-01	6.92E-01	KRT36	keratin 36	chr17q12-q21	214576_at	NM_003771
1.81	1.92	0.10	3.33E-01	6.92E-01	---	---	---	241147_at	---
6.27	6.85	0.57	3.34E-01	6.93E-01	APOD	apolipoprotein D	chr3q26.2-qter	201525_at	NM_001647
4.28	4.46	0.18	3.34E-01	6.93E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	215162_at	NM_014990 /// NM_194301
3.24	3.38	0.15	3.34E-01	6.93E-01	MGC57346	hypothetical LOC401884	chr17q21.31	1568987_at	XM_001722151 /// XM_001724623 /// XM_377476
2.77	2.92	0.15	3.34E-01	6.93E-01	---	---	---	231413_at	---
1.83	1.94	0.11	3.34E-01	6.93E-01	---	---	---	240811_at	---
4.86	5.05	0.19	3.34E-01	6.93E-01	---	---	---	228279_s_at	---
4.30	4.51	0.20	3.34E-01	6.93E-01	ANKRD57	ankyrin repeat domain 57	chr2q13	227034_at	NM_023016
4.38	4.53	0.14	3.34E-01	6.93E-01	METTL10	methyltransferase like 10	chr10q26.13	215061_at	NM_212554
3.47	3.84	0.37	3.34E-01	6.93E-01	---	---	---	233608_at	---
7.29	8.59	1.30	3.34E-01	6.93E-01	IGK@ /// IGKC	immunoglobulin kappa locus /// immunoglobulin kappa constant	chr2p12	221651_x_at	---
6.35	6.96	0.61	3.34E-01	6.93E-01	PSD3	pleckstrin and Sec7 domain containing 3	chr8pter-p23.3	203355_s_at	NM_015310 /// NM_206909
4.09	4.44	0.35	3.34E-01	6.93E-01	TBX2	T-box 2	chr17q23	213417_at	NM_005994
2.46	2.67	0.21	3.34E-01	6.93E-01	ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	chrXp11.4	201442_s_at	NM_005765
4.21	4.39	0.18	3.34E-01	6.93E-01	---	---	---	237735_at	---
2.99	3.17	0.18	3.34E-01	6.93E-01	LOC286254	hypothetical protein LOC286254	chr9q34.3	1559765_a_at	---
5.62	5.78	0.16	3.34E-01	6.93E-01	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	chr3p21	212128_s_at	NM_004393
4.77	4.91	0.14	3.34E-01	6.93E-01	LOC100129041 /// TGIF1	hypothetical protein LOC100129041 /// TGFB-induced factor homeobox 1	chr18p11.3 /// chr18p11.31	244858_at	NM_003244 /// NM_170695 /// NM_173207 /// NM_173208 /// NM_173209 /// NM_173210 /// NM_173211 /// NM_174886 /// XM_001714794 /// XM_001715061 /// XM_001716775
2.05	2.17	0.12	3.34E-01	6.93E-01	RAVER2	ribonucleoprotein, PTB-binding 2	chr1p31.3	220680_at	NM_018211
1.80	1.89	0.10	3.34E-01	6.93E-01	---	---	---	1561110_at	---
9.93	10.33	0.40	3.34E-01	6.93E-01	GPX3	glutathione peroxidase 3 (plasma)	chr5q23	214091_s_at	NM_002084
2.15	2.27	0.12	3.34E-01	6.93E-01	KANK1	KN motif and ankyrin repeat domains 1	chr9p24.3	1565832_at	NM_015158 /// NM_153186
2.47	2.58	0.12	3.34E-01	6.93E-01	C6orf182 /// C6orf182P	chromosome 6 open reading frame 182 /// chromosome 6 open reading frame 182 pseudogene	chr10q22.1 /// chr6q21	1554019_s_at	NM_001083535 /// NM_173830
2.31	2.46	0.15	3.34E-01	6.93E-01	GOLT1A	golgi transport 1 homolog A (S. cerevisiae)	chr1q32.1	229372_at	NM_198447
3.22	3.51	0.29	3.34E-01	6.93E-01	NF1	neurofibromin 1	chr17q11.2	211914_x_at	NM_000267 /// NM_001042492 /// NM_001128147
8.56	8.82	0.26	3.34E-01	6.93E-01	EIF3M	eukaryotic translation initiation factor 3, subunit M	chr11p13	202231_at	NM_006360

2.79	2.93	0.14	3.34E-01	6.93E-01	FANCA	Fanconi anemia, complementation group A	chr16q24.3	203805_s_at	NM_000135 /// NM_001018112
2.62	2.80	0.19	3.35E-01	6.93E-01	APBA1	amyloid beta (A4) precursor protein-binding, family A, member 1	chr9q13-q21.1	228101_at	NM_001163
6.25	6.50	0.26	3.35E-01	6.93E-01	RSPO3	R-spondin 3 homolog (Xenopus laevis)	chr6q22.33	228186_s_at	NM_032784
2.94	3.09	0.16	3.35E-01	6.93E-01	ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	chr1q32	230549_at	NM_001973 /// NM_021795
2.13	2.25	0.12	3.35E-01	6.93E-01	LAMC2	laminin, gamma 2	chr1q25-q31	207517_at	NM_005562 /// NM_018891
1.75	1.86	0.10	3.35E-01	6.93E-01	ABCA13	ATP-binding cassette, sub-family A (ABC1), member 13	chr7p12.3	1553604_at	NM_152701
3.03	3.16	0.13	3.35E-01	6.93E-01	---	---	---	229769_at	---
3.12	3.36	0.24	3.35E-01	6.93E-01	---	---	---	232406_at	---
2.77	2.95	0.18	3.35E-01	6.93E-01	LOC440028	hypothetical gene supported by BC040853	chr11p15.4	1562606_a_at	---
2.54	2.71	0.16	3.35E-01	6.93E-01	---	---	---	243748_at	---
3.02	3.17	0.15	3.35E-01	6.93E-01	---	---	---	241071_at	---
2.26	2.38	0.12	3.35E-01	6.93E-01	LOC100129865	similar to PRO1405	chr4q21.1	224037_at	XM_001720788 /// XM_001720874 /// XM_001722391
1.98	2.09	0.11	3.35E-01	6.93E-01	GJB6	gap junction protein, beta 6, 30kDa	chr13q11-q12.1|13q12	231771_at	NM_001110219 /// NM_001110220 /// NM_001110221 /// NM_006783
4.48	4.87	0.39	3.35E-01	6.93E-01	SERBP1	SERPINE1 mRNA binding protein 1	chr1p31	228129_at	NM_001018067 /// NM_001018068 /// NM_001018069 /// NM_015640
2.09	2.25	0.16	3.35E-01	6.93E-01	FRMD4A	FERM domain containing 4A	chr10p13	1554034_a_at	NM_018027
4.39	4.54	0.15	3.35E-01	6.93E-01	NCAPH2	non-SMC condensin II complex, subunit H2	chr22q13.33	40640_at	NM_014551 /// NM_152299
2.89	3.08	0.19	3.35E-01	6.93E-01	CCDC40	coiled-coil domain containing 40	chr17q25.3	220592_at	NM_017950
2.13	2.22	0.10	3.35E-01	6.93E-01	---	---	---	234020_x_at	---
3.87	4.04	0.17	3.35E-01	6.93E-01	HILS1	histone linker H1 domain, spermatid-specific 1	chr17q21.33	231229_at	XR_040471 /// XR_040472 /// XR_040473
4.83	4.97	0.13	3.35E-01	6.93E-01	ZFAT	zinc finger and AT hook domain containing	chr8q24.22	226564_at	NM_001029939 /// NM_020863
4.63	4.94	0.31	3.35E-01	6.94E-01	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	chr21q22.3	203865_s_at	NM_001033049 /// NM_001112 /// NM_015833 /// NM_015834
5.08	5.57	0.48	3.35E-01	6.94E-01	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	chr8q13-q21.1	204226_at	NM_014393
2.24	2.34	0.10	3.35E-01	6.94E-01	DHX35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	chr20q11.22-q12	1561132_at	NM_021931
6.51	6.63	0.12	3.35E-01	6.94E-01	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	chr15q22-q24	236715_x_at	NM_001008224 /// NM_018003
3.46	3.64	0.17	3.35E-01	6.94E-01	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	chrXq28	207026_s_at	NM_001001344 /// NM_021949
5.22	5.38	0.17	3.35E-01	6.94E-01	RELT	RELT tumor necrosis factor receptor	chr11q13.4	227060_at	NM_032871 /// NM_152222
2.11	2.24	0.13	3.35E-01	6.94E-01	PCDHA2	protocadherin alpha 2	chr5q31	210572_at	NM_018905 /// NM_031495 /// NM_031496
2.16	2.32	0.16	3.35E-01	6.94E-01	---	---	---	233147_at	---
2.05	2.19	0.14	3.35E-01	6.94E-01	---	---	---	1560237_at	---
2.79	2.95	0.16	3.35E-01	6.94E-01	---	---	---	236940_at	---
3.07	3.23	0.16	3.35E-01	6.94E-01	MAPK11	mitogen-activated protein kinase 11	chr22q13.33	206040_s_at	NM_002751
3.58	3.82	0.24	3.35E-01	6.94E-01	IL4R	Interleukin 4 receptor	chr16p12.1-p11.2	242743_at	NM_000418 /// NM_001008699
10.02	10.30	0.28	3.36E-01	6.94E-01	TMEM59	transmembrane protein 59	chr1p36-p31	200620_at	NM_004872
2.73	2.91	0.18	3.35E-01	6.94E-01	GATA4	GATA binding protein 4	chr8p23.1-p22	243692_at	NM_002052
2.65	2.82	0.16	3.36E-01	6.94E-01	---	---	---	234520_at	---
2.04	2.18	0.14	3.36E-01	6.94E-01	---	---	---	242536_at	---
2.38	2.54	0.15	3.36E-01	6.94E-01	OR14J1	olfactory receptor, family 14, subfamily J, member 1	chr6p22.1	234545_at	NM_030946

4.68	4.82	0.15	3.36E-01	6.94E-01	---	---	---	244012_x_at	---
1.84	1.95	0.10	3.36E-01	6.94E-01	---	---	---	210893_at	---
2.93	3.12	0.19	3.36E-01	6.94E-01	OR1E1 /// OR1E2	olfactory receptor, family 1, subfamily E, member 1 /// olfactory receptor, family 1, subfamily E, member 2	chr17p13.3	208587_s_at	NM_003553 /// NM_003554
2.29	2.42	0.12	3.36E-01	6.94E-01	MAGEA5	melanoma antigen family A, 5	chrXq28	214642_x_at	NM_021049
4.72	5.20	0.48	3.36E-01	6.94E-01	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	chr7q21.3	221088_s_at	NM_017650
1.94	2.06	0.12	3.36E-01	6.94E-01	CNTNAP2	contactin associated protein-like 2	chr7q35-q36	219302_s_at	NM_014141
4.28	4.63	0.35	3.36E-01	6.94E-01	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	chr19p13.3	205349_at	NM_002068
1.99	2.10	0.12	3.36E-01	6.94E-01	---	---	---	1562464_at	---
3.31	3.51	0.21	3.36E-01	6.94E-01	LIM2	lens intrinsic membrane protein 2, 19kDa	chr19q13.4	220519_s_at	NM_030657
6.00	6.33	0.34	3.36E-01	6.95E-01	---	---	---	227484_at	---
2.94	3.19	0.25	3.36E-01	6.95E-01	TAS2R45	taste receptor, type 2, member 45	---	234042_at	NM_176886
2.70	2.88	0.18	3.36E-01	6.95E-01	---	---	---	231170_at	---
3.73	3.88	0.16	3.36E-01	6.95E-01	YSK4	yeast Sps1/Ste20-related kinase 4 (S. cerevisiae)	chr2q21.3	221180_at	NM_001018046 /// NM_025052
1.85	2.01	0.16	3.36E-01	6.95E-01	ZNF417	zinc finger protein 417	chr19q13.43	1552783_at	NM_152475
1.97	2.07	0.10	3.36E-01	6.95E-01	LOC147670	hypothetical protein LOC147670	chr19q13.43	1557430_at	XM_001718473 /// XM_001718506 /// XM_001719187
2.33	2.44	0.11	3.36E-01	6.95E-01	---	---	---	216772_at	---
4.81	5.00	0.20	3.36E-01	6.95E-01	KIAA1147	KIAA1147	chr7q34	223161_at	NM_001080392
6.68	7.13	0.45	3.36E-01	6.95E-01	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	chr2q33-q34	225144_at	NM_001204
4.04	4.24	0.20	3.36E-01	6.95E-01	CTRB1 /// CTRB2	chymotrypsinogen B1 /// chymotrypsinogen B2	chr16q23-q24.1 /// chr16q23.1	205971_s_at	NM_001025200 /// NM_001906 /// XM_001717935
3.11	3.27	0.16	3.36E-01	6.95E-01	NTN1	netrin 1	chr17p13-p12	227816_at	NM_004822
2.30	2.45	0.15	3.36E-01	6.95E-01	CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1	chr3p22-p21.3	232494_at	NM_004391
3.32	3.47	0.15	3.36E-01	6.95E-01	---	---	---	234279_at	---
2.14	2.26	0.12	3.37E-01	6.95E-01	TMC5	transmembrane channel-like 5	chr16p12.3	219580_s_at	NM_001105248 /// NM_001105249 /// NM_024780
2.17	2.40	0.23	3.37E-01	6.95E-01	---	---	---	1557805_at	---
2.57	2.78	0.21	3.37E-01	6.95E-01	SYT4	synaptotagmin IV	chr18q12.3	223529_at	NM_020783
2.55	2.73	0.17	3.37E-01	6.95E-01	ZNF576	Hypothetical LOC100170229	chr19q13.31	1565849_a_at	NM_024327
1.89	2.01	0.12	3.37E-01	6.95E-01	LOC286126	hypothetical protein LOC286126	chr8q24.3	233045_at	---
2.10	2.20	0.10	3.37E-01	6.95E-01	---	---	---	211437_at	---
5.49	6.03	0.54	3.37E-01	6.95E-01	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	chr2p14	1554390_s_at	NM_001005386 /// NM_005722
4.54	4.91	0.37	3.37E-01	6.95E-01	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	chr3q26.3	222679_s_at	NM_020640
2.01	2.14	0.13	3.37E-01	6.95E-01	TEX11	testis expressed 11	chrXq13.1	234296_s_at	NM_001003811 /// NM_031276
6.03	6.22	0.19	3.37E-01	6.95E-01	ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1	chr19q13.13	203055_s_at	NM_004706 /// NM_198977 /// NM_199002
4.69	5.24	0.56	3.37E-01	6.95E-01	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	chr10p13	221547_at	NM_003675
3.11	3.24	0.12	3.37E-01	6.95E-01	DCTN2	Dynactin 2 (p50)	chr12q13.2-q13.3	232505_at	NM_006400
2.05	2.19	0.14	3.37E-01	6.95E-01	SYNPO2L	synaptopodin 2-like	chr10q22.2	219804_at	NM_001114133 /// NM_024875
6.17	6.31	0.14	3.37E-01	6.95E-01	SPOP	speckle-type POZ protein	chr17q21.33	208927_at	NM_001007226 /// NM_001007227 /// NM_001007228 /// NM_001007229 /// NM_001007230 /// NM_003563
2.04	2.16	0.12	3.37E-01	6.95E-01	ZNF846	zinc finger protein 846	chr19p13.2	1569156_at	NM_001077624
4.52	4.69	0.17	3.37E-01	6.96E-01	FBXO36	F-box protein 36	chr2q36.3	236525_at	NM_174899
1.97	2.12	0.14	3.37E-01	6.96E-01	EIF3F	eukaryotic translation initiation factor 3, subunit F	chr11p15.4	200865_at	NM_003754
3.71	3.85	0.13	3.37E-01	6.96E-01	SSTR5	somatostatin receptor 5	chr16p13.3	214555_at	NM_001053

1.97	2.10	0.13	3.37E-01	6.96E-01	TOX3	TOX high mobility group box family member 3	chr16q12.1	215108_x_at	NM_001080430
4.62	4.78	0.15	3.37E-01	6.96E-01	---	---	---	232120_at	---
4.83	5.36	0.52	3.37E-01	6.96E-01	RNF146	ring finger protein 146	chr6q22.1-q22.33	221430_s_at	NM_030963
3.03	3.18	0.15	3.37E-01	6.96E-01	---	---	---	233137_at	---
2.38	2.52	0.14	3.37E-01	6.96E-01	FLJ35424	hypothetical protein FLJ35424	chr4p16.2	1553912_at	XR_040705 /// XR_040706 /// XR_040707
2.14	2.27	0.13	3.37E-01	6.96E-01	---	---	---	236310_at	---
1.91	2.01	0.10	3.37E-01	6.96E-01	BCL8	B-cell CLL/lymphoma 8	chr15q11-q13	1560683_at	XM_001125807
2.51	2.70	0.19	3.37E-01	6.96E-01	---	---	---	244338_at	---
3.63	4.15	0.52	3.38E-01	6.96E-01	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	chr5p14-p13	219789_at	NM_000908
2.52	2.65	0.13	3.38E-01	6.96E-01	TECTA	tectorin alpha	chr11q22-q24	221296_at	NM_005422
2.34	2.47	0.13	3.38E-01	6.96E-01	LOC100131414 /// TJP2	hypothetical protein LOC100131414 /// tight junction protein 2 (zona occludens 2)	chr9q13-q21 /// chr9q21.11	242991_at	NM_004817 /// NM_201629 /// XM_001714417 /// XM_001714741 /// XM_001715469
2.52	2.72	0.19	3.38E-01	6.96E-01	KLK10	kallikrein-related peptidase 10	chr19q13.3-q13.4	209792_s_at	NM_001077500 /// NM_002776 /// NM_145888
3.01	3.19	0.18	3.38E-01	6.96E-01	P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	chr12q24	207091_at	NM_002562
2.03	2.17	0.14	3.38E-01	6.96E-01	CBY3	chibby homolog 3 (Drosophila)	chr5q35.3	241712_at	XM_001724133 /// XM_928982 /// XM_936994
4.53	4.74	0.21	3.38E-01	6.96E-01	OXCT2	3-oxoacid CoA transferase 2	chr1p34	220256_s_at	NM_022120
2.97	3.16	0.19	3.38E-01	6.96E-01	MORN5	MORN repeat containing 5	chr9q33.2	229976_at	NM_198469
2.67	2.81	0.14	3.38E-01	6.96E-01	PROKR2	prokineticin receptor 2	chr20p12.3	234450_at	NM_144773
3.05	3.20	0.14	3.38E-01	6.96E-01	HCG9	HLA complex group 9	chr6p21.3	208287_at	NM_005844
6.50	6.63	0.13	3.38E-01	6.96E-01	---	---	---	215504_x_at	---
2.69	2.83	0.14	3.38E-01	6.96E-01	---	---	---	216159_s_at	---
3.22	3.50	0.28	3.38E-01	6.96E-01	FKTN	fukutin	chr9q31-q33	205283_at	NM_001079802 /// NM_006731
2.72	2.89	0.17	3.38E-01	6.96E-01	KLHL5	kelch-like 5 (Drosophila)	chr4p14	233866_at	NM_001007075 /// NM_015990 /// NM_199039
5.35	5.49	0.14	3.38E-01	6.96E-01	HLA-DOA	major histocompatibility complex, class II, DO alpha	chr6p21.3	211142_x_at	NM_002119
2.80	2.93	0.12	3.38E-01	6.96E-01	DDHD1	DDHD domain containing 1	chr14q21	243705_at	NM_030637
5.15	5.55	0.39	3.38E-01	6.96E-01	NIPBL	Nipped-B homolog (Drosophila)	chr5p13.2	213918_s_at	NM_015384 /// NM_133433
1.84	1.96	0.12	3.38E-01	6.96E-01	IL31RA	interleukin 31 receptor A	chr5q11.2	1555431_a_at	NM_139017
3.84	3.95	0.12	3.38E-01	6.96E-01	---	---	---	237858_s_at	---
2.54	2.74	0.19	3.38E-01	6.96E-01	---	---	---	1562283_at	---
2.51	2.64	0.13	3.38E-01	6.96E-01	---	---	---	1553355_at	---
3.62	3.84	0.22	3.38E-01	6.96E-01	---	---	---	237948_at	---
2.75	2.91	0.15	3.38E-01	6.96E-01	PRRG4	Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	chr11p13	238513_at	NM_024081
2.40	2.51	0.11	3.38E-01	6.96E-01	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	chr4p14	214013_s_at	NM_015173
2.58	2.75	0.18	3.39E-01	6.96E-01	INSL3 /// JAK3	insulin-like 3 (Leydig cell) /// Janus kinase 3 (a protein tyrosine kinase, leukocyte)	chr19p13.1 /// chr19p13.2-p12	214572_s_at	NM_000215 /// NM_005543
5.06	5.78	0.71	3.39E-01	6.97E-01	---	---	---	240245_at	---
5.58	6.27	0.70	3.39E-01	6.97E-01	FAM115A	family with sequence similarity 115, member A	chr7q35	212979_s_at	NM_014719
4.45	4.82	0.37	3.39E-01	6.97E-01	ZNF33A	zinc finger protein 33A	chr10p11.2	231864_at	NM_006954 /// NM_006974
3.38	3.66	0.28	3.39E-01	6.97E-01	MANEA	mannosidase, endo-alpha	chr6q16.1	222805_at	NM_024641
5.33	5.59	0.26	3.39E-01	6.97E-01	GATA2	GATA binding protein 2	chr3q21.3	209710_at	NM_032638
3.01	3.24	0.23	3.39E-01	6.97E-01	HRASLS5	HRAS-like suppressor family, member 5	chr11q13.2	231050_at	NM_054108
10.35	10.56	0.21	3.39E-01	6.97E-01	RAB11A	RAB11A, member RAS oncogene family	chr15q21.3-q22.31	200863_s_at	NM_004663
4.59	4.80	0.21	3.39E-01	6.97E-01	RIN3	Ras and Rab interactor 3	chr14q32.12	219456_s_at	NM_024832
2.79	2.96	0.17	3.39E-01	6.97E-01	---	---	---	1558193_at	---

2.79	2.96	0.17	3.39E-01	6.97E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	214516_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054
1.97	2.13	0.16	3.39E-01	6.97E-01	---	---	---	216735_x_at	---
3.28	3.44	0.16	3.39E-01	6.97E-01	KIAA1656	KIAA1656 protein	---	232933_at	XR_040413 /// XR_040414 /// XR_040415
2.67	2.83	0.16	3.39E-01	6.97E-01	---	---	---	235637_s_at	---
2.16	2.31	0.15	3.39E-01	6.97E-01	---	---	---	214862_x_at	---
2.71	2.86	0.15	3.39E-01	6.97E-01	TP63	tumor protein p63	chr3q28	207382_at	NM_001114978 /// NM_001114979 /// NM_001114980 /// NM_001114981 /// NM_001114982 /// NM_003722
2.38	2.53	0.14	3.39E-01	6.97E-01	CPNE8	copine VIII	chr12q12	243727_at	NM_153634
1.83	1.97	0.14	3.39E-01	6.97E-01	---	---	---	1558226_a_at	---
2.83	2.97	0.14	3.39E-01	6.97E-01	FGF14	fibroblast growth factor 14	chr13q34	230288_at	NM_004115 /// NM_175929
1.96	2.10	0.13	3.39E-01	6.97E-01	GABRR1	gamma-aminobutyric acid (GABA) receptor, rho 1	chr6q14-q21|6q13-q16.3	206525_at	NM_002042
2.88	3.01	0.13	3.39E-01	6.97E-01	LOC728613 /// PDCD6	programmed cell death 6 pseudogene /// programmed cell death 6	chr5p15.33	1568762_at	NM_013232 /// NR_003713 /// XM_001714855 /// XM_001720072 /// XM_001723249
1.96	2.09	0.12	3.39E-01	6.97E-01	---	---	---	233118_at	---
3.99	4.11	0.12	3.39E-01	6.97E-01	GUCA1A	guanylate cyclase activator 1A (retina)	chr6p21.1	231700_at	NM_000409
2.07	2.18	0.11	3.39E-01	6.97E-01	---	---	---	241483_at	---
2.02	2.12	0.11	3.39E-01	6.97E-01	---	---	---	1563389_at	---
3.59	3.80	0.20	3.39E-01	6.97E-01	---	---	---	236607_at	---
2.87	3.02	0.14	3.39E-01	6.97E-01	---	---	---	243798_at	---
1.99	2.11	0.13	3.39E-01	6.97E-01	---	---	---	1565769_at	---
4.83	5.34	0.50	3.39E-01	6.97E-01	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	chr4q21.1	206383_s_at	NM_012297 /// NM_203504 /// NM_203505
5.48	5.83	0.35	3.39E-01	6.97E-01	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	chr7p15-p13	214435_x_at	NM_005402
1.94	2.05	0.12	3.39E-01	6.97E-01	---	---	---	216069_at	---
6.49	6.73	0.25	3.39E-01	6.97E-01	LIPE	lipase, hormone-sensitive	chr19q13.2	208186_s_at	NM_005357
5.41	5.72	0.31	3.39E-01	6.97E-01	RBM45	RNA binding motif protein 45	chr2q31.2	228578_at	NM_152945
6.76	6.88	0.11	3.39E-01	6.97E-01	PSMD13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	chr11p15.5	201233_at	NM_002817 /// NM_175932
2.62	2.81	0.19	3.39E-01	6.97E-01	---	---	---	239946_at	---

4.55	4.73	0.18	3.39E-01	6.97E-01	LOC100128071	Similar to hCG41624	chr1p35.1	236874_at	XM_001724365 /// XM_001724643 /// XM_001724939
2.38	2.52	0.14	3.39E-01	6.97E-01	---	---	---	237387_at	---
2.03	2.14	0.11	3.39E-01	6.97E-01	---	---	---	233120_at	---
8.19	8.64	0.45	3.40E-01	6.97E-01	MBNL1	muscleblind-like (Drosophila)	chr3q25	201152_s_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297
3.12	3.27	0.16	3.40E-01	6.97E-01	---	---	---	216122_at	---
3.56	3.69	0.13	3.40E-01	6.97E-01	SFRP1	Secreted frizzled-related protein 1	chr8p12-p11.1	228413_s_at	NM_003012
2.16	2.29	0.12	3.40E-01	6.97E-01	---	---	---	1568883_at	---
8.29	8.64	0.35	3.40E-01	6.97E-01	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	chr1q25.3	211963_s_at	NM_005717
3.12	3.37	0.25	3.40E-01	6.97E-01	RAB3B	RAB3B, member RAS oncogene family	chr1p32-p31	205925_s_at	NM_002867
2.39	2.52	0.13	3.40E-01	6.97E-01	ADAM28	ADAM metallopeptidase domain 28	chr8p21.2	241446_at	NM_014265 /// NM_021777
2.08	2.24	0.17	3.40E-01	6.97E-01	ZNF442	zinc finger protein 442	chr19p13.2	208081_s_at	NM_030824
5.57	6.04	0.47	3.40E-01	6.97E-01	NFIB	nuclear factor I/B	chr9p24.1	213032_at	NM_005596
1.95	2.14	0.19	3.40E-01	6.97E-01	---	---	---	241808_at	---
4.13	4.31	0.18	3.40E-01	6.97E-01	TNNI2	troponin I type 2 (skeletal, fast)	chr11p15.5	206393_at	NM_003282
3.76	4.17	0.41	3.40E-01	6.97E-01	SMC4	structural maintenance of chromosomes 4	chr3q26.1	201663_s_at	NM_001002800 /// NM_005496
6.46	6.74	0.28	3.40E-01	6.97E-01	---	---	---	226993_at	---
2.91	3.09	0.18	3.40E-01	6.97E-01	CTLA4	cytotoxic T-lymphocyte-associated protein 4	chr2q33	234362_s_at	NM_001037631 /// NM_005214
2.19	2.32	0.14	3.40E-01	6.97E-01	C9orf93	chromosome 9 open reading frame 93	chr9p22.3	242821_at	NM_173550
2.58	2.72	0.14	3.40E-01	6.97E-01	HPYR1	Helicobacter pylori responsive 1	chr8q24.22	1566917_at	---
2.34	2.47	0.13	3.40E-01	6.97E-01	C20orf12	chromosome 20 open reading frame 12	chr20p11.23	1554818_s_at	NM_001099407
2.20	2.33	0.13	3.40E-01	6.97E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	208180_s_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054
2.84	2.97	0.13	3.40E-01	6.97E-01	CCPG1	cell cycle progression 1	chr15q21.1	221156_x_at	NM_004748 /// NM_020739
2.28	2.40	0.12	3.40E-01	6.97E-01	WDHD1	WD repeat and HMG-box DNA binding protein 1	chr14q22.3	204728_s_at	NM_001008396 /// NM_007086
3.65	3.77	0.12	3.40E-01	6.97E-01	CBLC	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	chr19q13.2	223668_at	NM_001130852 /// NM_012116
2.14	2.24	0.11	3.40E-01	6.97E-01	---	---	---	243847_at	---
4.34	4.55	0.21	3.40E-01	6.97E-01	CCDC149	coiled-coil domain containing 149	chr4p15.2	226141_at	NM_001130726 /// NM_173463
2.16	2.34	0.19	3.40E-01	6.97E-01	CXCL5	chemokine (C-X-C motif) ligand 5	chr4q12-q13	215101_s_at	NM_002994

2.30	2.47	0.17	3.40E-01	6.97E-01	POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	chr16p13.3	222766_at	NM_016310
2.33	2.50	0.17	3.40E-01	6.97E-01	---	---	---	1555723_at	---
2.41	2.57	0.16	3.40E-01	6.97E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	234427_at	---
2.25	2.41	0.15	3.40E-01	6.97E-01	---	---	---	240844_at	---
2.30	2.45	0.15	3.40E-01	6.97E-01	---	---	---	214405_at	---
3.16	3.29	0.13	3.40E-01	6.97E-01	KCNIP2	Kv channel interacting protein 2	chr10q24	221321_s_at	NM_014591 /// NM_173191 /// NM_173192 /// NM_173193 /// NM_173194 /// NM_173195 /// NM_173197
1.84	1.96	0.12	3.40E-01	6.97E-01	PDE6C	phosphodiesterase 6C, cGMP-specific, cone, alpha prime	chr10q24	211093_at	NM_006204
1.95	2.07	0.12	3.40E-01	6.97E-01	---	---	---	216740_at	---
3.37	3.53	0.15	3.41E-01	6.97E-01	---	---	---	216530_at	---
1.84	1.96	0.12	3.41E-01	6.97E-01	ALS2CR11	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	chr2q33.1	1553261_x_at	NM_152525
2.26	2.43	0.17	3.41E-01	6.97E-01	---	---	---	1561347_a_at	---
3.48	4.16	0.68	3.41E-01	6.97E-01	GUCY1A3	Guanylate cyclase 1, soluble, alpha 3	chr4q31.3-q33|4q31.1-q31.2	229530_at	NM_000856 /// NM_001130682 /// NM_001130683 /// NM_001130684 /// NM_001130685 /// NM_001130686 /// NM_001130687
3.17	3.35	0.18	3.41E-01	6.97E-01	ANGPTL6	angiopoietin-like 6	chr19p13.2	223967_at	NM_031917
2.79	2.93	0.14	3.41E-01	6.97E-01	---	---	---	228616_at	---
5.37	5.63	0.26	3.41E-01	6.97E-01	HSDL1	hydroxysteroid dehydrogenase like 1	chr16q24.1	223248_at	NM_031463
5.53	5.71	0.18	3.41E-01	6.97E-01	C16orf45	Chromosome 16 open reading frame 45	chr16p13.11	1565641_at	NM_033201
1.90	2.02	0.12	3.41E-01	6.97E-01	RAB7A	RAB7A, member RAS oncogene family	chr3q21.3	217267_s_at	NM_004637
3.32	3.52	0.19	3.41E-01	6.97E-01	CACNA1F	calcium channel, voltage-dependent, L type, alpha 1F subunit	chrXp11.23	208377_s_at	NM_005183
3.49	3.62	0.12	3.41E-01	6.97E-01	MSH3	mutS homolog 3 (E. coli)	chr5q11-q12	205887_x_at	NM_002439
2.60	2.71	0.11	3.41E-01	6.97E-01	GPR1	G protein-coupled receptor 1	chr2q33.3	214605_x_at	NM_001098199 /// NM_005279
4.71	4.93	0.21	3.41E-01	6.97E-01	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	chr20q13.1	201710_at	NM_002466
2.48	2.65	0.17	3.41E-01	6.97E-01	KIAA0574	KIAA0574 protein	chr15q12	213997_at	NM_015307 /// XM_001713870 /// XM_001716797
2.96	3.10	0.14	3.41E-01	6.97E-01	C13orf33	Chromosome 13 open reading frame 33	chr13q12.3	1565763_at	NM_032849
1.89	2.01	0.12	3.41E-01	6.97E-01	---	---	---	239825_at	---
2.45	2.56	0.11	3.41E-01	6.97E-01	---	---	---	237837_at	---
2.41	2.62	0.21	3.41E-01	6.97E-01	ODF2L	outer dense fiber of sperm tails 2-like	chr1p22.3	228577_x_at	NM_001007022 /// NM_020729
2.29	2.47	0.18	3.41E-01	6.97E-01	ZNF165	zinc finger protein 165	chr6p21.3	206683_at	NM_003447
3.06	3.20	0.15	3.41E-01	6.98E-01	U2AF1	U2 small nuclear RNA auxiliary factor 1	chr21q22.3	242499_at	NM_001025203 /// NM_001025204 /// NM_006758
3.64	3.83	0.19	3.41E-01	6.98E-01	HMCN2	hemicentin 2	chr9q34.11	235932_x_at	XM_001715154 /// XM_001726942
2.01	2.12	0.12	3.41E-01	6.98E-01	---	---	---	1560144_at	---
2.10	2.24	0.14	3.41E-01	6.98E-01	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	chr6p21.1-p11.2	244407_at	NM_016593
4.55	4.72	0.18	3.41E-01	6.98E-01	IGFBP5	insulin-like growth factor binding protein 5	chr2q33-q36	203424_s_at	NM_000599
2.00	2.15	0.15	3.41E-01	6.98E-01	---	---	---	1559404_a_at	---
1.82	1.95	0.13	3.41E-01	6.98E-01	LOC100130868	hypothetical protein LOC100130868	chr9p24.1	1560425_s_at	XM_001716332 /// XM_001717199 /// XM_001717751
8.90	9.17	0.27	3.41E-01	6.98E-01	SERINC3	serine incorporator 3	chr20q13.1-q13.3	211769_x_at	NM_006811 /// NM_198941

4.21	4.41	0.19	3.41E-01	6.98E-01	---	---	---	240238_at	---
1.88	2.02	0.14	3.42E-01	6.98E-01	LOC100127950	hypothetical LOC100127950	chr7p14.1	1560950_at	XM_001724104 /// XM_001725212 /// XM_001725247
1.83	1.94	0.11	3.42E-01	6.98E-01	---	---	---	232439_at	---
3.77	4.00	0.23	3.42E-01	6.98E-01	LTB4R	leukotriene B4 receptor	chr14q11.2-q12	216388_s_at	NM_181657
2.07	2.20	0.13	3.42E-01	6.98E-01	---	---	---	244014_x_at	---
5.06	5.44	0.38	3.42E-01	6.98E-01	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	chr17q24-q25|17q25.1	213501_at	NM_004035 /// NM_007292
3.80	4.12	0.33	3.42E-01	6.98E-01	TMEM41A	Transmembrane protein 41A	chr3q27.2	229771_at	NM_080652
5.42	5.63	0.20	3.42E-01	6.98E-01	---	---	---	231191_at	---
3.73	3.86	0.13	3.42E-01	6.98E-01	ZNF551	Zinc finger protein 551	chr19q13.43	242992_at	NM_138347
2.91	3.06	0.15	3.42E-01	6.98E-01	SOX10	SRY (sex determining region Y)-box 10	chr22q13.1	209842_at	NM_006941
2.09	2.20	0.11	3.42E-01	6.98E-01	---	---	---	237547_at	---
3.04	3.20	0.16	3.42E-01	6.98E-01	KIR3DX1	killer cell immunoglobulin-like receptor, three domains, X1	chr19q13.42	216492_at	NM_001047605
2.11	2.26	0.15	3.42E-01	6.98E-01	DNAH6 /// DNHL1 /// LOC200383	dynein, axonemal, heavy chain 6 /// dynein heavy chain-like 1 /// similar to Dynein heavy chain at 16F	chr2p11.2	1561617_at	NM_001370 /// NM_173645
2.65	2.81	0.16	3.42E-01	6.98E-01	RIPK4	receptor-interacting serine-threonine kinase 4	chr21q22.3	234730_s_at	NM_020639
3.64	4.13	0.49	3.42E-01	6.98E-01	SV2B	synaptic vesicle glycoprotein 2B	chr15q26.1	205551_at	NM_014848
7.85	8.18	0.33	3.42E-01	6.98E-01	VPS29	vacuolar protein sorting 29 homolog (S. cerevisiae)	chr12q24	223026_s_at	NM_016226 /// NM_057180
3.55	3.70	0.14	3.42E-01	6.98E-01	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal	chr11p15.4-p15.1	217171_at	NM_000543 /// NM_001007593
2.47	2.64	0.18	3.42E-01	6.98E-01	CLIC5	chloride intracellular channel 5	chr6p21.1-p12.1	217628_at	NM_001114086 /// NM_016929
1.93	2.03	0.10	3.42E-01	6.98E-01	---	---	---	234621_at	---
6.15	6.58	0.44	3.42E-01	6.98E-01	FNTA	farnesyltransferase, CAAX box, alpha	chr8p11	209471_s_at	NM_001018676 /// NM_001018677 /// NM_002027
6.52	6.80	0.28	3.42E-01	6.98E-01	LOC440434	hypothetical protein FLJ11822	chr17q12	215090_x_at	XM_001725426 /// XM_001725441
2.66	2.87	0.21	3.42E-01	6.98E-01	---	---	---	1557841_at	---
2.80	2.95	0.15	3.42E-01	6.98E-01	---	---	---	1557809_a_at	---
2.57	2.71	0.15	3.42E-01	6.98E-01	LCE2B	late cornified envelope 2B	chr1q21	207710_at	NM_014357
2.68	2.79	0.12	3.42E-01	6.98E-01	---	---	---	1561499_at	---
5.41	5.62	0.21	3.42E-01	6.98E-01	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	chr3q22.1	209934_s_at	NM_001001485 /// NM_001001486 /// NM_001001487 /// NM_014382
1.88	2.00	0.12	3.42E-01	6.98E-01	LRRC63	leucine rich repeat containing 63	chr13q14.12	1569124_at	XM_001714777 /// XM_001716651 /// XM_001718341
2.17	2.31	0.14	3.42E-01	6.98E-01	MAEL	maelstrom homolog (Drosophila)	chr1q24.1	229475_at	NM_032858
2.68	2.81	0.13	3.42E-01	6.98E-01	---	---	---	1562231_at	---
5.59	5.99	0.40	3.42E-01	6.98E-01	---	---	---	237626_at	---
4.52	4.90	0.38	3.42E-01	6.98E-01	PELI1	Pellino homolog 1 (Drosophila)	chr2p13.3	232304_at	NM_020651
2.86	3.05	0.18	3.42E-01	6.98E-01	CHRNA4	cholinergic receptor, nicotinic, alpha 4	chr20q13.2-q13.3	216886_at	NM_000744
2.39	2.51	0.13	3.42E-01	6.98E-01	CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle)	chr1q21	219645_at	NM_001231
2.04	2.16	0.12	3.42E-01	6.98E-01	LRRN4	leucine rich repeat neuronal 4	chr20p12.3	1553171_x_at	NM_152611
5.34	5.69	0.35	3.43E-01	6.98E-01	SPG20	spastic paraplegia 20 (Troyer syndrome)	chr13q13.3	212526_at	NM_015087
5.66	5.87	0.21	3.43E-01	6.98E-01	LAMA2	laminin, alpha 2	chr6q22-q23	216840_s_at	NM_000426 /// NM_001079823
2.83	3.00	0.17	3.43E-01	6.98E-01	REC8	REC8 homolog (yeast)	chr14q11.2-q12	229536_at	NM_001048205 /// NM_005132
3.00	3.15	0.15	3.43E-01	6.98E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	217138_x_at	---
2.40	2.54	0.14	3.43E-01	6.98E-01	---	---	---	232559_at	---

2.13	2.24	0.11	3.43E-01	6.98E-01	EFCAB6	EF-hand calcium binding domain 6	chr22q13.1-q13.33	233600_at	NM_022785 /// NM_198856
2.04	2.15	0.10	3.43E-01	6.98E-01	ZNF613	zinc finger protein 613	chr19q13.33	219851_at	NM_001031721 /// NM_024840
7.17	7.54	0.37	3.43E-01	6.98E-01	CDC26 /// LOC729948 /// LOC730314	cell division cycle 26 homolog (S. cerevisiae) /// similar to CDC26 subunit of anaphase promoting complex /// similar to CDC26 subunit of anaphase promoting complex	chr7q32.1 /// chr9q32	225422_at	NM_139286 /// XM_001720644 /// XM_001722195 /// XM_001726317 /// XM_001726511
3.57	3.77	0.20	3.43E-01	6.98E-01	LIMK1	LIM domain kinase 1	chr7q11.23	204356_at	NM_002314
2.01	2.11	0.10	3.43E-01	6.98E-01	RASSF6	Ras association (RalGDS/AF-6) domain family member 6	chr4q13.3	235638_at	NM_177532 /// NM_201431
3.96	4.15	0.19	3.43E-01	6.98E-01	---	---	---	231222_at	---
3.11	3.28	0.17	3.43E-01	6.98E-01	SPRED2	sprouty-related, EVH1 domain containing 2	chr2p14	212466_at	NM_001128210 /// NM_181784
2.76	2.91	0.15	3.43E-01	6.98E-01	LOC100134445	hypothetical protein LOC100134445	---	231811_at	XM_001720526
3.35	3.59	0.24	3.43E-01	6.99E-01	FGD5	FYVE, RhoGEF and PH domain containing 5	chr3p24.3	226984_at	NM_152536
5.30	5.49	0.19	3.43E-01	6.99E-01	CNOT4	CCR4-NOT transcription complex, subunit 4	chr7q22-qter	203291_at	NM_001008225 /// NM_013316
2.27	2.43	0.15	3.43E-01	6.99E-01	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	chrXq13.1-q21.1	211022_s_at	NM_000489 /// NM_138270
1.76	1.88	0.12	3.43E-01	6.99E-01	---	---	---	233847_x_at	---
1.96	2.06	0.11	3.43E-01	6.99E-01	---	---	---	205728_at	---
6.87	7.14	0.27	3.43E-01	6.99E-01	STMN3	stathmin-like 3	chr20q13.3	222557_at	NM_015894
4.95	5.19	0.24	3.43E-01	6.99E-01	C2orf18	chromosome 2 open reading frame 18	chr2p23.3	219783_at	NM_017877
2.58	2.75	0.16	3.43E-01	6.99E-01	---	---	---	1570496_at	---
2.45	2.60	0.15	3.43E-01	6.99E-01	QSER1	glutamine and serine rich 1	chr11p13	219705_at	NM_001076786
2.37	2.50	0.13	3.43E-01	6.99E-01	MGST3	Microsomal glutathione S-transferase 3	chr1q23	244122_at	NM_004528
2.55	2.68	0.13	3.43E-01	6.99E-01	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	chr6p12.2	244410_at	NM_138694 /// NM_170724
2.26	2.38	0.11	3.43E-01	6.99E-01	---	---	---	1570054_at	---
2.29	2.65	0.36	3.43E-01	6.99E-01	---	---	---	230917_at	---
2.58	2.68	0.10	3.43E-01	6.99E-01	---	---	---	233909_at	---
1.90	2.01	0.12	3.43E-01	6.99E-01	---	---	---	234368_at	---
3.93	4.36	0.43	3.44E-01	6.99E-01	---	---	---	1563364_at	---
5.23	5.65	0.42	3.44E-01	6.99E-01	CRYZL1	crystallin, zeta (quinone reductase)-like 1	chr21q21.3	219767_s_at	NM_145858
3.71	4.07	0.36	3.44E-01	6.99E-01	---	---	---	242068_at	---
4.36	4.64	0.29	3.44E-01	6.99E-01	GSTM5	glutathione S-transferase M5	chr1p13.3	205752_s_at	NM_000851
7.62	7.88	0.27	3.44E-01	6.99E-01	KIAA0265	KIAA0265 protein	chr7q32.2	210111_s_at	NM_014997
3.75	4.00	0.25	3.44E-01	6.99E-01	CMTM7	CKLF-like MARVEL transmembrane domain containing 7	chr3p22.3	1560754_at	NM_138410 /// NM_181472
4.34	4.56	0.22	3.44E-01	6.99E-01	ZBTB7A	zinc finger and BTB domain containing 7A	chr19p13.3	213299_at	NM_015898
2.22	2.40	0.18	3.44E-01	6.99E-01	---	---	---	244792_at	---
2.85	3.03	0.18	3.44E-01	6.99E-01	REPS1	RALBP1 associated Eps domain containing 1	---	215201_at	NM_001128617 /// NM_031922
6.75	6.92	0.18	3.43E-01	6.99E-01	GIPC1	GIPC PDZ domain containing family, member 1	chr19p13.1	207525_s_at	NM_005716 /// NM_202467 /// NM_202468 /// NM_202469 /// NM_202470 /// NM_202494
4.62	4.79	0.17	3.44E-01	6.99E-01	CTAGE4	CTAGE family, member 4	chr7q35	215549_x_at	NM_198495 /// XM_001713619 /// XM_001726736 /// XR_038147 /// XR_039265
2.74	2.89	0.15	3.43E-01	6.99E-01	PRCP	Prolylcarboxypeptidase (angiotensinase C)	chr11q14	231588_at	NM_005040 /// NM_199418
2.53	2.67	0.14	3.44E-01	6.99E-01	AJAP1	adherens junctions associated protein 1	chr1p36.32	215789_s_at	NM_001042478 /// NM_018836
2.10	2.23	0.13	3.44E-01	6.99E-01	---	---	---	1569439_at	---
2.43	2.56	0.13	3.44E-01	6.99E-01	---	---	---	1560744_at	---
2.00	2.13	0.13	3.44E-01	6.99E-01	---	---	---	243506_at	---

2.30	2.43	0.13	3.44E-01	6.99E-01	SYNE1	spectrin repeat containing, nuclear envelope 1	chr6q25	232027_at	NM_015293 /// NM_033071 /// NM_133650 /// NM_182961
2.76	2.89	0.13	3.44E-01	6.99E-01	LOC100130598	hypothetical protein LOC100130598	chr13q32.2	1570408_at	XM_001719254 /// XM_001720068 /// XM_001721180
2.45	2.56	0.12	3.44E-01	6.99E-01	MFAP3L	microfibrillar-associated protein 3-like	chr4q32.3	210493_s_at	NM_001009554 /// NM_021647
1.93	2.04	0.10	3.44E-01	6.99E-01	---	---	---	1563016_at	---
3.44	3.82	0.38	3.44E-01	6.99E-01	MAP2	microtubule-associated protein 2	chr2q34-q35	225540_at	NM_001039538 /// NM_002374 /// NM_031845 /// NM_031847
2.69	3.03	0.34	3.44E-01	6.99E-01	---	---	---	238169_at	---
3.83	4.10	0.27	3.44E-01	6.99E-01	PARVA	parvin, alpha	chr11p15.3	215418_at	NM_018222
7.40	7.67	0.26	3.44E-01	6.99E-01	CGGBP1	CGG triplet repeat binding protein 1	chr3p12-p11.1	224599_at	NM_001008390 /// NM_003663
3.01	3.19	0.17	3.44E-01	6.99E-01	CDRT1	CMT1A duplicated region transcript 1	chr17p12	208280_at	NM_006382
2.12	2.29	0.17	3.44E-01	6.99E-01	---	---	---	241807_x_at	---
2.00	2.12	0.12	3.44E-01	6.99E-01	CCDC89	coiled-coil domain containing 89	chr11q14.1	1553228_at	NM_152723
2.12	2.23	0.10	3.44E-01	6.99E-01	PPM1L	protein phosphatase 1 (formerly 2C)-like	chr3q26.1	236339_at	NM_139245
6.18	6.72	0.54	3.44E-01	6.99E-01	RABEP1	rabaptin, RAB GTPase binding effector protein 1	chr17p13.2	225092_at	NM_001083585 /// NM_004703
5.72	6.06	0.35	3.44E-01	6.99E-01	HEATR1	HEAT repeat containing 1	chr1q43	218594_at	NM_018072
3.59	3.89	0.30	3.44E-01	6.99E-01	IPP	intracisternal A particle-promoted polypeptide	chr1p34-p32	1554740_a_at	NM_005897
3.80	4.02	0.22	3.44E-01	6.99E-01	PDLIM7	PDZ and LIM domain 7 (enigma)	chr5q35.3	214266_s_at	NM_005451 /// NM_203352 /// NM_213636
2.28	2.45	0.18	3.44E-01	6.99E-01	FAM84B	Family with sequence similarity 84, member B	chr8q24.21	230817_at	NM_174911
9.59	9.77	0.17	3.44E-01	6.99E-01	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	chr7q11.23	222985_at	NM_012479
2.78	2.94	0.16	3.44E-01	6.99E-01	CRNN	cornulin	chr1q21	220090_at	NM_016190
2.32	2.47	0.15	3.44E-01	6.99E-01	CCR2 /// FLJ78302	chemokine (C-C motif) receptor 2 /// chemokine (C-C motif) receptor 2-like	chr3p21.31	207794_at	NM_000647 /// NM_000648 /// NM_001123041 /// NM_001123396 /// XM_001133430 /// XM_001133431
1.80	1.90	0.10	3.44E-01	6.99E-01	---	---	---	1570080_at	---
3.08	3.47	0.39	3.44E-01	6.99E-01	DST	dystonin	chr6p12.1	232098_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380
3.72	3.91	0.19	3.44E-01	6.99E-01	KIAA1618	KIAA1618	chr17q25.3	232155_at	NM_020954
2.80	2.98	0.18	3.44E-01	6.99E-01	---	---	---	243393_at	---
2.03	2.14	0.10	3.44E-01	6.99E-01	NCOA3	Nuclear receptor coactivator 3	chr20q12	1562439_at	NM_006534 /// NM_181659
2.56	2.70	0.14	3.44E-01	6.99E-01	---	---	---	237178_at	---
2.57	2.77	0.20	3.44E-01	6.99E-01	GRIK5	glutamate receptor, ionotropic, kainate 5	chr19q13.2	1553168_at	NM_002088
3.10	3.27	0.16	3.44E-01	6.99E-01	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	chr7p15.1-p14.3	216869_at	NM_005020
2.29	2.43	0.13	3.44E-01	6.99E-01	---	---	---	1570424_at	---
2.72	2.85	0.13	3.44E-01	6.99E-01	---	---	---	1554043_a_at	---
1.87	1.99	0.12	3.44E-01	6.99E-01	---	---	---	1555928_at	---
2.45	2.56	0.12	3.44E-01	6.99E-01	---	---	---	243417_at	---
5.00	5.31	0.30	3.45E-01	6.99E-01	BBS9	Bardet-Biedl syndrome 9	chr7p14	209958_s_at	NM_001033604 /// NM_001033605 /// NM_014451 /// NM_198428
2.34	2.49	0.15	3.45E-01	6.99E-01	---	---	---	240885_at	---
2.58	2.74	0.16	3.45E-01	6.99E-01	---	---	---	232850_at	---
2.02	2.15	0.14	3.45E-01	6.99E-01	---	---	---	1567703_at	---
2.04	2.17	0.13	3.45E-01	6.99E-01	---	---	---	1566162_x_at	---
3.78	4.54	0.76	3.45E-01	6.99E-01	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	chr12q12	214007_s_at	NM_002822

5.69	5.95	0.27	3.45E-01	6.99E-01	SP110	SP110 nuclear body protein	chr2q37.1	209762_x_at	NM_004509 /// NM_004510 /// NM_080424
6.72	6.97	0.25	3.45E-01	6.99E-01	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	chr19q13.33	223237_x_at	NM_014203 /// NM_130787
4.06	4.25	0.19	3.45E-01	6.99E-01	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	chr4q25	226402_at	NM_183075
2.13	2.26	0.13	3.45E-01	6.99E-01	---	---	---	237134_at	---
2.45	2.60	0.15	3.45E-01	6.99E-01	ADARB2	adenosine deaminase, RNA-specific, B2 (RED2 homolog rat)	chr10p15.3	220648_at	NM_018702
2.83	3.05	0.22	3.45E-01	6.99E-01	---	---	---	222271_at	---
2.94	3.13	0.19	3.45E-01	7.00E-01	---	---	---	1556413_a_at	---
2.92	3.08	0.16	3.45E-01	7.00E-01	FZD1	frizzled homolog 1 (Drosophila)	chr7q21	204452_s_at	NM_003505
2.48	2.66	0.18	3.45E-01	7.00E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	210832_x_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719
2.31	2.48	0.17	3.45E-01	7.00E-01	---	---	---	1558626_at	---
3.56	3.70	0.14	3.45E-01	7.00E-01	PKNOX2	PBX/knotted 1 homeobox 2	---	222185_at	NM_022062
2.91	3.05	0.13	3.45E-01	7.00E-01	FMN1	formin 1	chr15q13.3	238621_at	NM_001103184
2.10	2.21	0.12	3.45E-01	7.00E-01	---	---	---	1564244_a_at	---
2.36	2.45	0.10	3.45E-01	7.00E-01	CCDC38	coiled-coil domain containing 38	chr12q22-q23.1	1557620_a_at	NM_182496
6.68	7.00	0.32	3.45E-01	7.00E-01	ZC3H14	zinc finger CCCH-type containing 14	chr14q31.3	204216_s_at	NM_024824 /// NM_207660 /// NM_207661 /// NM_207662
2.24	2.43	0.19	3.45E-01	7.00E-01	---	---	---	1560905_at	---
2.24	2.39	0.15	3.45E-01	7.00E-01	PUNC	putative neuronal cell adhesion molecule	chr15q22.3-q23	230960_at	NM_004884
2.11	2.22	0.11	3.45E-01	7.00E-01	---	---	---	242054_s_at	---
4.35	4.64	0.29	3.45E-01	7.00E-01	CAMK2N2	calcium/calmodulin-dependent protein kinase II inhibitor 2	chr3q27.1	230706_s_at	NM_033259
3.37	3.59	0.23	3.45E-01	7.00E-01	CLASP1	Cytoplasmic linker associated protein 1	chr2q14.2-q14.3	240757_at	NM_015282
5.63	5.82	0.19	3.45E-01	7.00E-01	LUZP1	leucine zipper protein 1	chr1p36	221832_s_at	NM_033631
5.13	5.31	0.17	3.45E-01	7.00E-01	APC2	adenomatosis polyposis coli 2	chr19p13.3	205320_at	NM_005883
2.11	2.24	0.13	3.45E-01	7.00E-01	---	---	---	238393_at	---
2.74	2.87	0.13	3.45E-01	7.00E-01	LAMA3	laminin, alpha 3	chr18q11.2	1568879_a_at	NM_000227 /// NM_001127717 /// NM_001127718 /// NM_198129
2.38	2.51	0.13	3.45E-01	7.00E-01	FLJ40759	hypothetical gene supported by AK098078	chr3q25.1	1562562_at	XM_374058 /// XM_374059 /// XM_934736 /// XM_942041
2.99	3.17	0.18	3.46E-01	7.00E-01	TBX15	T-box 15	chr1p11.1	230438_at	NM_152380
2.42	2.52	0.10	3.45E-01	7.00E-01	HCRTR2	hypocretin (orexin) receptor 2	chr6p12	207393_at	NM_001526
4.79	5.29	0.49	3.46E-01	7.00E-01	SLC30A5	solute carrier family 30 (zinc transporter), member 5	chr5q12.1	232432_s_at	NM_022902 /// NM_024055
2.57	2.74	0.17	3.46E-01	7.00E-01	---	---	---	1557610_at	---
3.41	3.57	0.16	3.46E-01	7.00E-01	---	---	---	1562723_at	---
6.58	6.74	0.16	3.46E-01	7.00E-01	MEF2D	myocyte enhancer factor 2D	chr1q12-q23	203003_at	NM_005920
2.94	3.13	0.19	3.46E-01	7.00E-01	---	---	---	239782_at	---
2.62	2.75	0.13	3.46E-01	7.00E-01	PART1	prostate androgen-regulated transcript 1	chr5q12.1	205834_s_at	XR_040430 /// XR_040431 /// XR_040432
2.57	2.70	0.14	3.46E-01	7.00E-01	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	chr9q22.1	214680_at	NM_001007097 /// NM_001018064 /// NM_001018065 /// NM_001018066 /// NM_006180
3.15	3.29	0.13	3.46E-01	7.00E-01	---	---	---	1569316_at	---
3.20	3.36	0.16	3.46E-01	7.00E-01	TMLHE	trimethyllysine hydroxylase, epsilon	chrXq28	218790_s_at	NM_018196

3.05	3.20	0.16	3.46E-01	7.00E-01	ZC3H18	zinc finger CCCH-type containing 18	chr16q24.2-q24.3	238416_x_at	NM_144604																				
2.00	2.11	0.12	3.46E-01	7.00E-01	---	---	---	234538_at	---																				
11.12	11.45	0.33	3.46E-01	7.00E-01	RPL6	ribosomal protein L6	chr12q24.1	200034_s_at	NM_000970 /// NM_001024662																				
4.88	5.38	0.50	3.46E-01	7.00E-01	WAPAL	wings apart-like homolog (Drosophila)	chr10q23.2	1554441_a_at	NM_015045																				
1.98	2.11	0.13	3.46E-01	7.00E-01	---	---	---	1565978_a_at	---																				
2.47	2.62	0.15	3.46E-01	7.00E-01	ZBED4	zinc finger, BED-type containing 4	chr22q13.33	214747_at	NM_014838																				
6.77	7.01	0.24	3.46E-01	7.00E-01	PEA15	phosphoprotein enriched in astrocytes 15	chr1q21.1	200787_s_at	NM_003768																				
3.70	3.91	0.22	3.46E-01	7.00E-01	---	---	---	244000_at	---																				
2.73	2.90	0.17	3.46E-01	7.00E-01	---	---	---	1566967_at	---																				
3.37	3.53	0.16	3.46E-01	7.00E-01	C12orf39	chromosome 12 open reading frame 39	chr12p12.1	221067_s_at	NM_030572																				
2.54	2.68	0.15	3.46E-01	7.00E-01	---	---	---	238512_at	---																				
3.25	3.37	0.12	3.46E-01	7.00E-01	ZBTB40	zinc finger and BTB domain containing 40	chr1pter-q31.3	1559728_at	NM_001083621 /// NM_014870																				
5.39	5.76	0.38	3.46E-01	7.00E-01	CTNS	cystinosis, nephropathic	chr17p13	204925_at	NM_001031681 /// NM_004937																				
8.02	8.21	0.19	3.46E-01	7.00E-01	GOSR1	golgi SNAP receptor complex member 1	chr17q11	204630_s_at	NM_001007024 /// NM_001007025 /// NM_004871																				
2.06	2.22	0.16	3.46E-01	7.00E-01	---	---	---	234569_at	---																				
2.11	2.25	0.14	3.46E-01	7.00E-01	---	---	---	216642_at	---																				
2.11	2.23	0.12	3.46E-01	7.00E-01	---	---	---	241657_at	---																				
2.54	2.69	0.15	3.46E-01	7.00E-01	---	---	---	1570568_at	---																				
3.62	4.15	0.53	3.47E-01	7.01E-01	KLRB1	killer cell lectin-like receptor subfamily B, member 1	chr12p13	214470_at	NM_002258																				
2.12	2.23	0.11	3.47E-01	7.01E-01	LOC340094	hypothetical LOC340094	chr5p15.32	1557877_s_at	XR_040086 /// XR_040087 /// XR_040088																				
2.79	2.92	0.13	3.47E-01	7.01E-01	---	---	---	1570624_at	---																				
2.40	2.54	0.14	3.47E-01	7.01E-01	OR8D2	olfactory receptor, family 8, subfamily D, member 2	chr11q24.2	234766_at	NM_001002918																				
3.06	3.27	0.22	3.47E-01	7.01E-01	---	---	---	1564317_at	---																				
6.00	6.34	0.34	3.47E-01	7.01E-01	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	chr2p13.3-p13.1	218660_at	NM_001130455 /// NM_001130976 /// NM_001130977 /// NM_001130978 /// NM_001130979 /// NM_001130980 /// NM_001130981 /// NM_001130982 /// NM_001130983 /// NM_001130984 /// NM_001130985 /// NM_001130986 /// NM_001130987 /// NM_003494																				
5.74	5.97	0.24	3.47E-01	7.01E-01	DKFZp547E087	hypothetical gene LOC283846	chr18p11.21	235060_at	XM_496136 /// XM_931802 /// XM_931808 /// XM_931814 /// XM_931818 /// XM_931827 /// XM_931837 /// XM_931840																				
7.76	7.99	0.23	3.47E-01	7.01E-01	MRPS22	mitochondrial ribosomal protein S22	chr3q23	228059_x_at	NM_020191																				
6.10	6.32	0.22	3.47E-01	7.01E-01	TCF15	transcription factor 15 (basic helix-loop-helix)	chr20p13	207306_at	NM_004609																				
3.10	3.26	0.16	3.47E-01	7.01E-01	TLE6	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)	chr19p13.3	1553812_at	NM_024760																				

2.41	2.57	0.16	3.47E-01	7.01E-01	TF	transferrin	chr3q22.1	203400_s_at	NM_001063
2.62	2.77	0.15	3.47E-01	7.01E-01	---	---	---	1566295_at	---
2.52	2.66	0.13	3.47E-01	7.01E-01	---	---	---	239504_at	---
2.05	2.18	0.12	3.47E-01	7.01E-01	---	---	---	1558383_at	---
4.37	4.49	0.12	3.47E-01	7.01E-01	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	chr12p11	211360_s_at	NM_002223
2.63	2.75	0.12	3.47E-01	7.01E-01	FGF2	fibroblast growth factor 2 (basic)	chr4q26-q27	204421_s_at	NM_002006
2.18	2.28	0.10	3.47E-01	7.01E-01	---	---	---	1566256_s_at	---
3.00	3.19	0.19	3.47E-01	7.01E-01	OR51I1	olfactory receptor, family 51, subfamily I, member 1	chr11p15.4	234626_at	NM_001005288
5.93	6.23	0.30	3.47E-01	7.01E-01	BCR	breakpoint cluster region	chr22q11|22q11.23	202315_s_at	NM_004327 /// NM_021574
4.08	4.40	0.32	3.47E-01	7.01E-01	IGSF3	immunoglobulin superfamily, member 3	chr1p13	202421_at	NM_001007237 /// NM_001542
4.54	4.65	0.11	3.47E-01	7.01E-01	---	---	---	1562979_at	---
2.63	2.80	0.16	3.47E-01	7.01E-01	ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2	---	1553989_a_at	NM_001039362 /// NM_144583
4.69	4.93	0.24	3.47E-01	7.01E-01	KIAA1219	KIAA1219	chr20q11.23	224678_at	NM_020336
2.36	2.54	0.18	3.47E-01	7.01E-01	LOC729178	hypothetical protein LOC729178	chr6q24.3	238685_at	XR_041025 /// XR_041026 /// XR_041027
1.84	1.93	0.09	3.47E-01	7.01E-01	---	---	---	217443_at	---
2.50	2.68	0.19	3.47E-01	7.01E-01	CHD6	chromodomain helicase DNA binding protein 6	chr20q12	234681_s_at	NM_032221
1.96	2.07	0.11	3.47E-01	7.01E-01	---	---	---	224109_at	---
1.74	1.84	0.10	3.47E-01	7.01E-01	GPRIN3	GPRIN family member 3	chr4q22.1	1556697_at	NM_198281
5.97	6.27	0.30	3.47E-01	7.01E-01	---	---	---	239815_at	---
2.09	2.25	0.15	3.47E-01	7.01E-01	---	---	---	241758_at	---
6.02	6.43	0.41	3.48E-01	7.01E-01	KLF9	Kruppel-like factor 9	chr9q13	203542_s_at	NM_001206
2.99	3.16	0.17	3.47E-01	7.01E-01	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	chr13q32.2	1562425_at	NM_001001715 /// NM_005766
3.13	3.29	0.16	3.48E-01	7.01E-01	RPL13	Ribosomal protein L13	chr16q24.3|17p11.2	1565758_at	NM_000977 /// NM_033251
3.15	3.31	0.16	3.48E-01	7.01E-01	TNN	tenascin N	chr1q23-q24	215271_at	NM_022093
4.53	4.68	0.16	3.48E-01	7.01E-01	CARD14	caspase recruitment domain family, member 14	chr17q25	224113_at	NM_024110 /// NM_052819
2.21	2.36	0.15	3.47E-01	7.01E-01	CPD	Carboxypeptidase D	chr17q11.2	229600_s_at	NM_001304
2.99	3.14	0.15	3.48E-01	7.01E-01	KIAA1632	KIAA1632	chr18q12.3-q21.1	234048_s_at	NM_020964
2.04	2.15	0.12	3.48E-01	7.01E-01	---	---	---	233332_at	---
2.49	2.60	0.11	3.47E-01	7.01E-01	ZNF704	zinc finger protein 704	chr8q21.13	241963_at	NM_001033723
3.88	4.06	0.18	3.48E-01	7.01E-01	ENTPD4 /// LOXL2	ectonucleoside triphosphate diphosphohydrolase 4 /// lysyl oxidase-like 2	chr8p21.3 /// chr8p21.3-p21.2	202997_s_at	NM_001128930 /// NM_002318 /// NM_004901
6.55	7.04	0.48	3.48E-01	7.01E-01	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	chr2q14.3	224714_at	NM_032390
9.24	9.46	0.22	3.48E-01	7.01E-01	TRAM1	translocation associated membrane protein 1	chr8q13.3	201398_s_at	NM_014294 /// XM_001721007 /// XM_001721035 /// XM_001721065
7.89	8.09	0.19	3.48E-01	7.01E-01	ORMDL2	ORM1-like 2 (S. cerevisiae)	chr12q13.2	218556_at	NM_014182
3.15	3.31	0.16	3.48E-01	7.01E-01	LOC400581	GRB2-related adaptor protein-like	chr17p11.2	239074_at	NM_001129778 /// XM_001720657 /// XM_001723190
2.12	2.23	0.11	3.48E-01	7.01E-01	HMHB1	histocompatibility (minor) HB-1	chr5q32	208302_at	NM_021182
4.92	5.36	0.43	3.48E-01	7.01E-01	CCDC5	coiled-coil domain containing 5 (spindle associated)	chr18q21.1	225297_at	NM_138443
2.91	3.07	0.16	3.48E-01	7.01E-01	C3orf31	chromosome 3 open reading frame 31	chr3p25.2	234697_x_at	NM_138807
4.79	5.02	0.24	3.48E-01	7.02E-01	ZNF507	zinc finger protein 507	chr19q13.11	226327_at	NM_014910
2.01	2.11	0.10	3.48E-01	7.02E-01	TLL1	tolloid-like 1	chr4q32-q33	206415_at	NM_012464
2.49	2.66	0.17	3.48E-01	7.02E-01	ZNF385B	zinc finger protein 385B	chr2q31.2-q31.3	1555800_at	NM_001113397 /// NM_001113398 /// NM_152520
2.66	2.86	0.20	3.48E-01	7.02E-01	---	---	---	1562745_at	---
2.52	2.66	0.15	3.48E-01	7.02E-01	---	---	---	229029_at	---
2.22	2.34	0.13	3.48E-01	7.02E-01	---	---	---	1565690_at	---
3.48	3.74	0.26	3.48E-01	7.02E-01	UBXN2B	UBX domain protein 2B	chr8q12.1	238903_at	NM_001077619
5.94	6.16	0.21	3.48E-01	7.02E-01	C22orf25	chromosome 22 open reading frame 25	chr22q11.21	235396_at	NM_152906

3.52	3.72	0.21	3.48E-01	7.02E-01	LOC730432 /// STYX	similar to serine/threonine/tyrosine interacting protein /// serine/threonine/tyrosine interacting protein	---	244030_at	NM_001130701 /// NM_145251 /// XM_001125680																			
2.83	3.01	0.19	3.48E-01	7.02E-01	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	chr18q21.3-q22	216257_at	NM_012397																				
2.25	2.42	0.18	3.48E-01	7.02E-01	TSPYL6	TSPY-like 6	chr2p16.2	231339_at	NM_001003937																				
1.95	2.10	0.15	3.48E-01	7.02E-01	---	---	---	1562880_at	---																				
3.87	4.25	0.38	3.48E-01	7.02E-01	HEY1	hairy/enhancer-of-split related with YRPW motif 1	chr8q21	44783_s_at	NM_001040708 /// NM_012258																				
9.29	9.43	0.14	3.48E-01	7.02E-01	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	chr20q13.33	201114_x_at	NM_002792																				
6.92	7.06	0.14	3.48E-01	7.02E-01	THUMPD3	THUMP domain containing 3	chr3p25.3	242377_x_at	NM_001114092 /// NM_015453																				
1.77	1.87	0.09	3.48E-01	7.02E-01	---	---	---	234755_x_at	---																				
1.94	2.06	0.13	3.48E-01	7.02E-01	---	---	---	1570448_at	---																				
2.02	2.14	0.12	3.48E-01	7.02E-01	---	---	---	232872_at	---																				
2.67	2.82	0.15	3.49E-01	7.02E-01	OTOF	otoferlin	chr2p23.1	1555251_a_at	NM_004802 /// NM_194248 /// NM_194322 /// NM_194323																				
5.65	5.95	0.30	3.49E-01	7.02E-01	---	---	---	236383_at	---																				
6.26	6.52	0.27	3.49E-01	7.02E-01	RFWD2	ring finger and WD repeat domain 2	chr1q25.1-q25.2	234950_s_at	NM_001001740 /// NM_022457																				
3.83	4.05	0.22	3.49E-01	7.02E-01	41526	septin 9	chr17q25	207425_s_at	NM_001113491 /// NM_001113492 /// NM_001113493 /// NM_001113494 /// NM_001113495 /// NM_001113496 /// NM_006640																				
2.51	2.71	0.20	3.49E-01	7.02E-01	ZNF548	zinc finger protein 548	chr19q13.43	1558622_a_at	NM_152909																				
3.18	3.36	0.18	3.49E-01	7.02E-01	TP53BP1	tumor protein p53 binding protein 1	chr15q15-q21	1569098_s_at	NM_005657																				
2.06	2.23	0.17	3.49E-01	7.02E-01	NCR1	natural cytotoxicity triggering receptor 1	chr19q13.42	207860_at	NM_004829																				
2.85	3.00	0.15	3.49E-01	7.02E-01	LOC100134259 /// LOC150837	similar to hCG1987718 /// hypothetical protein LOC150837	chr2p21	230799_at	XM_001725422																				
2.30	2.44	0.14	3.49E-01	7.02E-01	LOC286382	hypothetical protein LOC286382	chr9q21.13	240545_at	---																				
2.51	2.66	0.14	3.49E-01	7.02E-01	SPINK5	serine peptidase inhibitor, Kazal type 5	chr5q32	205185_at	NM_001127698 /// NM_001127699 /// NM_006846																				
2.73	2.87	0.14	3.49E-01	7.02E-01	---	---	---	1556683_x_at	---																				
2.17	2.29	0.13	3.49E-01	7.02E-01	RNF180	ring finger protein 180	chr5q12.2	236644_at	NM_001113561 /// NM_178532																				
4.23	4.35	0.12	3.49E-01	7.02E-01	TPM1	Tropomyosin 1 (alpha)	chr15q22.1	238688_at	NM_000366 /// NM_001018004 /// NM_001018005 /// NM_001018006 /// NM_001018007 /// NM_001018008 /// NM_001018020																				
2.01	2.11	0.10	3.49E-01	7.02E-01	TOX	thymocyte selection-associated high mobility group box	chr8q12.1	204529_s_at	NM_014729																				
2.26	2.36	0.10	3.49E-01	7.02E-01	---	---	---	1562856_at	---																				
4.52	4.85	0.32	3.49E-01	7.02E-01	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	chr17p13.3	211547_s_at	NM_000430																				
5.71	6.14	0.43	3.49E-01	7.02E-01	CTSK	cathepsin K	chr1q21	202450_s_at	NM_000396																				
4.92	5.15	0.24	3.49E-01	7.02E-01	GPC1	glypican 1	chr2q35-q37	202755_s_at	NM_002081																				
1.96	2.11	0.14	3.49E-01	7.02E-01	---	---	---	244093_at	---																				
2.48	2.62	0.14	3.49E-01	7.02E-01	LOC100130219	similar to hCG2041987	chr12p13.33	236042_at	XM_001714414 /// XM_001716247																				

3.42	3.56	0.14	3.49E-01	7.02E-01	3.8-1	MHC class I mRNA fragment 3.8-1	chr6p21.3	214186_s_at	NR_002812
5.77	6.26	0.49	3.49E-01	7.03E-01	SNW1	SNW domain containing 1	chr14q24.3	215424_s_at	NM_012245
2.12	2.26	0.14	3.49E-01	7.03E-01	RUFY1	RUN and FYVE domain containing 1	chr5q35.3	229179_at	NM_001040451 /// NM_001040452 /// NM_025158
3.75	3.91	0.16	3.49E-01	7.03E-01	---	---	---	230571_at	---
3.23	3.37	0.14	3.49E-01	7.03E-01	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	chr14q32.3-qter|14q32	236183_at	NM_001376
5.69	6.15	0.46	3.49E-01	7.03E-01	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	chr9q22.2	202278_s_at	NM_006415 /// NM_178324
4.89	5.31	0.42	3.49E-01	7.03E-01	USP47	ubiquitin specific peptidase 47	chr11p15.3	223117_s_at	NM_017944
3.13	3.29	0.16	3.49E-01	7.03E-01	C19orf23	chromosome 19 open reading frame 23	chr19p13.3	239126_at	NM_152480
2.64	2.75	0.11	3.49E-01	7.03E-01	MKI67	antigen identified by monoclonal antibody Ki-67	chr10q25-qter	212020_s_at	NM_002417
4.14	4.39	0.25	3.50E-01	7.03E-01	LOC730102	hypothetical protein LOC730102	chr1q25.2	241607_at	XR_015609 /// XR_015793 /// XR_041281
4.35	4.61	0.26	3.50E-01	7.03E-01	---	---	---	238944_at	---
2.36	2.50	0.13	3.50E-01	7.03E-01	---	---	---	233530_at	---
5.37	5.83	0.46	3.50E-01	7.03E-01	KIAA1958	KIAA1958	chr9q32	230166_at	NM_133465
2.62	2.81	0.19	3.50E-01	7.03E-01	CSH1 /// CSH2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// growth hormone 1	chr17q24.2	208342_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645
7.17	7.36	0.19	3.50E-01	7.03E-01	AAK1	AP2 associated kinase 1	chr2p14	225522_at	NM_014911
2.07	2.20	0.13	3.50E-01	7.03E-01	SLC35F4	solute carrier family 35, member F4	chr14q22.2	240799_at	NM_001080455
1.96	2.09	0.13	3.50E-01	7.03E-01	---	---	---	1556497_a_at	---
5.47	5.69	0.22	3.50E-01	7.03E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	244689_at	NM_001001928 /// NM_005036
2.67	2.86	0.19	3.50E-01	7.03E-01	---	---	---	234444_at	---
2.40	2.70	0.30	3.50E-01	7.03E-01	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	chr11p11.2	215363_x_at	NM_001014986 /// NM_004476
2.54	2.90	0.36	3.50E-01	7.03E-01	CDH13	cadherin 13, H-cadherin (heart)	chr16q24.2-q24.3	204726_at	NM_001257
4.44	4.60	0.16	3.50E-01	7.03E-01	---	---	---	239249_at	---
1.73	1.89	0.16	3.50E-01	7.03E-01	RGS13	regulator of G-protein signaling 13	chr1q31.2	1568752_s_at	NM_002927 /// NM_144766
2.08	2.22	0.14	3.50E-01	7.03E-01	DTNA	dystrobrevin, alpha	chr18q12	210611_s_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981
5.79	6.14	0.35	3.50E-01	7.03E-01	TMEM52	transmembrane protein 52	chr1p36.33	230467_at	NM_178545
2.75	2.98	0.23	3.50E-01	7.03E-01	EEF1DP3	Eukaryotic translation elongation factor 1 delta pseudogene 3	chr13q13.1	233356_at	---
2.48	2.64	0.16	3.50E-01	7.03E-01	---	---	---	237631_at	---
3.44	3.60	0.16	3.50E-01	7.03E-01	---	---	---	242376_at	---
2.08	2.22	0.14	3.50E-01	7.03E-01	---	---	---	1562073_at	---
1.95	2.05	0.10	3.50E-01	7.03E-01	---	---	---	242005_at	---
3.58	3.74	0.16	3.50E-01	7.03E-01	LPAR2	lysophosphatidic acid receptor 2	chr19p12	206723_s_at	NM_004720
2.81	2.97	0.16	3.50E-01	7.04E-01	KLK2	kallikrein-related peptidase 2	chr19q13.41	209854_s_at	NM_001002231 /// NM_005551
2.26	2.40	0.14	3.50E-01	7.04E-01	FSHR	follicle stimulating hormone receptor	chr2p21-p16	211201_at	NM_000145 /// NM_181446

7.26	7.58	0.32	3.50E-01	7.04E-01	DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	chr10q26.2	218198_at	NM_018180
2.34	2.52	0.18	3.50E-01	7.04E-01	---	---	---	215742_at	---
2.61	2.73	0.12	3.50E-01	7.04E-01	OR5L2	olfactory receptor, family 5, subfamily L, member 2	chr11q11	1567285_at	NM_001004739
12.62	12.78	0.16	3.50E-01	7.04E-01	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	chr6q14.1	213614_x_at	NM_001402
2.34	2.47	0.13	3.50E-01	7.04E-01	---	---	---	211193_at	---
4.16	4.44	0.27	3.51E-01	7.04E-01	SFRS2B	splicing factor, arginine/serine-rich 2B	chr11q22	238929_at	NM_032102
2.24	2.35	0.11	3.51E-01	7.04E-01	---	---	---	234161_at	---
3.53	3.76	0.23	3.51E-01	7.04E-01	GPR114	G protein-coupled receptor 114	chr16q13	1555447_at	NM_153837
1.99	2.20	0.21	3.51E-01	7.04E-01	ESR2	estrogen receptor 2 (ER beta)	chr14q23.2	1569554_at	NM_001040275 /// NM_001040276 /// NM_001437
3.76	3.92	0.16	3.51E-01	7.04E-01	POLN	polymerase (DNA directed) nu	chr4p16.3	233454_at	NM_181808
3.96	4.36	0.40	3.51E-01	7.04E-01	ARHGAP5	Rho GTPase activating protein 5	chr14q12	1552627_a_at	NM_001030055 /// NM_001173
2.02	2.13	0.11	3.51E-01	7.04E-01	SPAG11B	sperm associated antigen 11B	chr8p23-p22	1553579_a_at	NM_016512 /// NM_058200 /// NM_058201 /// NM_058202 /// NM_058203 /// NM_058206 /// NM_058207
3.49	3.81	0.32	3.51E-01	7.04E-01	RAB6A	RAB6A, member RAS oncogene family	chr11q13.3	201048_x_at	NM_002869 /// NM_198896
3.08	3.29	0.21	3.51E-01	7.04E-01	FAM65B	family with sequence similarity 65, member B	chr6p22.3-p21.32	206707_x_at	NM_014722 /// NM_015864
2.50	2.67	0.17	3.51E-01	7.04E-01	---	---	---	231687_at	---
2.92	3.05	0.14	3.51E-01	7.04E-01	SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	chr19q13.3-q13.4	232739_at	NM_003121
2.98	3.11	0.13	3.51E-01	7.04E-01	---	---	---	211411_at	---
2.31	2.44	0.13	3.51E-01	7.04E-01	LOC285733	hypothetical LOC285733	chr6q23.1	230716_at	XM_001724204 /// XM_379432 /// XM_944838
2.09	2.21	0.12	3.51E-01	7.04E-01	VPREB1	pre-B lymphocyte gene 1	chr22q11.2|22q11.22	221349_at	NM_007128
2.28	2.38	0.10	3.51E-01	7.04E-01	PAX2	paired box 2	chr10q24	206228_at	NM_000278 /// NM_003987 /// NM_003988 /// NM_003989 /// NM_003990
6.04	6.17	0.12	3.51E-01	7.04E-01	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	chr2q37.3	231948_s_at	NM_080678
1.95	2.07	0.12	3.51E-01	7.04E-01	NCBP1	nuclear cap binding protein subunit 1, 80kDa	chr9q34.1	209519_at	NM_002486
4.01	4.19	0.19	3.51E-01	7.04E-01	INTS10	integrator complex subunit 10	chr8p21.3	237504_at	NM_018142
4.61	4.99	0.38	3.51E-01	7.04E-01	APOOL	Apolipoprotein O-like	chrXq21.1	213289_at	NM_198450
3.49	3.64	0.14	3.51E-01	7.04E-01	FAM123A	family with sequence similarity 123A	chr13q12.13	1553720_a_at	NM_152704 /// NM_199138
7.83	8.16	0.34	3.51E-01	7.04E-01	SERBP1	SERPINE1 mRNA binding protein 1	chr1p31	209669_s_at	NM_001018067 /// NM_001018068 /// NM_001018069 /// NM_015640
5.79	6.01	0.21	3.51E-01	7.04E-01	PARD6A	par-6 partitioning defective 6 homolog alpha (C. elegans)	chr16q22.1	205245_at	NM_001037281 /// NM_016948
2.20	2.34	0.14	3.51E-01	7.04E-01	GLYATL1	glycine-N-acyltransferase-like 1	chr11q12.1	227794_at	NM_080661
2.54	2.70	0.16	3.51E-01	7.04E-01	FMNL3	Formin-like 3	chr12q13.12	231231_at	NM_175736 /// NM_198900
1.96	2.13	0.17	3.51E-01	7.04E-01	---	---	---	1557843_at	---
2.73	2.88	0.15	3.51E-01	7.04E-01	GALNT8	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8)	chr12p13.3	220929_at	NM_017417
4.86	5.00	0.14	3.51E-01	7.04E-01	LOC115110	hypothetical protein LOC115110	chr1p36.32	232190_x_at	---
5.06	5.25	0.20	3.51E-01	7.04E-01	TMEM204	transmembrane protein 204	chr16p13.3	222865_x_at	NM_024600

2.36	2.50	0.14	3.52E-01	7.04E-01	CTAG1A /// CTAG1B	cancer/testis antigen 1A /// cancer/testis antigen 1B	chrXq28	211674_x_at	NM_001327 /// NM_139250 /// XM_001719185
2.28	2.39	0.12	3.52E-01	7.04E-01	---	---	---	1561309_x_at	---
5.43	5.87	0.44	3.52E-01	7.04E-01	CALU	calumenin	chr7q32.1	214845_s_at	NM_001130674 /// NM_001219
5.43	5.75	0.32	3.52E-01	7.04E-01	C14orf65	chromosome 14 open reading frame 65	chr14q32.31	222809_x_at	XR_040689 /// XR_040690 /// XR_040691
2.27	2.39	0.12	3.52E-01	7.04E-01	---	---	---	217639_at	---
5.84	6.02	0.19	3.52E-01	7.04E-01	MEX3A	mex-3 homolog A (C. elegans)	chr1q22	227512_at	NM_001093725
4.09	4.27	0.18	3.52E-01	7.04E-01	SPAG8	sperm associated antigen 8	chr9p13.3	206816_s_at	NM_001039592 /// NM_172312
4.83	4.96	0.13	3.52E-01	7.04E-01	OBP2A	odorant binding protein 2A	chr9q34	234841_x_at	NM_014582
2.43	2.55	0.12	3.52E-01	7.04E-01	ZBTB11	zinc finger and BTB domain containing 11	chr3q12.3	242433_at	NM_014415
6.48	6.74	0.26	3.52E-01	7.04E-01	KIAA1279	KIAA1279	chr10q21.3	212453_at	NM_015634
2.02	2.13	0.11	3.52E-01	7.04E-01	CSN2	casein beta	chr4q21.1	207951_at	NM_001891
1.87	1.97	0.11	3.52E-01	7.05E-01	---	---	---	242908_x_at	---
6.03	6.44	0.41	3.52E-01	7.05E-01	GPSM1	G-protein signaling modulator 1 (AGS3-like, C. elegans)	chr9q34.3	226043_at	NM_015597
4.22	4.68	0.46	3.52E-01	7.05E-01	---	---	---	215390_at	---
1.98	2.10	0.12	3.52E-01	7.05E-01	RAG2	recombination activating gene 2	chr11p13	215117_at	NM_000536
4.38	4.69	0.31	3.52E-01	7.05E-01	MOCS1	molybdenum cofactor synthesis 1	chr6p21.3	211673_s_at	NM_001075098 /// NM_005942 /// NM_005943 /// NM_138928
7.32	7.55	0.23	3.52E-01	7.05E-01	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	chr22q12.2	221756_at	NM_052880
4.58	4.75	0.17	3.52E-01	7.05E-01	TMEM121	transmembrane protein 121	chr14q32.33	219663_s_at	NM_025268
2.27	2.40	0.13	3.52E-01	7.05E-01	---	---	---	205703_at	---
4.40	4.60	0.19	3.52E-01	7.05E-01	RARA	retinoic acid receptor, alpha	chr17q21	211605_s_at	NM_000964 /// NM_001024809
3.34	3.48	0.14	3.52E-01	7.05E-01	EFNA5	ephrin-A5	chr5q21	207301_at	NM_001962
4.42	4.99	0.57	3.52E-01	7.05E-01	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	chr9q22.1-q22.3	211679_x_at	NM_005458
7.22	7.56	0.34	3.52E-01	7.05E-01	GLS	glutaminase	chr2q32-q34	203159_at	NM_014905
2.24	2.41	0.17	3.52E-01	7.05E-01	---	---	---	215586_at	---
2.12	2.25	0.13	3.52E-01	7.05E-01	---	---	---	240685_at	---
2.52	2.66	0.13	3.52E-01	7.05E-01	AMAC1	acyl-malonyl condensing enzyme 1	chr17q12	1553471_at	NM_152462
2.00	2.14	0.13	3.52E-01	7.05E-01	---	---	---	237250_at	---
10.74	11.03	0.29	3.52E-01	7.05E-01	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	chr5q35	200063_s_at	NM_001037738 /// NM_002520 /// NM_199185
6.54	6.72	0.18	3.52E-01	7.05E-01	RRAGC	Ras-related GTP binding C	chr1p34	222514_at	NM_022157
3.47	3.89	0.43	3.52E-01	7.05E-01	---	---	---	232156_at	---
2.27	2.47	0.21	3.53E-01	7.05E-01	---	---	---	1558710_at	---
7.86	8.27	0.41	3.53E-01	7.05E-01	FBXL3	F-box and leucine-rich repeat protein 3	chr13q22	225132_at	NM_012158
5.99	6.26	0.27	3.53E-01	7.05E-01	USP8	ubiquitin specific peptidase 8	chr15q21.2	202745_at	NM_001128610 /// NM_001128611 /// NM_005154
2.65	2.81	0.16	3.53E-01	7.05E-01	LOC284898	hypothetical protein LOC284898	chr22q12.1	1562030_at	---
9.61	9.84	0.23	3.53E-01	7.05E-01	PPIF	peptidylprolyl isomerase F (cyclophilin F)	chr10q22-q23	201489_at	NM_005729
2.94	3.13	0.19	3.53E-01	7.05E-01	IRGQ	immunity-related GTPase family, Q	chr19q13.31	1569310_at	NM_001007561
4.42	4.58	0.16	3.53E-01	7.05E-01	SNX26	sorting nexin 26	chr19q13.12	213827_at	NM_052948
1.84	1.98	0.14	3.53E-01	7.05E-01	LRRC7	leucine rich repeat containing 7	chr1p31.1	233499_at	NM_020794
2.91	3.15	0.24	3.53E-01	7.05E-01	---	---	---	1557738_at	---
2.09	2.20	0.11	3.53E-01	7.05E-01	---	---	---	233838_at	---
2.53	2.82	0.28	3.53E-01	7.05E-01	NAPB	N-ethylmaleimide-sensitive factor attachment protein, beta	chr20p12.3-p11.21	1570441_at	NM_022080
10.72	10.94	0.22	3.53E-01	7.05E-01	LOC284889 /// MIF	hypothetical protein LOC284889 /// macrophage migration inhibitory factor (glycosylation-inhibiting factor)	chr22q11.23	217871_s_at	NM_002415
4.21	4.58	0.37	3.53E-01	7.05E-01	VRK1	vaccinia related kinase 1	chr14q32	203856_at	NM_003384
2.21	2.35	0.14	3.53E-01	7.06E-01	LOC646168	hypothetical protein LOC646168	chr3q26.1	1556920_s_at	XM_934868 /// XM_934869 /// XM_934871

2.07	2.20	0.13	3.53E-01	7.06E-01	LOC100129195	hypothetical protein LOC100129195	chr6p22.1	1557062_at	XM_001715702 /// XM_001719301 /// XM_001722758
4.15	4.27	0.13	3.53E-01	7.06E-01	ATP9B	ATPase, class II, type 9B	chr18q23	237766_at	NM_198531
2.48	2.65	0.18	3.53E-01	7.06E-01	---	---	---	240783_at	---
6.83	7.03	0.20	3.53E-01	7.06E-01	FLNB	filamin B, beta (actin binding protein 278)	chr3p14.3	208613_s_at	NM_001457
5.25	5.53	0.28	3.53E-01	7.06E-01	LOC286440	hypothetical protein LOC286440	chrXq22.3	209733_at	---
1.94	2.06	0.12	3.53E-01	7.06E-01	ANKRD30B	ankyrin repeat domain 30B	chr18p11.21	1562294_x_at	XM_001716904 /// XM_001717561 /// XM_001717810
1.95	2.07	0.12	3.53E-01	7.06E-01	RAB9P1	RAB9, member RAS oncogene family, pseudogene 1	chr5q21.2	208245_at	NR_000039
2.40	2.58	0.18	3.53E-01	7.06E-01	HRK	Harakiri, BCL2 interacting protein (contains only BH3 domain)	chr12q24.22	206865_at	NM_003806
2.78	2.94	0.16	3.53E-01	7.06E-01	PAX3	paired box 3	chr2q35-q37|2q35	207679_at	NM_000438 /// NM_001127366 /// NM_013942 /// NM_181457 /// NM_181458 /// NM_181459 /// NM_181460 /// NM_181461
2.63	2.77	0.15	3.53E-01	7.06E-01	FAM35A	family with sequence similarity 35, member A	chr10q23.2	233048_at	NM_019054
2.07	2.17	0.11	3.53E-01	7.06E-01	FKBP7	FK506 binding protein 7	chr2q31.2	223667_at	NM_181342
6.95	7.23	0.28	3.54E-01	7.06E-01	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	chr12q12	201745_at	NM_002822
3.77	3.99	0.22	3.54E-01	7.06E-01	HECA	headcase homolog (Drosophila)	chr6q23-q24	230529_at	NM_016217
2.55	2.71	0.15	3.54E-01	7.06E-01	---	---	---	244053_at	---
2.10	2.24	0.14	3.53E-01	7.06E-01	hCG_1795283	hCG1818123	chr13q31.2	232848_at	XM_930726 /// XM_942773
2.54	2.66	0.12	3.54E-01	7.06E-01	---	---	---	232858_at	---
2.67	2.78	0.11	3.54E-01	7.06E-01	KALRN	kalirin, RhoGEF kinase	chr3q21.1-q21.2	236651_at	NM_001024660 /// NM_003947 /// NM_007064
5.93	6.14	0.21	3.54E-01	7.06E-01	ALMS1	Alstrom syndrome 1	chr2p13	214707_x_at	NM_015120
2.93	3.09	0.16	3.54E-01	7.06E-01	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	chr16q22.1	214025_at	NM_018380
3.35	3.47	0.12	3.54E-01	7.06E-01	---	---	---	234528_at	---
4.40	4.68	0.28	3.54E-01	7.06E-01	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	chr14q24.1	225928_at	NM_006370
5.35	5.60	0.25	3.54E-01	7.06E-01	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	chr9q33-q34.1	230031_at	NM_005347
5.37	5.61	0.24	3.54E-01	7.06E-01	BOC	Boc homolog (mouse)	chr3q13.2	224184_s_at	NM_033254
2.75	2.90	0.15	3.54E-01	7.06E-01	BLK	B lymphoid tyrosine kinase	chr8p23-p22	210934_at	NM_001715
3.50	3.66	0.15	3.54E-01	7.06E-01	ALG2	Asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)	chr9q22.33	228166_at	NM_033087
5.70	5.86	0.15	3.54E-01	7.06E-01	---	---	---	241904_at	---
2.39	2.53	0.14	3.54E-01	7.06E-01	---	---	---	1560848_at	---
2.04	2.17	0.13	3.54E-01	7.06E-01	---	---	---	235937_at	---
1.99	2.16	0.17	3.54E-01	7.06E-01	---	---	---	243381_at	---
2.82	3.01	0.19	3.54E-01	7.06E-01	DSCR4	Down syndrome critical region gene 4	chr21q22.2	207258_at	NM_005867
2.31	2.44	0.13	3.54E-01	7.06E-01	---	---	---	233190_at	---
4.23	4.66	0.43	3.54E-01	7.06E-01	RECQL	RecQ protein-like (DNA helicase Q1-like)	chr12p12	210568_s_at	NM_002907 /// NM_032941
4.57	4.79	0.21	3.54E-01	7.06E-01	COMMD5	COMM domain containing 5	chr8q24-qter	232640_at	NM_001081003 /// NM_001081004 /// NM_014066
4.50	4.70	0.19	3.54E-01	7.06E-01	ZNF667	zinc finger protein 667	chr19q13.43	236635_at	NM_022103
2.38	2.55	0.17	3.54E-01	7.06E-01	---	---	---	1565881_at	---
3.17	3.32	0.16	3.54E-01	7.06E-01	GOLGA2LY1 /// GOLGA2LY2	golgi autoantigen, golgin subfamily a, 2-like, Y-linked 1 /// golgi autoantigen, golgin subfamily a, 2-like, Y-linked 2	chrYq11.223	234715_at	NR_001555 /// NR_002195
2.41	2.53	0.13	3.54E-01	7.06E-01	---	---	---	242495_at	---
1.81	1.92	0.11	3.54E-01	7.06E-01	---	---	---	1555601_at	---
1.76	1.86	0.10	3.54E-01	7.06E-01	---	---	---	1567379_at	---
2.28	2.41	0.14	3.54E-01	7.06E-01	---	---	---	1560118_at	---
1.92	2.04	0.11	3.54E-01	7.06E-01	SEMG1	semenogelin I	chr20q12-q13.2	206442_at	NM_003007 /// NM_198139
4.02	4.18	0.16	3.54E-01	7.06E-01	EGR4	Early growth response 4	chr2p13	231575_at	NM_001965
2.16	2.28	0.12	3.54E-01	7.06E-01	---	---	---	236063_at	---

6.00	6.19	0.19	3.54E-01	7.07E-01	HCCS	holocytochrome c synthase (cytochrome c heme-lyase)	chrXp22.3	203745_at	NM_001122608 /// NM_005333
3.34	3.55	0.21	3.55E-01	7.07E-01	BZRPL1	benzodiazapine receptor (peripheral)-like 1	chr6p21.1	215449_at	NM_001010873
4.93	5.19	0.25	3.55E-01	7.07E-01	SIGLEC11	sialic acid binding Ig-like lectin 11	chr19q13.33	1552911_at	NM_052884
5.08	5.27	0.19	3.55E-01	7.07E-01	---	---	---	1558515_at	---
2.90	3.09	0.19	3.55E-01	7.07E-01	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	chr12q13.3	206435_at	NM_001478
4.52	4.71	0.18	3.55E-01	7.07E-01	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	chr3p21.31	239772_x_at	NM_014966 /// NM_138615
2.25	2.39	0.14	3.55E-01	7.07E-01	RAB39B	RAB39B, member RAS oncogene family	chrXq28	230075_at	NM_171998
1.92	2.03	0.11	3.55E-01	7.07E-01	RP3-377H14.5	hypothetical protein FLJ35429	chr6p22.1	1562381_at	XR_039876 /// XR_039877 /// XR_039878 /// XR_039879 /// XR_039880
2.46	2.59	0.13	3.55E-01	7.07E-01	---	---	---	216581_at	---
3.30	3.42	0.12	3.55E-01	7.07E-01	CHERP	calcium homeostasis endoplasmic reticulum protein	chr19p13.1	202229_s_at	NM_006387
6.30	6.62	0.32	3.55E-01	7.07E-01	KIAA1797	KIAA1797	chr9p21	218503_at	NM_017794
1.92	2.03	0.11	3.55E-01	7.07E-01	HNRNPA3P1	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	chr10q11.21	206808_at	NR_002726
3.65	4.03	0.38	3.55E-01	7.07E-01	C12orf4	chromosome 12 open reading frame 4	chr12p13.3	218374_s_at	NM_020374
3.98	4.40	0.41	3.55E-01	7.07E-01	STAG1	stromal antigen 1	chr3q22.3	202293_at	NM_005862
2.63	2.86	0.23	3.55E-01	7.07E-01	---	---	---	235890_at	---
2.95	3.12	0.17	3.55E-01	7.07E-01	RGS9BP	regulator of G protein signaling 9 binding protein	chr19q13.11	1556199_a_at	NM_207391
3.73	3.88	0.15	3.55E-01	7.07E-01	IMP5	intramembrane protease 5	chr17q21.31	231253_at	NM_175882
2.81	2.94	0.13	3.55E-01	7.07E-01	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	chr12q13.2	235129_at	NM_006741
1.91	2.03	0.11	3.55E-01	7.07E-01	GLB1L3	galactosidase, beta 1-like 3	chr11q25	1569886_a_at	NM_001080407
1.96	2.07	0.12	3.55E-01	7.07E-01	GTF2A1L /// STON1 /// STON1-GTF2A1L	general transcription factor IIA, 1-like /// stonin 1 /// STON1-GTF2A1L	chr2p16.3	220190_s_at	NM_006872 /// NM_006873 /// NM_172196 /// NM_172311
4.23	4.84	0.61	3.55E-01	7.07E-01	ATR	ataxia telangiectasia and Rad3 related	chr3q22-q24	209902_at	NM_001184
7.03	7.40	0.37	3.55E-01	7.07E-01	RBMS1	RNA binding motif, single stranded interacting protein 1	chr2q24.2	209868_s_at	NM_002897 /// NM_016836 /// NM_016839
4.26	4.61	0.35	3.55E-01	7.07E-01	IGK@ /// IGKC /// LOC647506 /// LOC650405 /// LOC652493	immunoglobulin kappa locus /// immunoglobulin kappa constant /// similar to Ig kappa chain V-I region HK101 precursor /// similar to Ig kappa chain V-I region HK102 precursor /// similar to Ig kappa chain V-I region HK102 precursor	chr2p12	217157_x_at	XM_001713938 /// XM_001715827 /// XM_001724425
5.18	5.48	0.31	3.55E-01	7.07E-01	CNNM2	cyclin M2	chr10q24.32	206818_s_at	NM_017649 /// NM_199076 /// NM_199077
4.31	4.56	0.25	3.55E-01	7.07E-01	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	chr7p15	213786_at	NM_001079864 /// NM_006024
4.61	4.78	0.17	3.55E-01	7.07E-01	PDE6G	phosphodiesterase 6G, cGMP-specific, rod, gamma	chr17q25	210060_at	NM_002602
3.34	3.51	0.17	3.55E-01	7.07E-01	CCDC42	coiled-coil domain containing 42	chr17p13.1	230881_at	NM_144681
2.86	3.02	0.17	3.55E-01	7.07E-01	---	---	---	238024_at	---
7.83	7.99	0.16	3.55E-01	7.07E-01	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	chr19q13.1-q13.2	202201_at	NM_000713
2.21	2.36	0.16	3.55E-01	7.07E-01	---	---	---	233856_at	---
2.27	2.43	0.15	3.55E-01	7.07E-01	---	---	---	233981_at	---
1.93	2.08	0.14	3.55E-01	7.07E-01	---	---	---	243126_x_at	---
2.26	2.40	0.14	3.55E-01	7.07E-01	GABRA3	gamma-aminobutyric acid (GABA) A receptor, alpha 3	chrXq28	207210_at	NM_000808
2.53	2.67	0.14	3.55E-01	7.07E-01	ZNF154	zinc finger protein 154	chr19q13.4	216677_at	NM_001085384
2.71	2.84	0.13	3.55E-01	7.07E-01	---	---	---	1565730_at	---
2.93	3.06	0.13	3.55E-01	7.07E-01	---	---	---	1557410_at	---
2.18	2.30	0.12	3.55E-01	7.07E-01	---	---	---	1561706_at	---
2.11	2.22	0.11	3.55E-01	7.07E-01	---	---	---	1559807_at	---
2.20	2.31	0.11	3.55E-01	7.07E-01	ZNF808	zinc finger protein 808	chr19q13.41	1554476_x_at	NM_001039886
1.95	2.06	0.11	3.55E-01	7.07E-01	FSD1L	fibronectin type III and SPRY domain containing 1-like	chr9q31	223985_at	NM_031919 /// NM_207647
1.87	1.97	0.11	3.55E-01	7.07E-01	LOC285954	hypothetical protein LOC285954	chr7p13	1559163_at	---
9.38	9.87	0.50	3.56E-01	7.07E-01	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	chr5q35	221691_x_at	NM_001037738 /// NM_002520 /// NM_199185
2.83	3.04	0.21	3.56E-01	7.07E-01	---	---	---	241218_at	---

2.25	2.41	0.16	3.56E-01	7.07E-01	SPATS1 /// TMEM151B	spermatogenesis associated, serine-rich 1 /// transmembrane protein 151B	chr6p21.1	239870_at	NM_145026 /// XM_001723534 /// XM_001723740 /// XM_001725716
4.69	5.07	0.39	3.56E-01	7.07E-01	USP38	ubiquitin specific peptidase 38	---	223288_at	NM_032557
4.52	4.78	0.26	3.56E-01	7.07E-01	NUP50	nucleoporin 50kDa	chr22q13.31	218294_s_at	NM_007172 /// NM_153645
3.50	3.72	0.23	3.56E-01	7.07E-01	FLJ35220	Hypothetical protein FLJ35220	chr17q25.3	238400_at	NM_173627
5.35	5.52	0.17	3.56E-01	7.07E-01	TXNL4A	thioredoxin-like 4A	chr18q23	202835_at	NM_006701
2.33	2.46	0.13	3.56E-01	7.07E-01	SIGLECP3	sialic acid binding Ig-like lectin, pseudogene 3	chr19q13.3	232686_at	NR_002804
4.50	4.91	0.41	3.56E-01	7.07E-01	TTC37	tetratricopeptide repeat domain 37	chr5q15	203049_s_at	NM_014639
2.47	2.84	0.37	3.56E-01	7.07E-01	OSBPL6	oxysterol binding protein-like 6	chr2q31-q32.1	223805_at	NM_032523 /// NM_145739
3.58	3.72	0.14	3.56E-01	7.07E-01	MGC33556	Hypothetical LOC339541	chr1p34.1	238366_at	XR_039961 /// XR_039962 /// XR_039963
2.48	2.60	0.13	3.56E-01	7.07E-01	LOC100129482 /// ZNF37B	similar to zinc finger protein 37a (KOX 21) /// zinc finger protein 37B	chr10q11.21	215358_x_at	XR_037028 /// XR_037227 /// XR_039227 /// XR_040507 /// XR_040508 /// XR_040509 /// XR_040510 /// XR_040511 /// XR_040512
11.44	11.55	0.12	3.56E-01	7.07E-01	GNAS	GNAS complex locus	chr20q13.3	200981_x_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259
6.68	7.02	0.33	3.56E-01	7.07E-01	MRPS9	mitochondrial ribosomal protein S9	chr2q12.1	226749_at	NM_182640
5.41	5.58	0.17	3.56E-01	7.07E-01	APOL1	apolipoprotein L, 1	chr22q13.1	209546_s_at	NM_003661 /// NM_145343
4.74	4.89	0.15	3.56E-01	7.07E-01	---	---	---	233961_at	---
2.79	2.92	0.14	3.56E-01	7.07E-01	MN1	meningioma (disrupted in balanced translocation) 1	chr22q11|22q12.1	205330_at	NM_002430
2.24	2.37	0.13	3.56E-01	7.07E-01	FLJ45983	FLJ45983 protein	chr10p14	240192_at	NM_207423
2.26	2.37	0.12	3.56E-01	7.07E-01	KAP2.1B /// KRTAP2-4 /// LOC644350 /// LOC728285 /// LOC728934 /// LOC730755	keratin associated protein 2.1B /// keratin associated protein 2-4 /// hypothetical LOC644350 /// similar to keratin associated protein /// hypothetical LOC728934 /// similar to keratin associated protein 2-4	chr17q12-q21 /// chr17q21.2	220970_s_at	NM_033184 /// XM_001127070 /// XM_001127094 /// XM_001128836 /// XM_001714716 /// XM_927511
2.86	2.96	0.11	3.56E-01	7.07E-01	---	---	---	243223_at	---
2.15	2.26	0.10	3.56E-01	7.07E-01	LOC154822	hypothetical LOC154822	chr7q36.3	1559712_at	---
4.02	4.40	0.38	3.56E-01	7.07E-01	APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	chr3p21.1-p14.3	222538_s_at	NM_012096
4.87	5.25	0.37	3.56E-01	7.07E-01	LPHN2	latrophilin 2	chr1p31.1	206953_s_at	NM_012302
2.04	2.17	0.13	3.56E-01	7.07E-01	---	---	---	1561592_at	---
2.21	2.35	0.14	3.56E-01	7.08E-01	---	---	---	244562_s_at	---
2.14	2.29	0.15	3.56E-01	7.08E-01	GPR174	G protein-coupled receptor 174	chrXq21.1	224285_at	NM_032553 /// XM_001715858
3.17	3.30	0.13	3.56E-01	7.08E-01	---	---	---	244278_at	---
2.15	2.27	0.12	3.57E-01	7.08E-01	---	---	---	1557581_x_at	---
2.03	2.15	0.13	3.57E-01	7.08E-01	HNF4G	hepatocyte nuclear factor 4, gamma	chr8q21.11	207456_at	NM_004133
3.96	4.13	0.16	3.57E-01	7.08E-01	EZR	ezrin	chr6q25.2-q26	217230_at	NM_001111077 /// NM_003379
3.55	3.69	0.14	3.57E-01	7.08E-01	WASL	Wiskott-Aldrich syndrome-like	chr7q31.3	230340_s_at	NM_003941
2.56	2.68	0.12	3.57E-01	7.08E-01	ARRDC1	arrestin domain containing 1	chr9q34.3	234607_at	NM_152285
2.15	2.27	0.11	3.57E-01	7.08E-01	LOC400891	similar to chromosome 14 open reading frame 166B	chr22q11.21	1569213_at	XR_041652 /// XR_041653 /// XR_041654
1.91	2.01	0.10	3.57E-01	7.08E-01	---	---	---	237138_at	---
1.92	2.01	0.09	3.57E-01	7.08E-01	PLCE1	Phospholipase C, epsilon 1	chr10q23	239904_at	NM_016341

8.15	8.58	0.44	3.57E-01	7.08E-01	SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	chr19q13.3	206293_at	NM_003167
6.11	6.40	0.30	3.57E-01	7.08E-01	GATC	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	chr12q24.31	225430_at	NM_176818
3.78	4.07	0.29	3.57E-01	7.08E-01	---	---	---	241928_at	---
2.39	2.58	0.19	3.57E-01	7.08E-01	CALB1	calbindin 1, 28kDa	chr8q21.3-q22.1	205626_s_at	NM_004929
4.24	4.41	0.17	3.57E-01	7.08E-01	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	chr19q13	204229_at	NM_020309
3.80	3.96	0.16	3.57E-01	7.08E-01	---	---	---	217715_x_at	---
2.99	3.14	0.15	3.57E-01	7.08E-01	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	chr12q24.2	228607_at	NM_001032731 /// NM_002535 /// NM_016817
2.34	2.48	0.14	3.57E-01	7.08E-01	---	---	---	237194_at	---
1.99	2.11	0.12	3.57E-01	7.08E-01	---	---	---	1560800_at	---
1.78	1.89	0.10	3.57E-01	7.08E-01	---	---	---	239478_x_at	---
3.93	4.19	0.26	3.57E-01	7.08E-01	SLC16A11	Solute carrier family 16, member 11 (monocarboxylic acid transporter 11)	chr17p13.1	241952_at	NM_153357
2.79	2.93	0.14	3.57E-01	7.08E-01	MAS1L	MAS1 oncogene-like	chr6p21	234820_at	NM_052967
2.34	2.48	0.14	3.57E-01	7.08E-01	AP1GBP1	AP1 gamma subunit binding protein 1	chr17q12	232982_at	NM_007247 /// NM_080550
1.96	2.07	0.11	3.57E-01	7.08E-01	---	---	---	233318_at	---
5.70	5.86	0.16	3.57E-01	7.08E-01	DKFZp667G2110	hypothetical protein DKFZp667G2110	chr3q11.2	214030_at	NM_153605
2.07	2.21	0.14	3.57E-01	7.08E-01	FOXJ2	forkhead box J2	chr12p13.31	1555305_at	NM_018416
6.71	7.00	0.29	3.57E-01	7.08E-01	NPM2	nucleophosmin/nucleoplasmin, 2	chr8p21.3	230977_at	NM_182795
2.98	3.17	0.19	3.57E-01	7.08E-01	ACSM2A /// ACSM2B	acyl-CoA synthetase medium-chain family member 2A /// acyl-CoA synthetase medium-chain family member 2B	chr16p12.3	214069_at	NM_001010845 /// NM_001105069 /// NM_182617 /// XM_001724180 /// XM_001724186 /// XM_001724187
2.34	2.46	0.12	3.57E-01	7.08E-01	ADRB1	adrenergic, beta-1-, receptor	chr10q24-q26	208214_at	NM_000684
7.19	7.60	0.41	3.57E-01	7.08E-01	CAST	calpastatin	chr5q15	208908_s_at	NM_001042440 /// NM_001042441 /// NM_001042442 /// NM_001042443 /// NM_001042444 /// NM_001042445 /// NM_001042446 /// NM_001750 /// NM_173060 /// NM_173061 /// NM_173063
5.28	5.46	0.18	3.57E-01	7.08E-01	---	---	---	236679_x_at	---
4.27	4.52	0.24	3.58E-01	7.08E-01	C10orf84	chromosome 10 open reading frame 84	chr10q26.11	234947_s_at	NM_001134672 /// NM_022063
4.71	4.88	0.17	3.58E-01	7.08E-01	CBX8	chromobox homolog 8 (Pc class homolog, Drosophila)	chr17q25.3	219755_at	NM_020649
3.33	3.46	0.14	3.58E-01	7.08E-01	---	---	---	244129_at	---
5.55	6.17	0.62	3.58E-01	7.08E-01	CCDC151	coiled-coil domain containing 151	chr19p13.2	230807_at	NM_145045
4.41	4.68	0.27	3.58E-01	7.08E-01	TMEM37	transmembrane protein 37	chr2q14.2	1554485_s_at	NM_183240
3.20	3.38	0.18	3.58E-01	7.08E-01	---	---	---	1564778_at	---
3.91	4.09	0.18	3.58E-01	7.08E-01	---	---	---	217472_at	---
2.97	3.15	0.18	3.58E-01	7.08E-01	PLEKHG4B	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	chr5p15.33	236255_at	NM_052909
3.05	3.21	0.16	3.58E-01	7.08E-01	---	---	---	234225_at	---
2.06	2.18	0.12	3.58E-01	7.08E-01	LOC100131691	hypothetical protein LOC100131691	chr19q13.43	1568864_at	XM_001718612 /// XM_001718643 /// XM_001719058
1.89	1.99	0.10	3.58E-01	7.08E-01	CAPN14	calpain 14	chr2p23.1-p21	1557321_a_at	XR_017761 /// XR_040604 /// XR_040605

6.36	6.72	0.36	3.58E-01	7.08E-01	PRNP	prion protein	chr20p13	215707_s_at	NM_000311 /// NM_001080121 /// NM_001080122 /// NM_001080123 /// NM_183079																				
4.14	4.43	0.29	3.58E-01	7.08E-01	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	chr5q22.2	244777_at	NM_152624																				
6.12	6.60	0.48	3.58E-01	7.08E-01	IPO5	importin 5	chr13q32.2	211954_s_at	NM_002271																				
3.32	3.48	0.16	3.58E-01	7.08E-01	EHMT1	euchromatic histone-lysine N-methyltransferase 1	chr9q34.3	219339_s_at	NM_024757																				
3.36	3.53	0.17	3.58E-01	7.08E-01	RIPK4	receptor-interacting serine-threonine kinase 4	chr21q22.3	221215_s_at	NM_020639																				
1.91	2.06	0.15	3.58E-01	7.08E-01	ARPP-21 /// LOC100130503	cyclic AMP-regulated phosphoprotein, 21 kD /// hypothetical protein LOC100130503	chr3p22.3	1556599_s_at	NM_001025068 /// NM_001025069 /// NM_016300 /// NM_198399 /// XM_001717149 /// XM_001717791 /// XM_001718042																				
3.16	3.28	0.12	3.58E-01	7.08E-01	NMNAT2	nicotinamide nucleotide adenylyltransferase 2	chr1q25	1562818_at	NM_015039 /// NM_170706																				
2.18	2.30	0.12	3.58E-01	7.08E-01	---	---	---	239671_at	---																				
8.59	8.85	0.26	3.58E-01	7.08E-01	CCDC69	coiled-coil domain containing 69	chr5q33.1	212886_at	NM_015621																				
2.09	2.22	0.12	3.58E-01	7.08E-01	---	---	---	1556387_at	---																				
2.28	2.40	0.12	3.58E-01	7.08E-01	CDC25C	cell division cycle 25 homolog C (S. pombe)	chr5q31	216914_at	NM_001790 /// NM_022809																				
1.92	2.02	0.11	3.58E-01	7.08E-01	CASC2	cancer susceptibility candidate 2	chr10q26.11	1564371_a_at	XR_041332 /// XR_041333 /// XR_041334																				
4.07	4.19	0.12	3.58E-01	7.09E-01	C5orf27	chromosome 5 open reading frame 27	chr5q15	239380_at	XR_040298 /// XR_040299 /// XR_040300 /// XR_040301 /// XR_040302 /// XR_040303																				
2.07	2.18	0.12	3.58E-01	7.09E-01	ADAM23	ADAM metallopeptidase domain 23	chr2q33	1559268_at	NM_003812																				
3.39	3.81	0.42	3.58E-01	7.09E-01	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	chr7p11	205311_at	NM_000790 /// NM_001082971																				
5.11	5.41	0.30	3.58E-01	7.09E-01	---	---	---	230178_s_at	---																				
5.68	5.91	0.23	3.58E-01	7.09E-01	EHD2	EH-domain containing 2	chr19q13.3	205341_at	NM_014601																				
4.95	5.18	0.23	3.58E-01	7.09E-01	LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	chr3q29	223200_s_at	NM_018385																				
3.57	3.72	0.15	3.58E-01	7.09E-01	C15orf42	chromosome 15 open reading frame 42	chr15q26.1	232475_at	NM_152259																				
1.97	2.14	0.16	3.58E-01	7.09E-01	LOC283484	hypothetical protein LOC283484	chr13q33.3	1556940_at	---																				
2.08	2.20	0.12	3.58E-01	7.09E-01	---	---	---	216108_at	---																				
2.45	2.56	0.11	3.58E-01	7.09E-01	BTBD16	BTB (POZ) domain containing 16	chr10q26.13	1552566_at	NM_144587																				
2.81	2.97	0.16	3.58E-01	7.09E-01	CAPRIN1	cell cycle associated protein 1	chr11p13	243370_at	NM_005898 /// NM_203364																				
2.61	2.76	0.15	3.58E-01	7.09E-01	---	---	---	1566543_at	---																				
4.80	5.19	0.39	3.59E-01	7.09E-01	---	---	---	242363_at	---																				
2.48	2.84	0.37	3.59E-01	7.09E-01	POU2AF1	POU class 2 associating factor 1	chr11q23.1	205267_at	NM_006235																				
2.67	2.81	0.14	3.59E-01	7.09E-01	---	---	---	1569341_at	---																				
4.03	4.41	0.38	3.59E-01	7.09E-01	---	---	---	237864_at	---																				
3.08	3.30	0.22	3.59E-01	7.09E-01	---	---	---	235065_at	---																				

7.77	7.95	0.18	3.59E-01	7.09E-01	hCG_2015956 /// LOC100127893 /// LOC100130892 /// LOC100131085 /// LOC388401 /// LOC441896 /// LOC641900 /// LOC728380 /// LOC728843 /// RPL7	hCG2015956 /// similar to ribosomal protein L7 /// hypothetical protein LOC100130892 /// hypothetical LOC100131085 /// similar to ribosomal protein L7 /// similar to ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// hypothetical LOC728380 /// hypothetical LOC728843 /// ribosomal protein L7	chr17q21.33 /// chr1p13.3 /// chr2p22.2 /// chr5q14.1 /// chr5q34 /// chr6p22.3 /// chr7q31.1 /// chr8q21.11	217092_x_at	NM_000971 /// XM_001719048 /// XM_001720172 /// XM_001722435 /// XM_001722574 /// XM_001725978 /// XM_943842 /// XR_015391 /// XR_015500 /// XR_015600 /// XR_015705 /// XR_016234 /// XR_016879 /// XR_018042 /// XR_018794 /// XR_038286 /// XR_038691 /// XR_038779 /// XR_038885 /// XR_038901 /// XR_038947 /// XR_039043 /// XR_039090 /// XR_039345 /// XR_039473 /// XR_039795
2.79	2.94	0.15	3.59E-01	7.09E-01	LOC126536	hypothetical protein LOC126536	chr19p13.12	237242_at	XR_041168 /// XR_041169 /// XR_041170
3.21	3.35	0.14	3.59E-01	7.09E-01	ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4	chr11q23.3	207593_at	NM_022169
6.09	6.39	0.30	3.59E-01	7.09E-01	UBXN7	UBX domain protein 7	chr3q29	212840_at	NM_015562
4.85	5.08	0.23	3.59E-01	7.09E-01	COL1A1	collagen, type I, alpha 1	chr17q21.33	217430_x_at	NM_000088
2.83	3.00	0.17	3.59E-01	7.09E-01	TTC23	tetratricopeptide repeat domain 23	chr15q26.3	240716_at	NM_001040655 /// NM_001040656 /// NM_001040657 /// NM_001040658 /// NM_001040659 /// NM_001040660 /// NM_022905
1.99	2.12	0.13	3.59E-01	7.09E-01	---	---	---	240544_at	---
5.32	5.80	0.49	3.59E-01	7.09E-01	FASTKD2	FAST kinase domains 2	chr2q33.3	216996_s_at	NM_014929
4.89	5.27	0.39	3.59E-01	7.09E-01	UHRF1BP1L	UHRF1 binding protein 1-like	chr12q23.1	213118_at	NM_001006947 /// NM_015054
2.53	2.90	0.37	3.59E-01	7.09E-01	RHOJ	ras homolog gene family, member J	chr14q23.2	235489_at	NM_020663
2.23	2.37	0.15	3.59E-01	7.09E-01	---	---	---	1557389_at	---
2.22	2.36	0.13	3.59E-01	7.09E-01	---	---	---	240015_at	---
2.29	2.42	0.13	3.59E-01	7.09E-01	RBL1	retinoblastoma-like 1 (p107)	chr20q11.2	1555003_at	NM_002895 /// NM_183404
2.75	2.97	0.22	3.59E-01	7.10E-01	ERAP2	Endoplasmic reticulum aminopeptidase 2	chr5q15	227462_at	NM_001130140 /// NM_022350
4.03	4.22	0.20	3.59E-01	7.10E-01	FAM71A	family with sequence similarity 71, member A	chr1q32.3	1552383_at	NM_153606
2.22	2.41	0.19	3.59E-01	7.10E-01	---	---	---	1559131_a_at	---
4.66	4.83	0.17	3.59E-01	7.10E-01	BMF	Bcl2 modifying factor	chr15q14	226530_at	NM_001003940 /// NM_001003942 /// NM_001003943 /// NM_033503
2.09	2.24	0.15	3.59E-01	7.10E-01	NSUN7	NOL1/NOP2/Sun domain family, member 7	chr4p14	220194_at	NM_024677
2.53	2.68	0.15	3.59E-01	7.10E-01	---	---	---	220687_at	---
2.16	2.30	0.14	3.59E-01	7.10E-01	---	---	---	236315_at	---

3.82	3.95	0.13	3.59E-01	7.10E-01	RP3-439I14.1	Hypothetical protein LOC100129852	chr6q21	244175_at	XM_001715197 /// XM_001716786 /// XM_001719481																				
1.95	2.07	0.12	3.60E-01	7.10E-01	---	---	---	231489_x_at	---																				
4.08	4.21	0.12	3.60E-01	7.10E-01	---	---	---	244055_at	---																				
6.65	7.01	0.36	3.60E-01	7.10E-01	---	---	---	236685_at	---																				
3.91	4.10	0.20	3.60E-01	7.10E-01	FN1	fibronectin 1	chr2q34	214701_s_at	NM_002026 /// NM_054034 /// NM_212474 /// NM_212475 /// NM_212476 /// NM_212478 /// NM_212482																				
3.78	3.93	0.15	3.60E-01	7.10E-01	CEP27	centrosomal protein 27kDa	chr15q15.1	229208_at	NM_001130447 /// NM_018097																				
7.59	7.73	0.14	3.60E-01	7.10E-01	NPEPL1	aminopeptidase-like 1	chr20q13.32	89476_r_at	NM_024663																				
3.99	4.12	0.12	3.60E-01	7.10E-01	ZNF335	zinc finger protein 335	chr20q11.21-q13.12	78330_at	NM_022095																				
5.01	5.50	0.49	3.60E-01	7.10E-01	LIN7C	lin-7 homolog C (C. elegans)	chr11p14	219399_at	NM_018362																				
3.06	3.21	0.15	3.60E-01	7.10E-01	HGFAC	HGF activator	chr4p16	207027_at	NM_001528																				
2.30	2.43	0.13	3.60E-01	7.10E-01	WDR64	WD repeat domain 64	chr1q43	1553373_at	NM_144625																				
5.15	5.45	0.30	3.60E-01	7.10E-01	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	chr7q21.3	233985_x_at	NM_017650																				
2.50	2.70	0.21	3.60E-01	7.10E-01	LOC729085	hypothetical protein LOC729085	chr3p22.1	232124_at	NM_001129908 /// XM_001133294 /// XM_001724952 /// XM_001725043																				
5.43	5.61	0.18	3.60E-01	7.10E-01	NEIL1	nei endonuclease VIII-like 1 (E. coli)	chr15q24.2	241477_at	NM_024608																				
6.03	6.18	0.15	3.60E-01	7.10E-01	CNOT1	CCR4-NOT transcription complex, subunit 1	chr16q21	200861_at	NM_016284 /// NM_206999																				
3.49	3.62	0.14	3.60E-01	7.10E-01	ZFR2	zinc finger RNA binding protein 2	chr19p13.3	215419_at	NM_015174																				
5.55	5.83	0.27	3.60E-01	7.10E-01	RRAS2	related RAS viral (r-ras) oncogene homolog 2	chr11p15.2	212590_at	NM_001102669 /// NM_012250																				
2.59	3.18	0.59	3.60E-01	7.10E-01	AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	chr4q25	221008_s_at	NM_031279																				
3.05	3.16	0.11	3.60E-01	7.10E-01	ZNF100	zinc finger protein 100	chr19p12	238791_at	NM_173531																				
2.09	2.20	0.11	3.60E-01	7.10E-01	---	---	---	243767_at	---																				
1.83	1.93	0.10	3.60E-01	7.10E-01	LOC90925	hypothetical protein LOC90925	chr14q32.33	210450_at	XR_017976																				
5.51	5.84	0.33	3.60E-01	7.10E-01	HSPA9	heat shock 70kDa protein 9 (mortalin)	chr5q31.1	200690_at	NM_004134																				
2.11	2.23	0.11	3.60E-01	7.10E-01	---	---	---	238899_at	---																				
5.09	5.42	0.33	3.61E-01	7.10E-01	---	---	---	244646_at	---																				
3.11	3.35	0.25	3.60E-01	7.10E-01	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	chr1p34	208433_s_at	NM_001018054 /// NM_004631 /// NM_017522 /// NM_033300																				
2.88	3.07	0.19	3.61E-01	7.10E-01	FAM176A	family with sequence similarity 176, member A	chr2p12	227828_s_at	NM_032181																				
4.51	4.69	0.18	3.60E-01	7.10E-01	TRPV4	transient receptor potential cation channel, subfamily V, member 4	chr12q24.1	219516_at	NM_021625 /// NM_147204																				
3.30	3.48	0.18	3.60E-01	7.10E-01	GK	glycerol kinase	chrXp21.3	207387_s_at	NM_000167 /// NM_001128127 /// NM_203391																				
2.30	2.48	0.18	3.61E-01	7.10E-01	APOB	apolipoprotein B (including Ag(x) antigen)	chr2p24-p23	205108_s_at	NM_000384																				
3.51	3.67	0.16	3.61E-01	7.10E-01	---	---	---	1561538_at	---																				
2.65	2.79	0.14	3.61E-01	7.10E-01	---	---	---	238200_at	---																				
2.88	3.02	0.14	3.60E-01	7.10E-01	TFCP2L1	Transcription factor CP2-like 1	chr2q14	227642_at	NM_014553																				
2.35	2.50	0.14	3.60E-01	7.10E-01	SERP2	Stress-associated endoplasmic reticulum protein family member 2	chr13q14.11	240667_at	NM_001010897																				
2.54	2.68	0.14	3.61E-01	7.10E-01	---	---	---	234596_at	---																				
1.89	2.03	0.14	3.60E-01	7.10E-01	PCDHB17	protocadherin beta 17 pseudogene	chr5q31	216313_at	NR_001280																				
2.40	2.54	0.13	3.60E-01	7.10E-01	FAM161A	family with sequence similarity 161, member A	chr2p15	1557385_at	NM_032180																				
5.60	5.73	0.13	3.61E-01	7.10E-01	---	---	---	221947_at	---																				
3.64	3.77	0.13	3.60E-01	7.10E-01	LOC283177	hypothetical protein LOC283177	chr11q25	238112_at	---																				
2.77	2.89	0.13	3.61E-01	7.10E-01	SPRY3	sprouty homolog 3 (Drosophila)	chrXq28 and Yq12	232157_at	NM_005840																				
2.07	2.19	0.13	3.60E-01	7.10E-01	hCG_1983896	hCG1983896	chr16p13.13	1564327_at	XR_041489 /// XR_041490 /// XR_041491																				
2.89	3.01	0.12	3.61E-01	7.10E-01	MTAP	methylthioadenosine phosphorylase	chr9p21	211364_at	NM_002451																				
2.28	2.39	0.12	3.60E-01	7.10E-01	---	---	---	225714_s_at	---																				

1.92	2.03	0.11	3.61E-01	7.10E-01	---	---	---	241296_at	---
1.99	2.09	0.10	3.61E-01	7.10E-01	AGBL4	ATP/GTP binding protein-like 4	chr1p33	1569570_at	NM_032785
2.29	2.39	0.10	3.61E-01	7.10E-01	TMEM155	transmembrane protein 155	chr4q27	230137_at	NM_152399
2.04	2.14	0.10	3.60E-01	7.10E-01	HEPACAM2	HEPACAM family member 2	chr7q21.3	242601_at	NM_001039372 /// NM_198151
2.47	2.56	0.09	3.60E-01	7.10E-01	---	---	---	232823_at	---
6.13	6.37	0.24	3.61E-01	7.10E-01	SERTAD2	SERTA domain containing 2	chr2p14	202656_s_at	NM_014755
2.26	2.44	0.18	3.61E-01	7.10E-01	MCCC2	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	chr5q12-q13	233231_at	NM_022132
3.26	3.47	0.21	3.61E-01	7.10E-01	TRH	thyrotropin-releasing hormone	chr3q13.3-q21	206622_at	NM_007117
6.97	7.38	0.41	3.61E-01	7.10E-01	GNS	glucosamine (N-acetyl)-6-sulfatase	chr12q14	203676_at	NM_002076
2.42	2.54	0.12	3.61E-01	7.10E-01	MAP1LC3B2	microtubule-associated protein 1 light chain 3 beta 2	chr12q24.22	234238_at	NM_001085481
6.15	6.50	0.35	3.61E-01	7.10E-01	C1orf21	chromosome 1 open reading frame 21	chr1q25	223126_s_at	NM_030806
3.06	3.19	0.13	3.61E-01	7.10E-01	SPATA4	spermatogenesis associated 4	chr4q34.2	231178_at	NM_144644
3.02	3.25	0.22	3.61E-01	7.10E-01	LOC100131848	FP2025	chr10q26.11	1557729_at	XM_001721551 /// XM_001726142 /// XM_001726336
3.50	3.69	0.19	3.61E-01	7.10E-01	SIX1	SIX homeobox 1	chr14q23.1	230911_at	NM_005982
2.38	2.54	0.16	3.61E-01	7.10E-01	---	---	---	242262_x_at	---
2.15	2.29	0.15	3.61E-01	7.10E-01	---	---	---	228936_at	---
3.52	3.67	0.15	3.61E-01	7.10E-01	TSSK6	testis-specific serine kinase 6	chr19p13.11	230989_s_at	NM_032037
2.60	2.72	0.12	3.61E-01	7.10E-01	NCRNA00029	non-protein coding RNA 29	chr20q13.33	231760_at	---
3.55	3.72	0.16	3.61E-01	7.10E-01	KRT32	keratin 32	chr17q12-q21	207146_at	NM_002278
2.71	2.85	0.14	3.61E-01	7.10E-01	FAM66C /// LOC100132923	family with sequence similarity 66, member C /// similar to hCG1993470	chr12p13.31 /// chr8p23.1	1559952_x_at	XM_001716286 /// XR_040642 /// XR_040643
2.17	2.31	0.14	3.61E-01	7.10E-01	DSCR6	Down syndrome critical region gene 6	chr21q22.2	207267_s_at	NM_018962
3.79	4.08	0.29	3.61E-01	7.10E-01	ZNF317	zinc finger protein 317	---	1555337_a_at	NM_020933
2.17	2.29	0.12	3.61E-01	7.10E-01	LOC100133905 /// TLK1	hypothetical protein LOC100133905 /// tousled-like kinase 1	chr2q31.1	241642_x_at	NM_012290 /// XM_001713704
2.54	2.69	0.14	3.61E-01	7.10E-01	---	---	---	238991_at	---
2.34	2.45	0.11	3.61E-01	7.10E-01	SOSTDC1	sclerostin domain containing 1	chr7p21.1	213456_at	NM_015464
1.97	2.08	0.11	3.61E-01	7.10E-01	---	---	---	237885_at	---
3.33	3.53	0.20	3.62E-01	7.10E-01	---	---	---	238152_at	---
2.91	3.09	0.18	3.62E-01	7.10E-01	ZBTB7A	zinc finger and BTB domain containing 7A	chr19p13.3	222082_at	NM_015898
2.25	2.36	0.11	3.62E-01	7.10E-01	LOC440905	hypothetical protein LOC440905	chr2q21.1	241895_at	XM_001722749 /// XM_001722847 /// XM_001723708
5.76	6.09	0.33	3.62E-01	7.10E-01	---	---	---	227836_at	---
2.70	2.89	0.18	3.62E-01	7.10E-01	TMEM72	transmembrane protein 72	chr10q11.21	1558324_a_at	NM_001123376 /// XM_001717287 /// XM_926597 /// XM_937160
3.54	3.69	0.15	3.62E-01	7.11E-01	TTR	transthyretin	chr18q12.1	209660_at	NM_000371
2.07	2.21	0.14	3.62E-01	7.11E-01	---	---	---	1556867_at	---
1.74	1.86	0.12	3.62E-01	7.11E-01	---	---	---	1558480_at	---
2.04	2.39	0.35	3.62E-01	7.11E-01	FREM2	FRAS1 related extracellular matrix protein 2	chr13q13.3	230964_at	NM_207361
2.79	2.99	0.20	3.62E-01	7.11E-01	SMTNL2	smoothelin-like 2	chr17p13.2	229730_at	NM_001114974 /// NM_198501
5.73	6.12	0.40	3.62E-01	7.11E-01	ZNF451	zinc finger protein 451	chr6p12.1	212557_at	NM_001031623 /// NM_015555
3.16	3.48	0.32	3.62E-01	7.11E-01	KIF13A	kinesin family member 13A	chr6p23	220777_at	NM_001105566 /// NM_001105567 /// NM_001105568 /// NM_022113
5.39	5.62	0.22	3.62E-01	7.11E-01	C9orf86	chromosome 9 open reading frame 86	chr9q34.3	225377_at	NM_017995 /// NM_024718
2.74	2.91	0.17	3.62E-01	7.11E-01	SMA4	glucuronidase, beta pseudogene	chr5q13	215599_at	---
3.43	3.57	0.14	3.62E-01	7.11E-01	POLH	polymerase (DNA directed), eta	chr6p21.1	231115_at	NM_006502
3.14	3.28	0.14	3.62E-01	7.11E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	201335_s_at	NM_015313
2.00	2.14	0.14	3.62E-01	7.11E-01	---	---	---	243694_at	---
2.04	2.14	0.10	3.62E-01	7.11E-01	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	chr1q32	217552_x_at	NM_000573 /// NM_000651
7.11	7.64	0.53	3.62E-01	7.11E-01	TANK	TRAF family member-associated NFKB activator	chr2q24-q31	207616_s_at	NM_004180 /// NM_133484

7.72	8.18	0.46	3.62E-01	7.11E-01	TRIP12	thyroid hormone receptor interactor 12	chr2q36.3	201546_at	NM_004238
2.51	2.68	0.17	3.62E-01	7.11E-01	HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	chr7p14.1-p13	210331_at	NM_015052
1.93	2.03	0.10	3.62E-01	7.11E-01	LAMA2	Laminin, alpha 2	chr6q22-q23	216839_at	NM_000426 /// NM_001079823
3.87	4.04	0.17	3.62E-01	7.11E-01	CATSPER2 /// CATSPER2P1	cation channel, sperm associated 2 /// cation channel, sperm associated 2 pseudogene 1	chr15q15.3	217588_at	NM_054020 /// NM_172095 /// NM_172096 /// NM_172097 /// NR_002318
2.32	2.43	0.11	3.62E-01	7.11E-01	---	---	---	1561474_at	---
5.37	5.79	0.42	3.62E-01	7.11E-01	PYROXD1	Pyridine nucleotide-disulphide oxidoreductase domain 1	chr12p12.1	213878_at	NM_024854
1.86	1.97	0.11	3.62E-01	7.11E-01	---	---	---	244586_x_at	---
2.03	2.18	0.15	3.62E-01	7.11E-01	---	---	---	237602_at	---
3.67	3.88	0.22	3.62E-01	7.11E-01	---	---	---	232979_at	---
2.19	2.31	0.12	3.62E-01	7.11E-01	ATP8B3	ATPase, class I, type 8B, member 3	chr19p13.3	215319_at	NM_138813
2.76	2.89	0.13	3.62E-01	7.11E-01	---	---	---	232022_at	---
4.87	5.09	0.23	3.63E-01	7.11E-01	DOK2	docking protein 2, 56kDa	chr8p21.3	214054_at	NM_003974
2.46	2.58	0.12	3.63E-01	7.11E-01	CCDC79	coiled-coil domain containing 79	chr16q22.1	1553451_at	XM_001130007 /// XM_001717087 /// XM_001717868
2.31	2.44	0.12	3.63E-01	7.11E-01	TCTEX1D1	Tctex1 domain containing 1	chr1p31.3	1553635_s_at	NM_152665
4.17	4.38	0.21	3.63E-01	7.11E-01	CCDC134	coiled-coil domain containing 134	chr22q13.2	220077_at	NM_024821
2.98	3.15	0.18	3.63E-01	7.11E-01	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	chr19q13.4	208179_x_at	NM_014511 /// NM_015868
3.43	3.59	0.16	3.63E-01	7.11E-01	RNF186	ring finger protein 186	chr1p36.13	219739_at	NM_019062
2.57	2.72	0.15	3.63E-01	7.11E-01	FLJ30064	hypothetical protein LOC644975	chr7q21.3	222676_at	NM_001039906
2.60	2.72	0.12	3.63E-01	7.11E-01	INSL6	insulin-like 6	chr9p24	221403_s_at	NM_007179
1.98	2.09	0.11	3.63E-01	7.11E-01	---	---	---	211567_at	---
3.69	3.85	0.17	3.63E-01	7.11E-01	FGF18	fibroblast growth factor 18	chr5q34	211485_s_at	NM_003862
2.69	2.84	0.16	3.63E-01	7.11E-01	BCL2L14	BCL2-like 14 (apoptosis facilitator)	chr12p13-p12	234191_at	NM_030766 /// NM_138722 /// NM_138723 /// NM_138724
2.18	2.33	0.15	3.63E-01	7.11E-01	---	---	---	240946_at	---
2.07	2.24	0.16	3.63E-01	7.11E-01	---	---	---	241826_x_at	---
2.07	2.19	0.12	3.63E-01	7.11E-01	VN1R2	vomeronasal 1 receptor 2	chr19q13.41	1553549_at	NM_173856
2.99	3.14	0.15	3.63E-01	7.12E-01	C1QTNF3	C1q and tumor necrosis factor related protein 3	chr5p13	220988_s_at	NM_030945 /// NM_181435
2.96	3.11	0.14	3.63E-01	7.12E-01	HBEGF	Heparin-binding EGF-like growth factor	chr5q23	222076_at	NM_001945
5.99	6.38	0.39	3.63E-01	7.12E-01	TTC27	tetratricopeptide repeat domain 27	chr2p22.3	218710_at	NM_017735
5.43	5.71	0.27	3.63E-01	7.12E-01	CCDC55	coiled-coil domain containing 55	chr17q11.2	223236_at	NM_032141
4.71	4.94	0.23	3.63E-01	7.12E-01	MMP28	matrix metallopeptidase 28	chr17q11-q21.1	224207_x_at	NM_001032278 /// NM_024302
2.71	2.86	0.15	3.63E-01	7.12E-01	C7orf26	Chromosome 7 open reading frame 26	chr7p22.1	222002_at	NM_024067
3.08	3.21	0.12	3.63E-01	7.12E-01	ZNF518B	Zinc finger protein 518B	chr4p16.1	241580_at	NM_053042
2.31	2.43	0.12	3.63E-01	7.12E-01	---	---	---	243515_at	---
2.79	2.91	0.11	3.63E-01	7.12E-01	WNT6	Wingless-type MMTV integration site family, member 6	chr2q35	222086_s_at	NM_006522
2.21	2.45	0.25	3.63E-01	7.12E-01	---	---	---	1566624_at	---
3.34	3.71	0.37	3.63E-01	7.12E-01	---	---	---	239210_at	---
3.17	3.44	0.28	3.63E-01	7.12E-01	---	---	---	1565689_at	---
2.84	3.02	0.18	3.63E-01	7.12E-01	LYRM7	Lyrm7 homolog (mouse)	chr5q31.1	239960_x_at	NM_181705
2.93	3.06	0.13	3.63E-01	7.12E-01	FAM148B	Family with sequence similarity 148, member B	chr15q22.2	229306_at	NM_001007595
2.56	2.69	0.13	3.63E-01	7.12E-01	---	---	---	1556717_at	---
2.30	2.41	0.11	3.63E-01	7.12E-01	---	---	---	237918_at	---
2.27	2.43	0.15	3.63E-01	7.12E-01	---	---	---	233290_at	---
4.45	4.61	0.16	3.63E-01	7.12E-01	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	chr12q24	214209_s_at	NM_019624 /// NM_019625 /// NM_203444
2.05	2.17	0.12	3.63E-01	7.12E-01	DHRS7	dehydrogenase/reductase (SDR family) member 7	chr14q23.1	201789_at	NM_016029
2.78	2.88	0.10	3.63E-01	7.12E-01	PTTG3	pituitary tumor-transforming 3	chr8q13.1	208511_at	NR_002734
2.02	2.12	0.10	3.63E-01	7.12E-01	IPMK	inositol polyphosphate multikinase	chr10q21.1	239878_at	NM_152230
5.28	5.62	0.34	3.64E-01	7.12E-01	KLHL9	kelch-like 9 (Drosophila)	chr9p22	213117_at	NM_018847
2.49	2.63	0.14	3.64E-01	7.12E-01	POLR1E	polymerase (RNA) I polypeptide E, 53kDa	chr9p13.2	231041_at	NM_022490
1.96	2.09	0.12	3.64E-01	7.12E-01	CD47	CD47 molecule	chr3q13.1-q13.2	213856_at	NM_001025079 /// NM_001777 /// NM_198793
2.13	2.24	0.11	3.64E-01	7.12E-01	---	---	---	237973_at	---
4.31	4.84	0.53	3.64E-01	7.12E-01	CAV1	caveolin 1, caveolae protein, 22kDa	chr7q31.1	203065_s_at	NM_001753

6.12	6.34	0.22	3.64E-01	7.12E-01	KIAA2026	KIAA2026	chr9p24.1	228446_at	NM_001017969
2.94	3.12	0.18	3.64E-01	7.12E-01	---	---	---	240457_at	---
2.20	2.32	0.12	3.64E-01	7.12E-01	ZNF770	zinc finger protein 770	chr15q14	220608_s_at	NM_014106
4.15	4.28	0.13	3.64E-01	7.12E-01	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	chr19q12-q13.1	217270_s_at	NM_004714 /// NM_006483 /// NM_006484
2.04	2.17	0.13	3.64E-01	7.12E-01	ATP2B2 /// LOC100134286	ATPase, Ca++ transporting, plasma membrane 2 /// similar to ATPase, Ca++ transporting, plasma membrane 2	chr3p25.3	211586_s_at	NM_001001331 /// NM_001683 /// XM_001714571
2.01	2.12	0.11	3.64E-01	7.12E-01	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	chr13q14	210643_at	NM_003701 /// NM_033012
3.51	3.69	0.18	3.64E-01	7.12E-01	TMEM132C	transmembrane protein 132C	chr12q24.32	232313_at	XM_001715575 /// XM_044062 /// XM_941994
2.25	2.38	0.12	3.64E-01	7.12E-01	---	---	---	1563950_at	---
4.77	4.90	0.13	3.64E-01	7.12E-01	FAM84B	family with sequence similarity 84, member B	chr8q24.21	228870_at	NM_174911
6.08	6.29	0.21	3.64E-01	7.12E-01	FAM173A	family with sequence similarity 173, member A	chr16p13.3	219709_x_at	NM_023933
2.29	2.40	0.12	3.64E-01	7.12E-01	---	---	---	236952_at	---
4.10	4.21	0.11	3.64E-01	7.12E-01	---	---	---	242097_at	---
1.88	1.98	0.10	3.64E-01	7.12E-01	LOC100130964	similar to hCG2045185	chr8p11.22	238237_at	XM_001724267 /// XM_001724582 /// XM_001724994
5.89	6.23	0.34	3.64E-01	7.12E-01	KLHDC10	kelch domain containing 10	chr7q32.2	209255_at	NM_014997
3.40	3.59	0.19	3.64E-01	7.12E-01	CLDN19	claudin 19	chr1p34.2	1552535_at	NM_001123395 /// NM_148960
4.99	5.17	0.18	3.64E-01	7.12E-01	TMEM204	transmembrane protein 204	chr16p13.3	228947_x_at	NM_024600
2.30	2.45	0.15	3.64E-01	7.12E-01	IL23R	interleukin 23 receptor	chr1p31.3	1552912_a_at	NM_144701
6.99	7.11	0.12	3.64E-01	7.12E-01	---	---	---	208238_x_at	---
2.39	2.55	0.15	3.64E-01	7.12E-01	---	---	---	240740_at	---
2.64	2.76	0.12	3.64E-01	7.12E-01	ADCY2	adenylate cyclase 2 (brain)	chr5p15.3	217687_at	NM_020546
2.01	2.16	0.14	3.64E-01	7.12E-01	---	---	---	228643_at	---
4.32	4.48	0.16	3.64E-01	7.12E-01	RIMS4	regulating synaptic membrane exocytosis 4	chr20q13.12	233299_at	NM_182970
5.17	5.37	0.20	3.64E-01	7.12E-01	DOC2B	double C2-like domains, beta	chr17p13.3	207311_at	NM_003585
2.32	2.47	0.15	3.64E-01	7.12E-01	LOC100129406	hypothetical protein LOC100129406	chr1p13.2	240868_at	XM_001719974 /// XM_001722372 /// XM_001723170
2.40	2.61	0.21	3.64E-01	7.12E-01	---	---	---	1561658_at	---
3.84	4.04	0.20	3.64E-01	7.12E-01	---	---	---	1559491_at	---
2.39	2.51	0.12	3.64E-01	7.12E-01	NEK2	NIMA (never in mitosis gene a)-related kinase 2	chr1q32.2-q41	211080_s_at	NM_002497
2.02	2.13	0.11	3.65E-01	7.13E-01	---	---	---	1561962_at	---
3.99	4.20	0.20	3.65E-01	7.13E-01	ZNF22	zinc finger protein 22 (KOX 15)	chr10q11	218006_s_at	NM_006963
4.08	4.25	0.17	3.65E-01	7.13E-01	---	---	---	239088_at	---
2.22	2.36	0.14	3.65E-01	7.13E-01	C6orf182 /// C6orf182P	chromosome 6 open reading frame 182 /// chromosome 6 open reading frame 182 pseudogene	chr10q22.1 /// chr6q21	232152_at	NM_001083535 /// NM_173830
5.89	6.47	0.57	3.65E-01	7.13E-01	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	chr6q25.1-q25.3	210284_s_at	NM_015093
6.24	6.61	0.37	3.65E-01	7.13E-01	BXDC1	brix domain containing 1	chr6q21	225866_at	NM_032194
1.90	2.03	0.13	3.65E-01	7.13E-01	---	---	---	1561856_at	---
2.23	2.44	0.21	3.65E-01	7.13E-01	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	chr5q31.1-q33.1	206849_at	NM_000816 /// NM_198903 /// NM_198904
1.87	1.97	0.10	3.65E-01	7.13E-01	---	---	---	241560_at	---
5.40	5.59	0.19	3.65E-01	7.13E-01	CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6	chr19q13.2	207244_x_at	NM_000762
2.44	2.58	0.15	3.65E-01	7.13E-01	BRWD1	bromodomain and WD repeat domain containing 1	chr21q22.2	214820_at	NM_001007246 /// NM_018963 /// NM_033656
2.75	2.89	0.14	3.65E-01	7.13E-01	NLGN4X	neuroligin 4, X-linked	chrXp22.32-p22.31	1554689_a_at	NM_020742 /// NM_181332
2.56	2.68	0.12	3.65E-01	7.13E-01	C14orf148	chromosome 14 open reading frame 148	chr14q24.3	231566_at	NM_001113475 /// NM_138791
6.50	6.72	0.22	3.65E-01	7.13E-01	EGFL7	EGF-like-domain, multiple 7	chr9q34.3	218825_at	NM_016215 /// NM_201446
2.85	3.01	0.16	3.65E-01	7.13E-01	C1orf165	Chromosome 1 open reading frame 165	chr1p33	1558476_at	NM_024603
2.69	2.78	0.09	3.65E-01	7.13E-01	CP110	CP110 protein	chr16p12.3	1569353_at	NM_014711

7.39	7.73	0.34	3.65E-01	7.13E-01	ENAH	enabled homolog (Drosophila)	chr1q42.12	222433_at	NM_001008493 /// NM_018212
3.77	4.02	0.25	3.65E-01	7.13E-01	ATE1	arginyltransferase 1	chr10q26.13	225497_at	NM_001001976 /// NM_007041
5.36	6.11	0.75	3.65E-01	7.13E-01	UBXN4	UBX domain protein 4	chr2q21.3	212008_at	NM_014607
2.11	2.21	0.09	3.65E-01	7.13E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	1561615_s_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
3.68	3.83	0.15	3.65E-01	7.13E-01	---	---	---	240350_at	---
2.80	2.95	0.14	3.65E-01	7.13E-01	---	---	---	1552961_at	---
5.84	5.96	0.12	3.65E-01	7.13E-01	---	---	---	214902_x_at	---
3.42	3.62	0.19	3.65E-01	7.13E-01	TRPS1	trichorhinophalangeal syndrome I	chr8q24.12	234351_x_at	NM_014112
2.09	2.20	0.11	3.65E-01	7.13E-01	---	---	---	244582_at	---
3.07	3.39	0.32	3.65E-01	7.13E-01	ANGPT2	angiopoietin 2	chr8p23.1	211148_s_at	NM_001118887 /// NM_001118888 /// NM_001147
8.89	9.18	0.29	3.66E-01	7.13E-01	ZBTB20	zinc finger and BTB domain containing 20	chr3q13.2	235308_at	NM_015642
2.73	2.88	0.15	3.66E-01	7.13E-01	LOC199725	hypothetical protein LOC199725	chr19q13.2	232616_at	---
5.31	5.46	0.15	3.66E-01	7.13E-01	RHBDD3	rhomboid domain containing 3	chr22q12.1-q12.2	204402_at	NM_012265
1.86	1.97	0.12	3.66E-01	7.13E-01	---	---	---	1564950_at	---
1.82	1.92	0.10	3.66E-01	7.13E-01	---	---	---	1561775_at	---
3.84	3.99	0.15	3.66E-01	7.13E-01	ZNF821	zinc finger protein 821	chr16q22.3	242704_at	NM_017530
3.88	4.02	0.14	3.66E-01	7.13E-01	---	---	---	234911_at	---
2.58	2.71	0.12	3.66E-01	7.13E-01	C22orf24	chromosome 22 open reading frame 24	chr22q12.1-q12.3	207701_at	NM_015372
4.23	4.60	0.37	3.66E-01	7.13E-01	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	chrXp11.4	207620_s_at	NM_001126054 /// NM_001126055 /// NM_003688
2.87	3.02	0.15	3.66E-01	7.13E-01	TCF3	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	chr19p13.3	213732_at	NM_003200
2.92	3.07	0.15	3.66E-01	7.13E-01	---	---	---	1569644_at	---
5.33	5.49	0.16	3.66E-01	7.13E-01	NBR2	neighbor of BRCA1 gene 2	chr17q21	207631_at	NR_003108
7.71	7.91	0.20	3.66E-01	7.13E-01	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	chr3q12.2	201519_at	NM_014820
1.96	2.08	0.13	3.66E-01	7.13E-01	---	---	---	244505_at	---
2.70	2.87	0.17	3.66E-01	7.14E-01	FGF1	fibroblast growth factor 1 (acidic)	chr5q31	205117_at	NM_000800 /// NM_033136 /// NM_033137
6.69	6.83	0.14	3.66E-01	7.14E-01	RUFY1	RUN and FYVE domain containing 1	chr5q35.3	218243_at	NM_001040451 /// NM_001040452 /// NM_025158
4.37	4.49	0.12	3.66E-01	7.14E-01	ZNF71	zinc finger protein 71	chr19q13.4	234575_at	NM_021216
4.20	4.53	0.33	3.66E-01	7.14E-01	TRPM7	transient receptor potential cation channel, subfamily M, member 7	chr15q21	223324_s_at	NM_017672
2.14	2.24	0.10	3.66E-01	7.14E-01	TSHR	thyroid stimulating hormone receptor	chr14q31	215443_at	NM_000369 /// NM_001018036
2.75	2.92	0.17	3.66E-01	7.14E-01	COL6A1	Collagen, type VI, alpha 1	chr21q22.3	214200_s_at	NM_001848
3.03	3.16	0.13	3.66E-01	7.14E-01	---	---	---	1558847_at	---
3.22	3.33	0.12	3.66E-01	7.14E-01	FLJ33590	hypothetical protein FLJ33590	chr2q37.3	1560035_at	NM_173821
2.30	2.54	0.24	3.66E-01	7.14E-01	---	---	---	1561055_at	---
3.51	3.77	0.26	3.66E-01	7.14E-01	CUL3	cullin 3	chr2q36.2	201370_s_at	NM_003590
1.88	1.97	0.10	3.66E-01	7.14E-01	FAM70A	family with sequence similarity 70, member A	chrXq24	219895_at	NM_001104544 /// NM_001104545 /// NM_017938
2.15	2.33	0.18	3.66E-01	7.14E-01	---	---	---	1554224_at	---
3.52	3.71	0.19	3.66E-01	7.14E-01	---	---	---	229131_at	---
2.03	2.14	0.11	3.66E-01	7.14E-01	RIT2	Ras-like without CAAX 2	chr18q12.3	206984_s_at	NM_002930
4.52	4.88	0.36	3.66E-01	7.14E-01	CLIC4	chloride intracellular channel 4	chr1p36.11	221881_s_at	NM_013943
1.92	2.00	0.09	3.66E-01	7.14E-01	METT5D1	Methyltransferase 5 domain containing 1	chr11p14.1	1565900_at	NM_001113528 /// NM_152636
6.29	6.88	0.59	3.66E-01	7.14E-01	C10orf58	chromosome 10 open reading frame 58	chr10q23.1	228155_at	NM_032333

3.73	4.11	0.38	3.66E-01	7.14E-01	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	chr10p13	222233_s_at	NM_001033855 /// NM_001033857 /// NM_001033858 /// NM_022487																				
4.10	4.48	0.38	3.67E-01	7.14E-01	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	chr11q23.2	202886_s_at	NM_002716 /// NM_181699																				
4.49	4.87	0.37	3.67E-01	7.14E-01	RUFY3	RUN and FYVE domain containing 3	chr4q13.3	210251_s_at	NM_001037442 /// NM_001130709 /// NM_014961																				
6.07	6.25	0.17	3.66E-01	7.14E-01	NPAL3	NIPA-like domain containing 3	chr1p36.12-p35.1	225876_at	NM_020448																				
1.93	2.06	0.12	3.67E-01	7.14E-01	---	---	---	1564932_at	---																				
2.35	2.47	0.12	3.67E-01	7.14E-01	LOC554226	hypothetical protein LOC554226	chr2q21.2	237794_at	XR_017732 /// XR_040111 /// XR_042131																				
2.31	2.45	0.15	3.67E-01	7.14E-01	LOC728987	Hypothetical LOC728987	chr1q42.2	1566465_at	XM_001132417 /// XM_001132664 /// XM_001722952																				
6.23	6.47	0.24	3.67E-01	7.14E-01	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	chr10q22.3	221584_s_at	NM_001014797 /// NM_002247																				
4.13	4.33	0.20	3.67E-01	7.14E-01	CCL22	chemokine (C-C motif) ligand 22	chr16q13	207861_at	NM_002990																				
3.25	3.45	0.19	3.67E-01	7.14E-01	FLJ31713	hypothetical protein FLJ31713	chr9q32	1553429_at	XR_041881 /// XR_041882 /// XR_041883																				
2.48	2.62	0.14	3.67E-01	7.14E-01	---	---	---	240520_at	---																				
2.01	2.14	0.12	3.67E-01	7.14E-01	RNF17	ring finger protein 17	chr13q12.12	224383_at	NM_031277																				
6.36	6.56	0.19	3.67E-01	7.14E-01	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	chr4q12	226112_at	NM_000232																				
3.78	3.92	0.14	3.67E-01	7.14E-01	ANKFY1	ankyrin repeat and FYVE domain containing 1	chr17p13.3	239073_at	NM_016376 /// NM_020740																				
1.91	2.02	0.11	3.67E-01	7.14E-01	---	---	---	237530_at	---																				
1.78	1.89	0.10	3.67E-01	7.14E-01	---	---	---	1562491_at	---																				
1.83	1.93	0.10	3.67E-01	7.14E-01	---	---	---	233682_at	---																				
3.58	3.76	0.18	3.67E-01	7.14E-01	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	chr7p14.2	1569640_s_at	NM_030636																				
6.90	7.10	0.20	3.67E-01	7.14E-01	VASP	vasodilator-stimulated phosphoprotein	chr19q13.2-q13.3	202205_at	NM_003370																				
3.15	3.28	0.13	3.67E-01	7.14E-01	MUC17	mucin 17, cell surface associated	chr7q22.1	232407_at	NM_001040105 /// XM_001719956																				
6.15	6.47	0.32	3.67E-01	7.15E-01	STAG1	stromal antigen 1	chr3q22.3	202294_at	NM_005862																				
3.04	3.24	0.20	3.67E-01	7.15E-01	MEI1	meiosis inhibitor 1	chr22q13.2	1554208_at	NM_152513																				
2.38	2.51	0.13	3.67E-01	7.15E-01	FLJ45825	hypothetical protein LOC646888	chr6p21.2	242095_at	XR_041301 /// XR_041302 /// XR_041303																				
2.49	2.62	0.12	3.67E-01	7.15E-01	---	---	---	237366_at	---																				
1.95	2.06	0.12	3.67E-01	7.15E-01	---	---	---	1564690_at	---																				
2.68	2.87	0.19	3.67E-01	7.15E-01	---	---	---	237775_x_at	---																				
5.24	5.43	0.19	3.67E-01	7.15E-01	PEX12	peroxisomal biogenesis factor 12	chr17q12	205094_at	NM_000286																				
2.52	2.67	0.16	3.67E-01	7.15E-01	ARMC9	armadillo repeat containing 9	chr2q37.1	240639_at	NM_025139																				
3.15	3.29	0.14	3.67E-01	7.15E-01	---	---	---	231485_at	---																				
3.38	3.50	0.13	3.67E-01	7.15E-01	RPH3AL	rabphilin 3A-like (without C2 domains)	chr17p13.3	238120_at	NM_006987																				
3.99	4.13	0.14	3.67E-01	7.15E-01	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	chr7p13	213987_s_at	NM_003718 /// NM_031267																				
4.86	5.20	0.34	3.68E-01	7.15E-01	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	chr2q12	226039_at	NM_012214																				
4.91	5.06	0.16	3.68E-01	7.15E-01	FLJ33065	Hypothetical gene supported by AK057627; BC031275; BC045736	chr3p22.1	1556248_at	---																				
2.02	2.17	0.16	3.68E-01	7.15E-01	---	---	---	1561452_at	---																				
1.88	1.98	0.10	3.68E-01	7.15E-01	---	---	---	1565760_at	---																				
2.17	2.32	0.16	3.68E-01	7.15E-01	FLJ37673	hypothetical protein FLJ37673	chr4q25	1563581_at	XR_015418 /// XR_015518 /// XR_040677																				
2.43	2.56	0.13	3.68E-01	7.15E-01	---	---	---	243371_at	---																				
2.95	3.06	0.12	3.68E-01	7.15E-01	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	237944_at	NM_004735																				
2.32	2.47	0.15	3.68E-01	7.15E-01	---	---	---	233951_at	---																				
10.12	10.54	0.42	3.68E-01	7.15E-01	RDX	radixin	chr11q23	212397_at	NM_002906																				
4.48	4.67	0.19	3.68E-01	7.15E-01	OBSL1	Obscurin-like 1	chr2q35	238776_x_at	NM_015311																				

2.68	2.80	0.12	3.68E-01	7.15E-01	---	---	---	239943_x_at	---
2.64	2.83	0.19	3.68E-01	7.15E-01	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	chr7p15	205429_s_at	NM_016447
2.12	2.23	0.11	3.68E-01	7.15E-01	LOC145783	hypothetical LOC145783	chr15q21.3	1558202_at	XM_934388
1.74	1.83	0.09	3.68E-01	7.15E-01	---	---	---	215647_at	---
6.03	6.31	0.28	3.68E-01	7.15E-01	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	chr16q22.1	224614_at	NM_006141
3.52	3.69	0.17	3.68E-01	7.15E-01	MAP3K6	mitogen-activated protein kinase kinase kinase 6	chr1p36.11	1552631_a_at	NM_004672
4.10	4.37	0.27	3.68E-01	7.15E-01	APOOL	Apolipoprotein O-like	chrXq21.1	213282_at	NM_198450
3.07	3.25	0.17	3.68E-01	7.15E-01	---	---	---	215592_at	---
3.27	3.43	0.16	3.68E-01	7.15E-01	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	chr3p21.31	236844_at	NM_014966 /// NM_138615
3.12	3.54	0.42	3.68E-01	7.15E-01	---	---	---	232974_at	---
2.10	2.22	0.12	3.68E-01	7.15E-01	---	---	---	243008_at	---
4.01	4.71	0.70	3.68E-01	7.15E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	224942_at	NM_002581
2.65	2.80	0.15	3.68E-01	7.15E-01	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	chr7p15.1-p14.3	236344_at	NM_005020
2.59	2.72	0.13	3.68E-01	7.15E-01	---	---	---	1555085_at	---
4.99	5.40	0.41	3.68E-01	7.15E-01	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	chr15q26.3	203180_at	NM_000693
3.10	3.24	0.14	3.68E-01	7.15E-01	---	---	---	233331_at	---
2.05	2.18	0.13	3.69E-01	7.16E-01	KCND2	potassium voltage-gated channel, Shal-related subfamily, member 2	chr7q31	207103_at	NM_012281
3.67	3.86	0.19	3.69E-01	7.16E-01	PCM1	pericentriolar material 1	chr8p22-p21.3	228905_at	NM_006197
3.10	3.24	0.13	3.69E-01	7.16E-01	---	---	---	237187_at	---
2.24	2.36	0.13	3.69E-01	7.16E-01	ZNF321 /// ZNF816A	zinc finger protein 321 /// zinc finger protein 816A	chr19q13.41	217541_x_at	NM_001031665 /// NM_203307
7.29	7.66	0.36	3.69E-01	7.16E-01	RAB1A	RAB1A, member RAS oncogene family	chr2p14	207791_s_at	NM_004161
1.94	2.06	0.11	3.69E-01	7.16E-01	---	---	---	1569609_at	---
2.09	2.21	0.11	3.69E-01	7.16E-01	LOC150185	hypothetical LOC150185	chr22q11.21	1561707_at	XR_040370 /// XR_040371 /// XR_040372
2.07	2.17	0.11	3.69E-01	7.16E-01	AP4E1	adaptor-related protein complex 4, epsilon 1 subunit	chr15q21.2	220229_s_at	NM_007347
2.11	2.22	0.10	3.69E-01	7.16E-01	---	---	---	1561938_at	---
5.81	5.96	0.16	3.69E-01	7.16E-01	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	chr7q32	222419_x_at	NM_003344 /// NM_182697
4.66	4.86	0.20	3.69E-01	7.16E-01	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	chr1q21-q22	207629_s_at	NM_004723
5.76	6.17	0.42	3.69E-01	7.16E-01	UBQLN1	ubiquilin 1	chr9q22|9q21.2-q21.3	222991_s_at	NM_013438 /// NM_053067
6.39	6.75	0.36	3.69E-01	7.16E-01	C11orf46	chromosome 11 open reading frame 46	chr11p14.1	226383_at	NM_152316
4.57	4.92	0.34	3.69E-01	7.16E-01	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	chr12p11	202661_at	NM_002223
3.75	3.96	0.21	3.69E-01	7.16E-01	---	---	---	238204_at	---
4.84	5.01	0.17	3.69E-01	7.16E-01	HAPLN3	hyaluronan and proteoglycan link protein 3	chr15q26.1	227262_at	NM_178232
2.29	2.44	0.15	3.69E-01	7.16E-01	FAM3B	family with sequence similarity 3, member B	chr21q22.3	227194_at	NM_058186 /// NM_206964
2.05	2.19	0.14	3.69E-01	7.16E-01	GLYATL2	glycine-N-acyltransferase-like 2	chr11q12.1	1554712_a_at	NM_145016
2.48	2.62	0.14	3.69E-01	7.16E-01	LY9	lymphocyte antigen 9	chr1q21.3-q22	210370_s_at	NM_001033667 /// NM_002348
2.81	2.95	0.13	3.69E-01	7.16E-01	---	---	---	237343_at	---
2.94	3.07	0.13	3.69E-01	7.16E-01	CCDC18	coiled-coil domain containing 18	chr1p22.1	228022_at	NM_206886
2.26	2.39	0.13	3.69E-01	7.16E-01	CC2D2A	coiled-coil and C2 domain containing 2A	chr4p15.33	234933_at	NM_001080522 /// NM_020785 /// NR_024098
2.20	2.32	0.13	3.69E-01	7.16E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	207053_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
2.28	2.40	0.12	3.69E-01	7.16E-01	---	---	---	239456_at	---
2.44	2.55	0.11	3.69E-01	7.16E-01	BCLAF1	BCL2-associated transcription factor 1	chr6q22-q23	229454_at	NM_001077440 /// NM_001077441 /// NM_014739
2.55	2.65	0.11	3.69E-01	7.16E-01	---	---	---	1555014_x_at	---
2.58	2.67	0.09	3.69E-01	7.16E-01	ANPEP	Alanyl (membrane) aminopeptidase	chr15q25-q26	234458_at	NM_001150
4.02	4.20	0.18	3.69E-01	7.16E-01	HIST1H3F	histone cluster 1, H3f	chr6p22.1	214542_x_at	NM_021018
2.76	2.97	0.21	3.69E-01	7.16E-01	---	---	---	235654_at	---
2.44	2.57	0.13	3.69E-01	7.16E-01	KATNAL2	katanin p60 subunit A-like 2	chr18q21.1	233644_at	NM_031303
3.64	3.84	0.20	3.70E-01	7.16E-01	---	---	---	1560920_s_at	---
3.19	3.35	0.17	3.70E-01	7.16E-01	---	---	---	1556117_at	---
2.42	2.54	0.12	3.70E-01	7.16E-01	---	---	---	207755_at	---
4.41	4.52	0.11	3.70E-01	7.16E-01	GP9	glycoprotein IX (platelet)	chr3q21	206883_x_at	NM_000174
2.85	3.03	0.18	3.70E-01	7.16E-01	LOC27320 /// TNRC18	hypothetical protein LOC27320 /// trinucleotide repeat containing 18	chr7p22.1 /// chr7q11.21	1558238_at	NM_001080495 /// XM_376618 /// XM_499300

2.99	3.15	0.16	3.70E-01	7.16E-01	MKX	Mohawk homeobox	chr10p12.1	236014_at	NM_173576
2.12	2.24	0.13	3.70E-01	7.16E-01	FAM184A	family with sequence similarity 184, member A	chr6q22.31	1558523_at	NM_001100411 /// NM_024581
2.25	2.37	0.12	3.70E-01	7.16E-01	C12orf40	chromosome 12 open reading frame 40	chr12q12	1553424_at	NM_001031748
2.46	2.60	0.14	3.70E-01	7.16E-01	C18orf22	Chromosome 18 open reading frame 22	chr18q23	1558628_at	NM_024805
6.39	7.01	0.61	3.70E-01	7.16E-01	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	224582_s_at	NM_022731
6.29	6.56	0.27	3.70E-01	7.16E-01	EXOC3L2	exocyst complex component 3-like 2	chr19q13.32	1552889_a_at	NM_138568
3.98	4.20	0.22	3.70E-01	7.16E-01	C15orf55	chromosome 15 open reading frame 55	chr15q14	231338_at	NM_175741
3.06	3.23	0.17	3.70E-01	7.16E-01	UNQ1887	signal peptide peptidase 3	chr12q24.31	1554564_a_at	NM_139015
8.57	8.74	0.17	3.70E-01	7.16E-01	RAD23A	RAD23 homolog A (S. cerevisiae)	chr19p13.2	201046_s_at	NM_005053
2.14	2.29	0.15	3.70E-01	7.16E-01	TJP2	tight junction protein 2 (zona occludens 2)	chr9q13-q21	237132_at	NM_004817 /// NM_201629
2.11	2.26	0.15	3.70E-01	7.16E-01	GALP	galanin-like peptide	chr19q13.42	224242_at	NM_033106
2.02	2.15	0.14	3.70E-01	7.16E-01	DSE	Dermatan sulfate epimerase	chr6q22	1558867_at	NM_001080976 /// NM_013352
2.30	2.42	0.13	3.70E-01	7.16E-01	---	---	---	214618_at	---
3.38	3.51	0.13	3.70E-01	7.16E-01	SPANXC	SPANX family, member C	chrXq27.1	220217_x_at	NM_022661 /// XM_001713760
2.00	2.10	0.11	3.70E-01	7.16E-01	LOC286299	hypothetical protein LOC286299	chr9p22.2	1565999_at	---
2.01	2.10	0.09	3.70E-01	7.16E-01	SHCBP1	SHC SH2-domain binding protein 1	chr16q11.2	219493_at	NM_024745
1.88	1.98	0.10	3.70E-01	7.17E-01	DMRT3	doublesex and mab-3 related transcription factor 3	chr9p24.3	231800_s_at	NM_021240
2.50	2.64	0.14	3.70E-01	7.17E-01	DOK6	docking protein 6	chr18q22.2	241729_at	NM_152721
2.87	3.00	0.13	3.70E-01	7.17E-01	SAMD14	sterile alpha motif domain containing 14	chr17q21.33	1555819_s_at	NM_174920
1.90	2.02	0.12	3.70E-01	7.17E-01	---	---	---	1569929_at	---
2.21	2.33	0.11	3.70E-01	7.17E-01	---	---	---	233316_at	---
9.83	10.14	0.31	3.70E-01	7.17E-01	RBBP7	retinoblastoma binding protein 7	chrXp22.2	201092_at	NM_002893
2.11	2.22	0.12	3.70E-01	7.17E-01	EXOSC1	exosome component 1	chr10q24	1559044_at	NM_016046
3.13	3.24	0.11	3.70E-01	7.17E-01	GSTCD	glutathione S-transferase, C-terminal domain containing	chr4q24	235387_at	NM_001031720 /// NM_024751
2.29	2.41	0.12	3.70E-01	7.17E-01	OR10A3	olfactory receptor, family 10, subfamily A, member 3	chr11p15.4	1567251_at	NM_001003745
4.89	5.16	0.27	3.71E-01	7.17E-01	FAM101B	family with sequence similarity 101, member B	chr17p13	226876_at	NM_182705
2.04	2.16	0.12	3.71E-01	7.17E-01	---	---	---	1561860_at	---
6.71	6.94	0.22	3.71E-01	7.17E-01	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	chr10p12.2	212829_at	NM_005028
2.76	2.98	0.22	3.71E-01	7.17E-01	MARVELD1	MARVEL domain containing 1	chr10q24.2	234917_at	XR_041875 /// XR_041876 /// XR_041877
2.10	2.21	0.11	3.71E-01	7.17E-01	MYLK4	myosin light chain kinase family, member 4	chr6p25.2	1561503_at	NM_001012418
3.18	3.35	0.17	3.71E-01	7.17E-01	ARHGAP27	Rho GTPase activating protein 27	chr17q21.31	227057_at	NM_199282
3.75	4.03	0.28	3.71E-01	7.17E-01	UTRN	utrophin	chr6q24	213023_at	NM_007124
2.37	2.51	0.14	3.71E-01	7.17E-01	---	---	---	233964_at	---
2.91	3.02	0.10	3.71E-01	7.17E-01	STX6	syntaxin 6	chr1q25.3	244041_at	NM_005819
2.00	2.10	0.10	3.71E-01	7.17E-01	THAP5	THAP domain containing 5	chr7q31.1	244190_at	NM_001130475 /// NM_182529
1.82	1.92	0.10	3.71E-01	7.17E-01	---	---	---	234110_at	---
6.82	7.16	0.34	3.71E-01	7.17E-01	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	chrXp22.2	230264_s_at	NM_003916
6.26	6.58	0.32	3.71E-01	7.17E-01	TAOK3	TAO kinase 3	chr12q	220761_s_at	NM_016281
3.99	4.21	0.22	3.71E-01	7.17E-01	ZNF800	zinc finger protein 800	chr7q31.33	227101_at	NM_176814
3.92	4.12	0.20	3.71E-01	7.17E-01	PSEN2	presenilin 2 (Alzheimer disease 4)	chr1q31-q42	204261_s_at	NM_000447 /// NM_012486
2.17	2.33	0.16	3.71E-01	7.17E-01	B3GALT1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	chr2q24.3	220829_s_at	NM_020981
2.37	2.50	0.13	3.71E-01	7.17E-01	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	chr17p13.1	217415_at	NM_000937
1.89	2.00	0.11	3.71E-01	7.17E-01	---	---	---	1556794_at	---
2.28	2.43	0.15	3.71E-01	7.17E-01	LOC731852	hypothetical LOC731852	chr19p13.2	243412_at	XM_001131042 /// XM_001719170 /// XM_001726466
4.06	4.24	0.18	3.71E-01	7.17E-01	---	---	---	235628_x_at	---
4.69	4.86	0.17	3.71E-01	7.17E-01	---	---	---	236997_at	---
7.02	7.17	0.15	3.71E-01	7.17E-01	PCYT1A	Phosphate cytidylyltransferase 1, choline, alpha	chr3q29	225069_at	NM_005017
2.51	2.65	0.15	3.71E-01	7.17E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	231668_x_at	---
2.91	3.04	0.14	3.71E-01	7.17E-01	CCDC150	coiled-coil domain containing 150	chr2q33.1	243565_at	NM_001080539
2.05	2.18	0.13	3.71E-01	7.17E-01	TSLP	thymic stromal lymphopoietin	chr5q22.1	235737_at	NM_033035 /// NM_138551
1.98	2.11	0.13	3.71E-01	7.17E-01	---	---	---	1562634_at	---
2.10	2.21	0.11	3.71E-01	7.17E-01	CLDN8	claudin 8	chr21q22.11	214598_at	NM_199328
4.31	4.51	0.20	3.71E-01	7.17E-01	ALOX5	arachidonate 5-lipoxygenase	chr10q11.2	204445_s_at	NM_000698
3.09	3.25	0.15	3.71E-01	7.17E-01	ZNF775	Zinc finger protein 775	chr7q36.1	228294_s_at	NM_173680

8.47	8.61	0.13	3.72E-01	7.18E-01	NUDC	nuclear distribution gene C homolog (A. nidulans)	chr1p35-p34	210574_s_at	NM_006600
2.33	2.50	0.17	3.72E-01	7.18E-01	---	---	---	1570267_at	---
2.76	2.88	0.13	3.72E-01	7.18E-01	FAM131B	family with sequence similarity 131, member B	chr7q34	205368_at	NM_001031690 /// NM_014690
2.47	2.59	0.12	3.72E-01	7.18E-01	C6orf150	chromosome 6 open reading frame 150	chr6q13	1559051_s_at	NM_138441
3.98	4.16	0.17	3.72E-01	7.18E-01	LOC285965	hypothetical protein LOC285965	chr7q35	238263_at	---
4.10	4.34	0.24	3.72E-01	7.18E-01	---	---	---	239393_at	---
3.17	3.38	0.21	3.72E-01	7.18E-01	MMRN2	multimerin 2	chr10q23.2	222822_s_at	NM_024756
1.99	2.09	0.11	3.72E-01	7.18E-01	---	---	---	1562613_at	---
2.07	2.16	0.09	3.72E-01	7.18E-01	---	---	---	239639_at	---
3.59	3.76	0.17	3.72E-01	7.18E-01	FAM98B	family with sequence similarity 98, member B	chr15q14	1564637_a_at	NM_001042429 /// NM_173611
4.45	4.87	0.42	3.72E-01	7.18E-01	---	---	---	1556656_at	---
2.49	2.70	0.21	3.72E-01	7.18E-01	LOC646208 /// NUS1 /// YDD19	nuclear undecaprenyl pyrophosphate synthase 1 pseudogene /// nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae) /// YDD19 protein	chr13q12 /// chr13q12.12 /// chr6q22.2	215207_x_at	NM_138459 /// XR_016400 /// XR_019397 /// XR_038826
2.37	2.51	0.14	3.72E-01	7.18E-01	MEX3B	mex-3 homolog B (C. elegans)	chr15q25.2	223627_at	NM_032246
3.04	3.17	0.13	3.72E-01	7.18E-01	---	---	---	234552_at	---
2.29	2.40	0.11	3.72E-01	7.18E-01	---	---	---	239472_at	---
4.83	5.10	0.28	3.72E-01	7.18E-01	PAK1IP1	PAK1 interacting protein 1	chr6p24.2	218886_at	NM_017906
6.37	6.58	0.21	3.72E-01	7.18E-01	ABHD4	abhydrolase domain containing 4	chr14q11.2	218581_at	NM_022060
2.24	2.43	0.19	3.72E-01	7.18E-01	ZNF542	Zinc finger protein 542	chr19q13.43	229187_at	NR_003127 /// NR_024055 /// NR_024056 /// NR_024057 /// XR_017885 /// XR_017984
3.80	3.97	0.17	3.72E-01	7.18E-01	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	chr15q22	210421_s_at	NM_004727
2.45	2.61	0.16	3.72E-01	7.18E-01	---	---	---	243136_at	---
2.60	2.76	0.16	3.72E-01	7.18E-01	HHATL	hedgehog acyltransferase-like	chr3p22.1	223572_at	NM_020707
3.59	3.75	0.15	3.72E-01	7.18E-01	SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	chr2p25.3	1554198_at	NM_015677
2.33	2.48	0.15	3.72E-01	7.18E-01	ERBB2IP	Erbb2 interacting protein	chr5q12.3	232896_at	NM_001006600 /// NM_018695
2.93	3.08	0.15	3.72E-01	7.18E-01	---	---	---	237886_at	---
1.97	2.11	0.14	3.72E-01	7.18E-01	---	---	---	234588_at	---
3.00	3.14	0.13	3.72E-01	7.18E-01	LOC100128185	PNAS-19	chr2p25.3	224294_at	XM_001714745 /// XM_001720716 /// XM_001726477
2.17	2.30	0.13	3.72E-01	7.18E-01	---	---	---	1566080_at	---
2.06	2.18	0.12	3.72E-01	7.18E-01	---	---	---	1566538_at	---
3.64	3.76	0.12	3.72E-01	7.18E-01	---	---	---	216126_at	---
2.03	2.14	0.11	3.72E-01	7.18E-01	C12orf64	chromosome 12 open reading frame 64	chr12q21.31	1553746_a_at	NM_173591
2.42	2.54	0.11	3.72E-01	7.18E-01	RBMS3	RNA binding motif, single stranded interacting protein	chr3p24-p23	1560322_at	NM_001003792 /// NM_001003793 /// NM_014483
1.86	1.96	0.10	3.72E-01	7.18E-01	---	---	---	233465_at	---
2.17	2.27	0.10	3.72E-01	7.18E-01	LOC286154	Hypothetical protein LOC286154	chr8q22.3	1559029_at	---
1.87	1.97	0.10	3.72E-01	7.18E-01	---	---	---	1556491_at	---
3.90	4.60	0.70	3.73E-01	7.18E-01	TNC	tenascin C	chr9q33	201645_at	NM_002160
4.94	5.59	0.65	3.73E-01	7.18E-01	FAS	Fas (TNF receptor superfamily, member 6)	chr10q24.1	216252_x_at	NM_000043 /// NM_152871 /// NM_152872 /// NM_152873 /// NM_152874 /// NM_152875 /// NM_152876 /// NM_152877
4.19	4.59	0.40	3.73E-01	7.18E-01	CRIP1	cysteine-rich protein 1 (intestinal)	chr14q32.33	205081_at	NM_001311
2.46	2.64	0.18	3.73E-01	7.18E-01	RASIP1	Ras interacting protein 1	chr19q13.33	244830_at	NM_017805

5.56	5.74	0.18	3.73E-01	7.18E-01	HISPPD2A	histidine acid phosphatase domain containing 2A	chr15q15.3	204578_at	NM_001024463 /// NM_001130858 /// NM_001130859 /// NM_014659 /// XM_001723275
2.35	2.46	0.11	3.73E-01	7.18E-01	LOC100129410	hypothetical protein LOC100129410	chr4q13.3	216359_at	XM_001714842 /// XM_001715712 /// XM_001715812
2.05	2.15	0.11	3.73E-01	7.18E-01	---	---	---	232741_at	---
6.46	6.99	0.54	3.73E-01	7.18E-01	CDK6	cyclin-dependent kinase 6	chr7q21-q22	224851_at	NM_001259
4.07	4.23	0.16	3.73E-01	7.18E-01	PTGER1	Prostaglandin E receptor 1 (subtype EP1), 42kDa	chr19p13.1	231201_at	NM_000955
2.28	2.50	0.22	3.73E-01	7.18E-01	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	chr6p22-p21	209292_at	NM_001546
2.35	2.47	0.12	3.73E-01	7.18E-01	---	---	---	1563132_at	---
2.88	3.01	0.13	3.73E-01	7.18E-01	GBX2	gastrulation brain homeobox 2	chr2q37	210560_at	NM_001485
4.72	4.98	0.27	3.73E-01	7.18E-01	PXMP4	peroxisomal membrane protein 4, 24kDa	chr20q11.22	224210_s_at	NM_007238 /// NM_183397
1.98	2.11	0.12	3.73E-01	7.18E-01	---	---	---	1556462_a_at	---
2.06	2.16	0.10	3.73E-01	7.18E-01	---	---	---	237376_at	---
2.38	2.51	0.13	3.73E-01	7.18E-01	REG4	regenerating islet-derived family, member 4	chr1p13.1-p12	1554436_a_at	NM_032044
6.40	7.07	0.66	3.73E-01	7.18E-01	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	chrXp22.2-p22.1	205321_at	NM_001415
6.29	6.58	0.29	3.73E-01	7.18E-01	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	chr11q13.1	209356_x_at	NM_016938
2.00	2.11	0.10	3.73E-01	7.18E-01	ECT2	Epithelial cell transforming sequence 2 oncogene	chr3q26.1-q26.2	237241_at	NM_018098
1.71	1.82	0.11	3.73E-01	7.18E-01	---	---	---	1560540_x_at	---
4.29	4.58	0.29	3.73E-01	7.18E-01	NUP155	nucleoporin 155kDa	chr5p13.1	206550_s_at	NM_004298 /// NM_153485
3.37	3.52	0.15	3.73E-01	7.18E-01	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	chr3p14.1	1555262_a_at	NM_001033057 /// NM_004742 /// NM_015520
2.26	2.41	0.14	3.73E-01	7.19E-01	CCDC140	coiled-coil domain containing 140	chr2q36.1	1553485_at	NM_153038
1.97	2.09	0.12	3.73E-01	7.19E-01	C10orf40	chromosome 10 open reading frame 40	chr10q21.2	1556648_a_at	XM_001720081 /// XM_001720448 /// XM_001720595
2.51	2.64	0.13	3.73E-01	7.19E-01	---	---	---	240722_at	---
3.21	3.51	0.30	3.73E-01	7.19E-01	---	---	---	228471_at	---
2.72	2.93	0.21	3.73E-01	7.19E-01	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	chr12q22-q23	210393_at	NM_003667
4.81	5.05	0.24	3.73E-01	7.19E-01	---	---	---	242877_at	---
2.95	3.07	0.12	3.73E-01	7.19E-01	DTX3	deltex 3 homolog (Drosophila)	chr12q13.3	49051_g_at	NM_178502
4.15	4.35	0.20	3.74E-01	7.19E-01	SAMM50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	chr22q13.31	243239_at	NM_015380
2.88	3.02	0.13	3.74E-01	7.19E-01	SGMS2	sphingomyelin synthase 2	chr4q25	243141_at	NM_152621
2.15	2.27	0.11	3.74E-01	7.19E-01	ACADL	acyl-Coenzyme A dehydrogenase, long chain	chr2q34-q35	206069_s_at	NM_001608
4.73	5.56	0.83	3.74E-01	7.19E-01	MATR3	matrin 3	chr5q31.2	1558093_s_at	NM_018834 /// NM_199189
6.25	6.68	0.44	3.74E-01	7.19E-01	HMG2L1	high-mobility group protein 2-like 1	chr22q13.1	212596_s_at	NM_001003681 /// NM_005487 /// NM_014250
2.66	2.95	0.29	3.74E-01	7.19E-01	---	---	---	242496_at	---
5.17	5.41	0.25	3.74E-01	7.19E-01	HIP1	Huntingtin interacting protein 1	chr7q11.23	226364_at	NM_005338
6.95	7.19	0.24	3.74E-01	7.19E-01	TMCO1	transmembrane and coiled-coil domains 1	chr1q22-q25	211098_x_at	NM_019026
2.53	2.76	0.24	3.74E-01	7.19E-01	---	---	---	1558445_at	---
6.01	6.24	0.23	3.74E-01	7.19E-01	DOLPP1	dolichyl pyrophosphate phosphatase 1	chr9q34.1	221817_at	NM_020438
8.06	8.29	0.22	3.74E-01	7.19E-01	---	---	---	212498_at	---
4.29	4.51	0.21	3.74E-01	7.19E-01	---	---	---	244352_at	---
2.73	2.92	0.19	3.74E-01	7.19E-01	---	---	---	234264_at	---
3.47	3.66	0.19	3.74E-01	7.19E-01	---	---	---	241438_at	---
2.58	2.77	0.19	3.74E-01	7.19E-01	LOC348751	Hypothetical protein LOC348751	chr2q33.1	243744_at	XM_001716816 /// XM_929974 /// XM_936759
4.31	4.49	0.19	3.74E-01	7.19E-01	---	---	---	230586_s_at	---
2.61	2.77	0.16	3.74E-01	7.19E-01	---	---	---	1562621_at	---

3.29	3.44	0.16	3.74E-01	7.19E-01	MGC4294	hypothetical protein MGC4294	chr20q13.32	220698_at	XR_041174 /// XR_041175 /// XR_041176
3.53	3.69	0.16	3.74E-01	7.19E-01	IQCA1	IQ motif containing with AAA domain 1	chr2q37.2-q37.3	1562130_at	NM_024726
6.02	6.18	0.16	3.74E-01	7.19E-01	GLI1	glioma-associated oncogene homolog 1 (zinc finger protein)	chr12q13.2-q13.3	206646_at	NM_005269
3.37	3.52	0.15	3.74E-01	7.19E-01	---	---	---	240541_at	---
2.12	2.27	0.15	3.74E-01	7.19E-01	FAM19A1	family with sequence similarity 19 (chemokine (C-C motif)-like), member A1	chr3p14.1	230923_at	NM_213609
2.79	2.94	0.15	3.74E-01	7.19E-01	MAP3K11	mitogen-activated protein kinase kinase kinase 11	chr11q13.1-q13.3	1558984_at	NM_002419
2.28	2.42	0.14	3.74E-01	7.19E-01	---	---	---	216773_at	---
2.17	2.31	0.14	3.74E-01	7.19E-01	LOC574538	hypothetical protein LOC574538	chr12p13.33	1562251_a_at	---
3.83	3.96	0.13	3.74E-01	7.19E-01	NENF	neuron derived neurotrophic factor	chr1q32.3	218406_x_at	NM_013349
2.64	2.77	0.13	3.74E-01	7.19E-01	TCP11L1	t-complex 11 (mouse)-like 1	chr11p13	205796_at	NM_018393
2.72	2.84	0.12	3.74E-01	7.19E-01	LOC285281	hypothetical protein LOC285281	chr3p21.33	241717_at	---
2.53	2.65	0.12	3.74E-01	7.19E-01	C13orf28	chromosome 13 open reading frame 28	chr13q34	231405_at	NM_145248
2.00	2.12	0.12	3.74E-01	7.19E-01	FLJ42289	hypothetical LOC388182	chr15q26.3	1559298_a_at	XR_041191 /// XR_041192 /// XR_041193
2.48	2.60	0.13	3.74E-01	7.19E-01	C1orf104	Chromosome 1 open reading frame 104	chr1q22	230256_at	NM_001039517
2.05	2.16	0.12	3.74E-01	7.19E-01	---	---	---	1565830_at	---
2.24	2.39	0.15	3.74E-01	7.19E-01	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	chr17q21.32	206494_s_at	NM_000419
3.92	4.10	0.18	3.74E-01	7.19E-01	ARPC5	Actin related protein 2/3 complex, subunit 5, 16kDa	chr1q25.3	1569325_at	NM_005717
5.66	6.25	0.59	3.74E-01	7.19E-01	XRN2	5'-3' exoribonuclease 2	chr20p11.2-p11.1	233878_s_at	NM_012255
5.50	5.91	0.41	3.74E-01	7.19E-01	ARL8B	ADP-ribosylation factor-like 8B	chr3p26.2	222442_s_at	NM_018184
2.61	2.74	0.12	3.74E-01	7.19E-01	---	---	---	228533_at	---
2.40	2.57	0.17	3.74E-01	7.19E-01	SPATA6	spermatogenesis associated 6	chr1p33	238459_x_at	NM_019073
3.05	3.18	0.13	3.74E-01	7.19E-01	ZXDA /// ZXDB	zinc finger, X-linked, duplicated A /// zinc finger, X-linked, duplicated B	chrXp11.1 /// chrXp11.21	216014_s_at	NM_007156 /// NM_007157
2.32	2.43	0.11	3.74E-01	7.19E-01	---	---	---	237693_at	---
5.40	5.57	0.17	3.74E-01	7.19E-01	---	---	---	238044_at	---
2.18	2.34	0.16	3.75E-01	7.19E-01	---	---	---	1565895_at	---
2.17	2.31	0.13	3.75E-01	7.19E-01	---	---	---	1566879_at	---
4.25	4.58	0.33	3.75E-01	7.19E-01	SOD3	superoxide dismutase 3, extracellular	chr4p15.3-p15.1	205236_x_at	NM_003102
5.50	5.88	0.38	3.75E-01	7.19E-01	CDK5RAP2	CDK5 regulatory subunit associated protein 2	chr9q33.2	233540_s_at	NM_001011649 /// NM_018249
5.13	5.46	0.32	3.75E-01	7.19E-01	---	---	---	227579_at	---
3.25	3.39	0.14	3.75E-01	7.19E-01	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	chr21q22.3	207999_s_at	NM_001033049 /// NM_001112 /// NM_015833 /// NM_015834
3.79	3.91	0.13	3.75E-01	7.19E-01	MTMR3	myotubularin related protein 3	chr22q12.2	202198_s_at	NM_021090 /// NM_153050 /// NM_153051
1.94	2.06	0.12	3.75E-01	7.19E-01	GRIK3	glutamate receptor, ionotropic, kainate 3	chr1p34-p33	230593_at	NM_000831
1.92	2.03	0.10	3.75E-01	7.19E-01	---	---	---	242603_x_at	---
2.99	3.17	0.18	3.75E-01	7.19E-01	---	---	---	1567167_at	---
4.41	4.65	0.23	3.75E-01	7.19E-01	CRYZL1	crystallin, zeta (quinone reductase)-like 1	chr21q21.3	1554767_s_at	NM_145858
3.10	3.32	0.21	3.75E-01	7.19E-01	---	---	---	231087_at	---
8.71	8.89	0.18	3.75E-01	7.19E-01	---	---	---	224603_at	---
2.16	2.31	0.15	3.75E-01	7.19E-01	---	---	---	235172_at	---
2.52	2.66	0.14	3.75E-01	7.19E-01	---	---	---	231374_at	---
2.17	2.31	0.13	3.75E-01	7.19E-01	---	---	---	240207_at	---
2.23	2.37	0.13	3.75E-01	7.19E-01	CA5BL	carbonic anhydrase VB-like	chrXp22.2	238435_at	XM_001715245 /// XM_001716189 /// XM_001719208 /// XM_001719213
2.97	3.10	0.13	3.75E-01	7.19E-01	ZNF546	zinc finger protein 546	chr19q13.2	240429_at	NM_178544
2.16	2.27	0.12	3.75E-01	7.19E-01	---	---	---	242768_at	---
2.06	2.17	0.11	3.75E-01	7.19E-01	---	---	---	239479_x_at	---
1.96	2.06	0.10	3.75E-01	7.19E-01	SYTL3	synaptotagmin-like 3	chr6q25.3	1562255_at	NM_001009991
1.85	1.96	0.12	3.75E-01	7.19E-01	---	---	---	1561230_at	---
4.44	4.57	0.13	3.75E-01	7.19E-01	ZNF710	zinc finger protein 710	chr15q26.1	239335_at	NM_198526
2.71	2.88	0.17	3.75E-01	7.19E-01	CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	chr4q31.1	220671_at	NM_012118
6.54	6.96	0.43	3.75E-01	7.19E-01	PXMP3	peroxisomal membrane protein 3, 35kDa	chr8q21.1	210296_s_at	NM_000318 /// NM_001079867
2.29	2.40	0.11	3.75E-01	7.19E-01	---	---	---	235247_at	---
2.48	2.58	0.10	3.75E-01	7.19E-01	LRRC18	leucine rich repeat containing 18	chr10q11.22	1554331_a_at	NM_001006939

2.34	2.52	0.18	3.75E-01	7.19E-01	OPCML	opioid binding protein/cell adhesion molecule-like	chr11q25	214111_at	NM_001012393 /// NM_002545
2.60	2.77	0.17	3.75E-01	7.19E-01	---	---	---	237157_at	---
2.90	3.05	0.15	3.75E-01	7.19E-01	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	chr2p22-p21	242898_at	NM_002759
3.47	3.61	0.14	3.75E-01	7.19E-01	C5orf35	chromosome 5 open reading frame 35	chr5q11.2	240840_s_at	NM_153706
4.68	4.88	0.21	3.75E-01	7.19E-01	CALCOCO2	calcium binding and coiled-coil domain 2	chr17q21.32	238560_at	NM_005831
5.47	5.66	0.19	3.75E-01	7.19E-01	C2orf18	chromosome 2 open reading frame 18	chr2p23.3	1554444_s_at	NM_017877
2.35	2.48	0.13	3.75E-01	7.19E-01	ZFAND5	Zinc finger, AN1-type domain 5	chr9q13-q21	228317_at	NM_001102420 /// NM_001102421 /// NM_006007
2.08	2.19	0.11	3.75E-01	7.19E-01	---	---	---	240845_at	---
3.76	3.97	0.20	3.75E-01	7.20E-01	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	---	1559039_at	NM_001114397 /// NM_020865
7.58	8.02	0.44	3.76E-01	7.20E-01	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	chr2q35	208643_s_at	NM_021141
7.67	8.06	0.39	3.76E-01	7.20E-01	FH	fumarate hydratase	chr1q42.1	214170_x_at	NM_000143
6.37	6.74	0.37	3.76E-01	7.20E-01	THUMPD3	THUMP domain containing 3	chr3p25.3	223804_s_at	NM_001114092 /// NM_015453
2.64	2.82	0.18	3.76E-01	7.20E-01	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	chr6p21.3	208428_at	NM_000544 /// NM_018833
3.23	3.39	0.17	3.76E-01	7.20E-01	IGHD	immunoglobulin heavy constant delta	chr14q32.33	213674_x_at	---
2.82	2.97	0.15	3.76E-01	7.20E-01	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	---	234514_at	NM_080823
9.40	9.55	0.15	3.76E-01	7.20E-01	TMEM50A	transmembrane protein 50A	chr1p36.11	222401_s_at	NM_014313
3.45	3.58	0.14	3.76E-01	7.20E-01	---	---	---	1557584_at	---
1.95	2.08	0.13	3.76E-01	7.20E-01	---	---	---	242221_at	---
4.11	4.23	0.12	3.76E-01	7.20E-01	PSD2	pleckstrin and Sec7 domain containing 2	chr5q31.3	223536_at	NM_032289
3.08	3.18	0.11	3.76E-01	7.20E-01	---	---	---	215727_x_at	---
2.44	2.61	0.18	3.76E-01	7.20E-01	C9orf68	chromosome 9 open reading frame 68	chr9p24.2-p24.1	1554708_s_at	NM_001039395
2.75	2.86	0.11	3.76E-01	7.20E-01	RFC1	replication factor C (activator 1) 1, 145kDa	chr4p14-p13	208133_at	NM_002913
2.22	2.36	0.13	3.76E-01	7.20E-01	HDAC7	histone deacetylase 7	chr12q13.1	236326_at	NM_001098415 /// NM_001098416 /// NM_015401 /// NM_016596
4.97	5.50	0.53	3.76E-01	7.20E-01	ISLR	immunoglobulin superfamily containing leucine-rich repeat	chr15q23-q24	207191_s_at	NM_005545 /// NM_201526
5.29	5.51	0.22	3.76E-01	7.20E-01	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	chr19p13.3	206929_s_at	NM_005597 /// NM_205843
2.84	3.01	0.18	3.76E-01	7.20E-01	FAM71B	family with sequence similarity 71, member B	chr5q33.3	1553629_a_at	NM_130899
2.81	2.95	0.15	3.76E-01	7.20E-01	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	chr16q22-q23	209347_s_at	NM_001031804 /// NM_005360
2.29	2.41	0.11	3.76E-01	7.20E-01	---	---	---	237155_at	---
3.39	3.64	0.25	3.76E-01	7.20E-01	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	chr4p14-p13	213419_at	NM_173075
3.44	3.63	0.20	3.76E-01	7.20E-01	TPP2	tripeptidyl peptidase II	chr13q32-q33	1569857_s_at	NM_003291
8.83	9.46	0.62	3.76E-01	7.20E-01	SLC38A2	solute carrier family 38, member 2	chr12q	220924_s_at	NM_018976
5.46	5.97	0.51	3.76E-01	7.20E-01	FER1L3	fer-1-like 3, myoferlin (C. elegans)	chr10q24	211864_s_at	NM_013451 /// NM_133337
6.71	7.14	0.43	3.76E-01	7.20E-01	ANTXR2	anthrax toxin receptor 2	chr4q21.21	225524_at	NM_058172
4.28	4.58	0.30	3.76E-01	7.20E-01	HNMT	histamine N-methyltransferase	chr2q22.1	211732_x_at	NM_001024074 /// NM_001024075 /// NM_006895
6.69	6.94	0.26	3.76E-01	7.20E-01	UBE2K	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	chr4p14	225179_at	NM_001111112 /// NM_001111113 /// NM_005339
2.83	3.08	0.24	3.76E-01	7.20E-01	---	---	---	244487_at	---
4.35	4.57	0.22	3.76E-01	7.20E-01	N4BP2L2	NEDD4 binding protein 2-like 2	chr13q13.1	202259_s_at	NM_014887 /// NM_033111
6.46	6.68	0.22	3.76E-01	7.20E-01	RHOF	ras homolog gene family, member F (in filopodia)	chr12q24.31	219045_at	NM_019034
4.49	4.66	0.17	3.76E-01	7.20E-01	TMEM198	transmembrane protein 198	chr2q35	242782_x_at	NM_001005209
2.74	2.90	0.16	3.76E-01	7.20E-01	CENTG1	centaurin, gamma 1	chr12q14.1	215080_s_at	NM_001122772 /// NM_014770
2.65	2.79	0.14	3.77E-01	7.20E-01	LOC339874	hypothetical LOC339874	chr3q22.1	1561348_at	---
3.60	3.73	0.13	3.76E-01	7.20E-01	---	---	---	244088_at	---

2.52	2.65	0.13	3.76E-01	7.20E-01	PCDH11X /// PCDH11Y	protocadherin 11 X-linked /// protocadherin 11 Y-linked	chrXq21.3 /// chrYp11.2	1557880_at	NM_014522 /// NM_032967 /// NM_032968 /// NM_032969 /// NM_032971 /// NM_032972 /// NM_032973
1.94	2.07	0.13	3.76E-01	7.20E-01	SCN3A	sodium channel, voltage-gated, type III, alpha subunit	chr2q24	210432_s_at	NM_001081676 /// NM_001081677 /// NM_006922
2.48	2.60	0.12	3.76E-01	7.20E-01	GPR173	G protein-coupled receptor 173	chrXp11	221299_at	NM_018969
2.03	2.14	0.11	3.76E-01	7.20E-01	---	---	---	237700_at	---
2.12	2.22	0.11	3.76E-01	7.20E-01	---	---	---	240196_at	---
2.50	2.61	0.11	3.77E-01	7.20E-01	---	---	---	243840_at	---
1.66	1.77	0.11	3.76E-01	7.20E-01	---	---	---	1561959_x_at	---
6.39	6.50	0.11	3.76E-01	7.20E-01	SLC22A3	Solute carrier family 22 (extraneuronal monoamine transporter), member 3	chr6q26-q27	242578_x_at	NM_021977
2.38	2.48	0.10	3.77E-01	7.20E-01	C21orf82	chromosome 21 open reading frame 82	chr21q22.11	237326_at	---
2.31	2.42	0.11	3.77E-01	7.20E-01	ZNF233	zinc finger protein 233	chr19q13.31	230919_at	NM_181756
1.78	1.88	0.10	3.77E-01	7.20E-01	---	---	---	1563072_at	---
8.68	9.27	0.59	3.77E-01	7.20E-01	AOX1	aldehyde oxidase 1	chr2q33	205082_s_at	NM_001159
2.02	2.13	0.11	3.77E-01	7.20E-01	---	---	---	1568852_x_at	---
4.70	5.37	0.67	3.77E-01	7.20E-01	CLDN11	claudin 11	chr3q26.2-q26.3	228335_at	NM_005602
4.81	4.97	0.16	3.77E-01	7.20E-01	PRG2	plasticity-related gene 2	chr19p13.3	220798_x_at	NM_024888
2.49	2.60	0.12	3.77E-01	7.20E-01	---	---	---	234717_at	---
2.41	2.52	0.12	3.77E-01	7.20E-01	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	chr19p13.1	211108_s_at	NM_000215
3.33	3.54	0.21	3.77E-01	7.20E-01	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	chr17q11.2-q12|17q21.1	210930_s_at	NM_001005862 /// NM_004448
2.40	2.52	0.12	3.77E-01	7.20E-01	---	---	---	243068_at	---
6.67	7.00	0.34	3.77E-01	7.20E-01	---	---	---	243768_at	---
4.01	4.20	0.19	3.77E-01	7.21E-01	---	---	---	239263_at	---
2.01	2.11	0.10	3.77E-01	7.21E-01	DACH2	dachshund homolog 2 (Drosophila)	chrXq21.3	239738_at	NM_053281
3.82	4.08	0.26	3.77E-01	7.21E-01	NRTN	neurturin	chr19p13.3	210683_at	NM_004558
3.91	4.24	0.33	3.77E-01	7.21E-01	ZNF805	zinc finger protein 805	chr19q13.43	238437_at	XM_001718504 /// XM_001718548 /// XM_001719150
4.77	5.14	0.37	3.77E-01	7.21E-01	KRT8	keratin 8	chr12q13	209008_x_at	NM_002273
3.40	3.56	0.15	3.77E-01	7.21E-01	C17orf39	chromosome 17 open reading frame 39	chr17p11.2	220058_at	NM_024052
3.38	3.79	0.41	3.77E-01	7.21E-01	NEB	nebulin	chr2q22	205054_at	NM_004543
4.47	4.87	0.41	3.77E-01	7.21E-01	CDV3	CDV3 homolog (mouse)	chr3q22.1	213548_s_at	NM_001134422 /// NM_001134423 /// NM_017548
2.21	2.31	0.10	3.77E-01	7.21E-01	---	---	---	1556778_at	---
4.10	4.34	0.24	3.77E-01	7.21E-01	KIAA1305	KIAA1305	chr14q12	220911_s_at	NM_025081
6.27	6.88	0.61	3.77E-01	7.21E-01	MBNL2	Muscleblind-like 2 (Drosophila)	chr13q32.1	232138_at	NM_144778 /// NM_207304
2.68	2.86	0.18	3.78E-01	7.21E-01	SNCAIP	synuclein, alpha interacting protein	chr5q23.1-q23.3	237833_s_at	NM_005460
3.90	4.07	0.17	3.78E-01	7.21E-01	SPRR1A	small proline-rich protein 1A	chr1q21-q22	214549_x_at	NM_005987
3.61	3.75	0.14	3.78E-01	7.21E-01	KCNK4	potassium channel, subfamily K, member 4	chr11q13	224552_s_at	NM_033310
2.30	2.42	0.12	3.78E-01	7.21E-01	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	chr16q24.1-q24.2	204818_at	NM_002153
2.29	2.40	0.11	3.78E-01	7.21E-01	---	---	---	1569925_at	---
3.54	3.66	0.12	3.78E-01	7.21E-01	SLC38A10	solute carrier family 38, member 10	chr17q25.3	238347_at	NM_001037984 /// NM_138570
2.95	3.13	0.17	3.78E-01	7.21E-01	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	chr3q25	223374_s_at	NM_001038628 /// NM_003781 /// NM_033167 /// NM_033168 /// NM_033169
5.65	6.11	0.47	3.78E-01	7.21E-01	ATG12	ATG12 autophagy related 12 homolog (S. cerevisiae)	chr5q21-q22	213026_at	NM_004707
3.05	3.23	0.18	3.78E-01	7.21E-01	HCG27	HLA complex group 27	chr6p21.33	1559050_at	NM_181717

2.10	2.23	0.13	3.78E-01	7.22E-01	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2	chr1p13	239118_at	NM_004974
3.24	3.35	0.11	3.78E-01	7.22E-01	KIRREL2	kin of IRRE like 2 (Drosophila)	chr19q13.12	223755_at	NM_032123 /// NM_199179 /// NM_199180
3.54	3.69	0.15	3.78E-01	7.22E-01	---	---	---	243079_x_at	---
2.19	2.29	0.11	3.78E-01	7.22E-01	L3MBTL4	l(3)mbt-like 4 (Drosophila)	chr18p11.31	1554699_at	NM_173464
2.03	2.13	0.10	3.78E-01	7.22E-01	---	---	---	236791_at	---
2.37	2.48	0.11	3.78E-01	7.22E-01	SORCS1	sortilin-related VPS10 domain containing receptor 1	chr10q23-q25	1556891_at	NM_001013031 /// NM_052918
10.72	10.88	0.15	3.78E-01	7.22E-01	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	chr6p12	200064_at	NM_007355
3.43	3.66	0.22	3.78E-01	7.22E-01	FAM70B	family with sequence similarity 70, member B	chr13q34	238226_at	NM_182614 /// XM_001715788
5.28	5.44	0.15	3.78E-01	7.22E-01	---	---	---	235352_at	---
4.66	4.81	0.15	3.78E-01	7.22E-01	---	---	---	239565_at	---
6.54	7.03	0.50	3.79E-01	7.22E-01	CPNE3	copine III	chr8q21.3	202118_s_at	NM_003909
5.12	5.49	0.36	3.79E-01	7.22E-01	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	chr1q32	219960_s_at	NM_015984
5.11	5.28	0.17	3.79E-01	7.22E-01	ZNF207	zinc finger protein 207	chr17q11.2	244153_at	NM_001032293 /// NM_001098507 /// NM_003457
2.34	2.47	0.13	3.79E-01	7.22E-01	---	---	---	1563154_at	---
2.06	2.15	0.09	3.79E-01	7.22E-01	BCL8	B-cell CLL/lymphoma 8	chr15q11-q13	1560684_x_at	XM_001125807
3.20	3.35	0.15	3.79E-01	7.22E-01	SOS2	son of sevenless homolog 2 (Drosophila)	chr14q21	217576_x_at	NM_006939
6.57	6.71	0.14	3.79E-01	7.22E-01	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	chr12q22-qter	202366_at	NM_000017
1.97	2.10	0.14	3.79E-01	7.22E-01	GNAL	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	chr18p11.22-p11.21	206355_at	NM_002071 /// NM_182978
3.75	3.87	0.11	3.79E-01	7.22E-01	---	---	---	241724_x_at	---
3.77	4.04	0.27	3.79E-01	7.22E-01	SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	chr1p32-p31	209712_at	NM_015139
2.32	2.46	0.14	3.79E-01	7.22E-01	---	---	---	1560460_at	---
6.41	6.75	0.34	3.79E-01	7.22E-01	JAZF1	JAZF zinc finger 1	chr7p15.2-p15.1	225800_at	NM_175061
3.26	3.41	0.15	3.79E-01	7.22E-01	UNQ2963	hypothetical protein LOC283314	chr12p13.31	1560320_a_at	XR_039860 /// XR_039861 /// XR_039862
2.42	2.56	0.15	3.79E-01	7.22E-01	C18orf8	Chromosome 18 open reading frame 8	chr18q11.2	232348_at	NM_013326
2.61	2.78	0.16	3.79E-01	7.22E-01	PTPN1	Protein tyrosine phosphatase, non-receptor type 1	chr20q13.1-q13.2	217689_at	NM_002827
2.63	2.78	0.15	3.79E-01	7.22E-01	---	---	---	244286_at	---
2.12	2.25	0.13	3.79E-01	7.23E-01	---	---	---	233527_at	---
6.05	6.33	0.28	3.79E-01	7.23E-01	LYCAT	lysocardiolipin acyltransferase	chr2p23.1	226996_at	NM_001002257 /// NM_182551
2.34	2.51	0.17	3.79E-01	7.23E-01	SP140	SP140 nuclear body protein	chr2q37.1	207777_s_at	NM_001005176 /// NM_007237
3.86	4.04	0.17	3.79E-01	7.23E-01	---	---	---	239993_at	---
1.93	2.04	0.10	3.79E-01	7.23E-01	VN1R3	vomeronasal 1 receptor 3	chr16p11.2	224290_at	---
4.01	4.16	0.16	3.79E-01	7.23E-01	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	chr16q13	204763_s_at	NM_020988 /// NM_138736
2.00	2.10	0.10	3.79E-01	7.23E-01	---	---	---	244335_at	---
3.25	3.44	0.19	3.79E-01	7.23E-01	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	chr13q33	1557080_s_at	NM_004791
3.59	3.74	0.15	3.79E-01	7.23E-01	---	---	---	244408_at	---
4.29	4.89	0.60	3.79E-01	7.23E-01	LOC654433	Hypothetical LOC654433	chr2q13	227474_at	NR_015377 /// XR_041715 /// XR_041716 /// XR_041717
3.12	3.23	0.11	3.79E-01	7.23E-01	TTC23	tetratricopeptide repeat domain 23	chr15q26.3	1568821_at	NM_001040655 /// NM_001040656 /// NM_001040657 /// NM_001040658 /// NM_001040659 /// NM_001040660 /// NM_022905

4.42	4.57	0.15	3.80E-01	7.23E-01	LOC652755 /// NAIP	similar to Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein) /// NLR family, apoptosis inhibitory protein	chr5q13.1	204861_s_at	NM_004536 /// NM_022892 /// XM_001713981 /// XM_942384																				
4.03	4.21	0.18	3.80E-01	7.23E-01	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	chr7q36.1	232940_s_at	NM_170606																				
5.00	5.20	0.20	3.80E-01	7.23E-01	UNC13D	unc-13 homolog D (C. elegans)	chr17q25.1	228350_at	NM_199242																				
2.33	2.45	0.12	3.80E-01	7.23E-01	LOC100129449	PRO2055	chr2q23.3	224256_at	XM_001716723 /// XM_001716731 /// XM_001724506																				
5.92	6.27	0.35	3.80E-01	7.23E-01	TTYH2	tweety homolog 2 (Drosophila)	chr17q25.1	223741_s_at	NM_032646 /// NM_052869																				
8.80	9.05	0.25	3.80E-01	7.23E-01	SUB1	SUB1 homolog (S. cerevisiae)	chr5p13.3	212857_x_at	NM_006713																				
3.73	3.89	0.16	3.80E-01	7.23E-01	QRICH2	glutamine rich 2	chr17q25.1	232532_at	NM_032134																				
2.84	3.00	0.16	3.80E-01	7.23E-01	LCA5L	Leber congenital amaurosis 5-like	chr21q22.2	232196_at	NM_152505																				
2.10	2.25	0.15	3.80E-01	7.23E-01	---	---	---	241110_at	---																				
5.41	5.55	0.14	3.80E-01	7.23E-01	POU5F1P1	POU class 5 homeobox 1 pseudogene 1	chr8q24.21	214532_x_at	NR_002304																				
4.07	4.20	0.13	3.80E-01	7.23E-01	KRT79	keratin 79	chr12q13.13	1569909_at	NM_175834																				
3.09	3.22	0.13	3.80E-01	7.23E-01	---	---	---	239497_at	---																				
4.32	4.46	0.14	3.80E-01	7.23E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	1558631_at	NM_001001928 /// NM_005036																				
2.26	2.39	0.13	3.80E-01	7.23E-01	---	---	---	235251_at	---																				
9.43	9.55	0.13	3.80E-01	7.23E-01	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	chr7p22	208641_s_at	NM_006908 /// NM_018890 /// NM_198829																				
2.42	2.54	0.12	3.80E-01	7.23E-01	ACSM1	acyl-CoA synthetase medium-chain family member 1	chr16p12.2	234197_at	NM_052956																				
2.02	2.13	0.11	3.80E-01	7.23E-01	GH2	growth hormone 2	chr17q24.2	211508_s_at	NM_002059 /// NM_022556 /// NM_022557 /// NM_022558																				
3.01	3.11	0.10	3.80E-01	7.23E-01	---	---	---	216702_x_at	---																				
3.39	3.76	0.37	3.80E-01	7.23E-01	C5orf22	chromosome 5 open reading frame 22	chr5p13.3	1552660_a_at	NM_018356																				
4.20	4.39	0.19	3.80E-01	7.23E-01	---	---	---	244580_at	---																				
2.89	3.07	0.18	3.80E-01	7.23E-01	D21S2088E	D21S2088E	---	1559471_s_at	---																				
2.02	2.12	0.10	3.80E-01	7.23E-01	CCDC26	coiled-coil domain containing 26	chr8q24.21	1553849_at	NM_145050																				
5.38	5.69	0.31	3.80E-01	7.23E-01	INO80D	INO80 complex subunit D	chr2q33.3	227931_at	NM_017759																				
6.53	6.79	0.26	3.80E-01	7.23E-01	NMD3	NMD3 homolog (S. cerevisiae)	chr3q26.1	222497_x_at	NM_015938																				
4.90	5.16	0.26	3.80E-01	7.23E-01	PTGER1	prostaglandin E receptor 1 (subtype EP1), 42kDa	chr19p13.1	207650_x_at	NM_000955																				
2.07	2.19	0.12	3.80E-01	7.23E-01	---	---	---	1556764_s_at	---																				
4.05	4.23	0.18	3.80E-01	7.23E-01	---	---	---	230696_at	---																				
3.54	4.00	0.45	3.80E-01	7.23E-01	CEP57	centrosomal protein 57kDa	chr11q21	203491_s_at	NM_014679																				
3.56	3.98	0.43	3.80E-01	7.23E-01	ITM2A	integral membrane protein 2A	chrXq13.3-Xq21.2	202746_at	NM_004867																				

4.51	4.88	0.37	3.80E-01	7.23E-01	hCG_1998957 /// HLA-DQB1 /// HLA-DQB2 /// HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133583 /// LOC100133661 /// LOC100133811 /// LOC730415 /// LOC731718 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 5 /// major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647 /// hypothetical protein LOC730415 /// similar to HLA class II histocompatibility antigen, DRB1-7 beta chain precursor (MHC class I antigen DRB1*7) (DR-7) (DR7) /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749	chr14q24-q31 /// chr19q13.43 /// chr6p21 /// chr6p21.3	221491_x_at	NM_001023561 /// NM_002123 /// NM_002124 /// NM_002125 /// NM_002934 /// NM_021983 /// NM_022555 /// NR_003937 /// XM_001124749 /// XM_001713857 /// XM_001713867 /// XM_001714067 /// XM_001714074 /// XM_001718754 /// XM_001719473 /// XM_001720834 /// XM_001720835 /// XM_001720843 /// XM_001722124 /// XM_001722127 /// XM_001722253 /// XM_001723414 /// XM_001723417 /// XM_001723419 /// XM_001723447 /// XR_036846
3.81	4.08	0.26	3.80E-01	7.23E-01	PRDM1	PR domain containing 1, with ZNF domain	chr6q21-q22.1	228964_at	NM_001198 /// NM_182907
2.37	2.51	0.14	3.80E-01	7.23E-01	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	chr7q31	1555571_at	NM_032549
2.49	2.62	0.13	3.80E-01	7.23E-01	---	---	---	1566999_at	---
2.12	2.25	0.13	3.80E-01	7.23E-01	---	---	---	217244_at	---
4.79	5.48	0.68	3.81E-01	7.24E-01	SEL1L	Sel-1 suppressor of lin-12-like (C. elegans)	chr14q24.3-q31	230265_at	NM_005065
2.27	2.40	0.13	3.81E-01	7.24E-01	TCP11L2	t-complex 11 (mouse)-like 2	chr12q23.3	1559413_at	NM_152772
2.59	2.78	0.20	3.81E-01	7.24E-01	LOC153577	hypothetical protein LOC153577	chr5q35.3	1556750_at	---
3.98	4.12	0.14	3.81E-01	7.24E-01	---	---	---	231604_at	---
3.75	3.92	0.17	3.81E-01	7.24E-01	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	chr4p16.1	228140_s_at	NM_020416 /// NM_181876
2.71	2.85	0.14	3.81E-01	7.24E-01	---	---	---	237903_at	---
4.96	5.12	0.17	3.81E-01	7.24E-01	---	---	---	1558784_at	---
2.58	2.77	0.19	3.81E-01	7.24E-01	NCAN	neurocan	chr19p12	205143_at	NM_004386
3.81	4.00	0.19	3.81E-01	7.24E-01	BCL2L1	BCL2-like 1	chr20q11.21	215037_s_at	NM_001191 /// NM_138578
2.47	2.59	0.13	3.81E-01	7.24E-01	NKX6-2	NK6 homeobox 2	chr10q26	235832_at	NM_177400
7.06	7.23	0.17	3.81E-01	7.24E-01	SESN1	sestrin 1	chr6q21	218346_s_at	NM_014454
4.39	4.96	0.57	3.81E-01	7.24E-01	LOC400642	Hypothetical LOC400642	chr18p11.31	217506_at	---
5.46	5.80	0.34	3.81E-01	7.24E-01	MSH3	mutS homolog 3 (E. coli)	chr5q11-q12	210947_s_at	NM_002439
2.79	2.98	0.19	3.81E-01	7.24E-01	---	---	---	231508_s_at	---
3.44	3.63	0.19	3.81E-01	7.24E-01	KCNIP3	Kv channel interacting protein 3, calsenilin	chr2q21.1	1555694_a_at	NM_001034914 /// NM_013434
2.37	2.53	0.17	3.81E-01	7.24E-01	---	---	---	1566958_at	---
3.29	3.42	0.13	3.81E-01	7.24E-01	BRAF	v-raf murine sarcoma viral oncogene homolog B1	chr7q34	206044_s_at	NM_004333
2.21	2.33	0.12	3.81E-01	7.24E-01	GLYAT	glycine-N-acyltransferase	chr11q12.1	231683_at	NM_005838 /// NM_201648
2.10	2.20	0.10	3.81E-01	7.24E-01	FRG1B	Hypothetical protein LOC283788	chr20q11.1	243689_s_at	NR_003579
2.12	2.21	0.09	3.81E-01	7.24E-01	PHLDA2	Pleckstrin homology-like domain, family A, member 2	chr11p15.5	229494_s_at	NM_003311
1.86	1.95	0.09	3.81E-01	7.24E-01	---	---	---	1564097_at	---

5.57	5.83	0.26	3.81E-01	7.24E-01	CAPS	calcyphosine	chr19p13.3	226424_at	NM_004058 /// NM_080590
3.03	3.22	0.19	3.81E-01	7.24E-01	KLC3	kinesin light chain 3	chr19q13.2-q13.3	239853_at	NM_177417
1.91	2.07	0.16	3.81E-01	7.24E-01	THAP9	THAP domain containing 9	chr4q21.22	220360_at	NM_024672
3.02	3.15	0.13	3.81E-01	7.24E-01	SCTR	secretin receptor	chr2q14.1	210382_at	NM_002980
5.08	5.29	0.21	3.81E-01	7.24E-01	MGC45922	hypothetical gene MGC45922	chr19q13.33	1554222_at	XR_041434 /// XR_041435 /// XR_041436
6.67	7.04	0.37	3.82E-01	7.24E-01	CUGBP2	CUG triplet repeat, RNA binding protein 2	chr10p13	202157_s_at	NM_001025076 /// NM_001025077 /// NM_001083591 /// NM_006561
2.14	2.26	0.11	3.82E-01	7.24E-01	FLJ12120	hypothetical LOC388439	chr17p13.3	233210_at	---
1.98	2.08	0.10	3.81E-01	7.24E-01	RFPL3S	ret finger protein-like 3 antisense	chr22q12.3	214409_at	NR_001450 /// NR_002596
2.58	2.73	0.15	3.82E-01	7.24E-01	FLJ40473	hypothetical protein FLJ40473	chr3q21.3	1558987_at	XR_040377 /// XR_040378 /// XR_040379
2.00	2.12	0.12	3.82E-01	7.24E-01	ANLN	anillin, actin binding protein	chr7p15-p14	222608_s_at	NM_018685
4.29	4.41	0.12	3.82E-01	7.24E-01	---	---	---	234481_at	---
1.71	1.80	0.09	3.82E-01	7.24E-01	RTKN2	rhotekin 2	chr10q21.2	230469_at	NM_145307
7.06	7.31	0.26	3.82E-01	7.24E-01	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	chr16q12.1	209157_at	NM_005880
3.20	3.43	0.23	3.82E-01	7.24E-01	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	chr7p12.1	206805_at	NM_006080
2.62	2.75	0.14	3.82E-01	7.24E-01	EDN3	endothelin 3	chr20q13.2-q13.3	217154_s_at	NM_000114 /// NM_207032 /// NM_207033 /// NM_207034
4.40	4.53	0.13	3.82E-01	7.24E-01	---	---	---	1560883_s_at	---
1.76	1.86	0.10	3.82E-01	7.24E-01	---	---	---	233622_x_at	---
4.63	5.16	0.54	3.82E-01	7.24E-01	FLJ30901	hypothetical protein FLJ30901	chr22q13.31	1552388_at	---
3.84	4.43	0.59	3.82E-01	7.24E-01	GPM6B	glycoprotein M6B	chrXp22.2	209167_at	NM_001001994 /// NM_001001995 /// NM_001001996 /// NM_005278
7.80	7.97	0.17	3.82E-01	7.24E-01	HSPG2	heparan sulfate proteoglycan 2	chr1p36.1-p34	201655_s_at	NM_005529
2.04	2.15	0.11	3.82E-01	7.24E-01	HOXD13	homeobox D13	chr2q31.1	207397_s_at	NM_000523
5.40	5.58	0.18	3.82E-01	7.24E-01	SPTBN4	spectrin, beta, non-erythrocytic 4	chr19q13.13	224145_s_at	NM_020971 /// NM_025213
5.63	5.85	0.23	3.82E-01	7.25E-01	C20orf149	chromosome 20 open reading frame 149	chr20q13.33	218010_x_at	NM_024299
3.19	3.34	0.15	3.82E-01	7.25E-01	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	chr7q21.1	209961_s_at	NM_000601 /// NM_001010931 /// NM_001010932 /// NM_001010933 /// NM_001010934
2.33	2.44	0.11	3.82E-01	7.25E-01	CHD1L	Chromodomain helicase DNA binding protein 1-like	chr1q12	244848_at	NM_004284
1.94	2.05	0.11	3.82E-01	7.25E-01	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	chr5p15.1-p14	205533_s_at	NM_004932
2.70	2.84	0.14	3.82E-01	7.25E-01	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	chr4q21-q23	206262_at	NM_000669
1.97	2.08	0.11	3.82E-01	7.25E-01	SLC25A42	solute carrier family 25, member 42	chr19p13.11	242274_x_at	NM_178526
5.72	5.98	0.27	3.82E-01	7.25E-01	RELL1	RELT-like 1	chr4p14	226430_at	NM_001085399 /// NM_001085400
5.68	6.25	0.56	3.82E-01	7.25E-01	KLHL15	kelch-like 15 (Drosophila)	chrXp22.1-p21	226370_at	NM_030624
5.12	5.50	0.38	3.83E-01	7.25E-01	PWP1	PWP1 homolog (S. cerevisiae)	chr12q23.3	201607_at	NM_007062
4.20	4.45	0.25	3.83E-01	7.25E-01	---	---	---	236754_at	---
2.57	2.74	0.17	3.83E-01	7.25E-01	KRTAP17-1	keratin associated protein 17-1	chr17q12-q21	234680_at	NM_031964
2.61	2.78	0.17	3.82E-01	7.25E-01	GAGE3	G antigen 3	chrXp11.4-p11.2	207663_x_at	---
2.07	2.22	0.15	3.83E-01	7.25E-01	SMG1	PI-3-kinase-related kinase SMG-1	chr16p12.3	210057_at	NM_015092
4.30	4.45	0.14	3.83E-01	7.25E-01	FLJ33630	hypothetical LOC644873	chr5q23.3	230685_at	NR_015360 /// XM_932475
3.22	3.41	0.19	3.83E-01	7.25E-01	ZNF140	Zinc finger protein 140	chr12q24.32-q24.33	238631_at	NM_003440

2.21	2.36	0.15	3.83E-01	7.25E-01	C11orf9	chromosome 11 open reading frame 9	chr11q12-q13.1	217463_s_at	NM_001127392 /// NM_013279																				
4.08	4.27	0.19	3.83E-01	7.25E-01	GPATCH4	G patch domain containing 4	chr1q22	224633_s_at	NM_015590 /// NM_182679																				
3.23	3.38	0.15	3.83E-01	7.25E-01	---	---	---	243434_at	---																				
1.96	2.07	0.10	3.83E-01	7.25E-01	---	---	---	239102_s_at	---																				
3.29	3.53	0.24	3.83E-01	7.25E-01	---	---	---	227600_at	---																				
5.39	5.62	0.23	3.83E-01	7.25E-01	MAPKAP1	mitogen-activated protein kinase associated protein 1	chr9q33.3	229846_s_at	NM_001006617 /// NM_001006618 /// NM_001006619 /// NM_001006620 /// NM_001006621 /// NM_024117																				
5.05	5.21	0.16	3.83E-01	7.25E-01	CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	chr16p13.3	222960_at	NM_001005407 /// NM_021098																				
2.68	2.84	0.16	3.83E-01	7.25E-01	CCDC125	coiled-coil domain containing 125	chr5q13.2	1553542_at	NM_176816																				
2.90	3.03	0.13	3.83E-01	7.25E-01	---	---	---	1570084_at	---																				
3.49	3.61	0.12	3.83E-01	7.25E-01	---	---	---	233125_at	---																				
2.48	2.59	0.11	3.83E-01	7.25E-01	NF2	neurofibromin 2 (merlin)	chr22q12.2	211092_s_at	NM_000268 /// NM_016418 /// NM_181825 /// NM_181828 /// NM_181829 /// NM_181830 /// NM_181831 /// NM_181832 /// NM_181833																				
2.35	2.47	0.13	3.83E-01	7.25E-01	ZAR1	zygote arrest 1	chr4p11	1555774_at	NM_175619																				
5.45	6.04	0.59	3.83E-01	7.25E-01	FKBP5	FK506 binding protein 5	chr6p21.3-p21.2	204560_at	NM_004117																				
4.53	4.78	0.25	3.83E-01	7.25E-01	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene spi1	chr11p11.2	205312_at	NM_001080547 /// NM_003120																				
3.08	3.29	0.21	3.83E-01	7.25E-01	PHTF1	putative homeodomain transcription factor 1	chr1p13	215285_s_at	NM_006608																				
2.25	2.43	0.18	3.83E-01	7.25E-01	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	chr17q23.1-q24.2	222901_s_at	NM_018658 /// NM_170741 /// NM_170742																				
4.62	4.77	0.15	3.83E-01	7.25E-01	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	chr17q22	211802_x_at	NM_018896 /// NM_198376 /// NM_198377 /// NM_198378 /// NM_198379 /// NM_198380 /// NM_198382 /// NM_198383 /// NM_198384 /// NM_198385 /// NM_198386 /// NM_198387 /// NM_198388 /// NM_198396 /// NM_198397																				
2.34	2.45	0.12	3.83E-01	7.25E-01	FAM83A	family with sequence similarity 83, member A	chr8q24.13	238460_at	NM_032899 /// NM_207006																				
2.00	2.10	0.11	3.83E-01	7.25E-01	---	---	---	240442_at	---																				
2.01	2.11	0.10	3.83E-01	7.25E-01	VSTM2A	V-set and transmembrane domain containing 2A	chr7p11.2	230117_at	NM_182546																				
6.69	6.95	0.26	3.83E-01	7.25E-01	ARMCX3	armadillo repeat containing, X-linked 3	chrXq21.33-q22.2	222444_at	NM_016607 /// NM_177947 /// NM_177948																				
1.98	2.12	0.13	3.83E-01	7.25E-01	KCNV1	potassium channel, subfamily V, member 1	chr8q22.3-q24.1	220294_at	NM_014379																				
2.92	3.08	0.16	3.83E-01	7.25E-01	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	chr2p23.3	223505_s_at	NM_016544																				
6.58	6.72	0.14	3.83E-01	7.25E-01	SLC31A1	solute carrier family 31 (copper transporters), member 1	chr9q31-q32	235013_at	NM_001859																				
2.53	2.70	0.17	3.84E-01	7.26E-01	NPC1L1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	chr7p13	224305_s_at	NM_001101648 /// NM_013389																				
5.94	6.08	0.14	3.84E-01	7.26E-01	B4GALT4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	chr3q13.3	212876_at	NM_003778 /// NM_212543																				
2.43	2.54	0.11	3.84E-01	7.26E-01	KIAA1267	KIAA1267	chr17q21.31	224490_s_at	NM_015443																				
3.73	3.94	0.22	3.84E-01	7.26E-01	SNHG7	Small nucleolar RNA host gene 7 (non-protein coding)	chr9q34.3	1558619_at	NR_003672																				

2.56	2.68	0.13	3.84E-01	7.26E-01	STARD13	StAR-related lipid transfer (START) domain containing 13	chr13q12-q13	242686_at	NM_052851 /// NM_178006 /// NM_178007
5.61	6.00	0.39	3.84E-01	7.26E-01	BIRC6	baculoviral IAP repeat-containing 6	chr2p22-p21	224635_s_at	NM_016252
3.65	3.80	0.15	3.84E-01	7.26E-01	FAM83A	family with sequence similarity 83, member A	chr8q24.13	239586_at	NM_032899 /// NM_207006
2.91	3.05	0.14	3.84E-01	7.26E-01	MBP	myelin basic protein	chr18q23	209072_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385
1.96	2.07	0.12	3.84E-01	7.26E-01	CFTR	Cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	chr7q31.2	234702_x_at	NM_000492
2.11	2.21	0.11	3.84E-01	7.26E-01	---	---	---	238281_at	---
2.06	2.17	0.10	3.84E-01	7.26E-01	PLCZ1	phospholipase C, zeta 1	chr12p12.3	231425_at	NM_033123
1.96	2.06	0.10	3.84E-01	7.26E-01	SP8	Sp8 transcription factor	chr7p21.2	237449_at	NM_182700 /// NM_198956 /// NR_024112
5.42	5.55	0.13	3.84E-01	7.26E-01	EMX1	empty spiracles homeobox 1	chr2p14-p13	215265_at	NM_004097
2.43	2.56	0.12	3.84E-01	7.26E-01	OPN5	opsin 5	chr6p12.3	1568914_at	NM_001030051 /// NM_181744
2.33	2.54	0.21	3.84E-01	7.26E-01	---	---	---	238562_at	---
2.56	2.75	0.20	3.84E-01	7.26E-01	GRM3	glutamate receptor, metabotropic 3	chr7q21.1-q21.2	205814_at	NM_000840
2.13	2.27	0.14	3.84E-01	7.26E-01	COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	chr17p12-p11.2	216003_at	NM_001303
2.52	2.69	0.17	3.84E-01	7.26E-01	PGBD4	piggyBac transposable element derived 4	chr15q14	243815_at	NM_152595
2.28	2.41	0.13	3.84E-01	7.26E-01	---	---	---	1564626_at	---
2.27	2.36	0.09	3.84E-01	7.26E-01	IL11	interleukin 11	chr19q13.3-q13.4	206924_at	NM_000641
3.59	3.78	0.19	3.84E-01	7.26E-01	---	---	---	241152_at	---
6.21	6.67	0.45	3.84E-01	7.26E-01	ASNSD1	asparagine synthetase domain containing 1	chr2p24.3-q21.3	217987_at	NM_019048
5.09	5.45	0.37	3.84E-01	7.26E-01	HIST1H1C	histone cluster 1, H1c	chr6p21.3	209398_at	NM_005319
5.84	6.20	0.36	3.84E-01	7.26E-01	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	chr4q23-q25	209444_at	NM_001100426 /// NM_001100427 /// NM_001100428 /// NM_001100429 /// NM_001100430 /// NM_021159
4.96	5.30	0.34	3.84E-01	7.26E-01	C10orf46	chromosome 10 open reading frame 46	chr10q26.11	227257_s_at	NM_153810
2.95	3.08	0.13	3.84E-01	7.26E-01	---	---	---	230772_at	---
1.95	2.07	0.13	3.84E-01	7.26E-01	---	---	---	1566882_at	---
2.46	2.66	0.20	3.84E-01	7.26E-01	CASP14	caspase 14, apoptosis-related cysteine peptidase	chr19p13.1	231722_at	NM_012114
3.72	4.31	0.59	3.84E-01	7.26E-01	CALCRL	calcitonin receptor-like	chr2q32.1	206331_at	NM_005795
5.71	6.09	0.38	3.84E-01	7.26E-01	CCDC104	coiled-coil domain containing 104	chr2p16.1	224968_at	NM_080667
4.04	4.27	0.24	3.84E-01	7.26E-01	KIF26A	kinesin family member 26A	chr14q32.33	234307_s_at	NM_015656
2.92	3.08	0.16	3.84E-01	7.26E-01	IL16	interleukin 16 (lymphocyte chemoattractant factor)	chr15q26.3	209828_s_at	NM_004513 /// NM_172217
3.84	3.99	0.15	3.84E-01	7.26E-01	PRRG2	proline rich Gla (G-carboxyglutamic acid) 2	chr19q13.33	205617_at	NM_000951
5.65	5.79	0.14	3.85E-01	7.26E-01	B9D2	B9 protein domain 2	chr19q13.2	219766_at	NM_030578
2.46	2.60	0.14	3.84E-01	7.26E-01	---	---	---	235304_at	---
2.70	2.80	0.11	3.84E-01	7.26E-01	DDHD1	DDHD domain containing 1	chr14q21	225970_at	NM_030637
2.10	2.20	0.10	3.84E-01	7.26E-01	---	---	---	220897_at	---
3.76	3.89	0.13	3.85E-01	7.26E-01	RBM12B	RNA binding motif protein 12B	chr8q22.1	51228_at	NM_203390
1.92	2.01	0.09	3.85E-01	7.26E-01	---	---	---	215457_at	---
2.73	2.88	0.15	3.85E-01	7.26E-01	---	---	---	237622_at	---
2.74	2.86	0.13	3.85E-01	7.26E-01	ZNF391	Hypothetical protein LOC100128090	chr6p22.1	1561116_at	NM_001076781
2.13	2.23	0.10	3.85E-01	7.26E-01	---	---	---	1570099_at	---
5.87	6.21	0.34	3.85E-01	7.26E-01	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	chr3q25.31	222412_s_at	NM_007107
3.18	3.52	0.33	3.85E-01	7.26E-01	CCL5	chemokine (C-C motif) ligand 5	chr17q11.2-q12	1405_i_at	NM_002985
3.07	3.28	0.21	3.85E-01	7.26E-01	FAM159A	family with sequence similarity 159, member A	chr1p32.3	237033_at	NM_001042693
3.72	3.93	0.21	3.85E-01	7.26E-01	---	---	---	229370_at	---

3.09	3.28	0.19	3.85E-01	7.26E-01	---	---	---	237064_x_at	---
4.87	5.04	0.17	3.85E-01	7.26E-01	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	chr17q25.3	201167_x_at	NM_004309
2.80	2.95	0.16	3.85E-01	7.26E-01	---	---	---	231180_at	---
3.03	3.19	0.15	3.85E-01	7.26E-01	---	---	---	231097_at	---
5.07	5.22	0.15	3.85E-01	7.26E-01	MXD3	MAX dimerization protein 3	chr5q35.3	221250_s_at	NM_031300
2.60	2.74	0.14	3.85E-01	7.26E-01	---	---	---	240123_at	---
2.25	2.38	0.13	3.85E-01	7.26E-01	---	---	---	239571_at	---
2.04	2.15	0.11	3.85E-01	7.26E-01	FEZF2	FEZ family zinc finger 2	chr3p14.2	221086_s_at	NM_018008
1.93	2.03	0.11	3.85E-01	7.26E-01	DKFZp667F0711	hypothetical protein DKFZp667F0711	chr10p15.1	1559756_at	XM_001719944 /// XM_001723851 /// XM_001725021
2.46	2.57	0.10	3.85E-01	7.26E-01	---	---	---	236003_x_at	---
2.57	2.66	0.10	3.85E-01	7.26E-01	TMPRSS11E /// TMPRSS11E2	transmembrane protease, serine 11E /// transmembrane protease, serine 11E2	chr4q13.2	220431_at	NM_001099662 /// NM_014058
2.61	2.77	0.15	3.85E-01	7.26E-01	LOC339760	similar to hCG40442	chr2q14.3	237685_at	XM_001716464 /// XM_001717443 /// XM_295058
2.33	2.48	0.15	3.85E-01	7.27E-01	PCDHB19P	Protocadherin beta 19 pseudogene	chr5q31	230957_at	NR_001282
3.10	3.21	0.11	3.85E-01	7.27E-01	---	---	---	1559915_at	---
5.84	6.47	0.63	3.85E-01	7.27E-01	MAN2A1	mannosidase, alpha, class 2A, member 1	chr5q21-q22	205105_at	NM_002372
4.42	4.92	0.50	3.86E-01	7.27E-01	CEP57	centrosomal protein 57kDa	chr11q21	209862_s_at	NM_014679
6.12	6.46	0.34	3.85E-01	7.27E-01	CALU	calumenin	chr7q32.1	200756_x_at	NM_001130674 /// NM_001219
6.95	7.24	0.29	3.85E-01	7.27E-01	CFL2	cofilin 2 (muscle)	chr14q12	224352_s_at	NM_021914 /// NM_138638
4.85	5.11	0.26	3.86E-01	7.27E-01	---	---	---	232264_at	---
2.34	2.52	0.18	3.86E-01	7.27E-01	ORF1	hypothetical protein, clone pT-Adv JuaX22	chr18q23	234855_at	---
2.47	2.61	0.14	3.85E-01	7.27E-01	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	chr18q21.31	230262_at	NM_015879
2.71	2.86	0.14	3.85E-01	7.27E-01	ALOX12P2	arachidonate 12-lipoxygenase pseudogene 2	chr17p13	214340_at	NR_002710
2.38	2.50	0.12	3.85E-01	7.27E-01	SSH2	slingshot homolog 2 (Drosophila)	chr17q11.2	1555423_at	NM_033389
2.00	2.10	0.10	3.85E-01	7.27E-01	RPTN	repetin	chr1q21.3	1553454_at	NM_001122965 /// XM_001721513 /// XM_001724407 /// XM_937200
2.07	2.17	0.10	3.85E-01	7.27E-01	KIF2B	kinesin family member 2B	chr17q22	223926_at	NM_032559
2.76	2.90	0.14	3.86E-01	7.27E-01	LOC100130623 /// RP11-160N1.10	hypothetical protein LOC100130623 /// hypothetical LOC401522	chr20q11.1 /// chr9p11.2	243674_at	XM_001713846 /// XM_001721157
8.45	8.62	0.17	3.86E-01	7.27E-01	C8orf40	chromosome 8 open reading frame 40	chr8p11.21	225534_at	NM_138436
4.99	5.22	0.23	3.86E-01	7.27E-01	SOBP	sine oculis binding protein homolog (Drosophila)	chr6q21	229034_at	NM_018013
3.58	4.24	0.66	3.86E-01	7.27E-01	YTHDF3	YTH domain family, member 3	chr8q12.3	1564053_a_at	NM_152758
2.46	2.61	0.15	3.86E-01	7.27E-01	LOC100130344	hypothetical protein LOC100130344	chr9q22.1	244812_at	XM_001721006 /// XM_001721881 /// XM_001723399
5.37	5.56	0.19	3.86E-01	7.27E-01	ZNF473	zinc finger protein 473	chr19q13.33	213130_at	NM_001006656 /// NM_015428
2.75	2.91	0.16	3.86E-01	7.27E-01	FLJ11292	hypothetical protein FLJ11292	chr5q14.3	217342_x_at	NM_018382
2.88	3.03	0.15	3.86E-01	7.27E-01	---	---	---	242971_at	---
2.10	2.21	0.11	3.86E-01	7.27E-01	C21orf109	chromosome 21 open reading frame 109	chr21q22.11	1553608_a_at	---
3.96	4.11	0.15	3.86E-01	7.27E-01	CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	chr11q13	214014_at	NM_006779
4.15	4.38	0.24	3.86E-01	7.27E-01	PRKCB	protein kinase C, beta	chr16p11.2	209685_s_at	NM_002738 /// NM_212535
2.61	2.85	0.25	3.86E-01	7.27E-01	ARHGAP6	Rho GTPase activating protein 6	chrXp22.3	206167_s_at	NM_001174 /// NM_006125 /// NM_013422 /// NM_013423 /// NM_013427
4.57	4.79	0.22	3.86E-01	7.27E-01	VISA	virus-induced signaling adapter	chr20p13	231829_at	NM_020746
2.27	2.43	0.15	3.86E-01	7.27E-01	EXOSC1	exosome component 1	chr10q24	218369_s_at	NM_016046
2.27	2.40	0.13	3.86E-01	7.27E-01	ZNF681	zinc finger protein 681	chr19p12	238962_at	NM_138286
2.77	2.86	0.09	3.86E-01	7.27E-01	AAK1	AP2 associated kinase 1	chr2p14	238100_at	NM_014911
5.95	6.22	0.27	3.86E-01	7.27E-01	---	---	---	228333_at	---
7.58	7.98	0.40	3.86E-01	7.28E-01	TMED2	transmembrane emp24 domain trafficking protein 2	chr12q24.31	204427_s_at	NM_006815
6.97	7.19	0.23	3.86E-01	7.28E-01	TEX2	testis expressed 2	chr17q23.3	218099_at	NM_018469

1.98	2.13	0.15	3.86E-01	7.28E-01	IGHA1 /// IGHG1 /// IGHM /// IGHV4-31 /// IGHV@	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable group	chr14q32.33	217084_at	---
5.55	5.96	0.41	3.86E-01	7.28E-01	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	chr6q22.31	203428_s_at	NM_014034
3.46	3.60	0.14	3.87E-01	7.28E-01	---	---	---	1556553_at	---
6.76	7.13	0.37	3.87E-01	7.28E-01	GULP1	GULP, engulfment adaptor PTB domain containing 1	chr2q32.3-q33	204235_s_at	NM_016315
1.98	2.08	0.10	3.87E-01	7.28E-01	LOC100129890	similar to hCG1750329	chr21q22.3	234025_at	XM_001719878 /// XM_001722818 /// XM_001726288
3.68	3.91	0.23	3.87E-01	7.28E-01	STON2	stonin 2	chr14q31.1	227461_at	NM_033104
2.58	2.76	0.18	3.87E-01	7.28E-01	---	---	---	1567045_at	---
4.04	4.64	0.60	3.87E-01	7.28E-01	---	---	---	233691_at	---
5.37	5.75	0.38	3.87E-01	7.28E-01	MED6	mediator complex subunit 6	chr14q24.2	207079_s_at	NM_005466
2.93	3.16	0.22	3.87E-01	7.28E-01	---	---	---	220728_at	---
1.91	2.02	0.10	3.87E-01	7.28E-01	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	chr1p31.1	1555394_at	NM_005482
8.64	8.99	0.35	3.87E-01	7.28E-01	MEST	mesoderm specific transcript homolog (mouse)	chr7q32	202016_at	NM_002402 /// NM_177524 /// NM_177525
6.32	6.60	0.28	3.87E-01	7.28E-01	RBPJ	recombination signal binding protein for immunoglobulin kappa J region	chr4p15.2	207785_s_at	NM_005349 /// NM_015874 /// NM_203283 /// NM_203284
2.11	2.22	0.11	3.87E-01	7.28E-01	MAGEA2 /// MAGEA2B /// MAGEA6	melanoma antigen family A, 2 /// melanoma antigen family A, 2B /// melanoma antigen family A, 6	chrXq28	1553830_s_at	NM_005361 /// NM_005363 /// NM_153488 /// NM_175742 /// NM_175743 /// NM_175868
7.61	7.85	0.25	3.87E-01	7.28E-01	EMP3	epithelial membrane protein 3	chr19q13.3	203729_at	NM_001425
2.74	2.90	0.16	3.87E-01	7.28E-01	CDH4	cadherin 4, type 1, R-cadherin (retinal)	chr20q13.3	206866_at	NM_001794
2.01	2.12	0.10	3.87E-01	7.28E-01	FLJ44048	FLJ44048 protein	chr2q32.1	240028_at	NM_207482
6.77	6.98	0.22	3.87E-01	7.28E-01	ZNF322A	zinc finger protein 322A	chr6p22.1	227980_at	NM_024639
2.31	2.46	0.15	3.87E-01	7.28E-01	---	---	---	1561905_at	---
2.64	2.77	0.13	3.87E-01	7.28E-01	ESPNP /// LOC100133967	espin pseudogene /// hypothetical LOC100133967	chr1p36.13	234281_at	XR_036931
4.10	4.23	0.13	3.87E-01	7.28E-01	LINCR	likely ortholog of mouse lung-inducible Neutralized-related C3HC4 RING domain protein	chr2q11.2	232593_at	NM_001080535
1.93	2.04	0.10	3.87E-01	7.28E-01	ONECUT2	one cut homeobox 2	chr18q21.1-q21.2	233441_at	NM_004852
5.36	5.70	0.34	3.88E-01	7.28E-01	CGRRF1	cell growth regulator with ring finger domain 1	chr14q22.2	204605_at	NM_006568
3.54	3.64	0.10	3.88E-01	7.29E-01	NYX	nyctalopin	chrXp11.4	221684_s_at	NM_022567
4.91	5.44	0.53	3.88E-01	7.29E-01	TPP2	tripeptidyl peptidase II	chr13q32-q33	203374_s_at	NM_003291
6.29	6.78	0.50	3.88E-01	7.29E-01	PREPL	prolyl endopeptidase-like	chr2p21	212216_at	NM_001042385 /// NM_001042386 /// NM_006036
4.82	5.18	0.37	3.88E-01	7.29E-01	DOPEY1	dopey family member 1	chr6q15	213271_s_at	NM_015018
7.31	7.57	0.26	3.88E-01	7.29E-01	RBMS1	RNA binding motif, single stranded interacting protein 1	chr2q24.2	203748_x_at	NM_002897 /// NM_016836 /// NM_016839
3.64	3.89	0.24	3.88E-01	7.29E-01	PGF	placental growth factor	chr14q24-q31	209652_s_at	NM_002632
3.06	3.25	0.19	3.88E-01	7.29E-01	KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4	chr22q13.1	211451_s_at	NM_004981 /// NM_152868
2.85	3.01	0.16	3.88E-01	7.29E-01	BIRC5	baculoviral IAP repeat-containing 5	chr17q25	202094_at	NM_001012270 /// NM_001012271 /// NM_001168
3.30	3.45	0.14	3.88E-01	7.29E-01	---	---	---	239931_at	---
4.49	4.63	0.14	3.88E-01	7.29E-01	MAGIX	MAGI family member, X-linked	chrXp11.23	1565562_at	NM_001099680 /// NM_001099681 /// NM_001099682 /// NM_024859
2.09	2.18	0.09	3.88E-01	7.29E-01	---	---	---	233285_at	---
3.83	4.00	0.17	3.88E-01	7.29E-01	CEP27	centrosomal protein 27kDa	chr15q15.1	229181_s_at	NM_001130447 /// NM_018097

3.90	4.02	0.13	3.88E-01	7.29E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	211550_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284																					
2.89	2.99	0.10	3.88E-01	7.29E-01	TRIM10	tripartite motif-containing 10	chr6p21.3	221627_at	NM_006778 /// NM_052828																					
1.90	1.98	0.09	3.88E-01	7.29E-01	---	---	---	1556997_a_at	---																					
2.01	2.10	0.09	3.88E-01	7.29E-01	---	---	---	238898_at	---																					
2.04	2.16	0.12	3.88E-01	7.29E-01	LOC134466	hypothetical protein LOC134466	chr5q33.1	244289_at	XR_015962 /// XR_015967 /// XR_041597																					
10.08	10.20	0.12	3.88E-01	7.29E-01	ATP5H	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	chr17q25	210149_s_at	NM_001003785 /// NM_006356																					
3.43	3.69	0.27	3.88E-01	7.29E-01	RNASE4	ribonuclease, RNase A family, 4	chr14q11.1	205158_at	NM_002937 /// NM_194431																					
7.01	7.31	0.30	3.88E-01	7.29E-01	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	chr6p25-p24|18q21	209397_at	NM_002396																					
3.46	3.61	0.15	3.88E-01	7.29E-01	MARK1	MAP/microtubule affinity-regulating kinase 1	chr1q41	221047_s_at	NM_018650																					
5.32	5.51	0.19	3.88E-01	7.29E-01	CCDC43	coiled-coil domain containing 43	chr17q21.31	225607_at	NM_001099225 /// NM_144609																					
2.14	2.24	0.11	3.88E-01	7.29E-01	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	chr3q28	1556350_a_at	NM_001967																					
6.02	6.37	0.36	3.88E-01	7.29E-01	CUL1	cullin 1	chr7q36.1	207614_s_at	NM_003592																					
3.55	3.80	0.25	3.88E-01	7.29E-01	PGM2L1	phosphoglucomutase 2-like 1	chr11q13.4	238417_at	NM_173582																					
5.44	5.56	0.12	3.88E-01	7.29E-01	GTPBP1	GTP binding protein 1	chr22q13.1	205276_s_at	NM_004286																					
4.15	4.28	0.13	3.88E-01	7.29E-01	---	---	---	234076_at	---																					
2.22	2.38	0.16	3.88E-01	7.29E-01	---	---	---	1557789_at	---																					
4.66	4.86	0.19	3.88E-01	7.29E-01	TNRC6A	trinucleotide repeat containing 6A	chr16p11.2	233836_at	NM_014494																					
3.75	4.19	0.43	3.88E-01	7.29E-01	SRPK2	SFRS protein kinase 2	chr7q22-q31.1	1558254_s_at	NM_182691 /// NM_182692																					
3.04	3.30	0.26	3.88E-01	7.29E-01	DISP2	dispatched homolog 2 (Drosophila)	chr15q15.1	229579_s_at	NM_033510																					
2.67	2.83	0.16	3.88E-01	7.29E-01	---	---	---	1565581_at	---																					
2.60	2.76	0.15	3.88E-01	7.29E-01	ETV3	ets variant gene 3	chr1q21-q23	214480_at	NM_005240																					
8.69	8.88	0.19	3.89E-01	7.29E-01	VDAC3	voltage-dependent anion channel 3	chr8p11.2	208845_at	NM_005662																					
3.24	3.40	0.16	3.89E-01	7.29E-01	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	chr2q12	231283_at	NM_012214																					
2.48	2.64	0.16	3.89E-01	7.29E-01	WIT1	Wilms tumor upstream neighbor 1	chr11p13	206954_at	NM_015855 /// NR_023920																					
2.70	2.85	0.15	3.89E-01	7.29E-01	---	---	---	1569602_at	---																					
2.89	3.00	0.12	3.89E-01	7.29E-01	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	chr8p21.3	1555358_a_at	NM_001128930 /// NM_004901																					
2.62	2.80	0.18	3.89E-01	7.29E-01	FOXN4	forkhead box N4	chr12q24.11	241009_at	NM_213596																					
6.59	6.77	0.18	3.89E-01	7.29E-01	IGF2R	insulin-like growth factor 2 receptor	chr6q26	201392_s_at	NM_000876																					
7.28	7.44	0.16	3.89E-01	7.30E-01	METTL7A	methyltransferase like 7A	chr12q13.13	209703_x_at	NM_014033																					
2.05	2.15	0.10	3.89E-01	7.30E-01	---	---	---	241273_at	---																					
6.50	6.82	0.32	3.89E-01	7.30E-01	PDCD10	programmed cell death 10	chr3q26.1	210907_s_at	NM_007217 /// NM_145859 /// NM_145860																					
1.93	2.02	0.09	3.89E-01	7.30E-01	---	---	---	216097_at	---																					
6.73	7.03	0.30	3.89E-01	7.30E-01	TMEM32	transmembrane protein 32	chrXq26.3	225125_at	NM_173470																					
4.94	5.24	0.30	3.89E-01	7.30E-01	TRIB3	tribbles homolog 3 (Drosophila)	chr20p13-p12.2	218145_at	NM_021158																					
3.98	4.10	0.12	3.89E-01	7.30E-01	---	---	---	239947_at	---																					
1.85	1.94	0.09	3.89E-01	7.30E-01	TEX9	testis expressed 9	chr15q21.3	1566606_a_at	NM_198524																					
11.00	11.26	0.25	3.89E-01	7.30E-01	RPL7	ribosomal protein L7	chr8q21.11	212042_x_at	NM_000971																					
3.72	3.86	0.13	3.89E-01	7.30E-01	ARHGAP27	Rho GTPase activating protein 27	chr17q21.31	229424_s_at	NM_199282																					
9.42	9.85	0.43	3.89E-01	7.30E-01	EIF3E	eukaryotic translation initiation factor 3, subunit E	chr8q22-q23	208697_s_at	NM_001568																					
5.64	5.80	0.17	3.89E-01	7.30E-01	---	---	---	243131_x_at	---																					
2.24	2.35	0.11	3.89E-01	7.30E-01	LOC643187	hypothetical LOC643187	---	1569608_x_at	XM_001716758																					
2.77	3.11	0.34	3.89E-01	7.30E-01	RAB6B	RAB6B, member RAS oncogene family	chr3q22.1	210127_at	NM_016577																					
2.15	2.30	0.15	3.89E-01	7.30E-01	BXDC5	brix domain containing 5	chr1p22.3	234243_at	NM_025065																					
2.24	2.33	0.10	3.89E-01	7.30E-01	---	---	---	240585_at	---																					
2.60	2.73	0.13	3.89E-01	7.30E-01	CDCA2	cell division cycle associated 2	chr8p21.2	226661_at	NM_152562																					
4.44	4.58	0.14	3.89E-01	7.30E-01	JPH2	junctophilin 2	chr20q13.12	1553174_at	NM_020433 /// NM_175913																					
2.34	2.45	0.11	3.89E-01	7.30E-01	---	---	---	240242_at	---																					
6.34	6.44	0.10	3.90E-01	7.30E-01	ZCCHC17	zinc finger, CCHC domain containing 17	chr1p35.2	223108_s_at	NM_016505																					
3.34	3.46	0.12	3.90E-01	7.30E-01	---	---	---	244025_at	---																					
3.84	4.10	0.25	3.90E-01	7.30E-01	SHE	Src homology 2 domain containing E	chr1q21.3	238036_at	NM_001010846																					
2.29	2.39	0.09	3.90E-01	7.30E-01	DEFB105A /// DEFB105B	defensin, beta 105A /// defensin, beta 105B	chr8p23.1	1553002_at	NM_001040703 /// NM_152250																					
3.24	3.63	0.39	3.90E-01	7.30E-01	SMC3	structural maintenance of chromosomes 3	chr10q25	209257_s_at	NM_005445																					
2.08	2.19	0.11	3.90E-01	7.30E-01	TRIM42	tripartite motif-containing 42	chr3q23	1553620_at	NM_152616																					

2.31	2.47	0.16	3.90E-01	7.30E-01	ATE1	arginyltransferase 1	chr10q26.13	234874_at	NM_001001976 /// NM_007041
2.22	2.37	0.15	3.90E-01	7.30E-01	FLJ22536	hypothetical locus LOC401237	chr6p22.3	1562469_at	XM_379398
3.74	3.87	0.13	3.90E-01	7.30E-01	AURKAIP1	aurora kinase A interacting protein 1	chr1p36.33	225555_x_at	NM_001127229 /// NM_001127230 /// NM_017900
5.22	5.34	0.13	3.90E-01	7.30E-01	STK40	serine/threonine kinase 40	chr1p34.3	225015_s_at	NM_032017
4.17	4.52	0.35	3.90E-01	7.30E-01	---	---	---	236474_at	---
6.84	7.17	0.33	3.90E-01	7.30E-01	AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	chr9q22.31	205052_at	NM_001698
4.98	5.19	0.22	3.90E-01	7.30E-01	MUM1	melanoma associated antigen (mutated) 1	chr19p13.3	223347_at	NM_032853
4.69	4.88	0.19	3.90E-01	7.30E-01	CD3D	CD3d molecule, delta (CD3-TCR complex)	chr11q23	213539_at	NM_000732 /// NM_001040651
2.76	2.91	0.15	3.90E-01	7.30E-01	PCDHB9	protocadherin beta 9	chr5q31	223927_at	NM_019119
3.23	3.38	0.15	3.90E-01	7.30E-01	---	---	---	231660_at	---
2.55	2.68	0.13	3.90E-01	7.30E-01	---	---	---	235406_x_at	---
2.23	2.35	0.12	3.90E-01	7.30E-01	KIAA1109	KIAA1109	chr4q27	233227_at	NM_015312
1.99	2.11	0.11	3.90E-01	7.30E-01	---	---	---	238379_x_at	---
2.25	2.35	0.10	3.90E-01	7.30E-01	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	chr3q28-q29	223723_at	NM_005929 /// NM_033316
1.97	2.05	0.08	3.90E-01	7.30E-01	---	---	---	1569960_at	---
2.93	3.11	0.18	3.90E-01	7.30E-01	---	---	---	240993_at	---
3.01	3.15	0.14	3.90E-01	7.30E-01	PLEKHA3	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	chr2q31.2	227659_at	NM_019091
4.84	5.05	0.21	3.90E-01	7.30E-01	---	---	---	241595_at	---
2.07	2.21	0.14	3.90E-01	7.30E-01	LOC116437	hypothetical protein LOC116437	chr12q24.33	234493_at	XM_001134387 /// XM_001719993 /// XM_001722735
2.41	2.57	0.16	3.90E-01	7.30E-01	C6orf199	chromosome 6 open reading frame 199	chr6q21	1564002_a_at	NM_145025
2.08	2.18	0.10	3.90E-01	7.30E-01	---	---	---	1570575_at	---
2.69	2.84	0.15	3.90E-01	7.30E-01	---	---	---	230932_at	---
3.80	3.92	0.12	3.90E-01	7.31E-01	NOL6	nucleolar protein family 6 (RNA-associated)	chr9p13.3	228076_s_at	NM_022917 /// NM_139235
2.02	2.15	0.13	3.90E-01	7.31E-01	CLEC2D	C-type lectin domain family 2, member D	chr12p13	235522_at	NM_001004419 /// NM_013269
2.92	3.10	0.17	3.91E-01	7.31E-01	HNF4A	hepatocyte nuclear factor 4, alpha	chr20q12-q13.1	208429_x_at	NM_000457 /// NM_001030003 /// NM_001030004 /// NM_175914 /// NM_178849 /// NM_178850
4.35	4.49	0.14	3.91E-01	7.31E-01	KCTD18	potassium channel tetramerisation domain containing 18	chr2q33.1	1553136_at	NM_152387
2.20	2.31	0.11	3.91E-01	7.31E-01	GYPA	glycophorin A (MNS blood group)	chr4q28.2-q31.1	205838_at	NM_002099
2.54	2.69	0.16	3.91E-01	7.31E-01	---	---	---	241439_at	---
3.30	3.52	0.22	3.91E-01	7.31E-01	ZNF397 /// ZNF397OS	zinc finger protein 397 /// zinc finger protein 397 opposite strand	chr18q12.2	235271_s_at	NM_001112734 /// NM_032347 /// XM_001720071 /// XM_001722380 /// XM_001723235
2.85	3.04	0.19	3.91E-01	7.31E-01	OR2L1P	olfactory receptor, family 2, subfamily L, member 1 pseudogene	chr1q44	1567241_at	NR_002145
5.23	5.40	0.17	3.91E-01	7.31E-01	ZDHHC18	zinc finger, DHHC-type containing 18	chr1p36.11	212860_at	NM_032283
8.69	8.86	0.17	3.91E-01	7.31E-01	PSMC5	proteasome (prosome, macropain) 26S subunit, ATPase, 5	chr17q23-q25	209503_s_at	NM_002805
7.40	7.66	0.26	3.91E-01	7.31E-01	CCDC69	coiled-coil domain containing 69	chr5q33.1	1553102_a_at	NM_015621
4.25	4.46	0.21	3.91E-01	7.31E-01	OXNAD1	oxidoreductase NAD-binding domain containing 1	chr3p25-p24	227686_at	NM_138381
4.75	5.07	0.32	3.91E-01	7.31E-01	SPG3A	spastic paraplegia 3A (autosomal dominant)	chr14q22.1	223340_at	NM_001127713 /// NM_015915 /// NM_181598
4.97	5.13	0.16	3.91E-01	7.31E-01	---	---	---	216455_at	---
3.91	4.05	0.14	3.91E-01	7.31E-01	---	---	---	244371_at	---
2.18	2.32	0.14	3.91E-01	7.31E-01	C10orf79	chromosome 10 open reading frame 79	chr10q25.1	224251_at	NM_025145

5.96	6.35	0.39	3.91E-01	7.31E-01	RNF14	ring finger protein 14	chr5q23.3-q31.1	201823_s_at	NM_004290 /// NM_183398 /// NM_183399 /// NM_183400 /// NM_183401																				
3.02	3.18	0.15	3.91E-01	7.31E-01	---	---	---	234127_at	---																				
3.09	3.23	0.14	3.91E-01	7.31E-01	LOC100126784	hypothetical LOC100126784	chr11p15.1	239141_at	XR_040478 /// XR_040479 /// XR_040480																				
2.16	2.26	0.11	3.91E-01	7.31E-01	---	---	---	1560738_at	---																				
4.33	4.65	0.31	3.91E-01	7.31E-01	---	---	---	239979_at	---																				
2.95	3.12	0.16	3.91E-01	7.31E-01	KIAA1324L	KIAA1324-like	chr7q21.12	244317_at	NM_152748																				
6.22	6.62	0.39	3.91E-01	7.31E-01	UBA5	ubiquitin-like modifier activating enzyme 5	chr3q22.1	222578_s_at	NM_024818 /// NM_198329																				
11.68	11.85	0.17	3.91E-01	7.31E-01	B2M	beta-2-microglobulin	chr15q21-q22.2	216231_s_at	NM_004048																				
3.09	3.25	0.16	3.91E-01	7.31E-01	---	---	---	241668_s_at	---																				
2.63	2.73	0.11	3.91E-01	7.31E-01	ZNF287	zinc finger protein 287	chr17p11.2	216710_x_at	NM_020653																				
2.54	2.65	0.11	3.91E-01	7.31E-01	---	---	---	236698_at	---																				
1.73	1.81	0.09	3.91E-01	7.31E-01	PCDHGB7	protocadherin gamma subfamily B, 7	chr5q31	1552661_at	NM_018927 /// NM_032101																				
2.47	2.59	0.12	3.92E-01	7.31E-01	PSCA	prostate stem cell antigen	chr8q24.2	1560011_at	NM_005672																				
3.71	3.89	0.17	3.92E-01	7.31E-01	ZNF552	Zinc finger protein 552	chr19q13.43	232328_at	NM_024762																				
6.16	6.51	0.35	3.92E-01	7.31E-01	DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	chr15q22.31	235005_at	NM_133375																				
2.11	2.29	0.17	3.92E-01	7.31E-01	---	---	---	236520_at	---																				
4.09	4.23	0.14	3.92E-01	7.31E-01	IKZF4	IKAROS family zinc finger 4 (Eos)	chr12q13	208472_at	NM_022465																				
4.15	4.37	0.22	3.92E-01	7.31E-01	GPR56	G protein-coupled receptor 56	chr16q12.2-q21	206582_s_at	NM_005682 /// NM_201524 /// NM_201525																				
1.86	1.97	0.11	3.92E-01	7.31E-01	---	---	---	234808_x_at	---																				
5.25	5.69	0.45	3.92E-01	7.31E-01	USP15	ubiquitin specific peptidase 15	chr12q14	210681_s_at	NM_006313																				
3.74	3.91	0.17	3.92E-01	7.31E-01	SEZ6L	seizure related 6 homolog (mouse)-like	chr22q12.1	207873_x_at	NM_021115																				
2.02	2.12	0.11	3.92E-01	7.31E-01	FAM123A	family with sequence similarity 123A	chr13q12.13	235465_at	NM_152704 /// NM_199138																				
6.96	7.13	0.16	3.92E-01	7.31E-01	---	---	---	226806_s_at	---																				
3.96	4.13	0.17	3.92E-01	7.32E-01	PRDM11	PR domain containing 11	chr11p11	220571_at	NM_020229																				
3.98	4.18	0.20	3.92E-01	7.32E-01	SNCAIP	synuclein, alpha interacting protein	chr5q23.1-q23.3	219511_s_at	NM_005460																				
3.31	3.49	0.18	3.92E-01	7.32E-01	SOX15	SRY (sex determining region Y)-box 15	chr17p13	206122_at	NM_006942																				
7.31	7.73	0.43	3.92E-01	7.32E-01	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	chr11q12-q13.1	200986_at	NM_000062 /// NM_001032295																				
1.79	1.88	0.10	3.92E-01	7.32E-01	---	---	---	241770_x_at	---																				
5.79	6.10	0.30	3.92E-01	7.32E-01	GCOM1 /// GRINL1A	GRINL1A complex locus /// glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	chr15q21.3 /// chr15q22.1	212243_at	NM_001018090 /// NM_001018091 /// NM_001018100 /// NM_001018102 /// NM_001018103 /// NM_015532 /// NM_152451																				
3.63	3.75	0.12	3.92E-01	7.32E-01	LOC147080	hypothetical protein LOC147080	chr17q21.31	1559171_at	---																				
3.62	3.80	0.18	3.92E-01	7.32E-01	---	---	---	1560630_at	---																				
5.70	5.84	0.14	3.92E-01	7.32E-01	C9orf116	chromosome 9 open reading frame 116	chr9q34.3	221946_at	NM_001048265 /// NM_144654																				
3.68	3.81	0.13	3.92E-01	7.32E-01	C22orf31	chromosome 22 open reading frame 31	chr22q12.1	206839_at	NM_015370																				
1.98	2.11	0.12	3.92E-01	7.32E-01	---	---	---	233904_at	---																				
2.64	2.81	0.17	3.92E-01	7.32E-01	---	---	---	244701_at	---																				
2.67	2.78	0.11	3.92E-01	7.32E-01	VWA3B	von Willebrand factor A domain containing 3B	chr2q11.2	1564598_a_at	NM_144992																				
4.27	4.43	0.16	3.92E-01	7.32E-01	AZGP1 /// AZGP1P1	alpha-2-glycoprotein 1, zinc-binding /// alpha-2-glycoprotein 1, zinc-binding pseudogene 1	chr7q22.1	217014_s_at	NM_001185 /// XR_017216 /// XR_037935 /// XR_039311 /// XR_039317																				
3.52	3.65	0.13	3.92E-01	7.32E-01	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	chr10q21.3	1568814_at	NM_024045																				
4.01	4.43	0.42	3.93E-01	7.32E-01	CDC14B /// CDC14C	CDC14 cell division cycle 14 homolog B (S. cerevisiae) /// CDC14 cell division cycle 14 homolog C (S. cerevisiae)	chr7p12.3 /// chr9q22.33	208022_s_at	NM_001077181 /// NM_003671 /// NM_033331 /// NR_003595																				
3.14	3.32	0.18	3.93E-01	7.32E-01	ZNF414	zinc finger protein 414	chr19p13.2	227071_at	NM_032370																				
2.38	2.55	0.17	3.93E-01	7.32E-01	---	---	---	208139_s_at	---																				
6.72	6.87	0.15	3.93E-01	7.32E-01	---	---	---	216246_at	---																				
2.79	2.93	0.14	3.93E-01	7.32E-01	TTLL5	tubulin tyrosine ligase-like family, member 5	chr14q24.3	208099_x_at	NM_015072																				

2.73	2.87	0.14	3.93E-01	7.32E-01	ZNF483	zinc finger protein 483	chr9q31.3	1559988_at	NM_001007169 /// NM_133464
2.24	2.37	0.13	3.93E-01	7.32E-01	---	---	---	1560309_s_at	---
3.83	3.96	0.12	3.93E-01	7.32E-01	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	chr11p15	1557964_at	NM_001042559 /// NM_001418
2.26	2.38	0.12	3.93E-01	7.32E-01	---	---	---	206909_at	---
1.89	2.00	0.11	3.92E-01	7.32E-01	KLHL1	kelch-like 1 (Drosophila)	chr13q21	223810_at	NM_020866
1.94	2.04	0.10	3.92E-01	7.32E-01	---	---	---	216050_at	---
1.96	2.05	0.09	3.92E-01	7.32E-01	EFCAB5	EF-hand calcium binding domain 5	chr17q11.2	1558300_at	NM_198529
6.89	7.31	0.43	3.93E-01	7.32E-01	CGGBP1	CGG triplet repeat binding protein 1	chr3p12-p11.1	224600_at	NM_001008390 /// NM_003663
3.31	3.49	0.19	3.93E-01	7.32E-01	---	---	---	1558695_at	---
2.72	2.84	0.12	3.93E-01	7.32E-01	---	---	---	1570068_at	---
4.85	5.18	0.32	3.93E-01	7.32E-01	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	chr2q33-q34	209920_at	NM_001204
6.91	7.22	0.31	3.93E-01	7.32E-01	DNASE1L3	deoxyribonuclease I-like 3	chr3p21.1-p14.3	205554_s_at	NM_004944
3.26	3.43	0.17	3.93E-01	7.32E-01	NCR3	natural cytotoxicity triggering receptor 3	chr6p21.3	211010_s_at	NM_147130
2.11	2.23	0.12	3.93E-01	7.32E-01	---	---	---	243867_at	---
1.76	1.87	0.11	3.93E-01	7.32E-01	---	---	---	242175_at	---
3.28	3.48	0.20	3.93E-01	7.32E-01	---	---	---	1555084_at	---
2.24	2.42	0.19	3.93E-01	7.32E-01	---	---	---	229629_at	---
2.87	2.99	0.13	3.93E-01	7.32E-01	POU5F2	POU domain class 5, transcription factor 2	chr5q15	1553325_at	NM_153216
6.76	7.02	0.26	3.93E-01	7.32E-01	NDUFAF1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	chr15q11.2-q21.3	204125_at	NM_016013
3.40	3.59	0.19	3.93E-01	7.32E-01	---	---	---	220846_s_at	---
3.37	3.54	0.17	3.93E-01	7.32E-01	DNAH10	dynein, axonemal, heavy chain 10	chr12q24.31	229738_at	NM_001083900 /// NM_207437
5.22	5.38	0.15	3.93E-01	7.32E-01	WDR92	WD repeat domain 92	chr2p14	235071_at	NM_138458
2.76	2.97	0.22	3.93E-01	7.32E-01	---	---	---	238565_at	---
2.28	2.42	0.13	3.93E-01	7.32E-01	AGXT2	alanine-glyoxylate aminotransferase 2	chr5p13	229229_at	NM_031900
2.78	2.94	0.16	3.93E-01	7.32E-01	ARL4C	ADP-ribosylation factor-like 4C	chr2q37.1	213759_at	NM_005737
4.59	4.98	0.39	3.93E-01	7.32E-01	MRPS14	mitochondrial ribosomal protein S14	chr1q23-q25	203801_at	NM_022100
1.95	2.05	0.10	3.93E-01	7.33E-01	---	---	---	1561478_at	---
2.54	2.66	0.12	3.93E-01	7.33E-01	---	---	---	243684_at	---
3.49	3.67	0.17	3.94E-01	7.33E-01	---	---	---	230617_at	---
2.77	3.04	0.26	3.94E-01	7.33E-01	NTSR2	neurotensin receptor 2	chr2p25.1	206899_at	NM_012344
2.23	2.35	0.12	3.94E-01	7.33E-01	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	chr2p21	239568_at	NM_172069
5.88	6.21	0.33	3.94E-01	7.33E-01	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	chr17q24-q25|17q25.1	209600_s_at	NM_004035 /// NM_007292
6.54	6.82	0.27	3.94E-01	7.33E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	210563_x_at	NM_001127183 /// NM_001127184 /// NM_003879
2.19	2.29	0.10	3.94E-01	7.33E-01	ATP1B4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	chrXq24	220556_at	NM_012069
1.81	1.92	0.11	3.94E-01	7.33E-01	CLCA3	chloride channel, calcium activated, family member 3	chr1p31-p22	220810_at	NM_004921
5.56	6.18	0.62	3.94E-01	7.33E-01	PRLR	Prolactin receptor	chr5p14-p13	227629_at	NM_000949
3.24	3.66	0.42	3.94E-01	7.33E-01	---	---	---	229193_at	---
4.04	4.30	0.26	3.94E-01	7.33E-01	DKFZP566E164	DKFZP566E164 protein	chr11q13.1	219883_at	NM_001039496
4.98	5.24	0.26	3.94E-01	7.33E-01	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	chr1q24-q25	231907_at	NM_001100108 /// NM_005158 /// NM_007314
4.38	4.55	0.17	3.94E-01	7.33E-01	ZNF853	zinc finger protein 853	chr7p22.1	228270_at	XM_001715278 /// XM_001716278 /// XM_001716628 /// XM_001723503
2.39	2.54	0.15	3.94E-01	7.33E-01	LOC100130998	hypothetical protein LOC100130998	chr5q13.2	1563970_at	XM_001715036 /// XM_001720994 /// XM_001721872
2.48	2.63	0.15	3.94E-01	7.33E-01	RFPL3	ret finger protein-like 3	chr22q12.3	207936_x_at	NM_001098535 /// NM_006604
2.15	2.26	0.11	3.94E-01	7.33E-01	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	chr11q14.3	236029_at	NM_001008781

5.06	5.32	0.26	3.94E-01	7.33E-01	IL32	interleukin 32	chr16p13.3	203828_s_at	NM_001012631 /// NM_001012632 /// NM_001012633 /// NM_001012634 /// NM_001012635 /// NM_001012636 /// NM_001012718 /// NM_004221
5.07	5.18	0.12	3.94E-01	7.33E-01	FLJ22596	hypothetical protein FLJ22596	chr11q13.3	220583_at	---
3.39	3.68	0.29	3.94E-01	7.34E-01	LOC100132884	hypothetical protein LOC100132884	chr7q36.1	228899_at	XM_001714056 /// XM_001714844 /// XM_001716924
7.73	7.99	0.25	3.94E-01	7.34E-01	F11R	F11 receptor	chr1q21.2-q21.3	223000_s_at	NM_016946 /// NM_144503
3.55	3.69	0.14	3.94E-01	7.34E-01	---	---	---	1570192_at	---
2.27	2.39	0.13	3.94E-01	7.34E-01	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	chr20p13	233630_at	NM_003818
2.45	2.58	0.12	3.94E-01	7.34E-01	MIAT	myocardial infarction associated transcript (non-protein coding)	chr22q12.1	237322_at	NR_003491
2.92	3.04	0.12	3.94E-01	7.34E-01	LOC254099	hypothetical protein LOC254099	chr1p36.33	1562788_at	---
1.98	2.08	0.11	3.94E-01	7.34E-01	---	---	---	1570623_at	---
2.40	2.51	0.10	3.94E-01	7.34E-01	---	---	---	232667_at	---
2.39	2.49	0.10	3.94E-01	7.34E-01	---	---	---	208187_s_at	---
7.28	7.45	0.17	3.95E-01	7.34E-01	CACNG4	calcium channel, voltage-dependent, gamma subunit 4	chr17q24	62987_r_at	NM_014405
2.25	2.35	0.10	3.95E-01	7.34E-01	ZNF578	Zinc finger protein 578	chr19q13.41	1562244_at	NM_001099694
1.92	2.01	0.10	3.95E-01	7.34E-01	---	---	---	1561535_at	---
4.56	4.71	0.15	3.95E-01	7.34E-01	USP46	ubiquitin specific peptidase 46	chr4q12	219943_s_at	NM_001134223 /// NM_022832
2.98	3.11	0.13	3.95E-01	7.34E-01	---	---	---	1561369_at	---
2.21	2.34	0.13	3.95E-01	7.34E-01	---	---	---	1565838_at	---
7.36	7.77	0.41	3.95E-01	7.34E-01	TM9SF3	transmembrane 9 superfamily member 3	chr10q24.1	224755_at	NM_020123
2.14	2.24	0.10	3.95E-01	7.34E-01	---	---	---	241334_at	---
4.23	4.95	0.72	3.95E-01	7.34E-01	---	---	---	226560_at	---
2.63	2.77	0.14	3.95E-01	7.34E-01	PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	chr6q21	214206_at	NM_001111298 /// NM_173672
2.15	2.25	0.10	3.95E-01	7.34E-01	---	---	---	243494_at	---
4.85	5.04	0.19	3.95E-01	7.34E-01	C19orf25	chromosome 19 open reading frame 25	chr19p13.3	226379_s_at	NM_152482
8.54	8.66	0.11	3.95E-01	7.34E-01	NUDC	nuclear distribution gene C homolog (A. nidulans)	chr1p35-p34	201173_x_at	NM_006600
2.35	2.46	0.11	3.95E-01	7.34E-01	PRMT2	protein arginine methyltransferase 2	chr21q22.3	210384_at	NM_001535 /// NM_206962
5.92	6.29	0.37	3.95E-01	7.34E-01	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	chr1p36.12	201935_s_at	NM_003760
2.99	3.22	0.23	3.95E-01	7.34E-01	---	---	---	216849_at	---
4.13	4.34	0.21	3.95E-01	7.34E-01	MET	met proto-oncogene (hepatocyte growth factor receptor)	chr7q31	211599_x_at	NM_000245 /// NM_001127500
2.60	2.78	0.18	3.95E-01	7.34E-01	RGS3	regulator of G-protein signaling 3	chr9q32	220300_at	NM_017790 /// NM_021106 /// NM_130795 /// NM_134427 /// NM_144488 /// NM_144489
4.36	4.53	0.17	3.95E-01	7.34E-01	LILRB5	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	chr19q13.4	206856_at	NM_001081442 /// NM_001081443 /// NM_006840
2.35	2.47	0.12	3.95E-01	7.34E-01	LOC285286	hypothetical protein LOC285286	chr3p14.2	243954_at	---
3.37	3.49	0.12	3.95E-01	7.34E-01	SERP2	stress-associated endoplasmic reticulum protein family member 2	chr13q14.11	1558727_at	NM_001010897
2.47	2.58	0.11	3.95E-01	7.34E-01	---	---	---	1556679_at	---
1.89	1.99	0.10	3.95E-01	7.34E-01	EPHA3	EPH receptor A3	chr3p11.2	211164_at	NM_005233 /// NM_182644
2.34	2.44	0.10	3.95E-01	7.34E-01	C8orf12	chromosome 8 open reading frame 12	chr8p23-p22	1552448_a_at	XR_041851 /// XR_041852 /// XR_041853
2.00	2.09	0.09	3.95E-01	7.34E-01	---	---	---	241191_at	---

2.51	2.72	0.21	3.95E-01	7.34E-01	FAM124B	family with sequence similarity 124B	chr2q36.2	220637_at	NM_001122779 /// NM_024785
6.39	6.59	0.20	3.95E-01	7.34E-01	C5orf4	chromosome 5 open reading frame 4	chr5q31-q32	48031_r_at	NM_016348 /// NM_032385
2.02	2.17	0.15	3.95E-01	7.34E-01	CGA	Glycoprotein hormones, alpha polypeptide	chr6q12-q21	233615_at	NM_000735
1.93	2.03	0.10	3.95E-01	7.34E-01	CCDC83	coiled-coil domain containing 83	chr11q14.1-q14.2	237160_at	NM_173556
5.93	6.28	0.35	3.95E-01	7.34E-01	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	chr14q32	213305_s_at	NM_002719 /// NM_178586 /// NM_178587 /// NM_178588
2.77	2.93	0.16	3.95E-01	7.34E-01	STRBP	spermatid perinuclear RNA binding protein	chr9q33.3	233252_s_at	NM_018387
2.72	2.85	0.12	3.96E-01	7.34E-01	DKFZP434P211 /// LOC100133536 /// LOC440821 /// LOC646074 /// LOC729915 /// POM121L1 /// POM121L3	POM121-like protein /// similar to hCG2002956 /// similar to POM121 membrane glycoprotein-like 1 /// similar to POM121-like 1 /// hypothetical LOC729915 /// POM121 membrane glycoprotein-like 1 (rat) /// POM121 membrane glycoprotein-like 3 (rat)	chr20p11.21 /// chr22q11.22 /// chr22q11.23 /// chr5p13.3	1553817_at	NR_003714 /// XM_001719304 /// XM_001722873 /// XM_001724140 /// XM_929034 /// XR_019113 /// XR_036930 /// XR_038038
2.30	2.42	0.12	3.96E-01	7.34E-01	---	---	---	1570320_at	---
2.32	2.43	0.11	3.96E-01	7.34E-01	LOC387895	Hypothetical gene supported by BC040060	chr12q24.32	1560819_a_at	XM_373553 /// XM_945559
2.64	2.83	0.19	3.96E-01	7.34E-01	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	chr3q13.12	222520_s_at	NM_018010
2.21	2.30	0.09	3.96E-01	7.34E-01	---	---	---	238304_at	---
4.14	4.30	0.16	3.96E-01	7.34E-01	CYTH3	cytohesin 3	chr7p22.1	206523_at	NM_004227
3.62	3.95	0.32	3.96E-01	7.34E-01	TES	testis derived transcript (3 LIM domains)	chr7q31.2	202719_s_at	NM_015641 /// NM_152829
2.15	2.28	0.13	3.96E-01	7.34E-01	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	chr7p15.1-p14.3	207303_at	NM_005020
7.64	8.14	0.50	3.96E-01	7.34E-01	TRAM1	translocation associated membrane protein 1	chr8q13.3	201399_s_at	NM_014294 /// XM_001721007 /// XM_001721035 /// XM_001721065
2.87	3.01	0.15	3.96E-01	7.34E-01	CBS	cystathionine-beta-synthase	chr21q22.3	212816_s_at	NM_000071
2.05	2.19	0.14	3.96E-01	7.34E-01	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	chr6q23-q24	243254_at	NM_006734
5.57	5.75	0.18	3.96E-01	7.34E-01	PALM	paralemmin	chr19p13.3	203859_s_at	NM_001040134 /// NM_002579
2.40	2.56	0.16	3.96E-01	7.34E-01	CMYA5	cardiomyopathy associated 5	chr5q14.1	233520_s_at	NM_153610
2.23	2.36	0.13	3.96E-01	7.34E-01	CHML	Choroideremia-like (Rab escort protein 2)	chr1q42-qter	1565949_x_at	NM_001821
1.97	2.11	0.14	3.96E-01	7.34E-01	---	---	---	240995_at	---
2.73	2.85	0.11	3.96E-01	7.34E-01	---	---	---	1554404_a_at	---
2.09	2.19	0.10	3.96E-01	7.34E-01	---	---	---	230540_at	---
5.92	6.17	0.25	3.96E-01	7.34E-01	AKAP2 /// PALM2 /// PALM2-AKAP2	A kinase (PRKA) anchor protein 2 /// paralemmin 2 /// PALM2-AKAP2	chr9q31-q33	226694_at	NM_001004065 /// NM_001037293 /// NM_007203 /// NM_053016 /// NM_147150
2.88	3.11	0.23	3.96E-01	7.34E-01	HNF1B	HNF1 homeobox B	chr17cen-q21.3	208135_at	NM_000458
9.73	9.93	0.20	3.96E-01	7.34E-01	EIF3C /// EIF3CL	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation initiation factor 3, subunit C-like	chr16p11.2	215230_x_at	NM_001037808 /// NM_001099661 /// NM_003752
2.41	2.55	0.14	3.96E-01	7.34E-01	---	---	---	244402_at	---
2.82	2.92	0.10	3.96E-01	7.34E-01	---	---	---	232484_at	---
1.99	2.14	0.15	3.96E-01	7.34E-01	---	---	---	233932_at	---
2.90	3.05	0.14	3.96E-01	7.34E-01	---	---	---	241558_at	---
2.47	2.61	0.14	3.96E-01	7.34E-01	---	---	---	240796_at	---
2.79	2.91	0.12	3.96E-01	7.34E-01	ARHGAP22	Rho GTPase activating protein 22	chr10q11.22	1560764_at	NM_021226
2.39	2.51	0.12	3.96E-01	7.34E-01	SHOX	short stature homeobox	chrXpter-p22.32;Yp11.3	207570_at	NM_000451 /// NM_006883
2.06	2.17	0.12	3.96E-01	7.34E-01	FLJ35934	FLJ35934 protein	chr17p11.2	1557895_at	XR_041166
2.07	2.17	0.11	3.96E-01	7.34E-01	LOC729296	Similar to hCG2017976	chr20q13.33	237805_at	XM_001129872 /// XM_001130699 /// XM_001717168

6.14	6.57	0.43	3.96E-01	7.34E-01	USP16	ubiquitin specific peptidase 16	chr21q22.11	228822_s_at	NM_001001992 /// NM_001032410 /// NM_006447																				
2.28	2.37	0.09	3.96E-01	7.34E-01	---	---	---	240867_at	---																				
5.15	5.38	0.23	3.97E-01	7.34E-01	RSBN1L	round spermatid basic protein 1-like	chr7q11.23	226387_at	NM_198467																				
4.69	4.90	0.21	3.96E-01	7.34E-01	DHTKD1	dehydrogenase E1 and transketolase domain containing 1	chr10p14	209916_at	NM_018706																				
2.67	2.85	0.18	3.96E-01	7.34E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	1555944_at	NM_014612																				
2.82	2.98	0.17	3.96E-01	7.34E-01	---	---	---	237661_at	---																				
4.25	4.39	0.14	3.96E-01	7.34E-01	---	---	---	231827_at	---																				
2.21	2.34	0.14	3.97E-01	7.34E-01	ZNF44	zinc finger protein 44	chr19p13.2	206810_at	NM_016264 /// XM_001718561 /// XM_001719479 /// XM_001719639																				
2.37	2.49	0.12	3.96E-01	7.34E-01	ZFP2	zinc finger protein 2 homolog (mouse)	chr5q35.3	207757_at	NM_030613																				
2.03	2.12	0.10	3.96E-01	7.34E-01	---	---	---	1561525_at	---																				
2.50	2.63	0.14	3.97E-01	7.34E-01	C15orf56	chromosome 15 open reading frame 56	chr15q15.1	239470_at	NM_001039905																				
4.11	4.35	0.25	3.97E-01	7.34E-01	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	chrXq13.1-q21.1	221617_at	NM_015975																				
1.90	2.02	0.12	3.97E-01	7.34E-01	IFNK	interferon, kappa	---	224093_at	NM_020124																				
3.89	4.01	0.12	3.97E-01	7.34E-01	NTN2L	Netrin 2-like (chicken)	chr16p13.3	217034_at	NM_006181																				
6.56	7.04	0.47	3.97E-01	7.34E-01	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	chr14q24.3-q31	202061_s_at	NM_005065																				
1.90	2.03	0.12	3.97E-01	7.34E-01	---	---	---	237540_at	---																				
2.15	2.24	0.09	3.97E-01	7.35E-01	---	---	---	238938_at	---																				
2.17	2.31	0.14	3.97E-01	7.35E-01	DNASE1	deoxyribonuclease I	chr16p13.3	243127_x_at	NM_005223																				
2.06	2.15	0.10	3.97E-01	7.35E-01	LRRC28	Leucine rich repeat containing 28	chr15q26.3	238897_at	NM_144598																				
2.17	2.28	0.11	3.97E-01	7.35E-01	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	chr8p22-p21.3	210979_at	NM_001127505 /// NM_004315 /// NM_177924																				
10.34	10.61	0.27	3.97E-01	7.35E-01	SRP14	signal recognition particle 14kDa (homologous Alu RNA binding protein)	chr15q22	200007_at	NM_003134																				
3.21	3.35	0.13	3.97E-01	7.35E-01	---	---	---	237773_at	---																				
4.71	4.99	0.28	3.97E-01	7.35E-01	ANKRD28	ankyrin repeat domain 28	chr3p24.3	213035_at	NM_015199																				
1.96	2.11	0.15	3.97E-01	7.35E-01	TRDN	triadin	chr6q22-q23	1552791_a_at	NM_006073																				
2.11	2.25	0.13	3.97E-01	7.35E-01	DEFB125	defensin, beta 125	chr20p13	1552998_at	NM_153325																				
3.37	3.55	0.18	3.97E-01	7.35E-01	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	chr5q33.1	1557350_at	NM_005754 /// NM_198395																				
2.70	2.83	0.13	3.97E-01	7.35E-01	PPM1H	protein phosphatase 1H (PP2C domain containing)	chr12q14.1-q14.2	1558654_at	NM_020700																				
1.98	2.11	0.13	3.97E-01	7.35E-01	---	---	---	1561076_at	---																				
1.96	2.05	0.10	3.97E-01	7.35E-01	---	---	---	241750_x_at	---																				
3.94	4.14	0.20	3.97E-01	7.35E-01	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	chr22q11.23|22q11	228898_s_at	NM_001007468 /// NM_003073																				
2.06	2.20	0.14	3.97E-01	7.35E-01	CDC2	Cell division cycle 2, G1 to S and G2 to M	chr10q21.1	231534_at	NM_001130829 /// NM_001786 /// NM_033379																				
1.98	2.08	0.11	3.97E-01	7.35E-01	IGK@ /// IGKC /// LOC647506 /// LOC652694	immunoglobulin kappa locus /// immunoglobulin kappa constant /// similar to Ig kappa chain V-I region HK101 precursor /// similar to Ig kappa chain V-I region HK102 precursor	chr2p12	217145_at	XM_001713938 /// XM_942302																				
4.32	4.51	0.20	3.97E-01	7.35E-01	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	chr22q12	204152_s_at	NM_002405																				
8.80	9.32	0.52	3.97E-01	7.35E-01	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	chr5q31-q34	224959_at	NM_000112																				
4.45	4.85	0.40	3.97E-01	7.35E-01	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	chr12q15-q21	201604_s_at	NM_002480																				
2.63	2.75	0.12	3.97E-01	7.35E-01	STAB1	stabilin 1	chr3p21.1	1555319_at	NM_015136																				
2.84	2.95	0.11	3.97E-01	7.35E-01	LOC286109	hypothetical protein LOC286109	chr8q24.3	243304_at	---																				
2.65	2.76	0.11	3.97E-01	7.35E-01	---	---	---	238945_at	---																				
4.41	4.58	0.17	3.97E-01	7.35E-01	---	---	---	217406_at	---																				
3.49	3.65	0.16	3.97E-01	7.35E-01	GGT6	gamma-glutamyltransferase 6	chr17p13.2	236225_at	NM_001122890 /// NM_153338																				
3.14	3.28	0.14	3.97E-01	7.35E-01	LOC100129624	hypothetical LOC100129624	chr1p35.3	210748_at	XM_001722419 /// XM_001723959 /// XM_001724355																				

8.76	8.88	0.13	3.97E-01	7.35E-01	NOMO1 /// NOMO2 /// NOMO3	NODAL modulator 1 /// NODAL modulator 2 /// NODAL modulator 3	chr16p12.3 /// chr16p13 /// chr16p13.11	217225_x_at	NM_001004060 /// NM_001004067 /// NM_014287 /// NM_173614 /// XM_001716489 /// XM_001716493
1.94	2.03	0.09	3.97E-01	7.35E-01	---	---	---	1560111_at	---
2.42	2.54	0.12	3.97E-01	7.35E-01	---	---	---	244599_at	---
2.97	3.08	0.11	3.98E-01	7.35E-01	RHOXF1	Rhox homeobox family, member 1	chrXq24	1552724_at	NM_139282 /// XM_001715156
3.10	3.23	0.13	3.98E-01	7.35E-01	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	chr16p13.2	206534_at	NM_000833 /// NM_001134407 /// NM_001134408
7.14	7.68	0.54	3.98E-01	7.35E-01	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	chr5q11	212196_at	NM_002184 /// NM_175767
6.85	7.27	0.42	3.98E-01	7.35E-01	RB1CC1	RB1-inducible coiled-coil 1	chr8q11	202033_s_at	NM_001083617 /// NM_014781
3.36	3.57	0.21	3.98E-01	7.35E-01	CENTB1	centaurin, beta 1	chr17p13.1	205213_at	NM_014716
3.02	3.22	0.20	3.98E-01	7.35E-01	ZNF608	zinc finger protein 608	chr5q23.2	232303_at	NM_020747
4.02	4.20	0.18	3.98E-01	7.35E-01	HIGD1B	HIG1 domain family, member 1B	chr17q21.31	219719_at	NM_016438
4.62	4.79	0.18	3.98E-01	7.35E-01	KIAA1217	KIAA1217	chr10p12.2-p12.1	232046_at	NM_001098500 /// NM_001098501 /// NM_019590
3.17	3.34	0.16	3.98E-01	7.35E-01	TLN1	talin 1	chr9p13	236132_at	NM_006289
4.47	4.62	0.15	3.98E-01	7.35E-01	ADAM8	ADAM metallopeptidase domain 8	chr10q26.3	205180_s_at	NM_001109
2.26	2.40	0.14	3.98E-01	7.35E-01	---	---	---	1561097_at	---
2.04	2.16	0.12	3.98E-01	7.35E-01	TWF1	Twinfilin, actin-binding protein, homolog 1 (Drosophila)	chr12q12	243033_at	NM_002822
2.08	2.18	0.10	3.98E-01	7.35E-01	---	---	---	243401_at	---
3.56	3.90	0.34	3.98E-01	7.35E-01	NEK6	NIMA (never in mitosis gene a)-related kinase 6	chr9q33.3-q34.11	223159_s_at	NM_014397
4.30	4.46	0.16	3.98E-01	7.35E-01	RIMS4	regulating synaptic membrane exocytosis 4	chr20q13.12	227644_at	NM_182970
5.28	5.41	0.13	3.98E-01	7.35E-01	RCC1 /// SNHG3-RCC1	regulator of chromosome condensation 1 /// SNHG3-RCC1	chr1p36.1	215747_s_at	NM_001048194 /// NM_001048195 /// NM_001048197 /// NM_001048198 /// NM_001048199 /// NM_001269
11.66	11.78	0.12	3.98E-01	7.35E-01	B2M	beta-2-microglobulin	chr15q21-q22.2	201891_s_at	NM_004048
2.60	2.74	0.14	3.98E-01	7.35E-01	PITPNC1	Phosphatidylinositol transfer protein, cytoplasmic 1	chr17q24.2	227589_at	NM_012417 /// NM_181671
2.12	2.24	0.12	3.98E-01	7.35E-01	MAG	malignancy-associated gene	chr19q13.1	217105_at	---
3.94	4.40	0.46	3.98E-01	7.35E-01	---	---	---	242405_at	---
2.12	2.23	0.11	3.98E-01	7.35E-01	---	---	---	232839_at	---
2.00	2.10	0.10	3.98E-01	7.35E-01	FLJ35848	Hypothetical protein FLJ35848	chr17q21.31	1566478_at	NM_001033659
2.00	2.10	0.10	3.98E-01	7.35E-01	---	---	---	1561828_at	---
2.39	2.49	0.09	3.98E-01	7.35E-01	STYXL1	serine/threonine/tyrosine interacting-like 1	chr7q11.23	222591_at	NM_016086
4.52	4.71	0.20	3.98E-01	7.35E-01	OGN	osteoglycin	chr9q22	222722_at	NM_014057 /// NM_024416 /// NM_033014
2.56	2.68	0.12	3.98E-01	7.36E-01	ULBP3	UL16 binding protein 3	chr6q25	231748_at	NM_024518
7.18	7.34	0.15	3.98E-01	7.36E-01	LOC100133585 /// RABEP2	similar to RABEP2 protein /// rabaptin, RAB GTPase binding effector protein 2	chr16p11.2	77508_r_at	NM_024816 /// XM_001717918
1.87	1.95	0.08	3.98E-01	7.36E-01	---	---	---	236999_at	---
4.90	5.20	0.30	3.98E-01	7.36E-01	ZNF304	zinc finger protein 304	chr19q13.4	207753_at	NM_020657
6.58	7.22	0.63	3.99E-01	7.36E-01	---	---	---	232369_at	---
2.18	2.27	0.10	3.99E-01	7.36E-01	CCNC	cyclin C	chr6q21	1569126_at	NM_001013399 /// NM_005190
4.44	4.62	0.18	3.99E-01	7.36E-01	---	---	---	236666_s_at	---
1.93	2.03	0.10	3.99E-01	7.36E-01	TYRP1	tyrosinase-related protein 1	chr9p23	205694_at	NM_000550
2.19	2.28	0.09	3.99E-01	7.36E-01	DYDC2	DPY30 domain containing 2	chr10q23.1	239733_at	NM_032372

9.56	9.77	0.21	3.99E-01	7.36E-01	CTSA	cathepsin A	chr20q13.1	200661_at	NM_000308 /// NM_001127695
4.32	4.53	0.21	3.99E-01	7.36E-01	DAGLB	diacylglycerol lipase, beta	chr7p22.1	225828_at	NM_139179
3.17	3.30	0.13	3.99E-01	7.36E-01	LOC283177	hypothetical protein LOC283177	chr11q25	1557207_s_at	---
3.34	3.47	0.13	3.99E-01	7.36E-01	---	---	---	234062_at	---
6.20	6.46	0.26	3.99E-01	7.36E-01	GCLM	glutamate-cysteine ligase, modifier subunit	chr1p22.1	203925_at	NM_002061
2.80	2.93	0.13	3.99E-01	7.36E-01	---	---	---	1556856_at	---
2.26	2.55	0.29	3.99E-01	7.36E-01	---	---	---	228750_at	---
5.01	5.24	0.22	3.99E-01	7.36E-01	SSPN	sarcospan (Kras oncogene-associated gene)	chr12p11.2	204964_s_at	NM_005086
1.80	1.90	0.10	3.99E-01	7.36E-01	---	---	---	1564631_at	---
3.51	3.61	0.10	3.99E-01	7.36E-01	FAM129C	family with sequence similarity 129, member C	chr19p13.11	1569422_at	NM_001098524 /// NM_173544
4.64	5.20	0.57	3.99E-01	7.36E-01	---	---	---	1565597_at	---
2.51	2.72	0.21	3.99E-01	7.36E-01	---	---	---	242336_at	---
5.01	5.17	0.16	3.99E-01	7.36E-01	GLE1	GLE1 RNA export mediator homolog (yeast)	chr9q34.11	206920_s_at	NM_001003722 /// NM_001499
7.02	7.44	0.42	3.99E-01	7.36E-01	JARID1A	jumonji, AT rich interactive domain 1A	chr12p11	202040_s_at	NM_001042603 /// NM_005056
2.33	2.51	0.17	3.99E-01	7.36E-01	---	---	---	236230_at	---
2.12	2.21	0.09	3.99E-01	7.36E-01	---	---	---	1562215_at	---
2.25	2.38	0.13	3.99E-01	7.36E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	1561430_s_at	NM_033364
1.78	1.90	0.12	3.99E-01	7.36E-01	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	chr1q32.1	215168_at	NM_006335
1.73	1.82	0.09	4.00E-01	7.37E-01	SCEL	sciellin	chr13q22	232056_at	NM_003843 /// NM_144777
3.98	4.17	0.20	4.00E-01	7.37E-01	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	chr1q32.1	223229_at	NM_014176
2.18	2.29	0.11	4.00E-01	7.37E-01	FLJ30838	hypothetical gene supported by AL832565	chr2p16.1	1562326_at	XM_379096 /// XM_934421 /// XM_945691 /// XM_945693
5.52	5.62	0.10	4.00E-01	7.37E-01	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	chr21q22.3	1566670_at	NM_003681
3.04	3.23	0.19	4.00E-01	7.37E-01	---	---	---	243218_at	---
3.69	3.83	0.14	4.00E-01	7.37E-01	MYL7	myosin, light chain 7, regulatory	chr7p21-p11.2	219942_at	NM_021223
2.66	2.81	0.16	4.00E-01	7.37E-01	---	---	---	231594_at	---
2.48	2.63	0.15	4.00E-01	7.37E-01	CXXC4	CXXC finger 4	chr4q22-q24	229774_at	NM_025212
2.29	2.43	0.14	4.00E-01	7.37E-01	RNF17	ring finger protein 17	chr13q12.12	224384_s_at	NM_031277
2.53	2.75	0.21	4.00E-01	7.37E-01	PLXDC1	plexin domain containing 1	chr17q21.1	214081_at	NM_020405
1.95	2.04	0.10	4.00E-01	7.37E-01	---	---	---	1559222_at	---
2.53	2.63	0.11	4.00E-01	7.37E-01	HMGB3 /// LOC203510	high-mobility group box 3 /// similar to hCG1644442	chrXq23 /// chrXq28	217454_at	NM_005342 /// XM_001719132 /// XM_001719371 /// XM_001723892
4.19	4.35	0.16	4.00E-01	7.37E-01	SMAD6	SMAD family member 6	chr15q21-q22	209886_s_at	NM_005585
3.08	3.23	0.15	4.00E-01	7.37E-01	ATG9B	ATG9 autophagy related 9 homolog B (S. cerevisiae)	chr7q36.1	229252_at	NM_173681
3.95	4.08	0.13	4.00E-01	7.37E-01	SDCCAG3	Serologically defined colon cancer antigen 3	chr9q34.3	238111_at	NM_001039707 /// NM_001039708 /// NM_006643
2.12	2.25	0.13	4.00E-01	7.37E-01	CXorf30	chromosome X open reading frame 30	chrXp21.1	241538_at	NM_001098843 /// XM_001713662 /// XM_001713663 /// XM_001713664
6.50	6.79	0.28	4.00E-01	7.37E-01	TTLL12	tubulin tyrosine ligase-like family, member 12	chr22q13.31	216251_s_at	NM_015140
5.04	5.40	0.37	4.00E-01	7.37E-01	C10orf18	chromosome 10 open reading frame 18	chr10p15.1	227777_at	NM_017782
6.57	6.75	0.18	4.00E-01	7.37E-01	MINK1	misshapen-like kinase 1 (zebrafish)	chr17p13.2	209241_x_at	NM_001024937 /// NM_015716 /// NM_153827 /// NM_170663
4.05	4.19	0.13	4.00E-01	7.37E-01	RSHL1	radial spokehead-like 1	chr19q13.3	220965_s_at	NM_030785
1.97	2.07	0.10	4.00E-01	7.37E-01	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	chr4q13	217175_at	NM_001076
2.00	2.10	0.11	4.00E-01	7.37E-01	SH3GLP1	SH3-domain GRB2-like pseudogene 1	chr17q11.2	1566253_at	---
3.03	3.14	0.11	4.00E-01	7.37E-01	CCDC57	coiled-coil domain containing 57	chr17q25.3	1553248_at	NM_198082

1.99	2.11	0.13	4.00E-01	7.37E-01	---	---	---	237957_at	---
2.16	2.27	0.11	4.00E-01	7.37E-01	ESCO2	Establishment of cohesion 1 homolog 2 (S. cerevisiae)	chr8p21.1	1564473_at	NM_001017420
4.00	4.20	0.20	4.00E-01	7.37E-01	BTNL9	butyrophilin-like 9	chr5q35.3	1553279_at	NM_152547
6.35	6.65	0.30	4.01E-01	7.37E-01	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	chr7q22	213097_s_at	NM_001129887 /// NM_014377
2.13	2.24	0.12	4.01E-01	7.37E-01	---	---	---	234603_at	---
3.28	3.48	0.20	4.01E-01	7.37E-01	C20orf160	chromosome 20 open reading frame 160	chr20q11.2	1570070_at	NM_080625
2.28	2.44	0.16	4.01E-01	7.37E-01	PLXNA2	plexin A2	chr1q32.2	207290_at	NM_025179
3.44	3.59	0.15	4.01E-01	7.37E-01	BTRC	beta-transducin repeat containing	chr10q24.32	222374_at	NM_003939 /// NM_033637
6.65	6.80	0.15	4.01E-01	7.37E-01	---	---	---	233427_x_at	---
2.20	2.35	0.15	4.01E-01	7.37E-01	ZNF439	zinc finger protein 439	chr19p13.2	236562_at	NM_152262
2.17	2.30	0.12	4.01E-01	7.37E-01	---	---	---	1569780_at	---
2.19	2.29	0.11	4.01E-01	7.37E-01	DNASE1	deoxyribonuclease I	chr16p13.3	241854_at	NM_005223
1.86	1.97	0.11	4.01E-01	7.37E-01	DNM1L	Dynamin 1-like	chr12p11.21	237797_at	NM_005690 /// NM_012062 /// NM_012063
3.46	3.56	0.10	4.01E-01	7.37E-01	---	---	---	1562946_at	---
2.40	2.50	0.09	4.01E-01	7.37E-01	---	---	---	237612_at	---
2.31	2.45	0.14	4.01E-01	7.37E-01	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	chr16q22.2	210556_at	NM_004555 /// NM_173163 /// NM_173164 /// NM_173165
2.94	3.11	0.17	4.01E-01	7.37E-01	FAM104B	family with sequence similarity 104, member B	chrXp11.21	232990_at	NM_138362
2.59	2.72	0.13	4.01E-01	7.38E-01	---	---	---	237752_at	---
2.06	2.18	0.12	4.01E-01	7.38E-01	FAM13C1	family with sequence similarity 13, member C1	chr10q21.1	214914_at	NM_001001971 /// NM_198215
2.39	2.58	0.19	4.01E-01	7.38E-01	---	---	---	232384_s_at	---
2.22	2.34	0.12	4.01E-01	7.38E-01	CYP4F11	cytochrome P450, family 4, subfamily F, polypeptide 11	chr19p13.1	206153_at	NM_001128932 /// NM_021187
7.00	7.19	0.19	4.01E-01	7.38E-01	LAMP2	lysosomal-associated membrane protein 2	chrXq24	203042_at	NM_001122606 /// NM_002294 /// NM_013995
7.33	8.45	1.12	4.01E-01	7.38E-01	IGK@ /// IGKC	immunoglobulin kappa locus /// immunoglobulin kappa constant	chr2p12	221671_x_at	---
2.11	2.23	0.12	4.01E-01	7.38E-01	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	chr17q11.2	1554311_a_at	NM_003170
1.99	2.12	0.13	4.01E-01	7.38E-01	---	---	---	1568785_a_at	---
4.27	4.43	0.16	4.01E-01	7.38E-01	NLRP12	NLR family, pyrin domain containing 12	chr19q13.41	223944_at	NM_033297 /// NM_144687
2.04	2.14	0.10	4.01E-01	7.38E-01	SRP72	signal recognition particle 72kDa	chr4q11	208263_at	NM_006947
3.69	4.13	0.44	4.01E-01	7.38E-01	CD52	CD52 molecule	chr1p36	34210_at	NM_001803
3.72	4.06	0.34	4.01E-01	7.38E-01	---	---	---	233386_at	---
3.21	3.40	0.19	4.02E-01	7.38E-01	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	chr2q11.1-q11.2	240200_at	NM_001056 /// NM_176825
4.24	4.41	0.17	4.02E-01	7.38E-01	MMP14	matrix metallopeptidase 14 (membrane-inserted)	chr14q11-q12	202827_s_at	NM_004995
2.63	2.77	0.14	4.02E-01	7.38E-01	GPM6B	glycoprotein M6B	chrXp22.2	209168_at	NM_001001994 /// NM_001001995 /// NM_001001996 /// NM_005278
2.07	2.19	0.13	4.02E-01	7.38E-01	MUC4	mucin 4, cell surface associated	chr3q29	217110_s_at	NM_004532 /// NM_018406 /// NM_138297
1.92	2.04	0.11	4.01E-01	7.38E-01	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	chr5p15.1-p14	205532_s_at	NM_004932
1.87	1.98	0.11	4.02E-01	7.38E-01	---	---	---	240659_x_at	---
5.12	5.38	0.26	4.02E-01	7.38E-01	PHCA	phytoceramidase, alkaline	chr11q13.5	227776_at	NM_018367
3.42	3.56	0.14	4.02E-01	7.38E-01	---	---	---	231330_at	---
1.92	2.03	0.10	4.02E-01	7.38E-01	---	---	---	1559598_at	---
2.68	2.85	0.17	4.02E-01	7.38E-01	---	---	---	1567044_s_at	---
2.10	2.28	0.17	4.02E-01	7.38E-01	RFX6	regulatory factor X, 6	chr6q22.2	1552673_at	NM_173560
2.48	2.59	0.12	4.02E-01	7.38E-01	---	---	---	1561219_x_at	---
6.07	6.34	0.27	4.02E-01	7.38E-01	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	chr8q21.11	222657_s_at	NM_001001481 /// NM_018299
2.25	2.37	0.12	4.02E-01	7.38E-01	FLJ13224	hypothetical protein FLJ13224	chr12p11.21	220211_at	XR_040669 /// XR_040670 /// XR_040671
1.84	1.94	0.10	4.02E-01	7.38E-01	ABCA13	ATP-binding cassette, sub-family A (ABC1), member 13	chr7p12.3	1553295_at	NM_152701
6.76	6.93	0.17	4.02E-01	7.38E-01	---	---	---	202225_at	---
2.75	2.88	0.13	4.02E-01	7.38E-01	PAPOLG	Poly(A) polymerase gamma	chr2p16.1	1556929_at	NM_022894
2.03	2.14	0.11	4.02E-01	7.38E-01	---	---	---	1556531_at	---

2.21	2.31	0.10	4.02E-01	7.38E-01	---	---	---	235639_at	---
1.83	1.91	0.09	4.02E-01	7.38E-01	---	---	---	1559280_a_at	---
2.45	2.64	0.19	4.02E-01	7.38E-01	MED6	mediator complex subunit 6	chr14q24.2	207078_at	NM_005466
2.33	2.46	0.13	4.02E-01	7.38E-01	---	---	---	1561622_at	---
1.91	2.00	0.09	4.02E-01	7.38E-01	---	---	---	237150_at	---
3.67	4.02	0.35	4.02E-01	7.38E-01	LOC729970	Hypothetical LOC729970	chr1p21.3	235362_at	XM_001129522 /// XM_001134179 /// XM_001720397
2.90	3.04	0.14	4.02E-01	7.38E-01	---	---	---	244475_at	---
2.22	2.38	0.15	4.02E-01	7.38E-01	---	---	---	239278_at	---
2.25	2.39	0.14	4.02E-01	7.38E-01	---	---	---	1557484_at	---
2.44	2.56	0.12	4.02E-01	7.38E-01	IGHV7-81	immunoglobulin heavy variable 7-81	chr14q32.33	1555179_at	---
3.67	3.89	0.22	4.02E-01	7.38E-01	TUB	tubby homolog (mouse)	chr11p15.5	210737_at	NM_003320 /// NM_177972
2.09	2.19	0.10	4.02E-01	7.38E-01	FCRL1	Fc receptor-like 1	chr1q21-q22	235982_at	NM_052938
1.89	2.01	0.12	4.02E-01	7.38E-01	---	---	---	243421_at	---
3.00	3.17	0.16	4.02E-01	7.38E-01	RDH16	retinol dehydrogenase 16 (all-trans)	chr12q13.3	206753_at	NM_003708
3.10	3.24	0.14	4.02E-01	7.38E-01	KRT74	keratin 74	chr12q13.13	231583_at	NM_175053
3.25	3.38	0.13	4.02E-01	7.38E-01	LOC729556	similar to hCG2041598	chr16q22.3	237861_at	XM_001126071 /// XM_001130605 /// XM_001718257
2.43	2.55	0.12	4.02E-01	7.38E-01	---	---	---	231446_at	---
2.23	2.35	0.12	4.02E-01	7.38E-01	---	---	---	234437_at	---
1.90	1.99	0.09	4.02E-01	7.38E-01	PRO1596	hypothetical LOC29013	chr1p34.3	224083_s_at	---
2.40	2.54	0.14	4.02E-01	7.38E-01	KLF12	Kruppel-like factor 12	chr13q22	208467_at	NM_007249
2.27	2.37	0.10	4.02E-01	7.38E-01	---	---	---	1556231_a_at	---
4.37	4.53	0.16	4.02E-01	7.38E-01	PDE5A	phosphodiesterase 5A, cGMP-specific	chr4q25-q27	1562228_s_at	NM_001083 /// NM_033430 /// NM_033437
2.07	2.24	0.17	4.03E-01	7.39E-01	---	---	---	1559923_at	---
6.21	6.76	0.56	4.03E-01	7.39E-01	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	chr1p36.23-p34.3	218934_s_at	NM_014424
6.21	6.68	0.47	4.03E-01	7.39E-01	SAP18	Sin3A-associated protein, 18kDa	chr13q12.11	208740_at	NM_005870
8.94	9.30	0.35	4.03E-01	7.39E-01	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	chr5q11	212195_at	NM_002184 /// NM_175767
2.14	2.35	0.20	4.03E-01	7.39E-01	C17orf57	chromosome 17 open reading frame 57	chr17q21.32	1554772_at	NM_152347
3.56	3.74	0.18	4.03E-01	7.39E-01	FLJ10232	hypothetical protein FLJ10232	chr9q34.11	208160_at	XR_041437 /// XR_041438 /// XR_041439
3.04	3.20	0.16	4.03E-01	7.39E-01	---	---	---	243359_at	---
2.46	2.62	0.16	4.03E-01	7.39E-01	BMP8B	bone morphogenetic protein 8b	chr1p35-p32	207865_s_at	NM_001720
2.93	3.08	0.15	4.03E-01	7.39E-01	CLIC5	chloride intracellular channel 5	chr6p21.1-p12.1	243917_at	NM_001114086 /// NM_016929
4.38	4.53	0.15	4.03E-01	7.39E-01	CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit	chr22q13.1	211830_s_at	NM_001003406 /// NM_021096
2.74	2.89	0.15	4.03E-01	7.39E-01	BCL2L15	BCL2-like 15	chr1p13.2	236979_at	NM_001010922
2.58	2.72	0.14	4.03E-01	7.39E-01	LGR4	Leucine-rich repeat-containing G protein-coupled receptor 4	chr11p14-p13	230674_at	NM_018490
4.35	4.47	0.12	4.03E-01	7.39E-01	---	---	---	244208_at	---
2.32	2.44	0.12	4.03E-01	7.39E-01	---	---	---	243726_at	---
3.40	3.51	0.11	4.03E-01	7.39E-01	---	---	---	1561635_at	---
2.52	2.63	0.11	4.03E-01	7.39E-01	GSG1	germ cell associated 1	chr12p13.1	221252_s_at	NM_001080554 /// NM_001080555 /// NM_031289 /// NM_153823
1.96	2.07	0.11	4.03E-01	7.39E-01	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	chr5q31.1	239438_at	NM_016340
2.52	2.62	0.11	4.03E-01	7.39E-01	GADD45GIP1	Growth arrest and DNA-damage-inducible, gamma interacting protein 1	chr19p13.13	225495_x_at	NM_052850
2.26	2.36	0.11	4.03E-01	7.39E-01	TMIE	transmembrane inner ear	chr3p21	1553601_a_at	NM_147196
2.01	2.12	0.10	4.03E-01	7.39E-01	AKAP5	A kinase (PRKA) anchor protein 5	chr14q21-q24	207800_at	NM_004857
1.95	2.05	0.10	4.03E-01	7.39E-01	---	---	---	220851_at	---
1.88	1.99	0.10	4.03E-01	7.39E-01	HNF4G	hepatocyte nuclear factor 4, gamma	chr8q21.11	232271_at	NM_004133
2.12	2.21	0.09	4.03E-01	7.39E-01	---	---	---	238978_at	---
2.60	2.72	0.12	4.03E-01	7.39E-01	---	---	---	236828_at	---
2.04	2.15	0.10	4.03E-01	7.39E-01	CCDC123	coiled-coil domain containing 123	chr19q13.11	1554512_a_at	NM_032816
4.59	4.93	0.34	4.03E-01	7.39E-01	DPY19L3	dpy-19-like 3 (C. elegans)	chr19q13.11	225633_at	NM_207325

4.80	5.08	0.28	4.03E-01	7.39E-01	EIF4E3	eukaryotic translation initiation factor 4E family member 3	chr3p14	225941_at	NM_001134649 /// NM_001134650 /// NM_001134651 /// NM_173359																					
5.97	6.18	0.22	4.03E-01	7.39E-01	---	---	---	227367_at	---																					
3.03	3.17	0.14	4.03E-01	7.39E-01	BCAS4	breast carcinoma amplified sequence 4	chr20q13.13	220588_at	NM_001010974 /// NM_017843 /// NM_198799																					
4.87	5.00	0.13	4.03E-01	7.39E-01	BAD	BCL2-associated agonist of cell death	chr11q13.1	232660_at	NM_004322 /// NM_032989																					
4.40	4.53	0.12	4.03E-01	7.39E-01	MYL3	myosin, light chain 3, alkali; ventricular, skeletal, slow	chr3p21.3-p21.2	205589_at	NM_000258																					
2.45	2.53	0.09	4.03E-01	7.39E-01	TAS2R7	taste receptor, type 2, member 7	chr12p13	221396_at	NM_023919																					
4.19	4.38	0.19	4.03E-01	7.39E-01	TBCD	tubulin folding cofactor D	chr17q25.3	229191_at	NM_005993																					
3.83	3.96	0.13	4.03E-01	7.39E-01	CD209	CD209 molecule	chr19p13	207278_s_at	NM_021155																					
3.13	3.27	0.14	4.03E-01	7.39E-01	---	---	---	237650_at	---																					
4.73	4.86	0.13	4.03E-01	7.39E-01	C21orf2	Chromosome 21 open reading frame 2	chr21q22.3	203993_x_at	NM_004928																					
6.87	7.19	0.32	4.04E-01	7.39E-01	CRBN	cereblon	chr3p26.3	222533_at	NM_016302																					
8.61	8.83	0.22	4.04E-01	7.39E-01	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	chr5p13	201278_at	NM_001343																					
2.08	2.18	0.10	4.04E-01	7.39E-01	LOC284561	hypothetical protein LOC284561	chr1q21.3	232689_at	---																					
3.29	3.45	0.16	4.04E-01	7.39E-01	SAMD9L	sterile alpha motif domain containing 9-like	chr7q21.2-q21.3	230036_at	NM_152703																					
2.24	2.34	0.10	4.04E-01	7.39E-01	---	---	---	233153_at	---																					
5.30	5.50	0.20	4.04E-01	7.39E-01	STOML1	stomatin (EPB72)-like 1	chr15q24-q25	204701_s_at	NM_004809																					
5.60	5.85	0.24	4.04E-01	7.39E-01	FAM176B /// LOC100133999	family with sequence similarity 176, member B /// hypothetical protein LOC100133999	chr1p34.3	221710_x_at	NM_018166 /// XM_001716785																					
3.25	3.43	0.18	4.04E-01	7.39E-01	AMOTL1	angiomotin like 1	chr11q14.3	225459_at	NM_130847																					
3.69	3.84	0.15	4.04E-01	7.39E-01	---	---	---	238052_at	---																					
2.61	2.72	0.11	4.04E-01	7.39E-01	NMNAT2	nicotinamide nucleotide adenylyltransferase 2	chr1q25	1552712_a_at	NM_015039 /// NM_170706																					
3.49	3.66	0.17	4.04E-01	7.40E-01	CELSR3 /// SLC26A6	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) /// solute carrier family 26, member 6	chr3p21.3 /// chr3p24.1-p21.2	40020_at	NM_001040454 /// NM_001407 /// NM_022911 /// NM_134263 /// NM_134426																					
3.53	3.67	0.14	4.04E-01	7.40E-01	---	---	---	237337_at	---																					
3.55	3.68	0.13	4.04E-01	7.40E-01	---	---	---	222159_at	---																					
2.41	2.54	0.13	4.04E-01	7.40E-01	C11orf30	chromosome 11 open reading frame 30	chr11q13.5	219012_s_at	NM_020193																					
11.15	11.28	0.12	4.04E-01	7.40E-01	PSAP	prosaposin	chr10q21-q22	200871_s_at	NM_001042465 /// NM_001042466 /// NM_002778																					
2.06	2.18	0.12	4.04E-01	7.40E-01	---	---	---	1560887_a_at	---																					
2.61	2.73	0.12	4.04E-01	7.40E-01	VIT	vitrin	chr2p22-p21	227899_at	NM_053276																					
2.51	2.60	0.09	4.04E-01	7.40E-01	---	---	---	239858_at	---																					
2.31	2.46	0.14	4.04E-01	7.40E-01	ZNF365	zinc finger protein 365	chr10q21.2	1570121_at	NM_014951 /// NM_199450 /// NM_199451 /// NM_199452																					
4.45	4.73	0.29	4.04E-01	7.40E-01	ENY2	enhancer of yellow 2 homolog (Drosophila)	chr8q23.1	226775_at	NM_020189																					
3.19	3.42	0.24	4.04E-01	7.40E-01	TRA@	T cell receptor alpha locus	chr14q11.2	215540_at	---																					
4.20	4.39	0.20	4.04E-01	7.40E-01	---	---	---	242303_at	---																					
3.34	3.50	0.15	4.04E-01	7.40E-01	IL18RAP	interleukin 18 receptor accessory protein	chr2q12	207072_at	NM_003853																					
2.61	2.75	0.14	4.04E-01	7.40E-01	RAB3IP	RAB3A interacting protein (rabin3)	chr12q14.3	231399_at	NM_001024647 /// NM_022456 /// NM_175623 /// NM_175624 /// NM_175625																					
1.99	2.12	0.14	4.04E-01	7.40E-01	WHDC1L1 /// WHDC1L2	WAS protein homology region 2 domain containing 1-like 1 /// WAS protein homology region 2 domain containing 1-like 2	chr15q11.2 /// chr15q13.1	1560662_s_at	NR_003521 /// XM_926785 /// XR_042166																					
2.33	2.46	0.13	4.04E-01	7.40E-01	---	---	---	237787_at	---																					
6.33	6.64	0.32	4.05E-01	7.40E-01	COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	chr17p11.2	202078_at	NM_003653																					

3.77	4.06	0.29	4.05E-01	7.40E-01	CASP1 /// COP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase) /// caspase-1 dominant-negative inhibitor pseudo-ICE	chr11q23	1552703_s_at	NM_001017534 /// NM_001223 /// NM_033292 /// NM_033293 /// NM_033294 /// NM_033295 /// NM_052889
2.12	2.22	0.10	4.05E-01	7.40E-01	TDO2	Tryptophan 2,3-dioxygenase	chr4q31-q32	231702_at	NM_005651
7.89	8.17	0.28	4.05E-01	7.40E-01	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	chr2p23.2	212645_x_at	NM_004899 /// NM_199191 /// NM_199192 /// NM_199193 /// NM_199194
6.94	7.11	0.17	4.05E-01	7.40E-01	C14orf172	chromosome 14 open reading frame 172	chr14q32.33	52741_at	NM_152307
5.52	5.65	0.13	4.05E-01	7.40E-01	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	chr7q22	222017_x_at	NM_002319
3.78	3.88	0.11	4.05E-01	7.40E-01	C14orf48	Chromosome 14 open reading frame 48	chr14q32.13	234816_at	NM_152777
2.15	2.25	0.10	4.05E-01	7.40E-01	EHF	ets homologous factor	chr11p12	224189_x_at	NM_012153
4.24	4.37	0.13	4.05E-01	7.40E-01	PECAM1	platelet/endothelial cell adhesion molecule	chr17q23	1559921_at	NM_000442
1.86	1.98	0.12	4.05E-01	7.40E-01	---	---	---	241188_at	---
2.73	2.86	0.13	4.05E-01	7.40E-01	HIST1H2BN	histone cluster 1, H2bn	chr6p22-p21.3	207226_at	NM_003520
6.68	6.96	0.28	4.05E-01	7.40E-01	MCAM	melanoma cell adhesion molecule	chr11q23.3	211340_s_at	NM_006500
3.09	3.25	0.16	4.05E-01	7.40E-01	ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	chr6p21.3	214762_at	NM_130463 /// NM_138282
2.99	3.13	0.14	4.05E-01	7.40E-01	INS	insulin	chr11p15.5	206598_at	NM_000207
2.34	2.46	0.12	4.05E-01	7.40E-01	TP63	tumor protein p63	chr3q28	211195_s_at	NM_001114978 /// NM_001114979 /// NM_001114980 /// NM_001114981 /// NM_001114982 /// NM_003722
1.91	2.02	0.11	4.05E-01	7.40E-01	---	---	---	232817_at	---
5.21	5.55	0.34	4.05E-01	7.40E-01	FYN	FYN oncogene related to SRC, FGR, YES	chr6q21	210105_s_at	NM_002037 /// NM_153047 /// NM_153048
1.90	1.99	0.09	4.05E-01	7.40E-01	---	---	---	242401_x_at	---
2.53	2.67	0.14	4.05E-01	7.40E-01	---	---	---	236552_at	---
3.39	3.55	0.16	4.05E-01	7.40E-01	PGLYRP1	peptidoglycan recognition protein 1	chr19q13.2-q13.3	207384_at	NM_005091
2.42	2.53	0.11	4.05E-01	7.40E-01	CD160	CD160 molecule	chr1q21.1	207840_at	NM_007053
2.10	2.22	0.13	4.05E-01	7.40E-01	C18orf2	chromosome 18 open reading frame 2	---	224045_x_at	NM_031416 /// NR_023925 /// NR_023926 /// NR_023927 /// NR_023928
6.11	6.42	0.31	4.05E-01	7.40E-01	SLMO2	slowmo homolog 2 (Drosophila)	chr20q13.32	222441_x_at	NM_016045
5.15	5.24	0.09	4.05E-01	7.40E-01	CPM	Carboxypeptidase M	chr12q14.3	217557_s_at	NM_001005502 /// NM_001874 /// NM_198320
7.48	7.78	0.30	4.05E-01	7.40E-01	MEF2C	myocyte enhancer factor 2C	chr5q14	209199_s_at	NM_001131005 /// NM_002397
2.48	2.60	0.13	4.05E-01	7.40E-01	KIAA0892	KIAA0892	chr19p13.11	217652_at	NM_015329
1.86	1.96	0.09	4.05E-01	7.40E-01	---	---	---	230344_x_at	---
2.22	2.36	0.14	4.05E-01	7.40E-01	SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10	chr18q21.3	214539_at	NM_005024
7.73	8.25	0.52	4.06E-01	7.40E-01	EGR1	early growth response 1	chr5q31.1	201693_s_at	NM_001964
5.78	6.07	0.29	4.06E-01	7.40E-01	CHMP2B	chromatin modifying protein 2B	chr3p11.2	202538_s_at	NM_014043
3.44	3.66	0.22	4.06E-01	7.40E-01	CA12	carbonic anhydrase XII	chr15q22	214164_x_at	NM_001218 /// NM_206925
2.23	2.36	0.13	4.06E-01	7.40E-01	ETV1	ets variant gene 1	chr7p21.3	221910_at	NM_004956
1.82	1.91	0.09	4.06E-01	7.40E-01	---	---	---	1569981_at	---
5.44	5.72	0.28	4.06E-01	7.40E-01	NAV1	neuron navigator 1	chr1q32.3	224772_at	NM_020443
2.91	3.03	0.13	4.06E-01	7.41E-01	C12orf72	chromosome 12 open reading frame 72	chr12p11.21	1569792_a_at	NM_173802
2.95	3.11	0.15	4.06E-01	7.41E-01	---	---	---	238888_at	---
2.14	2.27	0.14	4.06E-01	7.41E-01	ABBA-1	actin-bundling protein with BAIAP2 homology	chr16q22.1	1556175_at	NM_138383
1.79	1.89	0.11	4.06E-01	7.41E-01	CCDC52	coiled-coil domain containing 52	chr3q13.2	215094_at	NM_144718

1.89	1.97	0.08	4.06E-01	7.41E-01	---	---	---	228502_at	---
6.01	6.18	0.18	4.06E-01	7.41E-01	ZNF548	zinc finger protein 548	chr19q13.43	1553718_at	NM_152909
4.69	4.77	0.08	4.06E-01	7.41E-01	LOC647070	hypothetical LOC647070	chr1q25.3	215467_x_at	XR_041237 /// XR_041238 /// XR_041239
3.38	3.64	0.26	4.06E-01	7.41E-01	---	---	---	1563130_a_at	---
2.70	2.88	0.18	4.06E-01	7.41E-01	---	---	---	235632_at	---
4.48	4.86	0.38	4.06E-01	7.41E-01	TRAM1	translocation associated membrane protein 1	chr8q13.3	210733_at	NM_014294 /// XM_001721007 /// XM_001721035 /// XM_001721065
4.59	4.79	0.20	4.06E-01	7.41E-01	CHD6	chromodomain helicase DNA binding protein 6	chr20q12	225031_at	NM_032221
2.88	3.06	0.18	4.06E-01	7.41E-01	FOXD2	forkhead box D2	chr1p34-p32	207653_at	NM_004474
2.62	2.77	0.15	4.06E-01	7.41E-01	C3orf71	chromosome 3 open reading frame 71	chr3p21.31	1559532_at	NM_001123040 /// XM_001724043 /// XM_929378
3.02	3.14	0.12	4.06E-01	7.41E-01	---	---	---	1557751_at	---
1.94	2.04	0.10	4.06E-01	7.41E-01	MYOZ2	myozenin 2	chr4q26-q27	213782_s_at	NM_016599
2.07	2.17	0.09	4.06E-01	7.41E-01	GRHL1	grainyhead-like 1 (Drosophila)	chr2p25.1	222830_at	NM_014552 /// NM_198182
2.89	3.05	0.15	4.06E-01	7.41E-01	LOC441617	Similar to hCG1820409	chr11q13.4	237393_at	XM_001717487 /// XM_497310 /// XM_940231
2.23	2.36	0.13	4.06E-01	7.41E-01	NF1	neurofibromin 1	chr17q11.2	211095_at	NM_000267 /// NM_001042492 /// NM_001128147
5.10	5.40	0.30	4.06E-01	7.41E-01	---	---	---	238652_at	---
2.72	2.87	0.15	4.06E-01	7.41E-01	FAM19A2	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	chr12q14.1	241399_at	NM_178539
4.85	4.97	0.12	4.06E-01	7.41E-01	ICAM1	intercellular adhesion molecule 1	chr19p13.3-p13.2	215485_s_at	NM_000201
2.39	2.50	0.11	4.06E-01	7.41E-01	---	---	---	242486_at	---
5.44	5.59	0.15	4.06E-01	7.41E-01	RARA	retinoic acid receptor, alpha	chr17q21	203750_s_at	NM_000964 /// NM_001024809
2.61	2.74	0.13	4.07E-01	7.41E-01	TRIM10	tripartite motif-containing 10	chr6p21.3	210578_at	NM_006778 /// NM_052828
2.69	2.82	0.13	4.07E-01	7.41E-01	---	---	---	236547_at	---
4.15	4.30	0.15	4.07E-01	7.41E-01	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	chr2q21.3	213530_at	NM_012233
4.09	4.21	0.12	4.07E-01	7.41E-01	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	chr22q11.21	206880_at	NM_005446
2.45	2.56	0.11	4.07E-01	7.41E-01	---	---	---	1570450_at	---
2.08	2.19	0.11	4.07E-01	7.41E-01	---	---	---	238368_at	---
1.95	2.05	0.10	4.07E-01	7.41E-01	---	---	---	240469_at	---
3.47	3.81	0.34	4.07E-01	7.41E-01	SFRS18	splicing factor, arginine/serine-rich 18	chr6q16.3	212177_at	NM_015491 /// NM_032870
1.86	1.96	0.10	4.07E-01	7.41E-01	---	---	---	1569779_at	---
3.84	4.24	0.40	4.07E-01	7.41E-01	USP34	ubiquitin specific peptidase 34	chr2p15	212065_s_at	NM_014709
2.67	2.88	0.21	4.07E-01	7.41E-01	---	---	---	1552867_at	---
2.78	2.91	0.13	4.07E-01	7.41E-01	NPHS1 /// PRODH2	nephrosis 1, congenital, Finnish type (nephrin) /// proline dehydrogenase (oxidase) 2	chr19q13.1	207673_at	NM_004646 /// NM_021232
3.47	3.59	0.12	4.07E-01	7.41E-01	---	---	---	239961_at	---
1.83	1.92	0.09	4.07E-01	7.41E-01	NECAB1	N-terminal EF-hand calcium binding protein 1	chr8q21.3	233305_at	NM_022351
4.25	4.61	0.36	4.07E-01	7.41E-01	GRAMD3	GRAM domain containing 3	chr5q23.2	238049_at	NM_023927
3.24	3.49	0.25	4.07E-01	7.41E-01	KIAA1333	KIAA1333	chr14q12	223255_at	NM_017769
3.15	3.30	0.16	4.07E-01	7.41E-01	SLC22A6	solute carrier family 22 (organic anion transporter), member 6	chr11q13.1-q13.2	216599_x_at	NM_004790 /// NM_153276 /// NM_153277 /// NM_153278
2.60	2.75	0.15	4.07E-01	7.41E-01	KCTD15	Potassium channel tetramerisation domain containing 15	chr19q13.11	229683_s_at	NM_001129994 /// NM_001129995 /// NM_024076
2.69	2.84	0.15	4.07E-01	7.41E-01	S1PR5	sphingosine-1-phosphate receptor 5	chr19p13.2	221417_x_at	NM_030760
2.77	2.91	0.14	4.07E-01	7.41E-01	---	---	---	234069_at	---
2.22	2.35	0.13	4.07E-01	7.41E-01	HNRNPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	chr4q21.1-q21.2	239040_at	NM_001003810 /// NM_002138 /// NM_031369 /// NM_031370

2.54	2.66	0.12	4.07E-01	7.41E-01	RASA3	RAS p21 protein activator 3	chr13q34	206221_at	NM_007368
2.37	2.49	0.12	4.07E-01	7.41E-01	PASD1	PAS domain containing 1	chrXq28	240687_at	NM_173493
1.98	2.08	0.10	4.07E-01	7.41E-01	C18orf33	chromosome 18 open reading frame 33	chr18q22.3	1563825_at	XM_001714254 /// XM_001721238 /// XM_001721257
2.16	2.27	0.10	4.07E-01	7.41E-01	RGS16	regulator of G-protein signaling 16	chr1q25-q31	242212_at	NM_002928
1.90	1.99	0.09	4.07E-01	7.41E-01	---	---	---	1560373_a_at	---
3.02	3.14	0.12	4.07E-01	7.41E-01	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	chr5q31.1	240846_at	NM_032151
2.71	2.81	0.10	4.07E-01	7.41E-01	---	---	---	232372_at	---
2.29	2.38	0.09	4.07E-01	7.41E-01	---	---	---	242347_at	---
4.99	5.31	0.33	4.08E-01	7.42E-01	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	chr7q32	204423_at	NM_013255
3.36	3.58	0.22	4.08E-01	7.42E-01	TNS1	tensin 1	chr2q35-q36	218863_s_at	NM_022648
6.83	7.00	0.17	4.08E-01	7.42E-01	KPNA1	karyopherin alpha 1 (importin alpha 5)	chr3q21	202059_s_at	NM_002264
3.04	3.20	0.16	4.08E-01	7.42E-01	---	---	---	1557479_at	---
2.13	2.23	0.09	4.08E-01	7.42E-01	GLRA3	glycine receptor, alpha 3	chr4q33-q34	210661_at	NM_001042543 /// NM_006529
8.09	8.39	0.30	4.08E-01	7.42E-01	MAPK1	mitogen-activated protein kinase 1	chr22q11.2|22q11.21	224621_at	NM_002745 /// NM_138957
5.39	5.68	0.29	4.08E-01	7.42E-01	C3orf38	chromosome 3 open reading frame 38	chr3p11.2	226524_at	NM_173824
4.31	4.59	0.27	4.08E-01	7.42E-01	---	---	---	227663_at	---
2.70	2.87	0.16	4.08E-01	7.42E-01	---	---	---	1556669_a_at	---
6.24	6.51	0.27	4.08E-01	7.42E-01	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	chr11q23.3	224833_at	NM_005238
3.08	3.26	0.18	4.08E-01	7.42E-01	LOC652637 /// WHDC1L1 /// WHDC1L2	similar to junction-mediating and regulatory protein /// WAS protein homology region 2 domain containing 1-like 1 /// WAS protein homology region 2 domain containing 1-like 2	chr15q11.2 /// chr15q13.1	1557261_at	NR_003521 /// XM_926785 /// XM_942188 /// XR_042166
7.89	8.07	0.19	4.08E-01	7.42E-01	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	chr1p13	201274_at	NM_002790
3.16	3.35	0.19	4.08E-01	7.42E-01	ZNF57	zinc finger protein 57	chr19p13.3	1554628_at	NM_173480
4.04	4.21	0.17	4.08E-01	7.42E-01	C20orf200	Chromosome 20 open reading frame 200	chr20q13.33	1553205_at	NM_152757
2.15	2.26	0.10	4.08E-01	7.42E-01	DEFA5	defensin, alpha 5, Paneth cell-specific	chr8pter-p21	207529_at	NM_021010
4.70	5.03	0.33	4.08E-01	7.42E-01	AKTIP	AKT interacting protein	chr16q12.2	223894_s_at	NM_001012398 /// NM_022476
3.12	3.38	0.26	4.08E-01	7.42E-01	---	---	---	209535_s_at	---
4.47	4.69	0.23	4.08E-01	7.42E-01	CLCN5	chloride channel 5	chrXp11.23-p11.22|Xp11.23	226274_at	NM_000084 /// NM_001127898 /// NM_001127899
4.33	4.53	0.20	4.08E-01	7.42E-01	HFE	hemochromatosis	chr6p21.3	211327_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
5.87	6.00	0.14	4.08E-01	7.42E-01	RNF122	ring finger protein 122	chr8p12	219897_at	NM_024787
2.83	2.94	0.11	4.08E-01	7.42E-01	RAET1E	retinoic acid early transcript 1E	chr6q25.1	1552777_a_at	NM_139165
1.96	2.06	0.10	4.08E-01	7.42E-01	OTX2	orthodenticle homeobox 2	chr14q21-q22	242128_at	NM_021728 /// NM_172337
2.54	2.64	0.09	4.08E-01	7.42E-01	---	---	---	244091_at	---
2.34	2.43	0.09	4.08E-01	7.42E-01	---	---	---	1566642_at	---
7.77	8.26	0.49	4.08E-01	7.42E-01	MRAP	melanocortin 2 receptor accessory protein	chr21q22.1	1555740_a_at	NM_178817 /// NM_206898
7.72	8.13	0.41	4.08E-01	7.42E-01	BCLAF1	BCL2-associated transcription factor 1	chr6q22-q23	201084_s_at	NM_001077440 /// NM_001077441 /// NM_014739
5.44	5.56	0.12	4.08E-01	7.42E-01	DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12	chr10q22.1	214338_at	NM_001002762 /// NM_017626
2.00	2.10	0.10	4.08E-01	7.42E-01	---	---	---	234587_at	---
2.13	2.22	0.09	4.08E-01	7.42E-01	ANKRD34C	ankyrin repeat domain 34C	chr15q25.1	216073_at	XM_001719889 /// XM_930512 /// XM_939324
3.89	4.49	0.59	4.08E-01	7.42E-01	LYZ	lysozyme (renal amyloidosis)	chr12q15	1555745_a_at	NM_000239
1.99	2.12	0.13	4.08E-01	7.42E-01	UNC13C	unc-13 homolog C (C. elegans)	chr15q21.3	1556096_s_at	NM_001080534

3.78	4.15	0.37	4.08E-01	7.42E-01	CUL4B	cullin 4B	chrXq23	210257_x_at	NM_001079872 /// NM_003588
5.54	5.77	0.23	4.08E-01	7.42E-01	LOC100131612 /// MED27	similar to cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa /// mediator complex subunit 27	chr9q34.1-q34.3	221598_s_at	NM_004269 /// XM_001715326
3.62	3.84	0.23	4.08E-01	7.42E-01	---	---	---	1565886_at	---
2.89	3.01	0.12	4.08E-01	7.42E-01	---	---	---	234591_at	---
4.37	4.75	0.37	4.09E-01	7.42E-01	EPB41L3	erythrocyte membrane protein band 4.1-like 3	chr18p11.32	212681_at	NM_012307
5.16	5.49	0.33	4.09E-01	7.42E-01	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	chr4q21.23	205709_s_at	NM_001263
2.44	2.54	0.10	4.09E-01	7.42E-01	WWC1	WW and C2 domain containing 1	chr5q35.1	237238_at	NM_015238
6.79	6.96	0.17	4.09E-01	7.42E-01	FURIN	furin (paired basic amino acid cleaving enzyme)	chr15q26.1	201945_at	NM_002569
2.46	2.60	0.14	4.09E-01	7.42E-01	CYTH4	cytohesin 4	chr22q12.3-q13.1	1554335_at	NM_013385
3.64	3.84	0.20	4.09E-01	7.42E-01	---	---	---	232493_at	---
2.16	2.28	0.12	4.09E-01	7.42E-01	SNAI3	snail homolog 3 (Drosophila)	chr16q24.3	1560228_at	NM_178310
3.74	3.95	0.21	4.09E-01	7.42E-01	GAB1	GRB2-associated binding protein 1	chr4q31.21	229114_at	NM_002039 /// NM_207123
2.74	2.84	0.10	4.09E-01	7.42E-01	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	chr15q26	221285_at	NM_006011
5.25	6.04	0.80	4.09E-01	7.42E-01	SLITRK4	SLIT and NTRK-like family, member 4	chrXq27.3	232636_at	NM_173078
3.74	4.01	0.27	4.09E-01	7.43E-01	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	chr3q24	203921_at	NM_004267
2.14	2.25	0.11	4.09E-01	7.43E-01	ACCN5	amiloride-sensitive cation channel 5, intestinal	chr4q31.3-q32	1564504_at	NM_017419
2.19	2.30	0.10	4.09E-01	7.43E-01	FMO5	flavin containing monooxygenase 5	chr1q21.1	1569688_at	NM_001461
3.04	3.18	0.13	4.09E-01	7.43E-01	MANEAL	Mannosidase, endo-alpha-like	chr1p34.3	231564_at	NM_001031740 /// NM_001113482 /// NM_152496
3.99	4.12	0.13	4.09E-01	7.43E-01	---	---	---	236210_at	---
4.71	4.92	0.21	4.09E-01	7.43E-01	FBXO3	F-box protein 3	chr11p13	238686_at	NM_012175 /// NM_033406
11.30	11.46	0.16	4.09E-01	7.43E-01	RPL11	ribosomal protein L11	chr1p36.1-p35	200010_at	NM_000975
4.35	4.48	0.13	4.09E-01	7.43E-01	---	---	---	230657_at	---
2.68	2.81	0.14	4.09E-01	7.43E-01	KIAA2026	KIAA2026	chr9p24.1	236306_at	NM_001017969
5.46	5.85	0.39	4.09E-01	7.43E-01	WARS2	tryptophanyl tRNA synthetase 2, mitochondrial	chr1p13.3-p13.1	222734_at	NM_015836 /// NM_201263
2.25	2.50	0.25	4.09E-01	7.43E-01	C15orf5	chromosome 15 open reading frame 5	chr15q23-q24	208109_s_at	XR_017877 /// XR_017977 /// XR_041829
6.89	7.13	0.24	4.09E-01	7.43E-01	FOXO3	forkhead box O3	chr6q21	224891_at	NM_001455 /// NM_201559
3.80	3.95	0.16	4.09E-01	7.43E-01	C21orf70 /// LOC729535	chromosome 21 open reading frame 70 /// hypothetical LOC729535	chr13q11 /// chr21q22.3	238703_at	NM_058190 /// XM_001129879 /// XM_001130539 /// XM_001715883
2.09	2.23	0.15	4.09E-01	7.43E-01	CCDC144A	coiled-coil domain containing 144A	chr17p11.2	216045_at	NM_014695
2.78	2.92	0.14	4.09E-01	7.43E-01	---	---	---	244514_at	---
3.40	3.51	0.11	4.09E-01	7.43E-01	GALNTL1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	chr14q24.1	232548_at	NM_020692
2.10	2.22	0.12	4.09E-01	7.43E-01	RPLP2	Ribosomal protein, large, P2	chr11p15.5-p15.4	217670_at	NM_001004
1.99	2.08	0.10	4.09E-01	7.43E-01	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	chr4q21	210738_s_at	NM_001098484 /// NM_001134742 /// NM_003759
3.68	3.90	0.22	4.10E-01	7.43E-01	---	---	---	244674_at	---
4.10	4.31	0.21	4.10E-01	7.43E-01	ZCCHC2	zinc finger, CCHC domain containing 2	chr18q21.33	219062_s_at	NM_017742
4.35	4.53	0.17	4.10E-01	7.43E-01	SCARB2	scavenger receptor class B, member 2	chr4q21.1	215754_at	NM_005506
3.27	3.43	0.16	4.10E-01	7.43E-01	UCN2	urocortin 2	chr3p21.3	232674_at	NM_033199
4.88	5.02	0.14	4.10E-01	7.43E-01	XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	chr7q36.1	207598_x_at	NM_005431
2.31	2.42	0.10	4.10E-01	7.43E-01	---	---	---	241523_at	---
2.80	2.94	0.14	4.10E-01	7.43E-01	---	---	---	1569805_at	---
6.70	6.95	0.25	4.10E-01	7.43E-01	RAB2A	RAB2A, member RAS oncogene family	chr8q12.1	208732_at	NM_002865
2.42	2.54	0.12	4.10E-01	7.43E-01	C18orf25	chromosome 18 open reading frame 25	chr18q21.1	217539_at	NM_001008239 /// NM_145055
1.93	2.04	0.11	4.10E-01	7.43E-01	---	---	---	241685_x_at	---
2.16	2.31	0.15	4.10E-01	7.43E-01	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	chr5q12	228962_at	NM_001104631 /// NM_006203
8.90	9.30	0.40	4.10E-01	7.43E-01	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	chr3p14	200760_s_at	NM_006407

8.32	8.61	0.29	4.10E-01	7.43E-01	SSBP1	single-stranded DNA binding protein 1	chr7q34	202591_s_at	NM_003143
5.07	5.28	0.21	4.10E-01	7.43E-01	STK32C	serine/threonine kinase 32C	chr10q26.3	227634_at	NM_173575
2.11	2.22	0.11	4.10E-01	7.43E-01	---	---	---	241655_at	---
2.29	2.45	0.16	4.10E-01	7.43E-01	LOC100128844	Hypothetical protein LOC100128844	chr9p22.1	229110_at	XM_001722718 /// XM_001722902 /// XM_001725276
2.84	2.95	0.11	4.10E-01	7.43E-01	LOC284240	hypothetical protein LOC284240	chr18q23	233474_at	---
2.34	2.43	0.09	4.10E-01	7.43E-01	CSTL1	cystatin-like 1	chr20p11.21	234803_at	NM_138283
2.37	2.52	0.15	4.10E-01	7.43E-01	---	---	---	236821_at	---
3.33	3.47	0.14	4.10E-01	7.43E-01	GSTCD	glutathione S-transferase, C-terminal domain containing	chr4q24	1554518_at	NM_001031720 /// NM_024751
3.75	3.90	0.15	4.10E-01	7.43E-01	LTK	leukocyte receptor tyrosine kinase	chr15q15.1-q21.1	217184_s_at	NM_002344 /// NM_206961
5.71	5.93	0.22	4.10E-01	7.43E-01	MAP6	microtubule-associated protein 6	chr11q13.5	228943_at	NM_033063 /// NM_207577
2.07	2.17	0.11	4.10E-01	7.43E-01	---	---	---	1561692_at	---
7.93	8.22	0.29	4.10E-01	7.43E-01	SON	SON DNA binding protein	chr21q22.1-q22.2|21q22.11	226465_s_at	NM_032195 /// NM_138927
10.01	10.26	0.25	4.10E-01	7.43E-01	PRDX3	peroxiredoxin 3	chr10q25-q26	201619_at	NM_006793 /// NM_014098
2.80	2.94	0.14	4.10E-01	7.43E-01	CLCN4	chloride channel 4	chrXp22.3	205149_s_at	NM_001830
2.25	2.35	0.09	4.10E-01	7.43E-01	---	---	---	236962_at	---
4.51	4.66	0.15	4.10E-01	7.44E-01	KRT17	keratin 17	chr17q12-q21	212236_x_at	NM_000422
6.92	7.31	0.39	4.11E-01	7.44E-01	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	chr17q24.2	202352_s_at	NM_002816
2.39	2.56	0.17	4.11E-01	7.44E-01	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	chr10q24.3-qter	209976_s_at	NM_000773
4.30	4.76	0.46	4.11E-01	7.44E-01	TUSC3	tumor suppressor candidate 3	chr8p22	209227_at	NM_006765 /// NM_178234
5.63	6.24	0.61	4.11E-01	7.44E-01	---	---	---	232584_at	---
2.00	2.10	0.10	4.11E-01	7.44E-01	IL23A	Enhancer of polycomb homolog 1 (Drosophila)	chr12q13.2	240766_at	NM_016584
7.93	8.08	0.15	4.11E-01	7.44E-01	PDHB	pyruvate dehydrogenase (lipoamide) beta	chr3p21.1-p14.2	208911_s_at	NM_000925
2.59	2.69	0.10	4.11E-01	7.44E-01	---	---	---	1560230_at	---
4.49	4.75	0.26	4.11E-01	7.44E-01	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	chr8q13-q21.1	227179_at	NM_014393
4.96	5.16	0.20	4.11E-01	7.44E-01	RNF216	ring finger protein 216	chr7p22.1	218426_s_at	NM_207111 /// NM_207116
5.62	5.82	0.19	4.11E-01	7.44E-01	EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA-specific	chr3q21.3	227540_at	NM_021937
2.98	3.12	0.14	4.11E-01	7.44E-01	MKI67	antigen identified by monoclonal antibody Ki-67	chr10q25-qter	212023_s_at	NM_002417
4.22	4.39	0.17	4.11E-01	7.44E-01	MCM5	minichromosome maintenance complex component 5	chr22q13.1	201755_at	NM_006739
2.24	2.32	0.08	4.11E-01	7.44E-01	---	---	---	1565825_at	---
2.14	2.25	0.11	4.11E-01	7.44E-01	---	---	---	239372_at	---
4.18	4.32	0.13	4.11E-01	7.44E-01	PCDHB13	protocadherin beta 13	chr5q31	221450_x_at	NM_018933
2.13	2.26	0.12	4.11E-01	7.44E-01	---	---	---	1563246_at	---
1.93	2.05	0.12	4.11E-01	7.44E-01	VENTXP1	VENT homeobox (Xenopus laevis) pseudogene 1	chrXp21.3	216722_at	NR_001559 /// XR_042160
1.86	1.96	0.09	4.11E-01	7.44E-01	FLJ40330 /// LOC730272	hypothetical LOC645784 /// similar to protein immuno-reactive with anti-PTH polyclonal antibodies	chr2p11.2	1569040_s_at	XR_015919 /// XR_041839 /// XR_041840 /// XR_041841
2.15	2.28	0.13	4.11E-01	7.44E-01	---	---	---	215392_at	---
4.09	4.75	0.66	4.11E-01	7.44E-01	XIST	X (inactive)-specific transcript (non-protein coding)	chrXq13.2	224589_at	NR_001564
2.70	2.88	0.18	4.11E-01	7.44E-01	---	---	---	1563473_at	---
6.97	7.14	0.17	4.11E-01	7.44E-01	CHD4	chromodomain helicase DNA binding protein 4	chr12p13	201183_s_at	NM_001273
3.15	3.29	0.14	4.11E-01	7.44E-01	SHANK1	SH3 and multiple ankyrin repeat domains 1	chr19q13.3	220563_s_at	NM_016148
2.04	2.16	0.12	4.11E-01	7.44E-01	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	215339_at	NM_005385
2.30	2.43	0.13	4.11E-01	7.44E-01	CXADRP1	coxsackie virus and adenovirus receptor pseudogene 1	chr21q11.2	239155_at	XR_016129 /// XR_038605
3.90	4.34	0.44	4.11E-01	7.44E-01	MGC39372	hypothetical protein MGC39372	chr6p25.2	239186_at	XM_001714336 /// XM_001718089 /// XM_001724093
5.41	5.65	0.23	4.11E-01	7.44E-01	RCHY1	ring finger and CHY zinc finger domain containing 1	chr4q21.1	214281_s_at	NM_001008925 /// NM_001009922 /// NM_015436
5.19	5.39	0.20	4.11E-01	7.44E-01	---	---	---	242021_at	---

11.67	11.87	0.20	4.11E-01	7.44E-01	NACA	nascent polypeptide-associated complex alpha subunit	chr12q23-q24.1	208635_x_at	NM_001113201 /// NM_001113202 /// NM_001113203 /// NM_005594
8.88	9.48	0.60	4.12E-01	7.44E-01	SLC38A2	solute carrier family 38, member 2	chr12q	218041_x_at	NM_018976
4.26	4.56	0.30	4.12E-01	7.44E-01	LRRC8C	leucine rich repeat containing 8 family, member C	chr1p22.2	1558517_s_at	NM_032270
4.25	4.49	0.24	4.12E-01	7.44E-01	---	---	---	235983_at	---
2.97	3.08	0.11	4.12E-01	7.44E-01	PPP1R2P9	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9	chrXp11.4-p11.3	207377_at	NR_002191
2.05	2.15	0.10	4.12E-01	7.44E-01	---	---	---	239862_at	---
1.96	2.06	0.10	4.12E-01	7.44E-01	---	---	---	1557883_a_at	---
2.00	2.09	0.09	4.12E-01	7.44E-01	FLJ39005	hypothetical protein FLJ39005	chr19q13.43	1560756_at	XR_041412 /// XR_041413 /// XR_041414
3.54	4.09	0.55	4.12E-01	7.44E-01	MYOM1	myomesin 1, 185kDa	chr18p11.31	205610_at	NM_003803 /// NM_019856
5.57	5.90	0.33	4.12E-01	7.44E-01	SLC4A1AP	solute carrier family 4 (anion exchanger), member 1, adaptor protein	chr2p23.2	218682_s_at	NM_018158
5.85	6.15	0.30	4.12E-01	7.44E-01	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	chr1p31.1	209707_at	NM_005482
2.93	3.05	0.12	4.12E-01	7.44E-01	---	---	---	236483_at	---
1.85	1.96	0.12	4.12E-01	7.44E-01	FAM124A	family with sequence similarity 124A	chr13q14.3	241829_at	NM_145019
4.99	5.17	0.19	4.12E-01	7.45E-01	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	chr16p13.1	202805_s_at	NM_004996 /// NM_019862 /// NM_019898 /// NM_019899 /// NM_019900
2.11	2.23	0.12	4.12E-01	7.45E-01	ZNF844	zinc finger protein 844	chr19p13.2	1558537_x_at	XR_015205 /// XR_015644 /// XR_041446
2.15	2.28	0.13	4.12E-01	7.45E-01	RNF157	Ring finger protein 157	chr17q25.1	230776_at	NM_052916
2.18	2.30	0.12	4.12E-01	7.45E-01	LOC613266	hypothetical LOC613266	chr20p12.1	1559459_at	NM_001033516
2.05	2.17	0.12	4.12E-01	7.45E-01	TMEM67	transmembrane protein 67	chr8q22.1	1552763_at	NM_153704
5.24	5.43	0.19	4.12E-01	7.45E-01	MTSS1	metastasis suppressor 1	chr8p22	203036_s_at	NM_014751
2.82	3.00	0.18	4.12E-01	7.45E-01	EP400	E1A binding protein p400	chr12q24.33	230629_s_at	NM_015409
3.75	3.91	0.16	4.12E-01	7.45E-01	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	chr18q23	224538_s_at	NM_032510
5.04	5.19	0.15	4.12E-01	7.45E-01	HTRA3	HtrA serine peptidase 3	chr4p16.1	226944_at	NM_053044
2.01	2.12	0.11	4.12E-01	7.45E-01	SOX30	SRY (sex determining region Y)-box 30	chr5q33	207678_s_at	NM_007017 /// NM_178424
2.61	2.72	0.11	4.12E-01	7.45E-01	---	---	---	231627_at	---
2.59	2.76	0.17	4.12E-01	7.45E-01	SCML4	sex comb on midleg-like 4 (Drosophila)	chr6q21	1556471_at	NM_198081
7.77	7.92	0.15	4.12E-01	7.45E-01	---	---	---	224653_at	---
1.95	2.07	0.11	4.12E-01	7.45E-01	---	---	---	1563116_at	---
3.85	4.02	0.17	4.13E-01	7.45E-01	---	---	---	1559715_at	---
2.70	2.82	0.12	4.13E-01	7.45E-01	---	---	---	234642_at	---
7.28	7.70	0.42	4.13E-01	7.45E-01	COPB1	coatomer protein complex, subunit beta 1	chr11p15.2	201359_at	NM_016451
3.39	3.56	0.17	4.13E-01	7.45E-01	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	chr13q12.12|13q12.1-q12.3	207367_at	NM_001676
2.21	2.35	0.14	4.13E-01	7.45E-01	---	---	---	1565896_at	---
1.85	1.96	0.11	4.13E-01	7.45E-01	LOC541471	Hypothetical LOC541471	chr2q13	1562876_s_at	XR_039885 /// XR_039886
2.37	2.48	0.11	4.13E-01	7.45E-01	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	chr5q31.1	1555247_a_at	NM_016340
3.20	3.33	0.13	4.13E-01	7.45E-01	LOC100129015	hypothetical protein LOC100129015	chr9q34.3	221936_x_at	XM_001715056 /// XM_001716341 /// XM_001716632
4.05	4.34	0.29	4.13E-01	7.45E-01	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	chr9p22	204918_s_at	NM_004529
4.28	4.41	0.13	4.13E-01	7.45E-01	MLX	MAX-like protein X	chr17q21.1	210752_s_at	NM_170607 /// NM_198204 /// NM_198205
2.64	2.76	0.12	4.13E-01	7.45E-01	---	---	---	1561091_at	---
2.23	2.35	0.11	4.13E-01	7.45E-01	SSH2	slingshot homolog 2 (Drosophila)	chr17q11.2	1555425_x_at	NM_033389
2.34	2.44	0.11	4.13E-01	7.45E-01	LOC200830	hypothetical protein LOC200830	chr3q26.1	1556898_at	---
3.28	3.44	0.15	4.13E-01	7.46E-01	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	chr20q12	216183_at	NM_004613 /// NM_198951
4.22	4.61	0.39	4.13E-01	7.46E-01	RABEP1	rabaptin, RAB GTPase binding effector protein 1	chr17p13.2	214552_s_at	NM_001083585 /// NM_004703
1.74	1.85	0.11	4.13E-01	7.46E-01	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	chr4q13.3	1553266_at	NM_144571
2.48	2.60	0.12	4.13E-01	7.46E-01	DDI1	DDI1, DNA-damage inducible 1, homolog 1 (S. cerevisiae)	chr11q22.3	239299_at	NM_001001711
5.31	5.47	0.16	4.13E-01	7.46E-01	KLF16	Kruppel-like factor 16	chr19p13.3	226328_at	NM_031918

3.82	3.97	0.15	4.13E-01	7.46E-01	NRF1	nuclear respiratory factor 1	chr7q32	211279_at	NM_001040110 /// NM_005011
3.20	3.33	0.13	4.13E-01	7.46E-01	---	---	---	242232_at	---
2.76	2.88	0.13	4.13E-01	7.46E-01	---	---	---	240515_at	---
2.54	2.66	0.12	4.13E-01	7.46E-01	TMEM206	transmembrane protein 206	chr1q32.3	218814_s_at	NM_018252
2.14	2.25	0.11	4.13E-01	7.46E-01	---	---	---	222300_at	---
5.84	6.09	0.24	4.13E-01	7.46E-01	NFX1	nuclear transcription factor, X-box binding 1	chr9p13.3	1553103_at	NM_002504 /// NM_147133 /// NM_147134
7.39	7.56	0.17	4.13E-01	7.46E-01	TRIAP1	TP53 regulated inhibitor of apoptosis 1	chr12q24.31	218403_at	NM_016399
2.32	2.46	0.14	4.14E-01	7.46E-01	APOB	apolipoprotein B (including Ag(x) antigen)	chr2p24-p23	223579_s_at	NM_000384
3.18	3.31	0.13	4.14E-01	7.46E-01	VPS45	vacuolar protein sorting 45 homolog (S. cerevisiae)	chr1q21.2	207967_at	NM_007259
3.07	3.20	0.14	4.14E-01	7.46E-01	---	---	---	242879_x_at	---
5.40	5.52	0.12	4.14E-01	7.46E-01	PAWR	PRKC, apoptosis, WT1, regulator	chr12q21	214237_x_at	NM_002583
2.34	2.46	0.12	4.14E-01	7.46E-01	---	---	---	237394_at	---
2.01	2.10	0.09	4.14E-01	7.46E-01	---	---	---	224116_at	---
7.25	7.62	0.37	4.14E-01	7.46E-01	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	chr16q13-q21	201069_at	NM_001127891 /// NM_004530
5.78	5.88	0.10	4.14E-01	7.46E-01	PFDN4	prefoldin subunit 4	chr20q13.2	205362_s_at	NM_002623
1.94	2.05	0.10	4.14E-01	7.46E-01	PTPRM	protein tyrosine phosphatase, receptor type, M	chr18p11.2	1555578_at	NM_001105244 /// NM_002845
4.93	5.08	0.15	4.14E-01	7.46E-01	SIX5	SIX homeobox 5	chr19q13.32	217661_x_at	NM_175875
7.89	8.63	0.74	4.14E-01	7.46E-01	COL1A1	collagen, type I, alpha 1	chr17q21.33	1556499_s_at	NM_000088
7.50	7.80	0.30	4.14E-01	7.46E-01	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	chr16q23	225771_at	NM_001030007 /// NM_001128
3.03	3.26	0.22	4.14E-01	7.46E-01	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	chr4q34.2	218817_at	NM_021928
2.80	2.99	0.19	4.14E-01	7.46E-01	---	---	---	1561574_at	---
1.95	2.11	0.16	4.14E-01	7.46E-01	DPPA3 /// STELLAR	developmental pluripotency associated 3 /// germ and embryonic stem cell enriched protein STELLA	chr12p13.31 /// chr14q13.3	231385_at	NM_199286 /// XR_017793 /// XR_017914 /// XR_041310
2.66	2.82	0.16	4.14E-01	7.46E-01	---	---	---	237525_at	---
2.59	2.71	0.12	4.14E-01	7.46E-01	LOC100132388	hypothetical protein LOC100132388	chr17q21.33	224241_s_at	XM_001723316 /// XM_001725330 /// XM_001726621
4.86	5.39	0.53	4.14E-01	7.46E-01	RIOK3	RIO kinase 3 (yeast)	chr18q11.2	202129_s_at	NM_003831
3.17	3.31	0.14	4.14E-01	7.46E-01	---	---	---	243510_at	---
2.05	2.16	0.10	4.14E-01	7.46E-01	---	---	---	1556749_at	---
2.42	2.52	0.11	4.14E-01	7.46E-01	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	chr22q12|7p14.3-p14.1	209956_s_at	NM_001220 /// NM_172078 /// NM_172079 /// NM_172080 /// NM_172081 /// NM_172082 /// NM_172083 /// NM_172084
6.65	6.77	0.11	4.14E-01	7.46E-01	ERN2	endoplasmic reticulum to nucleus signaling 2	chr16p12.2	214372_x_at	NM_033266
4.50	4.76	0.26	4.14E-01	7.46E-01	ENDOD1	endonuclease domain containing 1	chr11q21	212570_at	NM_015036
6.06	6.43	0.37	4.14E-01	7.46E-01	PPP6C	protein phosphatase 6, catalytic subunit	chr9q33.3	225429_at	NM_001123355 /// NM_001123369 /// NM_002721
2.58	2.70	0.12	4.14E-01	7.46E-01	ATP13A4	ATPase type 13A4	chr3q29	233535_at	NM_032279
2.79	2.90	0.11	4.14E-01	7.46E-01	---	---	---	243097_x_at	---
2.33	2.47	0.14	4.15E-01	7.46E-01	KIAA1609	KIAA1609	chr16q24.1	233423_at	NM_020947
4.03	4.16	0.13	4.15E-01	7.46E-01	LOC284385	hypothetical protein LOC284385	chr19p13.2	1557114_a_at	---
2.81	2.93	0.13	4.15E-01	7.46E-01	---	---	---	1561668_at	---
4.15	4.48	0.33	4.15E-01	7.46E-01	SDC2	syndecan 2	chr8q22-q23	212154_at	NM_002998
2.06	2.16	0.10	4.15E-01	7.46E-01	---	---	---	1569403_at	---
2.51	2.64	0.14	4.15E-01	7.46E-01	AFF2	AF4/FMR2 family, member 2	chrXq28	216364_s_at	NM_002025
6.23	6.39	0.16	4.15E-01	7.46E-01	EML2	echinoderm microtubule associated protein like 2	chr19q13.32	204398_s_at	NM_012155
6.27	6.58	0.31	4.15E-01	7.46E-01	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	chr13q14.3	224309_s_at	NM_001130912 /// NM_006704
2.41	2.57	0.16	4.15E-01	7.47E-01	---	---	---	1561000_at	---
2.07	2.20	0.13	4.15E-01	7.47E-01	---	---	---	1561560_at	---
5.18	5.30	0.12	4.15E-01	7.47E-01	FAM101A	family with sequence similarity 101, member A	chr12q24.31	227320_at	NM_181709
2.34	2.44	0.10	4.15E-01	7.47E-01	---	---	---	1562938_at	---
6.70	6.91	0.20	4.15E-01	7.47E-01	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	chr6q24-q25	205202_at	NM_005389

2.47	2.65	0.17	4.15E-01	7.47E-01	MAPK8IP3	Mitogen-activated protein kinase 8 interacting protein 3	chr16p13.3	230162_s_at	NM_001040439 /// NM_015133																					
3.02	3.19	0.17	4.15E-01	7.47E-01	FOXK1	forkhead box K1	chr7p22.1	230342_at	NM_001037165																					
2.56	2.71	0.15	4.15E-01	7.47E-01	FLJ42957	FLJ42957 protein	chr12q24.22	237591_at	NM_207436																					
6.07	6.20	0.14	4.15E-01	7.47E-01	NEU4	sialidase 4	chr2q37.3	222957_at	NM_080741																					
2.31	2.45	0.13	4.15E-01	7.47E-01	---	---	---	239312_at	---																					
2.02	2.13	0.11	4.15E-01	7.47E-01	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	chr11q21-q22.1	1561939_at	NM_001080463																					
5.68	6.00	0.32	4.15E-01	7.47E-01	ARFIP1	ADP-ribosylation factor interacting protein 1	chr4q31.3	218230_at	NM_001025593 /// NM_001025595 /// NM_014447																					
3.30	3.41	0.11	4.15E-01	7.47E-01	EPS8L3	EPS8-like 3	chr1p13.3	219404_at	NM_024526 /// NM_133181 /// NM_139053																					
2.19	2.30	0.11	4.15E-01	7.47E-01	LOC652993	hypothetical LOC652993	chr12q21	1556730_at	XR_018000 /// XR_042076																					
4.42	4.78	0.37	4.15E-01	7.47E-01	THOC2	THO complex 2	chrXq25-q26.3	212994_at	NM_001081550 /// NM_020449																					
3.24	3.38	0.14	4.15E-01	7.47E-01	GALK1	Galactokinase 1	chr17q24	229458_s_at	NM_000154																					
3.99	4.14	0.15	4.15E-01	7.47E-01	LOC646982	TTL/TEL fusion protein TTL-T	chr13q14.11	233432_at	XM_929953 /// XM_941294																					
2.11	2.23	0.13	4.15E-01	7.47E-01	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	chr4q11-q13	211533_at	NM_006206																					
4.14	4.47	0.33	4.15E-01	7.47E-01	PEX1	peroxisomal biogenesis factor 1	chr7q21.2	215023_s_at	NM_000466																					
3.34	3.53	0.18	4.15E-01	7.47E-01	---	---	---	236869_at	---																					
5.66	5.93	0.27	4.15E-01	7.47E-01	NIPBL	Nipped-B homolog (Drosophila)	chr5p13.2	212469_at	NM_015384 /// NM_133433																					
2.03	2.13	0.10	4.15E-01	7.47E-01	FLJ38576	hypothetical LOC651430	chr4q35.2	1559441_s_at	XM_001127939 /// XM_001723997 /// XM_940582																					
2.68	2.80	0.12	4.15E-01	7.47E-01	---	---	---	1566032_at	---																					
3.70	3.98	0.28	4.15E-01	7.47E-01	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	chr9q21.11	235484_at	NM_001099666																					
2.38	2.48	0.10	4.15E-01	7.47E-01	SIX6	SIX homeobox 6	chr14q22.3-q23	207250_at	NM_007374																					
2.90	3.11	0.21	4.16E-01	7.47E-01	GAS2L3	Growth arrest-specific 2 like 3	chr12q23.1	238756_at	NM_174942																					
2.30	2.42	0.12	4.16E-01	7.47E-01	FXR1	Fragile X mental retardation, autosomal homolog 1	chr3q28	1569171_a_at	NM_001013438 /// NM_001013439 /// NM_005087																					
5.22	5.38	0.17	4.16E-01	7.47E-01	EXTL3	exostoses (multiple)-like 3	chr8p21	209202_s_at	NM_001440																					
3.23	3.34	0.11	4.16E-01	7.47E-01	WWOX	WW domain containing oxidoreductase	chr16q23.3-q24.1	221147_x_at	NM_016373 /// NM_130791 /// NM_130844																					
2.01	2.13	0.11	4.16E-01	7.47E-01	TPH2	tryptophan hydroxylase 2	chr12q21.1	1555332_at	NM_173353																					
3.90	4.08	0.18	4.16E-01	7.47E-01	---	---	---	241997_at	---																					
4.31	4.47	0.16	4.16E-01	7.47E-01	GEFT /// SLC26A10	RhoA/RAC/CDC42 exchange factor /// solute carrier family 26, member 10	chr12q13 /// chr12q13.3	227427_at	NM_001111270 /// NM_133489 /// NM_182947																					
2.97	3.11	0.14	4.16E-01	7.47E-01	CCL28	chemokine (C-C motif) ligand 28	chr5p12	224240_s_at	NM_148672																					
2.31	2.41	0.09	4.16E-01	7.47E-01	---	---	---	240096_at	---																					
4.94	5.42	0.48	4.16E-01	7.47E-01	---	---	---	243495_s_at	---																					
3.66	3.96	0.30	4.16E-01	7.47E-01	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	chr12q13.2	205478_at	NM_006741																					
4.87	5.06	0.18	4.16E-01	7.47E-01	POMC	proopiomelanocortin	chr2p23.3	205720_at	NM_000939 /// NM_001035256																					
3.29	3.47	0.17	4.16E-01	7.47E-01	SHROOM1	Shroom family member 1	chr5q31.1	235140_at	NM_133456																					
2.76	2.93	0.17	4.16E-01	7.47E-01	MMP26	matrix metallopeptidase 26	chr11p15	220541_at	NM_021801																					
2.39	2.53	0.15	4.16E-01	7.47E-01	---	---	---	1560812_at	---																					
2.73	2.84	0.11	4.16E-01	7.47E-01	---	---	---	232465_at	---																					
2.48	2.62	0.14	4.16E-01	7.47E-01	MOGAT2	monoacylglycerol O-acyltransferase 2	chr11q13.5	232428_at	NM_025098																					

2.33	2.48	0.15	4.16E-01	7.47E-01	FLJ41278 /// TBC1D30	hypothetical gene supported by AK123272 /// TBC1 domain family, member 30	chr12q14.3	213912_at	XM_001129851 /// XM_001133877 /// XM_001716833 /// XM_001723805 /// XM_037557 /// XM_939476
3.86	4.02	0.16	4.16E-01	7.47E-01	CCDC103	coiled-coil domain containing 103	chr17q21.31	228300_at	NM_213607
2.11	2.19	0.09	4.16E-01	7.47E-01	---	---	---	243348_at	---
3.32	3.75	0.43	4.16E-01	7.47E-01	---	---	---	240861_at	---
5.35	5.59	0.24	4.16E-01	7.47E-01	---	---	---	242696_at	---
6.09	6.26	0.17	4.16E-01	7.47E-01	RARG	retinoic acid receptor, gamma	chr12q13	204189_at	NM_000966 /// NM_001042728
1.88	1.99	0.11	4.16E-01	7.47E-01	FLJ38379	hypothetical protein FLJ38379	chr2q37.3	1556473_at	XR_015732 /// XR_017906 /// XR_040034
4.47	5.00	0.54	4.16E-01	7.47E-01	---	---	---	232472_at	---
4.67	5.19	0.51	4.16E-01	7.47E-01	PTPN11	protein tyrosine phosphatase, non-receptor type 11	chr12q24	209895_at	NM_002834
4.09	4.27	0.17	4.16E-01	7.47E-01	TNRC6C	trinucleotide repeat containing 6C	chr17q25.3	222820_at	NM_018996
3.71	3.86	0.15	4.16E-01	7.47E-01	---	---	---	242167_at	---
3.46	3.85	0.39	4.16E-01	7.48E-01	---	---	---	1558397_at	---
3.00	3.36	0.36	4.16E-01	7.48E-01	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	chr21q21.3	229357_at	NM_007038
2.91	3.07	0.16	4.16E-01	7.48E-01	---	---	---	1566870_at	---
3.39	3.54	0.15	4.16E-01	7.48E-01	CETN1	centrin, EF-hand protein, 1	chr18p11.32	207209_at	NM_004066
2.37	2.49	0.12	4.16E-01	7.48E-01	---	---	---	221183_at	---
2.20	2.32	0.12	4.16E-01	7.48E-01	ANKRD18A	ankyrin repeat domain 18A	chr9p13.1	1559406_at	XM_001713970 /// XM_001717620 /// XM_001726105
3.91	4.04	0.13	4.17E-01	7.48E-01	SSH1	slingshot homolog 1 (Drosophila)	chr12q24.11	1554274_a_at	NM_018984
3.04	3.15	0.11	4.17E-01	7.48E-01	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	chr2p13.1	208124_s_at	NM_004263
1.99	2.09	0.10	4.17E-01	7.48E-01	---	---	---	242564_at	---
2.39	2.49	0.10	4.17E-01	7.48E-01	---	---	---	1561078_at	---
2.04	2.13	0.08	4.17E-01	7.48E-01	---	---	---	1562069_at	---
3.75	3.93	0.18	4.17E-01	7.48E-01	CASP10	caspase 10, apoptosis-related cysteine peptidase	chr2q33-q34	210708_x_at	NM_001230 /// NM_032974 /// NM_032977
2.14	2.24	0.10	4.17E-01	7.48E-01	GFM1	G elongation factor, mitochondrial 1	chr3q25.1-q26.2	220903_at	NM_024996
3.95	4.27	0.32	4.17E-01	7.48E-01	TRIM23	tripartite motif-containing 23	chr5q12.3	210994_x_at	NM_001656 /// NM_033227 /// NM_033228
2.91	3.03	0.12	4.17E-01	7.48E-01	MCPH1	microcephalin 1	chr8p23.1	1557347_at	NM_024596
5.48	5.98	0.50	4.17E-01	7.48E-01	SYTL2	synaptotagmin-like 2	chr11q14	225496_s_at	NM_032379 /// NM_032943 /// NM_206927 /// NM_206928 /// NM_206929 /// NM_206930
2.84	2.96	0.12	4.17E-01	7.48E-01	---	---	---	244658_at	---
2.20	2.32	0.12	4.17E-01	7.48E-01	---	---	---	243740_at	---
2.23	2.32	0.09	4.17E-01	7.48E-01	LRRC16A	leucine rich repeat containing 16A	chr6p22.2	1558931_at	NM_017640
7.69	7.86	0.16	4.17E-01	7.48E-01	ARL2BP	ADP-ribosylation factor-like 2 binding protein	chr16q13	202092_s_at	NM_012106
2.89	3.06	0.18	4.17E-01	7.48E-01	PNPLA3	patatin-like phospholipase domain containing 3	chr22q13.31	220675_s_at	NM_025225
3.08	3.17	0.09	4.17E-01	7.48E-01	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	chr1q32.1	216546_s_at	NM_001276
2.19	2.31	0.12	4.17E-01	7.48E-01	TPH1	tryptophan hydroxylase 1	chr11p15.3-p14	1553859_at	NM_004179
2.35	2.46	0.12	4.17E-01	7.48E-01	---	---	---	232454_at	---
2.91	3.01	0.11	4.17E-01	7.48E-01	---	---	---	239868_at	---
4.32	4.56	0.24	4.17E-01	7.48E-01	CD40	CD40 molecule, TNF receptor superfamily member 5	chr20q12-q13.2	215346_at	NM_001250 /// NM_152854

2.04	2.14	0.10	4.18E-01	7.48E-01	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	chr6p24	204654_s_at	NM_001032280 /// NM_001042425 /// NM_003220
2.53	2.63	0.10	4.18E-01	7.48E-01	RNF183	ring finger protein 183	chr9q32	235153_at	NM_145051
2.49	2.64	0.15	4.18E-01	7.49E-01	---	---	---	1569219_at	---
2.12	2.25	0.13	4.18E-01	7.49E-01	---	---	---	235267_at	---
1.96	2.04	0.09	4.18E-01	7.49E-01	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	chr19q13.2	206198_s_at	NM_006890
3.33	3.52	0.19	4.18E-01	7.49E-01	TCF7	transcription factor 7 (T-cell specific, HMG-box)	chr5q31.1	205254_x_at	NM_003202 /// NM_201632 /// NM_201633 /// NM_201634 /// NM_213648
2.31	2.42	0.12	4.18E-01	7.49E-01	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	chr9q32	221085_at	NM_005118
6.36	6.63	0.27	4.18E-01	7.49E-01	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	chr6p25-p24|18q21	210153_s_at	NM_002396
2.83	2.97	0.14	4.18E-01	7.49E-01	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	chr9q21.11	243995_at	NM_001099666
2.53	2.72	0.20	4.18E-01	7.49E-01	DIRAS1	DIRAS family, GTP-binding RAS-like 1	chr19p13.3	232854_at	NM_145173
1.96	2.06	0.10	4.18E-01	7.49E-01	---	---	---	240160_x_at	---
3.50	3.60	0.10	4.18E-01	7.49E-01	MGC45800	hypothetical protein LOC90768	chr4q35.1	232446_at	XR_017780 /// XR_039902 /// XR_039903
5.86	6.10	0.24	4.18E-01	7.49E-01	PTPRCAP	protein tyrosine phosphatase, receptor type, C-associated protein	chr11q13.3	204960_at	NM_005608
3.24	3.38	0.14	4.18E-01	7.49E-01	PTGES	prostaglandin E synthase	chr9q34.3	210367_s_at	NM_004878
3.03	3.15	0.12	4.18E-01	7.49E-01	C21orf9	chromosome 21 open reading frame 9	chr21q22.11	1554203_at	XR_041044 /// XR_041045 /// XR_041046
2.07	2.16	0.09	4.18E-01	7.49E-01	LOC285708	hypothetical protein LOC285708	chr5q21.2	1564282_a_at	---
2.18	2.31	0.13	4.18E-01	7.49E-01	NCRNA00051	non-protein coding RNA 51	chr8q24.3	1554976_a_at	---
3.42	3.68	0.26	4.18E-01	7.49E-01	---	---	---	222315_at	---
5.07	5.30	0.23	4.18E-01	7.49E-01	BTBD7	BTB (POZ) domain containing 7	chr14q32.12-q32.13	224945_at	NM_001002860 /// NM_018167
2.45	2.59	0.14	4.18E-01	7.49E-01	KNCN	kinocilin	chr1p33	1564044_at	NM_001097611
9.02	9.23	0.20	4.18E-01	7.49E-01	CD164	CD164 molecule, sialomucin	chr6q21	208405_s_at	NM_006016
4.68	5.05	0.37	4.19E-01	7.49E-01	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	chr1p13.2	202647_s_at	NM_002524
4.38	4.71	0.33	4.19E-01	7.49E-01	GRB10	growth factor receptor-bound protein 10	chr7p12-p11.2	209410_s_at	NM_001001549 /// NM_001001550 /// NM_001001555 /// NM_005311
2.35	2.47	0.12	4.19E-01	7.49E-01	---	---	---	1564933_at	---
3.74	3.94	0.19	4.19E-01	7.49E-01	JMJD6	jumonji domain containing 6	chr17q25	215233_at	NM_001081461 /// NM_015167
3.37	3.52	0.15	4.19E-01	7.49E-01	---	---	---	226138_s_at	---
4.98	5.13	0.15	4.19E-01	7.49E-01	SPHK2	sphingosine kinase 2	chr19q13.2	209857_s_at	NM_020126
2.11	2.21	0.10	4.19E-01	7.49E-01	PCDH7	protocadherin 7	chr4p15	205535_s_at	NM_002589 /// NM_032456 /// NM_032457
2.43	2.53	0.09	4.19E-01	7.49E-01	FLJ34651	hypothetical protein LOC646023	chr22q11.23	239513_at	XR_041159 /// XR_041160 /// XR_041161
3.10	3.33	0.23	4.19E-01	7.50E-01	---	---	---	1565743_at	---
8.77	9.13	0.36	4.19E-01	7.50E-01	ACAT1	acetyl-Coenzyme A acetyltransferase 1	chr11q22.3-q23.1	205412_at	NM_000019
3.53	3.68	0.15	4.19E-01	7.50E-01	LOC642032	hypothetical protein LOC642032	---	1560213_at	XM_001722894
3.12	3.26	0.14	4.19E-01	7.50E-01	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17p13.3	219794_at	NM_001128159 /// NM_018289
8.41	8.80	0.39	4.19E-01	7.50E-01	SET	SET nuclear oncogene	chr9q34	213047_x_at	NM_001122821 /// NM_003011
3.00	3.16	0.16	4.19E-01	7.50E-01	C12orf51	Chromosome 12 open reading frame 51	chr12q24.13	1561130_at	NM_001109662
3.84	3.97	0.13	4.19E-01	7.50E-01	ANKRD24	ankyrin repeat domain 24	chr19p13.3	1558398_at	NM_133475
2.75	2.86	0.11	4.19E-01	7.50E-01	IFRG15 /// TOR1AIP2	interferon responsive gene 15 /// torsin A interacting protein 2	chr1q25.2	1569676_at	NM_022347 /// NM_145034
5.74	6.09	0.35	4.19E-01	7.50E-01	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	chr10q24	204747_at	NM_001031683 /// NM_001549
2.94	3.04	0.10	4.19E-01	7.50E-01	ZDHHC1	Zinc finger, DHHC-type containing 1	chr16q22.1	244494_at	NM_013304

6.32	6.54	0.23	4.19E-01	7.50E-01	C10orf59	chromosome 10 open reading frame 59	chr10q23.31	223824_at	NM_001031709 /// NM_018363																					
2.00	2.12	0.11	4.19E-01	7.50E-01	---	---	---	244066_at	---																					
1.92	2.01	0.10	4.19E-01	7.50E-01	LOC149773	hypothetical protein LOC149773	chr20q13.32	1556901_s_at	XR_042084 /// XR_042085 /// XR_042086																					
3.62	3.83	0.21	4.19E-01	7.50E-01	NRD1	nardilysin (N-arginine dibasic convertase)	chr1p32.2-p32.1	229422_at	NM_001101662 /// NM_002525																					
4.56	4.92	0.36	4.19E-01	7.50E-01	INSIG2	insulin induced gene 2	chr2q14.1	209566_at	NM_016133																					
1.79	1.88	0.09	4.19E-01	7.50E-01	---	---	---	1562553_at	---																					
3.91	4.06	0.15	4.19E-01	7.50E-01	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	chr6p21	206160_at	NM_006789																					
2.50	2.67	0.17	4.19E-01	7.50E-01	LOC284578	hypothetical protein LOC284578	chr1q32.1	1557474_at	---																					
4.14	4.31	0.17	4.20E-01	7.50E-01	BTK	Bruton agammaglobulinemia tyrosine kinase	chrXq21.33-q22	205504_at	NM_000061																					
2.07	2.18	0.11	4.20E-01	7.50E-01	LOC100128727	hypothetical LOC100128727	chr7q33	240395_at	XM_001723393 /// XM_001724038 /// XM_001726684																					
5.07	5.22	0.15	4.20E-01	7.50E-01	LOC283663	hypothetical protein LOC283663	chr15q21.3	230648_at	XM_001133132 /// XM_001133281 /// XM_001726159																					
2.42	2.54	0.12	4.20E-01	7.50E-01	MAGIX	MAGI family member, X-linked	chrXp11.23	222944_s_at	NM_001099680 /// NM_001099681 /// NM_001099682 /// NM_024859																					
2.76	2.89	0.12	4.20E-01	7.50E-01	SLAMF7	SLAM family member 7	chr1q23.1-q24.1	234306_s_at	NM_021181																					
2.51	2.66	0.15	4.20E-01	7.50E-01	ZNF83	zinc finger protein 83	chr19q13.3	236429_at	NM_001105549 /// NM_001105550 /// NM_001105551 /// NM_001105552 /// NM_001105553 /// NM_001105554 /// NM_018300 /// NR_003936																					
2.25	2.35	0.10	4.20E-01	7.50E-01	NR2E3	nuclear receptor subfamily 2, group E, member 3	chr15q22.32	208388_at	NM_014249 /// NM_016346																					
2.10	2.20	0.10	4.20E-01	7.50E-01	---	---	---	1564595_at	---																					
3.12	3.32	0.20	4.20E-01	7.50E-01	FRMD4A	FERM domain containing 4A	chr10p13	1560031_at	NM_018027																					
2.59	2.71	0.12	4.20E-01	7.50E-01	MRPL19	mitochondrial ribosomal protein L19	chr2q11.1-q11.2	238448_at	NM_014763																					
4.29	4.46	0.17	4.20E-01	7.50E-01	C19orf45	chromosome 19 open reading frame 45	chr19p13.2	241842_x_at	NM_198534																					
3.95	4.11	0.16	4.20E-01	7.50E-01	BTBD12	BTB (POZ) domain containing 12	chr16p13.3	239687_at	NM_032444																					
4.97	5.16	0.18	4.20E-01	7.50E-01	EVC	Ellis van Creveld syndrome	chr4p16	210887_s_at	NM_153717																					
5.39	5.57	0.18	4.20E-01	7.50E-01	SAV1	salvador homolog 1 (Drosophila)	chr14q13-q23	218276_s_at	NM_021818																					
9.88	10.05	0.16	4.20E-01	7.50E-01	EIF3C /// EIF3CL	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation initiation factor 3, subunit C-like	chr16p11.2	200647_x_at	NM_001037808 /// NM_001099661 /// NM_003752																					
3.15	3.28	0.14	4.20E-01	7.50E-01	---	---	---	239756_at	---																					
1.87	1.94	0.08	4.20E-01	7.50E-01	---	---	---	216974_at	---																					
3.54	3.68	0.14	4.20E-01	7.50E-01	CSF3R	colony stimulating factor 3 receptor (granulocyte)	chr1p35-p34.3	203591_s_at	NM_000760 /// NM_156038 /// NM_156039 /// NM_172313																					
4.76	4.88	0.12	4.20E-01	7.50E-01	ADPRH	ADP-ribosylarginine hydrolase	chr3q13.31-q13.33	228042_at	NM_001125																					
5.78	6.31	0.52	4.20E-01	7.50E-01	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	chr1p22.2	231577_s_at	NM_002053																					
5.80	6.18	0.38	4.20E-01	7.50E-01	UBR5	ubiquitin protein ligase E3 component n-recognin 5	chr8q22	208884_s_at	NM_015902																					
5.11	5.39	0.28	4.20E-01	7.50E-01	---	---	---	242343_x_at	---																					
5.90	6.14	0.24	4.20E-01	7.50E-01	TGOLN2	trans-golgi network protein 2	chr2p11.2	212040_at	NM_006464																					

3.18	3.42	0.24	4.20E-01	7.50E-01	SH3D19	SH3 domain containing 19	chr4q31.3	1558647_at	NM_001009555 /// NM_001128923 /// NM_001128924																				
3.22	3.40	0.18	4.20E-01	7.50E-01	---	---	---	1565762_at	---																				
3.23	3.40	0.18	4.20E-01	7.50E-01	---	---	---	228465_at	---																				
2.70	2.87	0.17	4.20E-01	7.50E-01	---	---	---	1557346_a_at	---																				
2.96	3.12	0.16	4.20E-01	7.50E-01	LOC286114	hypothetical protein LOC286114	chr8p21.3	1562724_at	---																				
4.50	4.63	0.13	4.20E-01	7.50E-01	---	---	---	1562890_at	---																				
4.54	4.66	0.13	4.20E-01	7.50E-01	LLGL1	lethal giant larvae homolog 1 (Drosophila)	chr17p11.2	206123_at	NM_004140																				
2.94	3.07	0.12	4.20E-01	7.50E-01	GNG8	guanine nucleotide binding protein (G protein), gamma 8	chr19q13.2-q13.3	234284_at	NM_033258																				
2.50	2.61	0.12	4.20E-01	7.50E-01	SGPL1	sphingosine-1-phosphate lyase 1	chr10q21	208381_s_at	NM_003901																				
2.16	2.27	0.11	4.20E-01	7.50E-01	---	---	---	234901_at	---																				
2.10	2.19	0.09	4.20E-01	7.50E-01	---	---	---	233606_at	---																				
2.15	2.24	0.09	4.20E-01	7.50E-01	OR9A1P	olfactory receptor, family 9, subfamily A, member 1 pseudogene	chr7q34	1567248_at	---																				
6.11	6.28	0.17	4.21E-01	7.50E-01	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	chr1p13.2	224985_at	NM_002524																				
2.59	2.71	0.13	4.21E-01	7.50E-01	---	---	---	1557329_at	---																				
2.18	2.30	0.12	4.21E-01	7.50E-01	SYCP2L	synaptonemal complex protein 2-like	chr6p24.2	236337_at	NM_001040274																				
2.05	2.16	0.11	4.21E-01	7.50E-01	APOF	apolipoprotein F	chr12q13.2	207262_at	NM_001638																				
4.58	4.77	0.19	4.21E-01	7.50E-01	---	---	---	215799_at	---																				
4.20	4.35	0.15	4.21E-01	7.50E-01	VAC14	Vac14 homolog (S. cerevisiae)	chr16q22.1	216407_at	NM_018052 /// XM_001724197 /// XM_001724956 /// XM_001726731																				
2.02	2.13	0.11	4.21E-01	7.50E-01	LOC159110	hypothetical protein LOC159110	chrYq11.221	216786_at	---																				
2.86	2.99	0.13	4.21E-01	7.50E-01	STAB2	stabilin 2	chr12q23.3	220114_s_at	NM_017564																				
2.14	2.25	0.11	4.21E-01	7.50E-01	PDPN	podoplanin	chr1p36.21	208233_at	NM_001006624 /// NM_001006625 /// NM_006474 /// NM_198389																				
2.25	2.40	0.15	4.21E-01	7.51E-01	TRIO	Triple functional domain (PTPRF interacting)	chr5p15.2	244527_at	NM_007118 /// XM_001720067 /// XM_001721583 /// XM_001723929																				
2.07	2.19	0.12	4.21E-01	7.51E-01	---	---	---	1557775_a_at	---																				
4.49	4.61	0.12	4.21E-01	7.51E-01	---	---	---	216138_at	---																				
2.52	2.63	0.11	4.21E-01	7.51E-01	TRYX3	trypsin X3	chr7q34	237513_at	NM_001001317																				
5.22	5.42	0.20	4.21E-01	7.51E-01	WDR47	WD repeat domain 47	chr1p13.3	203855_at	NM_014969																				
3.13	3.31	0.18	4.21E-01	7.51E-01	SSTR4	somatostatin receptor 4	chr20p11.2	214556_at	NM_001052																				
2.06	2.18	0.12	4.21E-01	7.51E-01	---	---	---	242236_at	---																				
3.42	3.61	0.19	4.21E-01	7.51E-01	SRCAP	Snf2-related CREBBP activator protein	chr16p11.2	1552630_a_at	NM_006662																				
2.25	2.39	0.14	4.21E-01	7.51E-01	RP5-1000E10.4	suppressor of IKK epsilon	chr1p13.2	204666_s_at	NM_001102396 /// NM_025073																				
2.15	2.27	0.12	4.21E-01	7.51E-01	ZNF585A /// ZNF585B	zinc finger protein 585A /// zinc finger protein 585B	chr19q13.12	235262_at	NM_152279 /// NM_152655 /// NM_199126																				
2.31	2.42	0.11	4.21E-01	7.51E-01	GRM6	glutamate receptor, metabotropic 6	chr5q35	208035_at	NM_000843																				
4.32	4.73	0.41	4.21E-01	7.51E-01	UTRN	utrophin	chr6q24	213022_s_at	NM_007124																				
3.51	3.62	0.11	4.21E-01	7.51E-01	F12	coagulation factor XII (Hageman factor)	chr5q33-qter	205774_at	NM_000505																				
4.01	4.16	0.15	4.21E-01	7.51E-01	C11orf9	chromosome 11 open reading frame 9	chr11q12-q13.1	217462_at	NM_001127392 /// NM_013279																				
2.11	2.23	0.12	4.21E-01	7.51E-01	---	---	---	234213_at	---																				
2.20	2.31	0.10	4.21E-01	7.51E-01	---	---	---	231601_at	---																				
1.93	2.02	0.09	4.21E-01	7.51E-01	ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	chr5q12.1	1554882_at	NM_000082 /// NM_001007233 /// NM_001007234																				
1.83	1.91	0.08	4.21E-01	7.51E-01	---	---	---	1555939_at	---																				

3.14	3.32	0.18	4.21E-01	7.51E-01	LOC100128737	hypothetical protein LOC100128737	chr7q22.3	228753_at	XM_001715932 /// XM_001718329																				
2.03	2.13	0.10	4.21E-01	7.51E-01	PLCH1	phospholipase C, eta 1	chr3q25.31	214745_at	NM_001130960 /// NM_001130961 /// NM_014996																				
12.58	12.66	0.08	4.21E-01	7.51E-01	RPL39	ribosomal protein L39	chrXq22-q24	208695_s_at	NM_001000																				
6.14	6.29	0.15	4.22E-01	7.51E-01	AVEN	apoptosis, caspase activation inhibitor	chr15q13.1	219366_at	NM_020371																				
3.34	3.45	0.11	4.22E-01	7.51E-01	ZNF17	zinc finger protein 17	chr19q13.4	1558183_at	NM_006959																				
2.89	3.04	0.15	4.22E-01	7.51E-01	FLJ45224	FLJ45224 protein	chr9q34.3	1564431_a_at	NM_207510																				
2.46	2.60	0.14	4.22E-01	7.51E-01	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	chr1q42.13	1554306_at	NM_002221																				
4.88	5.04	0.17	4.22E-01	7.51E-01	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	chr4p14-p13	212970_at	NM_173075																				
3.07	3.19	0.12	4.22E-01	7.51E-01	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	chr6q24.3-q25.3	226907_at	NM_030949																				
6.33	6.67	0.34	4.22E-01	7.51E-01	FMO2	flavin containing monooxygenase 2 (non-functional)	chr1q23-q25	228268_at	NM_001460																				
2.59	2.69	0.10	4.22E-01	7.51E-01	---	---	---	232711_at	---																				
2.82	2.90	0.08	4.22E-01	7.51E-01	BEYLA	hypothetical LOC497634	---	240682_at	---																				
4.04	4.17	0.12	4.22E-01	7.51E-01	ANXA11	annexin A11	chr10q23	228727_at	NM_001157 /// NM_145868 /// NM_145869																				
2.73	2.88	0.15	4.22E-01	7.51E-01	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	chr6p21.32	210571_s_at	NR_002174																				
5.54	6.14	0.61	4.23E-01	7.52E-01	TXNDC1	thioredoxin domain containing 1	chr14q22.1	208097_s_at	NM_030755																				
6.07	6.56	0.48	4.23E-01	7.52E-01	PHF20L1	PHD finger protein 20-like 1	chr8q24.22	227523_s_at	NM_016018 /// NM_032205 /// NM_198513																				
3.28	3.53	0.25	4.22E-01	7.52E-01	---	---	---	240665_at	---																				
2.12	2.33	0.22	4.22E-01	7.52E-01	---	---	---	1560395_at	---																				
5.90	6.09	0.19	4.22E-01	7.52E-01	PHF20	PHD finger protein 20	chr20q11.22-q11.23	209422_at	NM_016436																				
5.54	5.71	0.17	4.23E-01	7.52E-01	CHERP	calcium homeostasis endoplasmic reticulum protein	chr19p13.1	1568704_a_at	NM_006387																				
3.03	3.20	0.17	4.22E-01	7.52E-01	SLIT1	slit homolog 1 (Drosophila)	chr10q23.3-q24	213601_at	NM_003061																				
2.63	2.78	0.15	4.23E-01	7.52E-01	---	---	---	233213_at	---																				
3.43	3.58	0.15	4.23E-01	7.52E-01	TBL1X	transducin (beta)-like 1X-linked	chrXp22.3	201868_s_at	NM_005647																				
2.17	2.31	0.13	4.23E-01	7.52E-01	SYT13	synaptotagmin XIII	chr11p12-p11	221859_at	NM_020826																				
2.24	2.37	0.13	4.22E-01	7.52E-01	LRP12	low density lipoprotein-related protein 12	chr8q22.2-q23.1	220253_s_at	NM_013437																				
2.43	2.56	0.13	4.22E-01	7.52E-01	---	---	---	236558_at	---																				
2.57	2.69	0.12	4.22E-01	7.52E-01	RHBDL3	Rhomboid, veinlet-like 3 (Drosophila)	chr17q11.2	233232_at	NM_138328																				
2.20	2.32	0.12	4.23E-01	7.52E-01	---	---	---	234288_at	---																				
2.33	2.45	0.12	4.22E-01	7.52E-01	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	chr15q26	239537_at	NM_006011																				
2.00	2.12	0.12	4.23E-01	7.52E-01	---	---	---	1569831_at	---																				
2.64	2.75	0.12	4.22E-01	7.52E-01	MAGEA10	melanoma antigen family A, 10	chrXq28	210295_at	NM_001011543 /// NM_021048																				
3.42	3.53	0.11	4.22E-01	7.52E-01	EMP2	epithelial membrane protein 2	chr16p13.2	238500_at	NM_001424																				
2.15	2.25	0.10	4.22E-01	7.52E-01	TMEM74	transmembrane protein 74	chr8q23.1	1552520_at	NM_153015																				
2.35	2.47	0.12	4.23E-01	7.52E-01	---	---	---	237696_at	---																				
2.29	2.43	0.14	4.23E-01	7.52E-01	DPP6	dipeptidyl-peptidase 6	chr7q36.2	228546_at	NM_001039350 /// NM_001936 /// NM_130797																				
2.09	2.21	0.12	4.23E-01	7.52E-01	KRTAP4-1	keratin associated protein 4-1	chr17q12-q21	234635_at	NM_033060																				
2.61	2.71	0.10	4.23E-01	7.52E-01	LOC644186	testis highly expressed protein 2	chr22q13.33	239854_at	NM_001123225 /// XM_001720205 /// XM_927380 /// XM_938334																				
2.38	2.48	0.10	4.23E-01	7.52E-01	---	---	---	1561857_at	---																				
1.96	2.05	0.09	4.23E-01	7.52E-01	---	---	---	224098_at	---																				
3.36	3.69	0.33	4.23E-01	7.52E-01	SYK	spleen tyrosine kinase	chr9q22	244023_at	NM_003177																				
2.71	2.81	0.10	4.23E-01	7.52E-01	---	---	---	236959_s_at	---																				
4.65	4.82	0.17	4.23E-01	7.52E-01	CAPS	calcyphosine	chr19p13.3	231729_s_at	NM_004058 /// NM_080590																				
5.88	6.00	0.12	4.23E-01	7.52E-01	EGLN2	egl nine homolog 2 (C. elegans)	chr19q13.2	223083_s_at	NM_053046 /// NM_080732																				

3.25	3.41	0.16	4.23E-01	7.52E-01	DNTT	deoxynucleotidyltransferase, terminal	chr10q23-q24	1566363_at	NM_001017520 /// NM_004088
2.02	2.11	0.09	4.23E-01	7.52E-01	---	---	---	1570117_at	---
3.69	3.84	0.15	4.23E-01	7.52E-01	KIAA0774	KIAA0774	chr13q12.3	244676_s_at	NM_001033602 /// NM_015233
2.06	2.18	0.12	4.23E-01	7.52E-01	---	---	---	1566863_at	---
1.91	2.01	0.10	4.23E-01	7.52E-01	TAS2R40	taste receptor, type 2, member 40	chr7q34	1553556_at	NM_176882
1.95	2.05	0.10	4.23E-01	7.52E-01	---	---	---	1563985_at	---
3.39	3.67	0.27	4.23E-01	7.52E-01	---	---	---	242225_at	---
2.66	2.80	0.14	4.23E-01	7.52E-01	---	---	---	1564552_at	---
2.42	2.52	0.10	4.23E-01	7.52E-01	---	---	---	237173_at	---
2.09	2.18	0.08	4.23E-01	7.52E-01	---	---	---	241461_at	---
4.00	4.12	0.13	4.24E-01	7.52E-01	APOA1	apolipoprotein A-I	chr11q23-q24	217073_x_at	NM_000039
4.53	5.03	0.50	4.24E-01	7.52E-01	---	---	---	233365_at	---
9.01	9.29	0.27	4.24E-01	7.52E-01	C1S	complement component 1, s subcomponent	chr12p13	208747_s_at	NM_001734 /// NM_201442
4.37	4.63	0.26	4.24E-01	7.52E-01	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	1556821_x_at	NR_002612
4.58	4.73	0.15	4.24E-01	7.52E-01	KRT8P12	keratin 8 pseudogene 12	chr3q26.1	222060_at	---
3.12	3.25	0.13	4.24E-01	7.52E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	1565818_s_at	NM_006060
2.29	2.41	0.12	4.24E-01	7.52E-01	IL31RA	interleukin 31 receptor A	chr5q11.2	1553032_at	NM_139017
2.30	2.40	0.11	4.24E-01	7.52E-01	LOC151760	hypothetical LOC151760	chr3q13.13	1564837_at	XR_041820 /// XR_041821 /// XR_041822
6.78	6.89	0.10	4.24E-01	7.52E-01	C18orf45	chromosome 18 open reading frame 45	chr18q11.2	244495_x_at	NM_032933
3.47	3.67	0.20	4.24E-01	7.52E-01	---	---	---	215306_at	---
4.82	4.98	0.16	4.24E-01	7.52E-01	NOL6	nucleolar protein family 6 (RNA-associated)	chr9p13.3	222554_s_at	NM_022917 /// NM_139235
2.55	2.66	0.11	4.24E-01	7.52E-01	PTPN23	protein tyrosine phosphatase, non-receptor type 23	chr3p21.3	223149_s_at	NM_015466
2.76	3.05	0.29	4.24E-01	7.53E-01	SMAD9	SMAD family member 9	chr13q12-q14	227719_at	NM_001127217 /// NM_005905
2.55	2.72	0.17	4.24E-01	7.53E-01	GPR83	G protein-coupled receptor 83	chr11q21	222953_at	NM_016540
3.97	4.12	0.14	4.24E-01	7.53E-01	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	chr19q13.1-q13.4	214339_s_at	NM_001042600 /// NM_007181
2.35	2.48	0.13	4.24E-01	7.53E-01	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	chr14q22.3	203764_at	NM_014750
2.21	2.34	0.13	4.24E-01	7.53E-01	RGS7BP	regulator of G-protein signaling 7 binding protein	chr5q12.3	237719_x_at	NM_001029875
2.62	2.83	0.21	4.24E-01	7.53E-01	PDE1A	phosphodiesterase 1A, calmodulin-dependent	chr2q32.1	242789_at	NM_001003683 /// NM_005019
3.18	3.38	0.20	4.24E-01	7.53E-01	APOL4	apolipoprotein L, 4	chr22q11.2-q13.2	1555600_s_at	NM_030643 /// NM_145660
5.20	5.32	0.13	4.24E-01	7.53E-01	LOC91316	similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific)	chr22q11.23	215202_at	XR_038140 /// XR_040205 /// XR_040206
2.93	3.08	0.15	4.24E-01	7.53E-01	SP3	Sp3 transcription factor	chr2q31	227537_s_at	NM_001017371 /// NM_003111
2.80	2.98	0.18	4.24E-01	7.53E-01	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	chr5q13.2	228043_at	NM_032175
2.67	2.83	0.16	4.24E-01	7.53E-01	CCDC61	Coiled-coil domain containing 61	chr19q13.32	228475_at	NM_001080402
5.84	6.12	0.28	4.24E-01	7.53E-01	PSME4	proteasome (prosome, macropain) activator subunit 4	chr2p16.2	212222_at	NM_014614
3.71	3.93	0.23	4.24E-01	7.53E-01	---	---	---	239167_at	---
5.66	6.06	0.41	4.24E-01	7.53E-01	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	chr11q23	211366_x_at	NM_001223 /// NM_033292 /// NM_033293 /// NM_033294 /// NM_033295
6.22	6.54	0.32	4.24E-01	7.53E-01	ZYG11B	Zyg-11 homolog B (C. elegans)	chr1p32.3	225338_at	NM_024646
2.54	2.67	0.13	4.24E-01	7.53E-01	---	---	---	241165_at	---
2.99	3.13	0.14	4.24E-01	7.53E-01	SUFU	suppressor of fused homolog (Drosophila)	chr10q24.32	224203_at	NM_016169
4.24	4.38	0.14	4.24E-01	7.53E-01	S100A7A	S100 calcium binding protein A7A	chr1q21.3	232220_at	NM_176823
2.54	2.65	0.11	4.24E-01	7.53E-01	PARK2	Parkinson disease (autosomal recessive, juvenile) 2, parkin	chr6q25.2-q27	1555668_a_at	NM_004562 /// NM_013987 /// NM_013988
2.55	2.66	0.11	4.24E-01	7.53E-01	UNC84A	unc-84 homolog A (C. elegans)	chr7p22.3	206487_at	NM_001130965 /// NM_025154
2.99	3.12	0.13	4.24E-01	7.53E-01	RUNDC2A	RUN domain containing 2A	chr16p13.13	232485_at	NM_032167
3.28	3.40	0.12	4.25E-01	7.53E-01	CA12	carbonic anhydrase XII	chr15q22	204508_s_at	NM_001218 /// NM_206925

3.92	4.08	0.16	4.25E-01	7.53E-01	ANTXR1	Anthrax toxin receptor 1	chr2p13.1	234832_at	NM_018153 /// NM_032208 /// NM_053034																				
1.97	2.09	0.12	4.25E-01	7.53E-01	---	---	---	1568190_at	---																				
5.69	6.16	0.47	4.25E-01	7.53E-01	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	chr11q22	202170_s_at	NM_015423																				
6.05	6.19	0.14	4.25E-01	7.53E-01	MUC1	mucin 1, cell surface associated	chr1q21	213693_s_at	NM_001018016 /// NM_001018017 /// NM_001044390 /// NM_001044391 /// NM_001044392 /// NM_001044393 /// NM_002456																				
2.57	2.68	0.11	4.25E-01	7.53E-01	C21orf88	chromosome 21 open reading frame 88	chr21q22.2	1553850_at	XR_040123 /// XR_040124 /// XR_040125 /// XR_040126 /// XR_040127 /// XR_040128 /// XR_040129																				
4.09	4.29	0.20	4.25E-01	7.53E-01	---	---	---	237398_at	---																				
2.58	2.72	0.15	4.25E-01	7.53E-01	EGO	eosinophil granule ontogeny	---	222314_x_at	NR_004428																				
2.37	2.50	0.13	4.25E-01	7.53E-01	---	---	---	244348_at	---																				
4.19	4.43	0.24	4.25E-01	7.53E-01	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D	chr7q22.1	226041_at	NM_001122838 /// NM_198990																				
4.17	4.32	0.15	4.25E-01	7.53E-01	---	---	---	238313_at	---																				
2.68	2.83	0.15	4.25E-01	7.53E-01	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	chr11q23.1	217002_s_at	NM_000869 /// NM_213621																				
2.14	2.27	0.14	4.25E-01	7.53E-01	---	---	---	1566539_at	---																				
3.66	3.79	0.13	4.25E-01	7.53E-01	SNRPE	small nuclear ribonucleoprotein polypeptide E	chr1q32	231112_at	NM_003094																				
4.33	4.45	0.12	4.25E-01	7.53E-01	---	---	---	1558504_at	---																				
2.88	2.99	0.12	4.25E-01	7.53E-01	DKFZp566F0947	hypothetical gene DKFZp566F0947	---	232634_at	---																				
3.36	3.47	0.11	4.25E-01	7.53E-01	LOC51233	hypothetical protein LOC51233	chr22q11.2	221108_at	NM_016449																				
2.24	2.34	0.10	4.25E-01	7.53E-01	C12orf61	chromosome 12 open reading frame 61	chr12q14.1	1557312_at	NM_175895																				
2.01	2.11	0.10	4.25E-01	7.53E-01	C1orf129	chromosome 1 open reading frame 129	chr1q24.3	221182_at	NM_025063																				
3.43	3.57	0.14	4.25E-01	7.53E-01	PSMD7	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	chr16q23-q24	238738_at	NM_002811																				
4.32	4.45	0.14	4.25E-01	7.53E-01	---	---	---	242466_at	---																				
2.39	2.55	0.16	4.25E-01	7.53E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	211909_x_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719																				
5.72	6.25	0.54	4.25E-01	7.53E-01	NOTCH3	Notch homolog 3 (Drosophila)	chr19p13.2-p13.1	203238_s_at	NM_000435																				
7.45	7.89	0.44	4.25E-01	7.53E-01	OSBPL9	oxysterol binding protein-like 9	chr1p32.3	218047_at	NM_024586 /// NM_148904 /// NM_148905 /// NM_148906 /// NM_148907 /// NM_148908 /// NM_148909																				
1.90	1.98	0.08	4.25E-01	7.53E-01	LOC389906	Hypothetical protein LOC441528	chrXp22.33	217712_at	XM_001713861 /// XM_928240 /// XM_942518																				

5.50	6.14	0.64	4.25E-01	7.54E-01	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	chr4q31.3-q33|4q31.1-q31.2	221942_s_at	NM_000856 /// NM_001130682 /// NM_001130683 /// NM_001130684 /// NM_001130685 /// NM_001130686 /// NM_001130687																				
2.85	3.00	0.15	4.25E-01	7.54E-01	STK38	Serine/threonine kinase 38	chr6p21	1557145_at	NM_007271																				
2.59	2.73	0.14	4.25E-01	7.54E-01	---	---	---	230773_at	---																				
2.58	2.69	0.11	4.25E-01	7.54E-01	---	---	---	1570126_at	---																				
2.38	2.52	0.14	4.26E-01	7.54E-01	---	---	---	1569828_at	---																				
2.50	2.64	0.13	4.26E-01	7.54E-01	RLN1	relaxin 1	chr9p24.1	211753_s_at	NM_006911																				
2.09	2.22	0.12	4.26E-01	7.54E-01	DEPDC7	DEP domain containing 7	chr11p13	228293_at	NM_001077242 /// NM_139160																				
4.06	4.18	0.12	4.26E-01	7.54E-01	ZMYND10	zinc finger, MYND-type containing 10	chr3p21.3	205714_s_at	NM_015896																				
2.11	2.24	0.12	4.26E-01	7.54E-01	---	---	---	1566461_at	---																				
3.00	3.10	0.09	4.26E-01	7.54E-01	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	chr10p12.1	219994_at	NM_019043																				
3.68	3.83	0.15	4.26E-01	7.54E-01	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	chr7q35-q36	205262_at	NM_000238 /// NM_172056 /// NM_172057																				
4.61	4.76	0.15	4.26E-01	7.54E-01	DLGAP3	discs, large (Drosophila) homolog-associated protein 3	chr1p35.3-p34.1	231151_at	NM_001080418																				
11.27	11.41	0.14	4.26E-01	7.54E-01	FTL	ferritin, light polypeptide	chr19q13.3-q13.4|19q13.3	213187_x_at	NM_000146																				
2.27	2.37	0.10	4.26E-01	7.54E-01	---	---	---	244418_at	---																				
5.44	5.59	0.15	4.26E-01	7.54E-01	STMN1	stathmin 1/oncoprotein 18	chr1p36.1-p35	217714_x_at	NM_005563 /// NM_203399 /// NM_203401																				
2.27	2.36	0.09	4.26E-01	7.54E-01	---	---	---	1559495_at	---																				
2.14	2.25	0.11	4.26E-01	7.54E-01	---	---	---	244174_at	---																				
2.17	2.27	0.10	4.26E-01	7.54E-01	OSGIN2	Oxidative stress induced growth inhibitor family member 2	chr8q21	214161_at	NM_001126111 /// NM_004337																				
2.12	2.24	0.12	4.26E-01	7.54E-01	FAM133B /// LOC728153 /// LOC728408	family with sequence similarity 133, member B /// similar to FAM133B protein /// similar to FAM133B protein	chr2p23.2 /// chr5q12.1 /// chr7q21.2	235469_at	NM_001040057 /// NM_152789 /// XM_001128002 /// XM_001722995 /// XR_015598 /// XR_015778 /// XR_039142																				
4.15	4.27	0.12	4.26E-01	7.54E-01	CEP250	Centrosomal protein 250kDa	chr20q11.22-q12	236424_at	NM_001035518 /// NM_007186																				
2.99	3.18	0.20	4.26E-01	7.54E-01	ZNF551	zinc finger protein 551	chr19q13.43	211721_s_at	NM_138347																				
8.31	8.79	0.48	4.26E-01	7.54E-01	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	chr9p13-p12	200881_s_at	NM_001539																				
5.51	5.82	0.31	4.26E-01	7.54E-01	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	chr6q21	218949_s_at	NM_018292																				
3.55	3.73	0.19	4.26E-01	7.54E-01	BICD1	Bicaudal D homolog 1 (Drosophila)	chr12p11.2-p11.1	228691_at	NM_001003398 /// NM_001714																				
2.57	2.74	0.17	4.26E-01	7.54E-01	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	chr3p25.3	215550_at	NM_001033117 /// NM_014850																				
4.45	4.61	0.16	4.26E-01	7.54E-01	CACNG6	calcium channel, voltage-dependent, gamma subunit 6	chr19q13.4	1552863_a_at	NM_031897 /// NM_145814 /// NM_145815																				
3.10	3.26	0.16	4.26E-01	7.54E-01	SPN	sialophorin	chr16p11.2	206057_x_at	NM_001030288 /// NM_003123																				
7.28	7.42	0.15	4.26E-01	7.54E-01	FAM128B	family with sequence similarity 128, member B	chr2q21.1	220720_x_at	NM_025029																				
3.18	3.31	0.13	4.26E-01	7.54E-01	CD79B	CD79b molecule, immunoglobulin-associated beta	chr17q23	1555748_x_at	NM_000626 /// NM_001039933 /// NM_021602																				
2.32	2.42	0.11	4.26E-01	7.54E-01	---	---	---	1557422_at	---																				
2.15	2.26	0.10	4.26E-01	7.54E-01	---	---	---	239692_at	---																				
2.10	2.23	0.13	4.26E-01	7.54E-01	---	---	---	1563397_at	---																				

7.16	7.31	0.16	4.26E-01	7.54E-01	TRIM44	tripartite motif-containing 44	chr11p13	217760_at	NM_017583																					
1.95	2.06	0.10	4.26E-01	7.54E-01	PRO2964	hypothetical protein PRO2964	chr2q32.1	220872_at	---																					
2.17	2.30	0.12	4.26E-01	7.54E-01	41334	Membrane-associated ring finger (C3HC4) 1	chr4q32.3	1562338_at	NM_017923																					
2.65	2.76	0.12	4.27E-01	7.54E-01	---	---	---	230984_s_at	---																					
6.71	6.98	0.28	4.27E-01	7.54E-01	LOC26010	viral DNA polymerase-transactivated protein 6	chr2q33.1	222154_s_at	NM_001100422 /// NM_001100423 /// NM_001100424 /// NM_015535																					
4.59	4.72	0.13	4.27E-01	7.54E-01	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	chr19q13.1-q13.2	217291_at	NM_004363																					
2.55	2.69	0.14	4.27E-01	7.54E-01	---	---	---	1563078_at	---																					
2.70	2.80	0.10	4.27E-01	7.54E-01	NEGR1	neuronal growth regulator 1	chr1p31.1	243357_at	NM_173808																					
2.09	2.18	0.09	4.27E-01	7.54E-01	---	---	---	1558587_at	---																					
2.43	2.53	0.10	4.27E-01	7.54E-01	E2F2	E2F transcription factor 2	chr1p36	207042_at	NM_004091																					
3.17	3.32	0.15	4.27E-01	7.54E-01	VPRBP	Vpr (HIV-1) binding protein	chr3p21.2	204377_s_at	NM_014703																					
3.19	3.35	0.16	4.27E-01	7.54E-01	POLQ	polymerase (DNA directed), theta	chr3q13.33	219510_at	NM_199420																					
2.65	2.79	0.14	4.27E-01	7.54E-01	---	---	---	234162_at	---																					
2.67	2.76	0.10	4.27E-01	7.54E-01	MEG3	Maternally expressed 3 (non-protein coding)	chr14q32	222328_x_at	NR_002766 /// NR_003530 /// NR_003531																					
4.77	5.07	0.31	4.27E-01	7.54E-01	PODN	podocan	chr1p32.3	226522_at	NM_153703																					
2.63	2.85	0.23	4.27E-01	7.54E-01	CTAGE5	CTAGE family, member 5	chr14q13.3	204055_s_at	NM_005930 /// NM_203354 /// NM_203355 /// NM_203356																					
3.05	3.20	0.14	4.27E-01	7.54E-01	IL6 /// LOC541472	interleukin 6 (interferon, beta 2) /// hypothetical LOC541472	chr7p21	243977_at	NM_000600 /// XR_039887 /// XR_039888 /// XR_039889 /// XR_039890																					
3.25	3.37	0.13	4.27E-01	7.54E-01	SLA2	Src-like-adaptor 2	chr20q11.23	1555688_s_at	NM_032214 /// NM_175077																					
2.00	2.11	0.11	4.27E-01	7.54E-01	FABP7	fatty acid binding protein 7, brain	chr6q22-q23	205029_s_at	NM_001446																					
2.17	2.27	0.10	4.27E-01	7.54E-01	---	---	---	238734_at	---																					
2.66	2.80	0.14	4.27E-01	7.54E-01	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	chr6p24.2	230788_at	NM_001491 /// NM_145649 /// NM_145655																					
2.79	2.90	0.11	4.27E-01	7.54E-01	DEFA6	defensin, alpha 6, Paneth cell-specific	chr8pter-p21	207814_at	NM_001926																					
2.47	2.57	0.10	4.27E-01	7.54E-01	---	---	---	1557274_at	---																					
1.98	2.07	0.10	4.27E-01	7.54E-01	FUT9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	chr6q16	214046_at	NM_006581																					
4.67	4.92	0.26	4.27E-01	7.54E-01	TMEM161B	transmembrane protein 161B	chr5q14.3	238783_at	NM_153354																					
2.61	2.79	0.18	4.27E-01	7.54E-01	---	---	---	217277_at	---																					
2.42	2.58	0.15	4.27E-01	7.54E-01	CSMD2	CUB and Sushi multiple domains 2	chr1p35.1-p34.3	1557143_at	NM_052896																					
3.20	3.35	0.15	4.27E-01	7.54E-01	MGEA5	Meningioma expressed antigen 5 (hyaluronidase)	chr10q24.1-q24.3	214972_at	NM_012215																					
3.49	3.64	0.15	4.27E-01	7.54E-01	BUD31	BUD31 homolog (S. cerevisiae)	chr7q22.1	215815_at	NM_003910																					
3.79	3.94	0.14	4.27E-01	7.54E-01	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	chr9q34.3	211125_x_at	NM_000832 /// NM_007327 /// NM_021569																					
2.58	2.70	0.13	4.27E-01	7.54E-01	ZNF567	zinc finger protein 567	chr19q13.12	238316_at	NM_152603																					
2.09	2.22	0.13	4.27E-01	7.54E-01	---	---	---	207371_at	---																					
2.22	2.34	0.13	4.27E-01	7.54E-01	---	---	---	1564262_at	---																					
2.72	2.82	0.11	4.27E-01	7.54E-01	---	---	---	204486_at	---																					
2.63	2.74	0.11	4.27E-01	7.54E-01	---	---	---	231498_at	---																					
2.00	2.10	0.10	4.27E-01	7.54E-01	---	---	---	1556329_a_at	---																					
3.43	3.60	0.17	4.27E-01	7.54E-01	IGF1R	insulin-like growth factor 1 receptor	chr15q26.3	243358_at	NM_000875																					
2.22	2.35	0.13	4.27E-01	7.55E-01	TGOLN2	trans-golgi network protein 2	chr2p11.2	1554608_at	NM_006464																					
3.78	4.04	0.26	4.28E-01	7.55E-01	IGHD	immunoglobulin heavy constant delta	chr14q32.33	214973_x_at	---																					
8.53	8.74	0.20	4.28E-01	7.55E-01	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	chr1p36.23	211749_s_at	NM_004781																					
3.87	4.03	0.16	4.28E-01	7.55E-01	---	---	---	235657_at	---																					
2.43	2.57	0.14	4.28E-01	7.55E-01	RNF148	ring finger protein 148	chr7q31.33	242925_at	NM_198085																					
5.06	5.17	0.12	4.28E-01	7.55E-01	CREBL1	cAMP responsive element binding protein-like 1	chr6p21.3	203168_at	NM_004381																					
2.67	2.82	0.15	4.28E-01	7.55E-01	TMEM139	transmembrane protein 139	chr7q34	229634_at	NM_153345																					
2.44	2.53	0.09	4.28E-01	7.55E-01	---	---	---	234768_at	---																					
6.45	6.58	0.13	4.28E-01	7.55E-01	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	chr3p21.3	202682_s_at	NM_003363 /// NM_199443																					
2.22	2.31	0.09	4.28E-01	7.55E-01	---	---	---	1562189_at	---																					
4.38	4.73	0.36	4.28E-01	7.55E-01	SCAMP1	secretory carrier membrane protein 1	chr5q13.3-q14.1	212417_at	NM_004866																					
2.38	2.50	0.12	4.28E-01	7.55E-01	---	---	---	228539_at	---																					
2.94	3.07	0.13	4.28E-01	7.55E-01	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	chr11q23.3	204909_at	NM_004397																					

7.25	7.37	0.12	4.28E-01	7.55E-01	AP2B1	adaptor-related protein complex 2, beta 1 subunit	chr17q11.2-q12	200612_s_at	NM_001030006 /// NM_001282																				
2.59	2.70	0.11	4.28E-01	7.55E-01	STIL	SCL/TAL1 interrupting locus	chr1q32|1p32	205339_at	NM_001048166 /// NM_003035																				
6.50	6.79	0.29	4.28E-01	7.55E-01	ZNF652	zinc finger protein 652	chr17q21.32	205594_at	NM_014897																				
3.27	3.40	0.13	4.28E-01	7.55E-01	SQSTM1	sequestosome 1	chr5q35	217255_at	NM_003900																				
2.03	2.14	0.11	4.28E-01	7.55E-01	---	---	---	1570391_at	---																				
5.15	5.50	0.35	4.28E-01	7.55E-01	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	chr2p15	219326_s_at	NM_006577																				
3.98	4.20	0.22	4.28E-01	7.55E-01	---	---	---	235494_at	---																				
3.86	4.07	0.21	4.28E-01	7.55E-01	FAF1	Fas (TNFRSF6) associated factor 1	chr1p33	222511_x_at	NM_007051																				
5.69	5.85	0.16	4.28E-01	7.55E-01	ZNF524	zinc finger protein 524	chr19q13.42	238683_at	NM_153219																				
3.27	3.38	0.11	4.28E-01	7.55E-01	SPOP	speckle-type POZ protein	chr17q21.33	238923_at	NM_001007226 /// NM_001007227 /// NM_001007228 /// NM_001007229 /// NM_001007230 /// NM_003563																				
2.63	2.86	0.23	4.28E-01	7.55E-01	GJC1	gap junction protein, gamma 1, 45kDa	chr17q21.31	228563_at	NM_001080383 /// NM_005497																				
3.66	3.81	0.15	4.28E-01	7.55E-01	IL13	interleukin 13	chr5q31	207844_at	NM_002188																				
2.46	2.58	0.11	4.28E-01	7.55E-01	TTC39B	tetratricopeptide repeat domain 39B	chr9p22.3	242477_at	NM_152574																				
6.35	6.48	0.13	4.28E-01	7.55E-01	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	chr17q25	217691_x_at	NM_001042422 /// NM_001042423 /// NM_004207																				
3.05	3.37	0.32	4.28E-01	7.55E-01	MGC13057	hypothetical protein MGC13057	chr2q32.2	228195_at	NM_001042519 /// NM_001042520 /// NM_001042521 /// NM_032321																				
2.83	2.95	0.12	4.28E-01	7.55E-01	CAPN2	calpain 2, (m/II) large subunit	chr1q41-q42	214888_at	NM_001748																				
2.70	2.81	0.11	4.28E-01	7.55E-01	ARSB	arylsulfatase B	chr5q11-q13	1554030_at	NM_000046 /// NM_198709																				
2.68	2.95	0.27	4.28E-01	7.55E-01	---	---	---	242714_at	---																				
6.23	6.34	0.11	4.28E-01	7.55E-01	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	chr22q11.21	206063_x_at	NM_014337 /// NM_148175 /// NM_148176																				
7.34	7.57	0.24	4.29E-01	7.55E-01	FAM129B	family with sequence similarity 129, member B	chr9q34.11	223019_at	NM_001035534 /// NM_022833																				
6.75	6.90	0.15	4.29E-01	7.55E-01	RHEB	Ras homolog enriched in brain	chr7q36	201452_at	NM_005614																				
2.31	2.45	0.14	4.29E-01	7.55E-01	SEZ6L	Seizure related 6 homolog (mouse)-like	chr22q12.1	231650_s_at	NM_021115																				
2.76	2.88	0.11	4.29E-01	7.55E-01	FSCN3	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)	chr7q31.3	220379_at	NM_020369																				
1.93	2.01	0.08	4.29E-01	7.55E-01	ALAS2	aminolevulinate, delta-, synthase 2	chrXp11.21	244205_at	NM_000032 /// NM_001037967 /// NM_001037968 /// NM_001037969																				
2.11	2.23	0.12	4.29E-01	7.56E-01	CREG2	cellular repressor of E1A-stimulated genes 2	chr2q11.2	1552714_at	NM_153836																				
2.50	2.61	0.11	4.29E-01	7.56E-01	---	---	---	241336_at	---																				
2.62	2.75	0.12	4.29E-01	7.56E-01	TRGC2	T cell receptor gamma constant 2	chr7p14	215806_x_at	---																				
2.93	3.12	0.19	4.29E-01	7.56E-01	---	---	---	230827_at	---																				
1.80	1.92	0.12	4.29E-01	7.56E-01	LOC401233	similar to HIV TAT specific factor 1; cofactor required for Tat activation of HIV-1 transcription	chr6p25.2	1558882_at	XR_040702 /// XR_040703 /// XR_040704																				
2.34	2.44	0.10	4.29E-01	7.56E-01	FAM163A	family with sequence similarity 163, member A	chr1q25.2	222095_s_at	NM_173509																				
2.10	2.22	0.13	4.29E-01	7.56E-01	---	---	---	1557803_at	---																				
4.81	5.20	0.39	4.29E-01	7.56E-01	HP /// HPR	haptoglobin /// haptoglobin-related protein	chr16q22.1	208470_s_at	NM_001126102 /// NM_005143 /// NM_020995																				

4.43	4.80	0.38	4.29E-01	7.56E-01	RANBP9	RAN binding protein 9	chr6p23	216125_s_at	NM_005493
6.76	7.10	0.34	4.30E-01	7.56E-01	CCAR1	cell division cycle and apoptosis regulator 1	chr10q21.3	224736_at	NM_018237
3.71	3.95	0.24	4.30E-01	7.56E-01	CDK8	cyclin-dependent kinase 8	chr13q12	204831_at	NM_001260
4.18	4.41	0.23	4.29E-01	7.56E-01	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	chr8q21.11	218521_s_at	NM_001001481 /// NM_018299
8.96	9.17	0.21	4.29E-01	7.56E-01	ZBTB20	zinc finger and BTB domain containing 20	chr3q13.2	205383_s_at	NM_015642
2.71	2.92	0.21	4.29E-01	7.56E-01	---	---	---	237232_at	---
3.98	4.15	0.17	4.29E-01	7.56E-01	KCNE2	potassium voltage-gated channel, Isk-related family, member 2	chr21q22.12	221095_s_at	NM_172201
2.50	2.67	0.17	4.30E-01	7.56E-01	---	---	---	243356_at	---
6.02	6.18	0.16	4.29E-01	7.56E-01	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	chr17q11.2	224958_at	NM_020772
2.80	2.96	0.16	4.29E-01	7.56E-01	CD27	CD27 molecule	chr12p13	206150_at	NM_001242
3.28	3.44	0.15	4.30E-01	7.56E-01	ZDHHC8P	zinc finger, DHHC-type containing 8 pseudogene	chr22q11.23	222274_at	NR_003950
6.30	6.45	0.15	4.29E-01	7.56E-01	RB1	retinoblastoma 1	chr13q14.2	203132_at	NM_000321
2.59	2.75	0.15	4.30E-01	7.56E-01	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	chr11q24.2	215710_at	NM_006278 /// XM_001714343 /// XM_001726541 /// XM_001726562
4.52	4.66	0.14	4.30E-01	7.56E-01	METRN	meteorin, glial cell differentiation regulator	chr16p13.3	228419_at	NM_024042
2.38	2.51	0.13	4.30E-01	7.56E-01	---	---	---	202280_at	---
2.30	2.43	0.13	4.29E-01	7.56E-01	---	---	---	239823_at	---
2.83	2.95	0.12	4.30E-01	7.56E-01	---	---	---	1561207_at	---
1.99	2.10	0.11	4.29E-01	7.56E-01	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	chr5q22.2	1555038_at	NM_022140
1.93	2.04	0.11	4.30E-01	7.56E-01	LOC284950	hypothetical protein LOC284950	chr2p11.2	1563680_at	---
4.33	4.44	0.11	4.30E-01	7.56E-01	ADPRHL1	ADP-ribosylhydrolase like 1	chr13q34	238054_at	NM_138430 /// NM_199162
2.28	2.38	0.10	4.29E-01	7.56E-01	PMCHL1	pro-melanin-concentrating hormone-like 1	chr5p14.3	224419_x_at	NR_003921
2.27	2.37	0.10	4.30E-01	7.56E-01	DOCK2	dedicator of cytokinesis 2	chr5q35.1	1554325_at	NM_004946
7.12	7.23	0.10	4.30E-01	7.56E-01	PLEC1	plectin 1, intermediate filament binding protein 500kDa	chr8q24	201373_at	NM_000445 /// NM_201378 /// NM_201379 /// NM_201380 /// NM_201381 /// NM_201382 /// NM_201383 /// NM_201384
3.44	3.54	0.10	4.30E-01	7.56E-01	MPPED1	metallophosphoesterase domain containing 1	chr22q13.31	241398_at	NM_001044370 /// XM_001713873 /// XM_001725743
2.90	3.00	0.10	4.29E-01	7.56E-01	---	---	---	232732_at	---
2.38	2.47	0.09	4.29E-01	7.56E-01	LYK5	Protein kinase LYK5	chr17q23.3	240905_at	NM_001003786 /// NM_001003787 /// NM_001003788 /// NM_153335
2.39	2.48	0.09	4.30E-01	7.56E-01	MBNL3	muscleblind-like 3	chrXq26.2	240561_at	XM_001715792 /// XM_001719734 /// XM_001720812
5.83	6.01	0.18	4.30E-01	7.56E-01	ZNF207	zinc finger protein 207	chr17q11.2	231848_x_at	NM_001032293 /// NM_001098507 /// NM_003457
2.09	2.65	0.56	4.30E-01	7.56E-01	SLC38A4	solute carrier family 38, member 4	chr12q13	220786_s_at	NM_018018
4.41	4.58	0.17	4.30E-01	7.56E-01	DCK	deoxycytidine kinase	chr4q13.3-q21.1	203302_at	NM_000788
3.24	3.39	0.15	4.30E-01	7.56E-01	---	---	---	1556510_at	---
2.21	2.31	0.10	4.30E-01	7.56E-01	MBD3L1	methyl-CpG binding domain protein 3-like 1	chr19p13.2	1552458_at	NM_145208
3.63	3.72	0.09	4.30E-01	7.56E-01	ZNF639	zinc finger protein 639	chr3q26.32	218413_s_at	NM_016331
4.28	4.46	0.18	4.30E-01	7.56E-01	C3orf38	chromosome 3 open reading frame 38	chr3p11.2	229174_at	NM_173824
3.69	3.82	0.14	4.30E-01	7.56E-01	ZNF169	zinc finger protein 169	chr9q22.32	1560921_at	NM_194320
2.85	2.97	0.12	4.30E-01	7.56E-01	C21orf29	chromosome 21 open reading frame 29	chr21q22.3	1555049_at	NM_144991
5.84	6.06	0.22	4.30E-01	7.56E-01	DERA	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	chr12p12.3	218102_at	NM_015954

3.36	3.54	0.18	4.30E-01	7.56E-01	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	chr2p23	218457_s_at	NM_022552 /// NM_153759 /// NM_175629 /// NM_175630
2.95	3.11	0.16	4.30E-01	7.56E-01	---	---	---	230950_at	---
5.73	6.10	0.37	4.30E-01	7.56E-01	DIXDC1	DIX domain containing 1	chr11q23.1	214724_at	NM_001037954 /// NM_033425
3.73	3.92	0.19	4.30E-01	7.56E-01	ZNF827	zinc finger protein 827	chr4q31.22	226764_at	NM_178835
3.09	3.24	0.15	4.30E-01	7.56E-01	---	---	---	1566527_at	---
5.34	5.62	0.27	4.30E-01	7.56E-01	---	---	---	222303_at	---
4.00	4.12	0.12	4.30E-01	7.56E-01	CCDC40	coiled-coil domain containing 40	chr17q25.3	229918_at	NM_017950
2.06	2.17	0.10	4.30E-01	7.56E-01	MDGA2	MAM domain containing glycosylphosphatidylinositol anchor 2	chr14q21.3	1570114_at	NM_001113498 /// NM_182830
2.01	2.09	0.08	4.30E-01	7.56E-01	ZPLD1	zona pellucida-like domain containing 1	chr3q12.3	1569777_a_at	NM_175056
4.06	4.23	0.16	4.31E-01	7.57E-01	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	chr15q11.2	225752_at	NM_144599
3.67	3.83	0.16	4.31E-01	7.57E-01	MAPK1	Mitogen-activated protein kinase 1	chr22q11.2|22q11.21	224620_at	NM_002745 /// NM_138957
2.27	2.41	0.14	4.31E-01	7.57E-01	SNX24	sorting nexin 24	chr5q23.2	239739_at	NM_014035
4.23	4.37	0.14	4.31E-01	7.57E-01	STK11	Serine/threonine kinase 11	chr19p13.3	231019_x_at	NM_000455
2.22	2.35	0.13	4.31E-01	7.57E-01	---	---	---	232254_at	---
2.36	2.48	0.13	4.31E-01	7.57E-01	---	---	---	239502_at	---
2.76	2.88	0.12	4.31E-01	7.57E-01	RAB7B	RAB7B, member RAS oncogene family	chr1q32	230266_at	NM_177403
2.41	2.53	0.12	4.31E-01	7.57E-01	---	---	---	239847_at	---
2.10	2.19	0.10	4.31E-01	7.57E-01	C10orf79	chromosome 10 open reading frame 79	chr10q25.1	243896_at	NM_025145
3.94	4.11	0.17	4.31E-01	7.57E-01	LOC283045	hypothetical protein LOC283045	chr10q21.3	1563853_at	---
1.92	2.02	0.10	4.31E-01	7.57E-01	---	---	---	242718_at	---
5.07	5.38	0.31	4.31E-01	7.57E-01	PPP6C	protein phosphatase 6, catalytic subunit	chr9q33.3	225426_at	NM_001123355 /// NM_001123369 /// NM_002721
4.27	4.50	0.23	4.31E-01	7.57E-01	---	---	---	239058_at	---
2.94	3.08	0.14	4.31E-01	7.57E-01	---	---	---	215428_at	---
6.59	6.92	0.34	4.31E-01	7.57E-01	SH3GLB1	SH3-domain GRB2-like endophilin B1	chr1p22	209090_s_at	NM_016009
3.22	3.44	0.22	4.31E-01	7.57E-01	---	---	---	238563_at	---
4.17	4.32	0.14	4.31E-01	7.57E-01	---	---	---	238183_at	---
2.23	2.36	0.13	4.31E-01	7.57E-01	---	---	---	215902_at	---
3.10	3.34	0.24	4.31E-01	7.57E-01	RHOJ	ras homolog gene family, member J	chr14q23.2	1555234_a_at	NM_020663
1.85	1.94	0.08	4.31E-01	7.57E-01	---	---	---	240724_at	---
6.11	6.39	0.28	4.31E-01	7.57E-01	PRKD3	protein kinase D3	chr2p21	218236_s_at	NM_005813
3.13	3.25	0.12	4.31E-01	7.57E-01	tcag7.929	hypothetical protein LOC286009	chr7q31.2	1562664_at	---
3.87	4.14	0.27	4.32E-01	7.57E-01	RXFP1	relaxin/insulin-like family peptide receptor 1	chr4q32.1	231804_at	NM_021634
2.88	3.03	0.15	4.31E-01	7.57E-01	KLHL31	kelch-like 31 (Drosophila)	chr6p12.1	234782_at	NM_001003760
2.45	2.58	0.12	4.31E-01	7.57E-01	MICALCL	MICAL C-terminal like	chr11p15.3	243611_at	NM_032867
2.71	2.83	0.12	4.31E-01	7.57E-01	---	---	---	1558874_a_at	---
3.71	3.82	0.12	4.31E-01	7.57E-01	RBM14	RNA binding motif protein 14	chr11q13.1	239635_at	NM_006328
2.61	2.72	0.11	4.31E-01	7.57E-01	---	---	---	1561639_at	---
1.96	2.05	0.09	4.32E-01	7.57E-01	---	---	---	1570101_at	---
4.64	4.84	0.21	4.32E-01	7.57E-01	RBM25	RNA binding motif protein 25	chr14q24.3	212027_at	NM_021239
1.98	2.10	0.13	4.32E-01	7.57E-01	NFYA	Nuclear transcription factor Y, alpha	chr6p21.3	228431_at	NM_002505 /// NM_021705 /// XM_001716589 /// XM_001717592 /// XM_001718396
5.97	6.15	0.19	4.32E-01	7.57E-01	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	chr3q22.1	212255_s_at	NM_001001485 /// NM_001001486 /// NM_001001487 /// NM_014382
4.77	4.95	0.18	4.32E-01	7.57E-01	---	---	---	237887_at	---
2.44	2.58	0.15	4.32E-01	7.57E-01	LOC254128	Hypothetical protein LOC254128	chr2q14.2	1557059_at	---
3.64	3.76	0.12	4.32E-01	7.57E-01	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	chr3q29	244268_x_at	NM_002577
5.20	5.39	0.19	4.32E-01	7.57E-01	KIAA0256	KIAA0256 gene product	chr15q21.1	212450_at	NM_014701
1.94	2.04	0.10	4.32E-01	7.57E-01	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	chr12q13.12	1553271_at	NM_173602
2.39	2.48	0.09	4.32E-01	7.57E-01	---	---	---	1561287_at	---
2.73	2.90	0.17	4.32E-01	7.57E-01	KIAA1549	KIAA1549	chr7q34	232921_at	NM_020910
3.53	3.71	0.18	4.32E-01	7.57E-01	---	---	---	1561436_at	---
3.46	3.59	0.13	4.32E-01	7.57E-01	---	---	---	215278_at	---
2.56	2.67	0.11	4.32E-01	7.57E-01	SPON1	spondin 1, extracellular matrix protein	chr11p15.2	224488_s_at	NM_006108

2.05	2.16	0.10	4.32E-01	7.57E-01	LOC121838	hypothetical protein LOC121838	chr13q14.11	232318_s_at	XR_040803 /// XR_040804 /// XR_040805																				
2.21	2.31	0.09	4.32E-01	7.57E-01	MDS1	myelodysplasia syndrome 1	chr3q26	208434_at	NM_004991																				
4.62	5.02	0.40	4.32E-01	7.57E-01	IGSF10	immunoglobulin superfamily, member 10	chr3q25.1	230670_at	NM_178822																				
3.48	3.86	0.37	4.32E-01	7.57E-01	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	chr5q31-q32	213849_s_at	NM_001127381 /// NM_004576 /// NM_181674 /// NM_181675 /// NM_181676 /// NM_181677 /// NM_181678																				
3.92	4.21	0.29	4.32E-01	7.57E-01	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	chrXq13.1-q21.1	221616_s_at	NM_015975																				
6.69	6.97	0.28	4.32E-01	7.57E-01	TMEM5	transmembrane protein 5	chr12q14.2	204808_s_at	NM_014254																				
6.76	6.99	0.23	4.32E-01	7.57E-01	CDC40	cell division cycle 40 homolog (S. cerevisiae)	chr6q21	203376_at	NM_015891																				
3.19	3.34	0.16	4.32E-01	7.57E-01	LOC730227	hypothetical protein LOC730227	chr1q32.1	215756_at	XR_041814 /// XR_041815 /// XR_041816																				
4.01	4.14	0.12	4.32E-01	7.57E-01	NR2E3	nuclear receptor subfamily 2, group E, member 3	chr15q22.32	208385_at	NM_014249 /// NM_016346																				
6.47	6.59	0.12	4.32E-01	7.57E-01	---	---	---	215604_x_at	---																				
2.90	3.00	0.10	4.32E-01	7.57E-01	---	---	---	240009_at	---																				
4.14	4.44	0.30	4.33E-01	7.58E-01	P2RY13	purinergic receptor P2Y, G-protein coupled, 13	chr3q24	220005_at	NM_023914 /// NM_176894																				
5.63	5.87	0.24	4.33E-01	7.58E-01	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	chr6q14-q15	217834_s_at	NM_006372																				
3.42	3.63	0.21	4.33E-01	7.58E-01	---	---	---	240432_x_at	---																				
5.08	5.30	0.22	4.33E-01	7.58E-01	BRAP	BRCA1 associated protein	chr12q24	41512_at	NM_006768																				
6.84	6.99	0.15	4.33E-01	7.58E-01	---	---	---	233775_x_at	---																				
2.41	2.55	0.13	4.33E-01	7.58E-01	RNF34	ring finger protein 34	chr12q24.31	236288_at	NM_025126 /// NM_194271																				
2.31	2.41	0.10	4.33E-01	7.58E-01	---	---	---	207751_at	---																				
2.50	2.65	0.15	4.33E-01	7.58E-01	C9orf80	chromosome 9 open reading frame 80	chr9q32	1560558_at	NM_021218																				
2.19	2.33	0.14	4.33E-01	7.58E-01	---	---	---	1561126_at	---																				
3.90	4.01	0.12	4.33E-01	7.58E-01	---	---	---	241202_at	---																				
5.31	5.67	0.36	4.33E-01	7.58E-01	TMEM187	transmembrane protein 187	chrXq28	204340_at	NM_003492																				
3.47	3.80	0.33	4.33E-01	7.58E-01	KYNU	kynureninase (L-kynurenine hydrolase)	chr2q22.2	217388_s_at	NM_001032998 /// NM_003937																				
6.68	6.82	0.14	4.33E-01	7.58E-01	MAP4	microtubule-associated protein 4	chr3p21	200836_s_at	NM_001134364 /// NM_001134365 /// NM_002375 /// NM_030884 /// NM_030885																				
3.79	3.93	0.14	4.33E-01	7.58E-01	CNTN2	contactin 2 (axonal)	chr1q32.1	206970_at	NM_005076																				
2.65	2.76	0.11	4.33E-01	7.58E-01	---	---	---	215144_at	---																				
2.00	2.11	0.11	4.33E-01	7.58E-01	---	---	---	1561544_at	---																				
2.07	2.17	0.10	4.33E-01	7.58E-01	---	---	---	1563099_at	---																				
2.80	2.97	0.17	4.33E-01	7.58E-01	C2orf51	chromosome 2 open reading frame 51	chr2p11.2	241430_at	NM_152670																				
2.87	3.00	0.13	4.33E-01	7.58E-01	LOC157931	hypothetical protein LOC157931	chr9q34.3	1561990_at	---																				
2.51	2.62	0.11	4.33E-01	7.58E-01	---	---	---	1562751_at	---																				
2.30	2.40	0.10	4.33E-01	7.58E-01	---	---	---	237949_at	---																				
2.10	2.19	0.09	4.33E-01	7.58E-01	HTN1	histatin 1	chr4q13	206639_x_at	NM_002159																				
2.07	2.16	0.09	4.33E-01	7.58E-01	---	---	---	233542_at	---																				
6.40	6.92	0.52	4.34E-01	7.58E-01	LOC647190	similar to 40S ribosomal protein S16	chr6p12.1	1566079_at	XM_001723027 /// XM_930224 /// XM_941815																				
3.31	3.59	0.29	4.34E-01	7.58E-01	ZNF224	zinc finger protein 224	chr19q13.2	220019_s_at	NM_013398																				
3.15	3.34	0.19	4.34E-01	7.58E-01	C3orf23	chromosome 3 open reading frame 23	chr3p21.33-p21.32	241666_at	NM_001029839 /// NM_001029840 /// NM_173826																				
2.72	2.90	0.18	4.33E-01	7.58E-01	LZTS1	leucine zipper, putative tumor suppressor 1	chr8p22	221721_s_at	NM_021020																				
4.82	4.99	0.17	4.34E-01	7.58E-01	MKRN2	makorin ring finger protein 2	chr3p25	222510_s_at	NM_014160																				
3.03	3.18	0.15	4.33E-01	7.58E-01	---	---	---	240555_at	---																				
3.03	3.16	0.13	4.34E-01	7.58E-01	PLCH1	phospholipase C, eta 1	chr3q25.31	216633_s_at	NM_001130960 /// NM_001130961 /// NM_014996																				
2.76	2.89	0.13	4.34E-01	7.58E-01	---	---	---	232555_at	---																				

2.63	2.76	0.13	4.34E-01	7.58E-01	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	chr11q11-q12	205513_at	NM_001062
2.43	2.55	0.12	4.34E-01	7.58E-01	LOC283682	hypothetical protein LOC283682	chr15q26.1-q26.2	1562308_at	XM_378544 /// XM_944000
3.26	3.38	0.12	4.34E-01	7.58E-01	---	---	---	238159_at	---
3.40	3.51	0.11	4.33E-01	7.58E-01	---	---	---	237309_at	---
2.24	2.35	0.11	4.34E-01	7.58E-01	IL3	interleukin 3 (colony-stimulating factor, multiple)	chr5q31.1	207906_at	NM_000588
2.57	2.67	0.10	4.34E-01	7.58E-01	---	---	---	233478_at	---
2.28	2.37	0.09	4.33E-01	7.58E-01	NOG	noggin	chr17q21-q22	231798_at	NM_005450
3.78	3.90	0.12	4.34E-01	7.58E-01	MBOAT2	membrane bound O-acyltransferase domain containing 2	chr2p25.1	213288_at	NM_138799
2.11	2.20	0.10	4.34E-01	7.58E-01	MTBP	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa	chr8q24.12	233211_at	NM_022045
3.29	3.42	0.14	4.34E-01	7.58E-01	EVC	Ellis van Creveld syndrome	chr4p16	234421_s_at	NM_153717
2.19	2.30	0.11	4.34E-01	7.58E-01	GPR158	G protein-coupled receptor 158	chr10p12.1	232195_at	NM_020752
2.50	2.67	0.17	4.34E-01	7.58E-01	---	---	---	240484_at	---
6.04	6.19	0.15	4.34E-01	7.58E-01	HAGHL	hydroxyacylglutathione hydrolase-like	chr16p13.3	223485_at	NM_032304 /// NM_207112
5.31	5.69	0.38	4.34E-01	7.58E-01	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	chr1q41	218909_at	NM_012424
7.40	7.63	0.22	4.34E-01	7.58E-01	RAB4B	RAB4B, member RAS oncogene family	chr19q13.2	228521_s_at	NM_016154
4.29	4.45	0.15	4.34E-01	7.58E-01	UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	chr2q14.3	222569_at	NM_001025777 /// NM_020120
5.10	5.72	0.62	4.34E-01	7.58E-01	41340	membrane-associated ring finger (C3HC4) 7	chr2q24.2	202654_x_at	NM_022826
3.90	4.17	0.27	4.34E-01	7.59E-01	---	---	---	238030_at	---
8.25	8.46	0.21	4.34E-01	7.59E-01	PCYOX1	prenylcysteine oxidase 1	chr2p13.3	225274_at	NM_016297
9.17	9.35	0.18	4.34E-01	7.59E-01	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	chr18p11.31-p11.2	202941_at	NM_021074
2.53	2.97	0.44	4.34E-01	7.59E-01	NPNT	nephronectin	chr4q24	225911_at	NM_001033047
5.95	6.29	0.34	4.34E-01	7.59E-01	NOL8	nucleolar protein 8	chr9q22.31	218244_at	NM_017948 /// NR_024020
4.18	4.37	0.19	4.34E-01	7.59E-01	RNF207	Ring finger protein 207	chr1p36.31	244759_x_at	NM_207396 /// XM_001716213 /// XM_001718203 /// XM_001719665
2.97	3.13	0.16	4.34E-01	7.59E-01	---	---	---	244890_at	---
3.10	3.24	0.14	4.35E-01	7.59E-01	---	---	---	230403_at	---
2.09	2.19	0.10	4.35E-01	7.59E-01	---	---	---	1564794_at	---
2.13	2.23	0.10	4.35E-01	7.59E-01	TXNDC3	thioredoxin domain containing 3 (spermatozoa)	chr7p14.1	220384_at	NM_016616
6.58	6.81	0.22	4.35E-01	7.59E-01	MCFD2	multiple coagulation factor deficiency 2	chr2p21	212246_at	NM_139279
2.69	2.87	0.18	4.35E-01	7.59E-01	LOC100132798	Similar to hCG1774772	chr15q26.2	242396_at	XM_001721122 /// XM_001722414 /// XM_001722478
2.61	2.76	0.15	4.35E-01	7.59E-01	LOC401577	Hypothetical protein LOC401577	chrXp22.33	239247_at	XM_001714655 /// XM_001716015 /// XM_001717305 /// XM_379694
4.03	4.24	0.20	4.35E-01	7.59E-01	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	chr5q35.2	201171_at	NM_003945
3.22	3.39	0.17	4.35E-01	7.59E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHG1 /// IGHG3 /// IGHM /// IGHV4-31 /// IGHV@ /// LOC100133739	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable group /// similar to hCG2038920	chr14q32.33	211641_x_at	XM_001718220
2.22	2.37	0.15	4.35E-01	7.59E-01	CRTC3	CREB regulated transcription coactivator 3	chr15q26.1	232879_at	NM_001042574 /// NM_022769
4.62	4.92	0.30	4.35E-01	7.60E-01	METTL9	Methyltransferase like 9	chr16p13-p12	226220_at	NM_001077180 /// NM_016025
6.53	6.81	0.28	4.35E-01	7.60E-01	CHN1	chimerin (chimaerin) 1	chr2q31-q32.1	212624_s_at	NM_001025201 /// NM_001822
4.04	4.31	0.27	4.35E-01	7.60E-01	C8orf83	chromosome 8 open reading frame 83	chr8q22.1	225599_s_at	NR_015339 /// XR_041349 /// XR_041350 /// XR_041351
5.97	6.16	0.19	4.35E-01	7.60E-01	PCIF1	PDX1 C-terminal inhibiting factor 1	chr20q13.12	221762_s_at	NM_022104

2.61	2.76	0.15	4.35E-01	7.60E-01	NIN	ninein (GSK3B interacting protein)	chr14q22.1	224303_x_at	NM_016350 /// NM_020921 /// NM_182944 /// NM_182946
2.94	3.06	0.12	4.35E-01	7.60E-01	RNF2	ring finger protein 2	chr1q25.3	205215_at	NM_007212
3.34	3.46	0.12	4.35E-01	7.60E-01	---	---	---	1564334_at	---
2.11	2.23	0.11	4.35E-01	7.60E-01	---	---	---	1560889_a_at	---
2.34	2.46	0.11	4.35E-01	7.60E-01	---	---	---	232747_at	---
2.65	2.76	0.11	4.35E-01	7.60E-01	---	---	---	1553498_at	---
2.42	2.53	0.11	4.35E-01	7.60E-01	---	---	---	1569564_at	---
2.18	2.28	0.10	4.35E-01	7.60E-01	DIAPH3	diaphanous homolog 3 (Drosophila)	chr13q21.2	232596_at	NM_001042517 /// NM_030932
2.31	2.46	0.16	4.36E-01	7.60E-01	C5orf40	chromosome 5 open reading frame 40	chr5q33.3	1554801_at	NM_001001343
5.66	5.79	0.13	4.36E-01	7.60E-01	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	chr6p21.3	208527_x_at	NM_003518 /// NM_003522 /// NM_003523 /// NM_003525 /// NM_003526
1.93	2.05	0.12	4.36E-01	7.60E-01	HELB	helicase (DNA) B	chr12q14.3	1552787_at	NM_033647
8.74	8.81	0.07	4.36E-01	7.60E-01	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	chr1p36.33	200745_s_at	NM_002074
2.38	2.50	0.12	4.36E-01	7.60E-01	NARG1	NMDA receptor regulated 1	chr4q31.1	1556382_a_at	NM_057175
5.72	6.12	0.41	4.36E-01	7.60E-01	CCDC132	coiled-coil domain containing 132	chr7q21.3	226031_at	NM_017667 /// NM_024553
6.41	6.80	0.38	4.36E-01	7.60E-01	SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	chrXq26.3	203909_at	NM_001042537 /// NM_006359
3.42	3.77	0.35	4.36E-01	7.60E-01	SCYL2	SCY1-like 2 (S. cerevisiae)	chr12q23.1	221220_s_at	NM_017988
2.43	2.54	0.11	4.36E-01	7.60E-01	---	---	---	239634_at	---
2.52	2.68	0.15	4.36E-01	7.60E-01	---	---	---	1556740_at	---
2.96	3.11	0.15	4.36E-01	7.60E-01	ZFYVE28	zinc finger, FYVE domain containing 28	chr4p16.3	1569383_s_at	NM_020972
7.80	8.05	0.25	4.36E-01	7.60E-01	IK	IK cytokine, down-regulator of HLA II	chr2p15-p14|5q31.3	200066_at	NM_006083
3.51	3.67	0.16	4.36E-01	7.60E-01	ARTN	artemin	chr1p33-p32	210237_at	NM_003976 /// NM_057090 /// NM_057091 /// NM_057160
3.01	3.17	0.16	4.36E-01	7.60E-01	hCG_17324	primary ciliary dyskinesia protein 1	chr2q14.2	237151_s_at	NM_001029996
2.58	2.70	0.11	4.36E-01	7.60E-01	---	---	---	242498_x_at	---
5.46	5.81	0.35	4.36E-01	7.60E-01	ZDHHC17	zinc finger, DHHC-type containing 17	chr12q21.2	212982_at	NM_015336
1.98	2.07	0.10	4.36E-01	7.60E-01	---	---	---	1563026_at	---
2.28	2.36	0.09	4.36E-01	7.60E-01	---	---	---	244626_at	---
5.75	6.37	0.62	4.36E-01	7.60E-01	MSH6	mutS homolog 6 (E. coli)	chr2p16	211450_s_at	NM_000179
2.71	2.82	0.10	4.36E-01	7.60E-01	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	chr14q32.3-qter|14q32	229042_s_at	NM_001376
1.87	2.03	0.16	4.36E-01	7.60E-01	---	---	---	242258_at	---
2.92	3.07	0.15	4.37E-01	7.60E-01	CASP2	caspase 2, apoptosis-related cysteine peptidase	chr7q34-q35	209811_at	NM_032982 /// NM_032983
2.76	2.90	0.14	4.36E-01	7.60E-01	PHOX2B	paired-like homeobox 2b	chr4p12	207009_at	NM_003924
2.56	2.69	0.13	4.37E-01	7.60E-01	---	---	---	237334_at	---
2.52	2.64	0.13	4.36E-01	7.60E-01	RTEL1 /// TNFRSF6B	regulator of telomere elongation helicase 1 /// tumor necrosis factor receptor superfamily, member 6b, decoy	chr20q13.3	211526_s_at	NM_003823 /// NM_016434 /// NM_032945 /// NM_032957
2.16	2.29	0.12	4.37E-01	7.60E-01	---	---	---	238221_at	---
1.95	2.04	0.09	4.36E-01	7.60E-01	DNAH3	Dynein, axonemal, heavy chain 3	chr16p12.2	216415_at	NM_017539
3.27	3.41	0.13	4.37E-01	7.60E-01	ZNF823	zinc finger protein 823	chr19p13.2	229732_at	NM_001080493
2.49	2.59	0.10	4.37E-01	7.60E-01	ECHDC2	Enoyl Coenzyme A hydratase domain containing 2	chr1p32.3	239836_at	NM_018281
2.26	2.37	0.11	4.37E-01	7.61E-01	FGF14	fibroblast growth factor 14	chr13q34	230231_at	NM_004115 /// NM_175929
3.29	3.46	0.17	4.37E-01	7.61E-01	ATXN8OS	ATXN8 opposite strand (non-protein coding)	chr13q21	216404_at	NR_002717
4.54	4.67	0.13	4.37E-01	7.61E-01	ANTXR2	anthrax toxin receptor 2	chr4q21.21	1555536_at	NM_058172
3.81	3.92	0.12	4.37E-01	7.61E-01	---	---	---	237947_at	---
2.64	2.75	0.11	4.37E-01	7.61E-01	---	---	---	225937_at	---
2.19	2.30	0.11	4.37E-01	7.61E-01	---	---	---	1560958_s_at	---
2.07	2.23	0.16	4.37E-01	7.61E-01	---	---	---	243858_at	---
3.45	3.60	0.15	4.37E-01	7.61E-01	UBL4B	ubiquitin-like 4B	chr1p13.3	1558584_at	NM_203412
2.59	2.72	0.14	4.37E-01	7.61E-01	LBR	lamin B receptor	chr1q42.1	220644_at	NM_002296 /// NM_194442

3.73	3.84	0.11	4.37E-01	7.61E-01	---	---	---	238863_x_at	---
2.26	2.36	0.11	4.37E-01	7.61E-01	PHKG2	phosphorylase kinase, gamma 2 (testis)	chr16p12.1-p11.2	1556368_at	NM_000294
2.16	2.26	0.10	4.37E-01	7.61E-01	---	---	---	231555_at	---
2.08	2.18	0.10	4.37E-01	7.61E-01	CRH	corticotropin releasing hormone	chr8q13	205630_at	NM_000756
2.67	2.81	0.14	4.37E-01	7.61E-01	LRRC43	leucine rich repeat containing 43	chr12q24.31	1553729_s_at	NM_001098519 /// NM_152759
2.35	2.44	0.09	4.37E-01	7.61E-01	LOC220077	docking protein 1-like protein	chr11q13.4	216386_at	XR_017002 /// XR_019008 /// XR_041797
1.99	2.09	0.10	4.37E-01	7.61E-01	---	---	---	241833_at	---
3.40	3.53	0.13	4.37E-01	7.61E-01	---	---	---	31799_at	---
1.90	2.00	0.10	4.37E-01	7.61E-01	SUGT1 /// SUGT1P	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) /// suppressor of G2 allele of SKP1 pseudogene (S. cerevisiae)	chr13q14.3 /// chr9p13.3	234686_at	NM_001130912 /// NM_006704 /// NR_003667 /// XR_000597
3.68	3.91	0.22	4.37E-01	7.61E-01	---	---	---	235825_at	---
2.58	2.72	0.14	4.37E-01	7.61E-01	---	---	---	1561534_at	---
2.34	2.46	0.11	4.38E-01	7.61E-01	---	---	---	1556805_at	---
2.94	3.06	0.13	4.38E-01	7.61E-01	MUC12	mucin 12, cell surface associated	chr7q22	226654_at	XM_001714400 /// XM_001724943 /// XM_379904 /// XM_936315
2.47	2.59	0.12	4.38E-01	7.61E-01	RORA	RAR-related orphan receptor A	chr15q21-q22	239550_at	NM_002943 /// NM_134260 /// NM_134261 /// NM_134262
2.17	2.25	0.08	4.38E-01	7.61E-01	---	---	---	1563569_at	---
1.86	1.94	0.08	4.38E-01	7.61E-01	C4orf22	chromosome 4 open reading frame 22	chr4q21.21	231565_at	NM_152770
4.23	4.40	0.17	4.38E-01	7.61E-01	---	---	---	233384_at	---
2.54	2.70	0.16	4.38E-01	7.61E-01	---	---	---	237848_at	---
2.23	2.33	0.10	4.38E-01	7.61E-01	---	---	---	235965_at	---
3.49	3.60	0.11	4.38E-01	7.61E-01	NBN	Nibrin	chr8q21	240510_at	NM_001024688 /// NM_002485
6.40	6.80	0.40	4.38E-01	7.61E-01	KIAA1370	KIAA1370	chr15q21.2	225327_at	NM_019600
3.75	3.86	0.12	4.38E-01	7.61E-01	PCDH24	protocadherin 24	chr5q35.2	220186_s_at	NM_017675
2.10	2.19	0.09	4.38E-01	7.61E-01	DNAJC24	DnaJ (Hsp40) homolog, subfamily C, member 24	chr11p13	1570048_at	NM_181706
4.54	4.65	0.11	4.38E-01	7.61E-01	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	chr3p23-p21	201073_s_at	NM_003074
2.10	2.21	0.10	4.38E-01	7.61E-01	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	chr22q13.32	237094_at	NM_001082967 /// NM_015381
2.57	2.67	0.10	4.38E-01	7.61E-01	PHF2	PHD finger protein 2	chr9q22.31	207138_at	NM_005392
4.48	4.79	0.31	4.38E-01	7.61E-01	SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	chr6q13-q15	225354_s_at	NM_031469
5.64	5.80	0.16	4.38E-01	7.61E-01	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	chr19q13.4	211135_x_at	NM_001081450 /// NM_006864
2.05	2.16	0.11	4.38E-01	7.62E-01	ABRA	actin-binding Rho activating protein	chr8q23.1	1552732_at	NM_139166
9.20	9.41	0.21	4.38E-01	7.62E-01	CCT4	chaperonin containing TCP1, subunit 4 (delta)	chr2p15	200877_at	NM_006430
2.40	2.49	0.09	4.38E-01	7.62E-01	OR51B4	olfactory receptor, family 51, subfamily B, member 4	chr11p15	234469_at	NM_033179
2.97	3.13	0.16	4.38E-01	7.62E-01	UNC13A	unc-13 homolog A (C. elegans)	chr19p13.11	227453_at	NM_001080421
3.89	4.01	0.11	4.38E-01	7.62E-01	FLJ23865	hypothetical protein FLJ23865	chr22q13.1	1553372_at	XM_001723522 /// XM_001725274 /// XM_001726751
4.11	4.31	0.20	4.38E-01	7.62E-01	FNBP1	formin binding protein 1	chr9q34	230389_at	NM_015033
3.17	3.31	0.14	4.38E-01	7.62E-01	LACRT	lacritin	chr12q13	224540_at	NM_033277
2.24	2.36	0.12	4.38E-01	7.62E-01	C1orf84 /// KIAA0467	chromosome 1 open reading frame 84 /// KIAA0467	chr1p34.2	1569709_at	NM_001012961 /// NM_015284
6.78	7.29	0.52	4.38E-01	7.62E-01	COL4A1	collagen, type IV, alpha 1	chr13q34	211981_at	NM_001845
5.08	5.24	0.16	4.38E-01	7.62E-01	LARGE	like-glycosyltransferase	chr22q12.3	215543_s_at	NM_004737 /// NM_133642
3.15	3.30	0.15	4.38E-01	7.62E-01	GOLGA1	Golgi autoantigen, golgin subfamily a, 1	chr9q33.3	214997_at	NM_002077
2.46	2.59	0.13	4.39E-01	7.62E-01	---	---	---	238126_at	---
4.05	4.14	0.09	4.39E-01	7.62E-01	RBM33	RNA binding motif protein 33	chr7q36.3	231834_at	NM_001008408 /// NM_053043
2.02	2.10	0.08	4.39E-01	7.62E-01	LOC144920	hypothetical protein LOC144920	chr13q33.2	1561540_at	---
4.07	4.24	0.17	4.39E-01	7.62E-01	MED17	mediator complex subunit 17	chr11q14	223115_at	NM_004268
2.15	2.24	0.09	4.39E-01	7.62E-01	LOC91431	prematurely terminated mRNA decay factor-like	chr4q25	228859_at	NM_001099776

6.65	7.01	0.36	4.39E-01	7.62E-01	PDLIM1	PDZ and LIM domain 1	chr10q22-q26.3	208690_s_at	NM_020992
6.10	6.25	0.15	4.39E-01	7.62E-01	ATAD3A /// ATAD3C	ATPase family, AAA domain containing 3A /// ATPase family, AAA domain containing 3C	chr1p36.33	219068_x_at	NM_001039211 /// NM_018188
1.92	2.02	0.10	4.39E-01	7.62E-01	---	---	---	244613_at	---
4.92	5.34	0.43	4.39E-01	7.62E-01	EMCN	Endomucin	chr4q23	227874_at	NM_016242
2.26	2.41	0.15	4.39E-01	7.62E-01	GUCA1C	guanylate cyclase activator 1C	chr3q13.1	233902_at	NM_005459
3.97	4.10	0.14	4.39E-01	7.62E-01	ZNF628	zinc finger protein 628	chr19q13.42	236269_at	NM_033113
2.31	2.43	0.13	4.39E-01	7.62E-01	GSDMB	Gasdermin B	chr17q12	215659_at	NM_001042471 /// NM_018530
2.29	2.41	0.11	4.39E-01	7.62E-01	---	---	---	224249_at	---
2.90	3.01	0.11	4.39E-01	7.62E-01	DENND2C	DENN/MADD domain containing 2C	chr1p13.2	230769_at	NM_198459
7.22	7.33	0.10	4.39E-01	7.62E-01	HN1L	hematological and neurological expressed 1-like	chr16p13.3	212115_at	NM_144570
2.02	2.11	0.09	4.39E-01	7.62E-01	LOC338651	hypothetical protein LOC338651	chr11p15.5	1566219_at	NR_021489
5.98	6.33	0.35	4.39E-01	7.62E-01	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	chr6p21.2-p21.1	201801_s_at	NM_001078174 /// NM_001078175 /// NM_001078176 /// NM_001078177 /// NM_004955
3.21	3.33	0.12	4.39E-01	7.62E-01	SLC22A8	solute carrier family 22 (organic anion transporter), member 8	chr11q11	221298_s_at	NM_004254
6.24	6.66	0.42	4.39E-01	7.62E-01	FAS	Fas (TNF receptor superfamily, member 6)	chr10q24.1	204780_s_at	NM_000043 /// NM_152871 /// NM_152872 /// NM_152873 /// NM_152874 /// NM_152875 /// NM_152876 /// NM_152877
2.27	2.40	0.13	4.39E-01	7.62E-01	---	---	---	216166_at	---
4.14	4.59	0.45	4.39E-01	7.62E-01	UEVLD	UEV and lactate/malate dehyrogenase domains	chr11p15.1	1554397_s_at	NM_001040697 /// NM_018314
2.63	2.78	0.15	4.39E-01	7.62E-01	NMT2	N-myristoyltransferase 2	chr10p13	205005_s_at	NM_004808
6.92	7.26	0.34	4.40E-01	7.63E-01	TTLL12	tubulin tyrosine ligase-like family, member 12	chr22q13.31	1552257_a_at	NM_015140
4.51	4.66	0.15	4.40E-01	7.63E-01	LOC100129827	hypothetical protein LOC100129827	chr11p15.4	231595_at	XM_001716326 /// XM_001716909 /// XM_001717832
2.41	2.55	0.14	4.40E-01	7.63E-01	ZNF569	zinc finger protein 569	chr19q13.12	1553696_s_at	NM_152484
2.45	2.57	0.13	4.39E-01	7.63E-01	CLEC4G	C-type lectin superfamily 4, member G	chr19p13.2	1559065_a_at	NM_198492
2.34	2.47	0.13	4.40E-01	7.63E-01	---	---	---	216168_at	---
2.92	3.02	0.10	4.40E-01	7.63E-01	---	---	---	236098_at	---
2.49	2.58	0.10	4.40E-01	7.63E-01	IGHA1	immunoglobulin heavy constant alpha 1	chr14q32.33	234477_at	---
3.37	3.63	0.26	4.40E-01	7.63E-01	EXOC5	exocyst complex component 5	chr14q23.1	228418_at	NM_006544
4.13	4.27	0.14	4.40E-01	7.63E-01	FOXO3	forkhead box O3	chr6q21	217399_s_at	NM_001455 /// NM_201559
2.81	2.91	0.10	4.40E-01	7.63E-01	---	---	---	240379_at	---
2.67	2.77	0.10	4.40E-01	7.63E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1565065_at	NM_153003
2.97	3.13	0.15	4.40E-01	7.63E-01	CCR10	chemokine (C-C motif) receptor 10	chr17q21.1-q21.3	220565_at	NM_016602
2.07	2.16	0.09	4.40E-01	7.63E-01	---	---	---	1561476_at	---
1.92	2.00	0.08	4.40E-01	7.63E-01	LOC100132788	Hypothetical protein LOC100132788	chr5p14.3	1558640_a_at	XM_001722155
4.79	4.97	0.18	4.40E-01	7.63E-01	---	---	---	233161_at	---
5.79	5.95	0.15	4.40E-01	7.63E-01	CYB5D1	cytochrome b5 domain containing 1	chr17p13.1	1552711_a_at	NM_144607
2.67	2.82	0.15	4.40E-01	7.63E-01	TRIM36	tripartite motif-containing 36	chr5q22.3	219736_at	NM_001017397 /// NM_001017398 /// NM_018700
4.07	4.20	0.13	4.40E-01	7.63E-01	FAM153A	family with sequence similarity 153, member A	chr5q35.3	211166_at	NM_173663
1.84	1.93	0.09	4.40E-01	7.63E-01	DEPDC1B	DEP domain containing 1B	chr5q12.1	226980_at	NM_018369
5.56	5.96	0.40	4.40E-01	7.63E-01	---	---	---	232081_at	---
3.66	3.91	0.25	4.40E-01	7.63E-01	---	---	---	230961_at	---
2.18	2.33	0.15	4.40E-01	7.63E-01	---	---	---	243972_at	---
3.56	3.68	0.12	4.40E-01	7.63E-01	---	---	---	234590_x_at	---
5.67	6.27	0.60	4.40E-01	7.63E-01	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	chr21q21.2	222162_s_at	NM_006988
6.98	7.27	0.29	4.40E-01	7.63E-01	FMOD	fibromodulin	chr1q32	202709_at	NM_002023
8.77	9.02	0.25	4.40E-01	7.63E-01	FKBP1A	FK506 binding protein 1A, 12kDa	chr20p13	200709_at	NM_000801 /// NM_054014
2.22	2.34	0.12	4.40E-01	7.63E-01	---	---	---	1562544_at	---

4.52	4.76	0.23	4.40E-01	7.63E-01	MAK10	MAK10 homolog, amino-acid N-acetyltransferase subunit (S. cerevisiae)	chr9q21.33	219362_at	NM_024635
3.40	3.53	0.13	4.40E-01	7.63E-01	---	---	---	243104_at	---
4.46	4.54	0.09	4.40E-01	7.63E-01	SCAMP4	secretory carrier membrane protein 4	chr19p13.3	235073_at	NM_079834
2.38	2.94	0.56	4.41E-01	7.63E-01	RP13-102H20.1	hypothetical protein FLJ30058	chrXq26.1	238047_at	NM_144967
5.66	5.80	0.14	4.41E-01	7.63E-01	SFXN1	sideroflexin 1	---	218392_x_at	NM_022754
7.29	7.40	0.11	4.41E-01	7.63E-01	BAG1	BCL2-associated athanogene	chr9p12	211475_s_at	NM_004323
4.94	5.19	0.25	4.41E-01	7.63E-01	PAPD1	PAP associated domain containing 1	chr10p11.23	218947_s_at	NM_018109
4.00	4.43	0.43	4.41E-01	7.63E-01	COL5A2	collagen, type V, alpha 2	chr2q14-q32	221730_at	NM_000393
2.50	2.60	0.10	4.41E-01	7.63E-01	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	chr11q21-q22	204259_at	NM_002423
5.53	5.70	0.17	4.41E-01	7.63E-01	PERLD1	per1-like domain containing 1	chr17q12	221811_at	NM_033419
6.79	7.12	0.33	4.41E-01	7.63E-01	PLVAP	plasmalemma vesicle associated protein	chr19p13.2	221529_s_at	NM_031310
3.81	4.10	0.29	4.41E-01	7.63E-01	MIA3	melanoma inhibitory activity family, member 3	chr1q41	212310_at	NM_198551
2.92	3.08	0.16	4.41E-01	7.63E-01	---	---	---	240506_at	---
1.97	2.07	0.10	4.41E-01	7.63E-01	---	---	---	1556832_at	---
2.90	3.00	0.09	4.41E-01	7.63E-01	---	---	---	243741_at	---
3.23	3.80	0.57	4.41E-01	7.64E-01	FRZB	frizzled-related protein	chr2qter	203697_at	NM_001463
3.35	3.60	0.25	4.41E-01	7.64E-01	---	---	---	242171_at	---
4.72	4.89	0.18	4.41E-01	7.64E-01	RNF126P1	ring finger protein 126 pseudogene 1	chr17q22	222349_x_at	NR_002818
3.66	3.81	0.15	4.41E-01	7.64E-01	TFB2M	transcription factor B2, mitochondrial	chr1q44	1566931_at	NM_022366
3.59	3.71	0.12	4.41E-01	7.64E-01	---	---	---	244417_at	---
2.38	2.49	0.12	4.41E-01	7.64E-01	---	---	---	1559282_at	---
5.48	5.59	0.11	4.41E-01	7.64E-01	CDH22	cadherin-like 22	chr20q13.1	1569679_at	NM_021248
2.04	2.15	0.11	4.41E-01	7.64E-01	ZNF396	zinc finger protein 396	chr18q12	1570030_at	NM_145756
2.00	2.10	0.10	4.41E-01	7.64E-01	---	---	---	240921_at	---
2.89	3.03	0.14	4.41E-01	7.64E-01	KIAA1751	KIAA1751	chr1p36.33	216781_at	NM_001080484
2.27	2.40	0.14	4.41E-01	7.64E-01	PRO1768	PRO1768 protein	chr14q32.11	220852_at	XR_041811 /// XR_041812 /// XR_041813
2.47	2.60	0.13	4.41E-01	7.64E-01	LPIN1	lipin 1	chr2p25.1	212272_at	NM_145693
2.59	2.72	0.13	4.41E-01	7.64E-01	FARP2	FERM, RhoGEF and pleckstrin domain protein 2	chr2q37.3	1554337_at	NM_014808
1.92	2.03	0.11	4.41E-01	7.64E-01	C11orf87	chromosome 11 open reading frame 87	chr11q22.3	236532_at	NM_207645
1.89	1.99	0.10	4.41E-01	7.64E-01	---	---	---	233755_at	---
2.49	2.58	0.09	4.41E-01	7.64E-01	---	---	---	233521_at	---
2.20	2.29	0.09	4.41E-01	7.64E-01	---	---	---	1565601_at	---
6.74	6.83	0.09	4.41E-01	7.64E-01	GRIPAP1	GRIP1 associated protein 1	chrXp11	225451_at	NM_020137 /// NM_207672
6.25	6.63	0.39	4.41E-01	7.64E-01	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	chr2q31.2	211932_at	NM_194247
3.86	3.97	0.10	4.41E-01	7.64E-01	MYH14	myosin, heavy chain 14	chr19q13.33	232977_x_at	NM_001077186 /// NM_024729
3.60	3.81	0.21	4.41E-01	7.64E-01	---	---	---	240652_at	---
2.63	2.76	0.13	4.42E-01	7.64E-01	LOC653192 /// TRIM43	Tripartite motif-containing protein 43-like protein 1 /// tripartite motif-containing 43	chr2q11.1	1553618_at	NM_138800 /// XM_926437
2.31	2.41	0.10	4.42E-01	7.64E-01	CD200	CD200 molecule	chr3q12-q13	209582_s_at	NM_001004196 /// NM_005944
2.19	2.28	0.09	4.42E-01	7.64E-01	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	chr2q11.1-q11.2	205343_at	NM_001056 /// NM_176825
5.33	5.52	0.19	4.42E-01	7.64E-01	NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1	chr11q12	228424_at	NM_005468
2.99	3.15	0.16	4.42E-01	7.64E-01	B2M	Beta-2-microglobulin	chr15q21-q22.2	232311_at	NM_004048
4.94	5.16	0.22	4.42E-01	7.64E-01	WDR25	WD repeat domain 25	chr14q32.2	219609_at	NM_024515
2.17	2.28	0.11	4.42E-01	7.64E-01	TBX18	T-box 18	chr6q14-q15	1559840_s_at	NM_001080508
2.30	2.40	0.10	4.42E-01	7.64E-01	---	---	---	244101_at	---
4.93	5.16	0.23	4.42E-01	7.64E-01	RBM8A	RNA binding motif protein 8A	chr1q12	217856_at	NM_005105
2.18	2.31	0.12	4.42E-01	7.64E-01	C5orf42	chromosome 5 open reading frame 42	chr5p13.2	1562387_at	NM_023073
2.19	2.33	0.14	4.42E-01	7.64E-01	---	---	---	233201_at	---
3.14	3.26	0.12	4.42E-01	7.64E-01	CLEC4A	C-type lectin domain family 4, member A	chr12p13	221724_s_at	NM_016184 /// NM_194447 /// NM_194448 /// NM_194450
2.91	3.01	0.11	4.42E-01	7.64E-01	---	---	---	231089_at	---
2.32	2.47	0.15	4.42E-01	7.64E-01	AFAP1L2	actin filament associated protein 1-like 2	chr10q25.3	226829_at	NM_001001936 /// NM_032550
1.84	1.92	0.08	4.42E-01	7.64E-01	---	---	---	1560775_at	---
3.02	3.25	0.23	4.42E-01	7.64E-01	---	---	---	1565804_at	---
2.33	2.45	0.12	4.42E-01	7.64E-01	---	---	---	1570270_at	---
2.45	2.57	0.12	4.42E-01	7.64E-01	CCR4	chemokine (C-C motif) receptor 4	chr3p24	208376_at	NM_005508
2.36	2.45	0.09	4.42E-01	7.64E-01	SLITRK5	SLIT and NTRK-like family, member 5	chr13q31.2	214930_at	NM_015567
2.23	2.32	0.09	4.42E-01	7.64E-01	TSPAN2	tetraspanin 2	chr1p13.2	227236_at	NM_005725
2.43	2.57	0.14	4.42E-01	7.64E-01	MMP28	matrix metallopeptidase 28	chr17q11-q21.1	219909_at	NM_001032278 /// NM_024302
4.90	5.15	0.25	4.42E-01	7.64E-01	SKAP2	src kinase associated phosphoprotein 2	chr7p21-p15	204361_s_at	NM_003930

4.10	4.43	0.33	4.43E-01	7.64E-01	CCDC50	coiled-coil domain containing 50	chr3q28	235051_at	NM_174908 /// NM_178335
6.00	6.24	0.23	4.43E-01	7.65E-01	C17orf80	chromosome 17 open reading frame 80	chr17q25.1	223351_at	NM_001100621 /// NM_001100622 /// NM_017941
2.53	2.66	0.13	4.43E-01	7.65E-01	GLYATL1	glycine-N-acyltransferase-like 1	chr11q12.1	227695_at	NM_080661
3.48	3.86	0.37	4.43E-01	7.65E-01	SULF1	sulfatase 1	chr8q13.2-q13.3	212344_at	NM_001128204 /// NM_001128205 /// NM_001128206 /// NM_015170
2.15	2.26	0.11	4.43E-01	7.65E-01	FBXO42	F-box protein 42	chr1p36.23-p36.11	1559566_at	NM_018994
2.92	3.04	0.11	4.43E-01	7.65E-01	---	---	---	238781_at	---
7.37	7.58	0.21	4.43E-01	7.65E-01	APP	amyloid beta (A4) precursor protein	chr21q21.2|21q21.3	211277_x_at	NM_000484 /// NM_201413 /// NM_201414
2.11	2.22	0.11	4.43E-01	7.65E-01	LOC282980	hypothetical protein LOC282980	chr10p15.3	1564209_at	---
2.56	2.72	0.16	4.43E-01	7.65E-01	---	---	---	237364_at	---
5.46	5.97	0.51	4.43E-01	7.65E-01	COL5A1	collagen, type V, alpha 1	chr9q34.2-q34.3	212488_at	NM_000093
2.50	2.61	0.11	4.43E-01	7.65E-01	KIAA1648	KIAA1648 protein	chr22q12.1	232246_at	XM_001720903 /// XM_001723353 /// XM_001726321
5.40	5.65	0.25	4.43E-01	7.65E-01	SNX4	sorting nexin 4	chr3q21.2	212652_s_at	NM_003794
4.61	4.92	0.30	4.43E-01	7.65E-01	COPG2	coatomer protein complex, subunit gamma 2	chr7q32	223457_at	NM_012133
2.75	2.89	0.14	4.43E-01	7.65E-01	BMP8A	bone morphogenetic protein 8a	chr1p34.2	207866_at	NM_181809
4.48	4.61	0.14	4.43E-01	7.65E-01	PRKCG	protein kinase C, gamma	chr19q13.4	206270_at	NM_002739
2.40	2.52	0.13	4.43E-01	7.65E-01	OR10H3	olfactory receptor, family 10, subfamily H, member 3	chr19p13.1	208520_at	NM_013938
6.40	6.57	0.16	4.43E-01	7.65E-01	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	chrXq28	229436_x_at	NM_001018055 /// NM_024332
2.02	2.10	0.08	4.43E-01	7.65E-01	LOC400620	Hypothetical LOC400620	chr17q25.1	1562000_at	---
2.00	2.15	0.16	4.43E-01	7.65E-01	MANEA	mannosidase, endo-alpha	chr6q16.1	219003_s_at	NM_024641
4.92	5.29	0.37	4.43E-01	7.65E-01	SLC30A5	solute carrier family 30 (zinc transporter), member 5	chr5q12.1	218989_x_at	NM_022902 /// NM_024055
4.23	4.44	0.21	4.43E-01	7.65E-01	---	---	---	1559401_a_at	---
3.67	3.82	0.15	4.43E-01	7.65E-01	LOC100134081	similar to 3-phosphoinositide dependent protein kinase-1	---	244630_at	XM_001715304
5.69	5.80	0.12	4.43E-01	7.65E-01	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	chr16p12.3	213877_x_at	NM_007108 /// NM_207013
2.70	2.84	0.14	4.43E-01	7.65E-01	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	chr5q22.2	228259_s_at	NM_022140
2.73	2.84	0.11	4.43E-01	7.65E-01	LMO4	LIM domain only 4	chr1p22.3	227155_at	NM_006769
2.58	2.68	0.10	4.43E-01	7.65E-01	---	---	---	237258_at	---
2.45	2.56	0.10	4.43E-01	7.65E-01	BEST2	bestrophin 2	chr19p13.13	207432_at	NM_017682
2.51	2.60	0.09	4.43E-01	7.65E-01	---	---	---	211369_at	---
2.93	3.05	0.12	4.43E-01	7.65E-01	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	chr3p14.3-p14.2	233785_at	NM_182920
4.26	4.54	0.28	4.44E-01	7.65E-01	FBXO6	F-box protein 6	chr1p36.23-p36.11	231769_at	NM_018438
2.13	2.23	0.10	4.44E-01	7.65E-01	BAI3	brain-specific angiogenesis inhibitor 3	chr6q12	205638_at	NM_001704
6.72	7.04	0.32	4.44E-01	7.65E-01	UBL3	ubiquitin-like 3	chr13q12-q13	201535_at	NM_007106
3.06	3.14	0.09	4.44E-01	7.65E-01	C3orf36	chromosome 3 open reading frame 36	chr3q22.1	221175_at	NM_025041
2.67	2.83	0.16	4.44E-01	7.65E-01	LOC100134743	similar to PRO2751	---	224030_s_at	XM_001726727
3.79	4.14	0.36	4.44E-01	7.65E-01	C10orf128	chromosome 10 open reading frame 128	chr10q11.22	228372_at	NM_001010863
2.87	3.13	0.26	4.44E-01	7.65E-01	GLRB	glycine receptor, beta	chr4q31.3	205279_s_at	NM_000824
5.70	5.92	0.21	4.44E-01	7.65E-01	FLJ21438	hypothetical protein FLJ21438	chr19p13.12	228677_s_at	NM_022904
2.73	2.90	0.17	4.44E-01	7.65E-01	C20orf118	chromosome 20 open reading frame 118	chr20q11.23	233829_at	NM_080628
3.07	3.21	0.14	4.44E-01	7.65E-01	TMEM44	transmembrane protein 44	chr3q29	228054_at	NM_001011655 /// NM_138399
2.92	3.06	0.14	4.44E-01	7.65E-01	SETDB2	SET domain, bifurcated 2	chr13q14	1564970_at	NM_031915
2.17	2.31	0.13	4.44E-01	7.65E-01	TXK	TXK tyrosine kinase	chr4p12	206828_at	NM_003328
2.83	2.96	0.13	4.44E-01	7.65E-01	PSTK	phosphoseryl-tRNA kinase	chr10q26.13	240040_at	NM_153336
2.49	2.59	0.10	4.44E-01	7.65E-01	MED30	Mediator complex subunit 30	chr8q24.11	230555_s_at	NM_080651
2.88	2.98	0.10	4.44E-01	7.65E-01	HSPD1	Heat shock 60kDa protein 1 (chaperonin)	chr2q33.1	243845_at	NM_002156 /// NM_199440
3.10	3.19	0.10	4.44E-01	7.65E-01	---	---	---	243670_at	---
2.04	2.14	0.09	4.44E-01	7.65E-01	UNC5C	unc-5 homolog C (C. elegans)	chr4q21-q23	1555341_at	NM_003728

9.03	9.12	0.09	4.44E-01	7.65E-01	MRPL51	mitochondrial ribosomal protein L51	chr12p13.3-p13.1	223086_x_at	NM_016497
2.17	2.26	0.09	4.44E-01	7.65E-01	---	---	---	1558804_at	---
2.09	2.18	0.08	4.44E-01	7.65E-01	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	chr16q12.2	217213_at	NM_001043
3.55	3.96	0.41	4.44E-01	7.65E-01	ZNF160	zinc finger protein 160	chr19q13.41	1567032_s_at	NM_001102603 /// NM_033288 /// NM_198893
4.83	4.97	0.14	4.44E-01	7.65E-01	---	---	---	233779_x_at	---
2.66	2.80	0.14	4.44E-01	7.65E-01	PRR19	proline rich 19	chr19q13.2	231176_at	NM_199285
2.05	2.16	0.11	4.44E-01	7.65E-01	---	---	---	1560495_at	---
4.32	4.79	0.47	4.44E-01	7.65E-01	SNX4	sorting nexin 4	chr3q21.2	205329_s_at	NM_003794
1.88	1.97	0.09	4.44E-01	7.65E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	211751_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359
4.64	4.79	0.14	4.44E-01	7.65E-01	TMEM17	transmembrane protein 17	chr2p15	1557137_at	NM_198276
2.20	2.31	0.11	4.44E-01	7.65E-01	---	---	---	236659_x_at	---
4.99	5.16	0.17	4.44E-01	7.65E-01	TRAF2	TNF receptor-associated factor 2	chr9q34	204413_at	NM_021138
6.48	6.64	0.17	4.44E-01	7.65E-01	VAC14	Vac14 homolog (S. cerevisiae)	chr16q22.1	218169_at	NM_018052 /// XM_001724197 /// XM_001724956 /// XM_001726731
5.32	5.53	0.21	4.44E-01	7.65E-01	RCAN1	regulator of calcineurin 1	chr21q22.1-q22.2|21q22.12	208370_s_at	NM_004414 /// NM_203417 /// NM_203418
3.71	3.91	0.20	4.44E-01	7.65E-01	TNPO1	Transportin 1	chr5q13.2	1556116_s_at	NM_002270 /// NM_153188
5.66	5.76	0.10	4.44E-01	7.65E-01	---	---	---	213813_x_at	---
3.96	4.20	0.24	4.45E-01	7.66E-01	LMOD1	leiomodin 1 (smooth muscle)	chr1q32	211562_s_at	NM_012134
4.40	4.56	0.16	4.45E-01	7.66E-01	---	---	---	1556748_x_at	---
2.32	2.45	0.13	4.45E-01	7.66E-01	CDC6	cell division cycle 6 homolog (S. cerevisiae)	chr17q21.3	203968_s_at	NM_001254
2.35	2.47	0.12	4.45E-01	7.66E-01	RAG1	recombination activating gene 1	chr11p13	206591_at	NM_000448
3.81	4.01	0.20	4.45E-01	7.66E-01	SOBP	Sine oculis binding protein homolog (Drosophila)	chr6q21	234098_at	NM_018013
3.00	3.11	0.11	4.45E-01	7.66E-01	ROPN1	ropporin, rhophilin associated protein 1	chr3q21.1	231535_x_at	NM_017578
7.01	7.15	0.14	4.45E-01	7.66E-01	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	chr1q21-q22	204648_at	NM_000906
7.48	7.73	0.25	4.45E-01	7.66E-01	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	chr9q33-q34.1	201809_s_at	NM_000118 /// NM_001114753
3.73	3.91	0.17	4.45E-01	7.66E-01	LOC100131642	PP5241	chr20p12.1	1555410_at	XM_001724379 /// XM_001725610 /// XM_001725624
2.99	3.15	0.16	4.45E-01	7.66E-01	SLFN11	schlafen family member 11	chr17q12	226743_at	NM_001104587 /// NM_001104588 /// NM_001104589 /// NM_001104590 /// NM_152270
4.30	4.46	0.16	4.45E-01	7.66E-01	NTF3	neurotrophin 3	chr12p13	206706_at	NM_001102654 /// NM_002527
2.81	2.92	0.10	4.45E-01	7.66E-01	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	chr4q25-q27	236707_at	NM_014395
4.91	5.22	0.31	4.45E-01	7.66E-01	GIMAP8	GTPase, IMAP family member 8	chr7q36.1	235306_at	NM_175571
2.73	2.88	0.14	4.45E-01	7.66E-01	APOL5	apolipoprotein L, 5	chr22q12.3	220478_at	NM_030642
8.08	8.31	0.23	4.45E-01	7.66E-01	RAB9A	RAB9A, member RAS oncogene family	chrXp22.2	221808_at	NM_004251
3.78	3.95	0.18	4.45E-01	7.66E-01	LOC283501	hypothetical protein LOC283501	chr13q34	1556855_a_at	---
3.99	4.15	0.16	4.45E-01	7.66E-01	LMF1	lipase maturation factor 1	chr16p13.3	1569048_s_at	NM_022773
2.49	2.61	0.13	4.45E-01	7.66E-01	FBXL13	F-box and leucine-rich repeat protein 13	chr7q22.1	1553798_a_at	NM_001111038 /// NM_145032
2.63	2.72	0.09	4.45E-01	7.66E-01	RAB20	RAB20, member RAS oncogene family	chr13q34	237373_at	NM_017817
2.33	2.48	0.15	4.45E-01	7.66E-01	---	---	---	224120_at	---
1.95	2.05	0.10	4.45E-01	7.66E-01	---	---	---	244854_at	---
4.33	4.59	0.25	4.46E-01	7.66E-01	MBTPS2	membrane-bound transcription factor peptidase, site 2	chrXp22.13	206473_at	NM_015884
2.33	2.43	0.10	4.46E-01	7.66E-01	LOC100132078	hypothetical protein LOC100132078	chr11q23.1	1556844_at	XM_001725779

4.25	4.52	0.26	4.46E-01	7.66E-01	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	chr9p12	218943_s_at	NM_014314
1.88	1.98	0.09	4.46E-01	7.66E-01	---	---	---	240952_at	---
2.73	2.83	0.09	4.46E-01	7.66E-01	TGM7	transglutaminase 7	chr15q15.2	237288_at	NM_052955
4.02	4.38	0.36	4.46E-01	7.67E-01	---	---	---	237945_at	---
2.23	2.36	0.13	4.46E-01	7.67E-01	LOC285043	hypothetical protein LOC285043	chr2p23.3	1559605_a_at	---
3.48	3.63	0.15	4.46E-01	7.67E-01	LOC90393	hypothetical protein LOC90393	chr15q25.2	229668_at	---
2.29	2.40	0.11	4.46E-01	7.67E-01	---	---	---	240035_at	---
2.16	2.27	0.11	4.46E-01	7.67E-01	SLFNL1	schlafen-like 1	chr1p34.2	1553315_at	NM_144990
3.25	3.36	0.11	4.46E-01	7.67E-01	BNC2	basonuclin 2	chr9p22.3-p22.2	229942_at	NM_017637
2.01	2.09	0.08	4.46E-01	7.67E-01	---	---	---	1564368_a_at	---
4.19	4.67	0.47	4.46E-01	7.67E-01	DOCK5	Dedicator of cytokinesis 5	chr8p21.2	230263_s_at	NM_024940
3.83	3.98	0.16	4.46E-01	7.67E-01	RAB7A	RAB7A, member RAS oncogene family	chr3q21.3	223760_s_at	NM_004637
3.63	3.75	0.12	4.46E-01	7.67E-01	GPR35	G protein-coupled receptor 35	chr2q37.3	210264_at	NM_005301
2.09	2.19	0.10	4.46E-01	7.67E-01	---	---	---	242630_at	---
2.06	2.16	0.10	4.46E-01	7.67E-01	---	---	---	239123_at	---
2.77	2.89	0.11	4.46E-01	7.67E-01	CST11	cystatin 11	chr20p11.21	233968_at	NM_080830 /// NM_130794
2.69	2.84	0.15	4.46E-01	7.67E-01	LOC441009	Hypothetical LOC441009	chr4p15.33	1561471_at	XM_001723280 /// XM_498965 /// XM_944418
2.09	2.20	0.11	4.46E-01	7.67E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	217063_x_at	---
4.47	4.62	0.16	4.46E-01	7.67E-01	GNGT2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	chr17q21	235139_at	NM_031498
4.93	5.05	0.12	4.46E-01	7.67E-01	TFCP2	Transcription factor CP2	chr12q13	227637_at	NM_005653
3.96	4.12	0.16	4.46E-01	7.67E-01	HSPC111	hypothetical protein HSPC111	chr5q35.2	209327_s_at	NM_016391
3.13	3.29	0.16	4.46E-01	7.67E-01	---	---	---	1556206_at	---
2.68	2.79	0.12	4.46E-01	7.67E-01	C6orf25	chromosome 6 open reading frame 25	chr6p21.33	221342_at	NM_025260 /// NM_138272 /// NM_138273 /// NM_138274 /// NM_138275 /// NM_138277
6.39	6.67	0.28	4.47E-01	7.67E-01	---	---	---	231069_at	---
5.31	5.52	0.21	4.46E-01	7.67E-01	CLEC11A	C-type lectin domain family 11, member A	chr19q13.3	210783_x_at	NM_002975
2.95	3.14	0.19	4.47E-01	7.67E-01	GTF2H2B	general transcription factor IIH, polypeptide 2B	chr5q13.2	215470_at	NM_001098729
4.81	4.99	0.18	4.47E-01	7.67E-01	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	chr18q22.3	227049_at	NM_175907
2.84	3.02	0.17	4.46E-01	7.67E-01	GTSF1	gametocyte specific factor 1	chr12q13.2	227711_at	NM_144594
3.85	3.99	0.15	4.47E-01	7.67E-01	USP42	ubiquitin specific peptidase 42	chr7p22.1	226176_s_at	NM_032172
3.10	3.22	0.11	4.47E-01	7.67E-01	DEFB1	defensin, beta 1	chr8p23.2-p23.1	210397_at	NM_005218
1.96	2.07	0.10	4.47E-01	7.67E-01	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	chrYq11	1570359_at	NM_001122665 /// NM_004660
2.20	2.32	0.12	4.47E-01	7.67E-01	LST-3TM12 /// SLCO1B1 /// SLCO1B3	organic anion transporter LST-3b /// solute carrier organic anion transporter family, member 1B1 /// solute carrier organic anion transporter family, member 1B3	chr12p /// chr12p12 /// chr12p12.2	206354_at	NM_001009562 /// NM_006446 /// NM_019844
3.72	3.84	0.12	4.47E-01	7.67E-01	LOC90520	hypothetical protein LOC90520	chr7q36.1	233342_at	---
7.49	8.60	1.11	4.47E-01	7.67E-01	IGK@ /// IGKC	immunoglobulin kappa locus /// immunoglobulin kappa constant	chr2p12	224795_x_at	---
5.24	5.60	0.35	4.47E-01	7.67E-01	WDR48	WD repeat domain 48	chr3p21.33	222157_s_at	NM_020839
4.21	4.54	0.33	4.47E-01	7.67E-01	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	chr13q32	208499_s_at	NM_006260
2.26	2.41	0.15	4.47E-01	7.67E-01	---	---	---	1557709_at	---
2.94	3.06	0.12	4.47E-01	7.67E-01	---	---	---	229987_at	---
2.28	2.39	0.11	4.47E-01	7.67E-01	SLC28A1	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	chr15q25-q26	231187_at	NM_004213 /// NM_201651
2.07	2.16	0.09	4.47E-01	7.67E-01	RNF165	ring finger protein 165	chr18q21.1	1557545_s_at	NM_152470
1.85	1.93	0.08	4.47E-01	7.67E-01	---	---	---	241109_at	---
2.83	2.91	0.09	4.47E-01	7.67E-01	---	---	---	1556339_a_at	---
4.82	4.97	0.15	4.47E-01	7.67E-01	---	---	---	220033_at	---
2.22	2.32	0.10	4.47E-01	7.67E-01	---	---	---	1569698_s_at	---
4.93	5.32	0.39	4.47E-01	7.67E-01	PHF20L1	PHD finger protein 20-like 1	chr8q24.22	222133_s_at	NM_016018 /// NM_032205 /// NM_198513
3.50	3.63	0.13	4.47E-01	7.67E-01	NCR1	natural cytotoxicity triggering receptor 1	chr19q13.42	217095_x_at	NM_004829
7.98	8.10	0.12	4.47E-01	7.67E-01	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7	chr2q37.3	213465_s_at	NM_002712
2.81	2.92	0.11	4.47E-01	7.67E-01	---	---	---	237445_at	---
4.18	4.27	0.10	4.47E-01	7.67E-01	PAX8	paired box 8	chr2q12-q14	207923_x_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992
2.00	2.09	0.09	4.47E-01	7.67E-01	---	---	---	216669_at	---
6.38	6.60	0.22	4.47E-01	7.67E-01	RBM26	RNA binding motif protein 26	chr13q31.1	218422_s_at	NM_022118

3.57	3.76	0.19	4.47E-01	7.67E-01	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	chr2q33-q34	236356_at	NM_005006
3.75	3.92	0.17	4.47E-01	7.67E-01	TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	chr6p21.1	1556978_a_at	NM_138572
2.37	2.53	0.16	4.47E-01	7.67E-01	PHF11	PHD finger protein 11	chr13q14.3	242060_x_at	NM_001040443 /// NM_001040444
7.10	7.25	0.15	4.47E-01	7.67E-01	C6orf47	chromosome 6 open reading frame 47	chr6p21.3	204968_at	NM_021184
3.01	3.16	0.15	4.47E-01	7.67E-01	---	---	---	243113_at	---
4.54	4.68	0.14	4.47E-01	7.67E-01	PPP1R3F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	chrXp11.23	229365_at	NM_033215
2.73	2.86	0.13	4.47E-01	7.67E-01	---	---	---	241087_at	---
3.35	3.47	0.13	4.47E-01	7.67E-01	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	chr8q13	1556227_at	NM_025054
3.25	3.37	0.12	4.47E-01	7.67E-01	ANKMY1	ankyrin repeat and MYND domain containing 1	chr2q37.3	210486_at	NM_016552 /// NM_017844
2.32	2.43	0.11	4.47E-01	7.67E-01	IRX1	iroquois homeobox 1	chr5p15.3	230472_at	NM_024337
2.96	3.06	0.11	4.47E-01	7.67E-01	TSC22D2	TSC22 domain family, member 2	chr3q25.1	210953_at	NM_014779
1.96	2.05	0.09	4.48E-01	7.67E-01	THADA	thyroid adenoma associated	chr2p21	1554492_at	NM_001083953 /// NM_022065
2.21	2.34	0.13	4.48E-01	7.67E-01	MCM10	minichromosome maintenance complex component 10	chr10p13	220651_s_at	NM_018518 /// NM_182751
2.47	2.60	0.12	4.48E-01	7.67E-01	---	---	---	243391_x_at	---
5.43	5.78	0.35	4.48E-01	7.67E-01	SEC23IP	SEC23 interacting protein	chr10q25-q26	216392_s_at	NM_007190
1.82	1.92	0.10	4.48E-01	7.67E-01	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	chr1q32.1	1555444_a_at	NM_002481 /// NM_032103 /// NM_032104 /// NM_032105
2.15	2.25	0.10	4.48E-01	7.68E-01	ZNF235	zinc finger protein 235	chr19q13.2	210595_at	NM_004234
2.89	3.03	0.14	4.48E-01	7.68E-01	---	---	---	237801_at	---
2.05	2.14	0.09	4.48E-01	7.68E-01	LOC100132234	Similar to hCG2020055	chr13q12.2	232448_at	XM_001720013 /// XM_001723160 /// XM_001724063
6.85	6.96	0.11	4.48E-01	7.68E-01	LYRM1	LYR motif containing 1	chr16p11.2	203897_at	NM_001128301 /// NM_001128302 /// NM_020424
3.61	3.91	0.30	4.48E-01	7.68E-01	---	---	---	227610_at	---
6.42	6.70	0.28	4.48E-01	7.68E-01	---	---	---	226128_at	---
6.34	6.61	0.27	4.48E-01	7.68E-01	RNF14	ring finger protein 14	chr5q23.3-q31.1	201824_at	NM_004290 /// NM_183398 /// NM_183399 /// NM_183400 /// NM_183401
2.10	2.22	0.12	4.48E-01	7.68E-01	---	---	---	1568832_a_at	---
3.40	3.52	0.12	4.48E-01	7.68E-01	---	---	---	1568894_at	---
2.73	2.84	0.11	4.48E-01	7.68E-01	---	---	---	235921_at	---
1.93	2.02	0.09	4.48E-01	7.68E-01	TRAT1	T cell receptor associated transmembrane adaptor 1	chr3q13	217147_s_at	NM_016388
3.12	3.24	0.12	4.48E-01	7.68E-01	C21orf105	chromosome 21 open reading frame 105	chr21q22.3	232191_at	---
2.74	2.85	0.11	4.48E-01	7.68E-01	SLC26A1	solute carrier family 26 (sulfate transporter), member 1	chr4p16.3	1552843_at	NM_022042 /// NM_134425 /// NM_213613
2.84	3.02	0.18	4.48E-01	7.68E-01	COL12A1	collagen, type XII, alpha 1	chr6q12-q13	231879_at	NM_004370 /// NM_080645
2.68	2.82	0.14	4.48E-01	7.68E-01	---	---	---	238293_at	---
1.90	1.99	0.09	4.48E-01	7.68E-01	SLC10A4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	chr4p12	239913_at	NM_152679
3.09	3.27	0.18	4.49E-01	7.68E-01	PRAMEF11	PRAME family member 11	chr1p36.21	217365_at	XM_001714028 /// XM_001714837 /// XM_001715375
3.48	3.60	0.12	4.49E-01	7.68E-01	SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	chr6p23	221010_s_at	NM_012241 /// NM_031244
2.86	2.97	0.11	4.49E-01	7.68E-01	LIPH	lipase, member H	chr3q27	235871_at	NM_139248
2.65	2.77	0.11	4.49E-01	7.68E-01	---	---	---	240095_at	---
2.21	2.30	0.09	4.49E-01	7.68E-01	---	---	---	243169_at	---
1.90	1.99	0.09	4.49E-01	7.68E-01	LRRFIP2	Leucine rich repeat (in FLII) interacting protein 2	chr3p22.2	232673_at	NM_001134369 /// NM_006309 /// NM_017724

2.12	2.20	0.09	4.49E-01	7.68E-01	RP3-398D13.1	hypothetical protein FLJ33708	chr6p25.1	1553428_at	NM_173675																					
2.07	2.20	0.13	4.49E-01	7.68E-01	CASC1	cancer susceptibility candidate 1	chr12p12.1	220168_at	NM_001082972 /// NM_001082973 /// NM_018272																					
2.72	2.86	0.14	4.49E-01	7.68E-01	GRIK3	glutamate receptor, ionotropic, kainate 3	chr1p34-p33	207454_at	NM_000831																					
2.21	2.32	0.11	4.49E-01	7.68E-01	---	---	---	237135_at	---																					
6.18	6.34	0.16	4.49E-01	7.68E-01	ELP3	elongation protein 3 homolog (S. cerevisiae)	chr8p21.1	227075_at	NM_018091																					
2.41	2.55	0.15	4.49E-01	7.68E-01	---	---	---	1569542_at	---																					
2.95	3.07	0.12	4.49E-01	7.68E-01	---	---	---	1559567_at	---																					
6.53	6.76	0.23	4.49E-01	7.68E-01	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	chr16q13	221090_s_at	NM_018233																					
3.35	3.48	0.14	4.49E-01	7.68E-01	LOC100131040 /// TRIM36	hypothetical protein LOC100131040 /// tripartite motif-containing 36	chr5q22.3	1565814_at	NM_001017397 /// NM_001017398 /// NM_018700 /// XM_001714504 /// XM_001715034 /// XM_001716984																					
3.38	3.52	0.14	4.49E-01	7.68E-01	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	chr21q22.3	219723_x_at	NM_001037553 /// NM_020132																					
2.24	2.36	0.12	4.49E-01	7.68E-01	LOC100132178	similar to hCG2008275	chr19q13.42	223872_at	XM_001725491 /// XM_001725533 /// XM_001726429																					
3.76	3.96	0.20	4.49E-01	7.69E-01	PRICKLE1	Prickle homolog 1 (Drosophila)	chr12q12	230708_at	NM_153026																					
2.48	2.56	0.08	4.49E-01	7.69E-01	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	chr9q22.33	211348_s_at	NM_001077181 /// NM_003671 /// NM_033331																					
5.94	6.33	0.39	4.49E-01	7.69E-01	INTS12	integrator complex subunit 12	chr4q24	218616_at	NM_020395																					
2.30	2.40	0.10	4.49E-01	7.69E-01	CA10	carbonic anhydrase X	chr17q21.33	223550_s_at	NM_001082533 /// NM_001082534 /// NM_020178																					
5.57	5.87	0.30	4.49E-01	7.69E-01	ZNF281	zinc finger protein 281	chr1q32.1	222619_at	NM_012482																					
2.20	2.31	0.11	4.49E-01	7.69E-01	SFRS4	splicing factor, arginine/serine-rich 4	chr1p35.3	239511_s_at	NM_005626																					
2.05	2.16	0.11	4.49E-01	7.69E-01	PPP3R2	protein phosphatase 3 (formerly 2B), regulatory subunit B, beta isoform	chr9q31.1	244782_at	NM_147180																					
2.83	2.97	0.13	4.49E-01	7.69E-01	LOC100131509	similar to inward rectifying K+ channel negative regulator Kir2.2v	---	208566_at	XM_001718636																					
1.96	2.04	0.08	4.49E-01	7.69E-01	NT5DC4	5'-nucleotidase domain containing 4	chr2q13	1562019_at	XM_001715677 /// XM_001716359 /// XM_001716541																					
4.73	4.85	0.12	4.49E-01	7.69E-01	SNF8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	chr17q21.32	242790_at	NM_007241																					
2.42	2.53	0.10	4.50E-01	7.69E-01	ADAM17	ADAM metallopeptidase domain 17	chr2p25	237897_at	NM_003183																					
2.38	2.48	0.09	4.50E-01	7.69E-01	OPRM1	opioid receptor, mu 1	chr6q24-q25	207994_s_at	NM_000914 /// NM_001008503 /// NM_001008504 /// NM_001008505																					
2.29	2.40	0.11	4.50E-01	7.69E-01	C6orf118	chromosome 6 open reading frame 118	chr6q27	232777_s_at	NM_144980																					
4.82	4.99	0.18	4.50E-01	7.69E-01	NPAS2	neuronal PAS domain protein 2	chr2q11.2	205459_s_at	NM_002518																					
3.75	4.02	0.27	4.50E-01	7.69E-01	---	---	---	215435_at	---																					
4.18	4.37	0.19	4.50E-01	7.69E-01	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	chr20q12	211003_x_at	NM_004613 /// NM_198951																					
1.76	1.84	0.08	4.50E-01	7.69E-01	---	---	---	1569663_at	---																					
5.30	5.43	0.12	4.50E-01	7.69E-01	HSD11B1L	hydroxysteroid (11-beta) dehydrogenase 1-like	chr19p13.3	228757_at	NM_198533 /// NM_198704 /// NM_198705 /// NM_198706 /// NM_198707 /// NM_198708																					
2.86	2.99	0.13	4.50E-01	7.69E-01	EHD4	EH-domain containing 4	chr15q11.1	1556608_a_at	NM_139265																					
4.44	4.55	0.11	4.50E-01	7.69E-01	C6orf15	chromosome 6 open reading frame 15	chr6p21.3	221100_at	NM_014070																					

2.44	2.58	0.14	4.50E-01	7.69E-01	ALG5	asparagine-linked glycosylation 5 homolog (S. cerevisiae, dolichyl-phosphate beta-glucosyltransferase)	chr13q13.3	222556_at	NM_013338
2.86	2.97	0.12	4.50E-01	7.69E-01	C6orf12	chromosome 6 open reading frame 12	chr6p21.33	234445_at	XR_041144 /// XR_041145
2.59	2.76	0.18	4.50E-01	7.69E-01	---	---	---	232320_at	---
3.56	3.70	0.14	4.50E-01	7.69E-01	PIGO	phosphatidylinositol glycan anchor biosynthesis, class O	chr9p13.3	214990_at	NM_032634 /// NM_152850
1.94	2.07	0.13	4.50E-01	7.69E-01	---	---	---	237101_at	---
2.22	2.34	0.12	4.50E-01	7.69E-01	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	chr6p12.3	204161_s_at	NM_014936
2.75	2.85	0.10	4.50E-01	7.69E-01	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	chr8q13	234988_at	NM_025054
2.35	2.49	0.14	4.50E-01	7.69E-01	MAP1A	microtubule-associated protein 1A	chr15q13-qter	215391_at	NM_002373
2.31	2.43	0.12	4.50E-01	7.69E-01	---	---	---	1562742_at	---
2.17	2.28	0.10	4.50E-01	7.69E-01	LOC100131662	hypothetical LOC100131662	chr2q11.1	236973_at	XM_001714052 /// XM_001716469 /// XM_001717290
7.98	8.19	0.21	4.50E-01	7.69E-01	EIF5A	eukaryotic translation initiation factor 5A	chr17p13-p12	201122_x_at	NM_001970 /// XM_001724572
2.72	2.83	0.11	4.50E-01	7.69E-01	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	chr14q24.3	203982_s_at	NM_005050 /// NR_003256
3.01	3.11	0.10	4.50E-01	7.69E-01	KCNJ11	potassium inwardly-rectifying channel, subfamily J, member 11	chr11p15.1	231740_at	NM_000525
2.62	2.74	0.12	4.50E-01	7.69E-01	---	---	---	1562007_at	---
2.84	2.97	0.13	4.50E-01	7.69E-01	GJA5	gap junction protein, alpha 5, 40kDa	chr1q21.1	214466_at	NM_005266 /// NM_181703
2.09	2.24	0.15	4.51E-01	7.69E-01	---	---	---	231654_s_at	---
6.39	6.68	0.29	4.51E-01	7.70E-01	VEZF1	vascular endothelial zinc finger 1	chr17q22	202173_s_at	NM_007146
4.20	4.31	0.11	4.51E-01	7.70E-01	---	---	---	240550_at	---
2.36	2.44	0.08	4.51E-01	7.70E-01	---	---	---	210848_at	---
5.00	5.42	0.42	4.51E-01	7.70E-01	BACE2	beta-site APP-cleaving enzyme 2	chr21q22.3	222446_s_at	NM_012105 /// NM_138991 /// NM_138992
2.04	2.13	0.09	4.51E-01	7.70E-01	CLCA2	CLCA family member 2, chloride channel regulator	chr1p31-p22	206166_s_at	NM_006536
4.10	4.24	0.15	4.51E-01	7.70E-01	FAM109B	family with sequence similarity 109, member B	chr22q13.2	226504_at	NM_001002034
5.05	5.32	0.27	4.51E-01	7.70E-01	C21orf91	chromosome 21 open reading frame 91	chr21q21.1	226109_at	NM_001100420 /// NM_001100421 /// NM_017447
7.86	8.07	0.21	4.51E-01	7.70E-01	RWDD1	RWD domain containing 1	chr6q13-q22.33	219598_s_at	NM_001007464 /// NM_015952 /// NM_016104
4.55	4.92	0.37	4.51E-01	7.70E-01	FH	fumarate hydratase	chr1q42.1	203032_s_at	NM_000143
4.81	4.96	0.15	4.51E-01	7.70E-01	GGT1	gamma-glutamyltransferase 1	chr22q11.23	211417_x_at	NM_001032364 /// NM_001032365 /// NM_005265 /// NM_013430
3.33	3.47	0.14	4.51E-01	7.70E-01	TTTY7	testis-specific transcript, Y-linked 7	chrYp11.2	233151_s_at	NR_001534
3.86	3.98	0.12	4.51E-01	7.70E-01	MBP	myelin basic protein	chr18q23	207323_s_at	NM_001025081 /// NM_001025090 /// NM_001025092 /// NM_001025100 /// NM_001025101 /// NM_002385

2.17	2.28	0.11	4.51E-01	7.70E-01	TTC23	tetratricopeptide repeat domain 23	chr15q26.3	232734_at	NM_001040655 /// NM_001040656 /// NM_001040657 /// NM_001040658 /// NM_001040659 /// NM_001040660 /// NM_022905
1.93	2.02	0.09	4.51E-01	7.70E-01	---	---	---	1560063_a_at	---
2.66	2.74	0.08	4.51E-01	7.70E-01	---	---	---	231476_at	---
2.39	2.54	0.16	4.51E-01	7.70E-01	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	chr6p21.1-p11.2	220432_s_at	NM_016593
2.88	2.99	0.11	4.51E-01	7.70E-01	CALML3	calmodulin-like 3	chr10pter-p13	210019_at	NM_005185
2.06	2.15	0.09	4.51E-01	7.70E-01	COL29A1	collagen, type XXIX, alpha 1	chr3q22.1	1553835_a_at	NM_153264 /// NR_022012
2.14	2.22	0.08	4.51E-01	7.70E-01	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	chr2q24	208288_at	NM_003742
2.62	2.74	0.11	4.51E-01	7.70E-01	CD3G	CD3g molecule, gamma (CD3-TCR complex)	chr11q23	206804_at	NM_000073
4.20	4.40	0.19	4.51E-01	7.70E-01	MYNN	myoneurin	chr3q26.2	218926_at	NM_018657
2.62	2.73	0.11	4.51E-01	7.70E-01	---	---	---	1562678_at	---
2.70	2.85	0.15	4.51E-01	7.70E-01	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	chr10p13	232473_at	NM_003675
2.26	2.38	0.12	4.51E-01	7.70E-01	---	---	---	228818_at	---
2.37	2.49	0.12	4.52E-01	7.70E-01	---	---	---	1569952_x_at	---
2.36	2.46	0.10	4.52E-01	7.70E-01	RPGRIP1L	RPGRIP1-like	chr16q12.2	241028_at	NM_001127897 /// NM_015272
1.98	2.12	0.14	4.52E-01	7.70E-01	---	---	---	1570628_at	---
3.13	3.27	0.14	4.52E-01	7.70E-01	SLC34A1	solute carrier family 34 (sodium phosphate), member 1	chr5q35	208177_at	NM_003052
1.80	1.90	0.10	4.52E-01	7.70E-01	LOC100134365	hypothetical protein LOC100134365	---	238464_at	XM_001715832
3.16	3.24	0.09	4.52E-01	7.70E-01	---	---	---	233016_at	---
2.33	2.41	0.08	4.52E-01	7.70E-01	TAS2R4	taste receptor, type 2, member 4	chr7q31.3-q32	221392_at	NM_016944
6.56	6.94	0.38	4.52E-01	7.70E-01	PIK3C3	phosphoinositide-3-kinase, class 3	chr18q12.3	204297_at	NM_002647
4.02	4.19	0.17	4.52E-01	7.70E-01	CD86	CD86 molecule	chr3q21	205685_at	NM_006889 /// NM_175862
2.52	2.63	0.12	4.52E-01	7.70E-01	C2orf46	chromosome 2 open reading frame 46	chr2p25.1	1562717_at	XR_040099 /// XR_040100 /// XR_040101
4.21	4.40	0.19	4.52E-01	7.70E-01	---	---	---	232952_at	---
3.78	3.94	0.16	4.52E-01	7.70E-01	---	---	---	240887_at	---
3.84	3.95	0.11	4.52E-01	7.70E-01	C7orf30	chromosome 7 open reading frame 30	chr7p15.3	244641_at	NM_138446
2.23	2.34	0.10	4.52E-01	7.70E-01	---	---	---	244369_at	---
2.78	2.93	0.14	4.52E-01	7.70E-01	---	---	---	242826_at	---
2.42	2.52	0.11	4.52E-01	7.70E-01	FSCB	fibrous sheath CABYR binding protein	chr14q21.3	224274_at	NM_032135
6.44	6.81	0.37	4.52E-01	7.70E-01	FXYD5	FXYD domain containing ion transport regulator 5	chr19q12-q13.1	218084_x_at	NM_014164 /// NM_144779
4.48	4.58	0.10	4.52E-01	7.70E-01	CFC1B	Cripto, FRL-1, cryptic family 1B	chr2q21.1	228878_s_at	NM_001079530
2.42	2.52	0.10	4.52E-01	7.70E-01	---	---	---	1554813_at	---
4.05	4.18	0.13	4.52E-01	7.70E-01	MAT1A	methionine adenosyltransferase I, alpha	chr10q22	205813_s_at	NM_000429
2.04	2.16	0.12	4.52E-01	7.70E-01	MYO1D	myosin ID	chr17q11-q12	1555397_at	NM_015194
3.38	3.50	0.12	4.52E-01	7.70E-01	B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	chr11q13.4	1552833_at	NM_138706
4.69	5.33	0.63	4.52E-01	7.70E-01	NAMPT	nicotinamide phosphoribosyltransferase	chr7q22.2	1555167_s_at	NM_005746
4.90	5.21	0.31	4.52E-01	7.70E-01	CLRN1	clarin 1	chr3q25	1555695_a_at	NM_052995 /// NM_174878
2.99	3.28	0.29	4.52E-01	7.70E-01	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	chr3q24-q25.1	206637_at	NM_001081455 /// NM_014879
3.90	4.15	0.25	4.52E-01	7.70E-01	---	---	---	239619_at	---
6.07	6.29	0.23	4.52E-01	7.70E-01	FIG4	FIG4 homolog (S. cerevisiae)	chr6q21	203656_at	NM_014845
3.22	3.39	0.17	4.52E-01	7.70E-01	SPATA18	spermatogenesis associated 18 homolog (rat)	chr4q12	230723_at	NM_145263
2.10	2.24	0.14	4.52E-01	7.70E-01	---	---	---	1566695_at	---
2.94	3.08	0.13	4.52E-01	7.70E-01	---	---	---	237627_at	---
3.45	3.56	0.11	4.52E-01	7.70E-01	TYRO3	TYRO3 protein tyrosine kinase	chr15q15.1-q21.1	211431_s_at	NM_006293
2.99	3.10	0.11	4.52E-01	7.70E-01	LOC401442	hypothetical gene supported by BC028401	chr8p23.3	1568827_at	XR_040277 /// XR_040278 /// XR_040279
2.16	2.27	0.11	4.52E-01	7.70E-01	LOC100130452	similar to hCG1777700	chr2q33.1	244518_at	XM_001715212 /// XM_001723842 /// XM_001723860
2.29	2.40	0.10	4.52E-01	7.70E-01	---	---	---	1569904_x_at	---

2.75	2.85	0.10	4.52E-01	7.70E-01	KRTAP19-3	keratin associated protein 19-3	chr21q22.1	240967_at	NM_181609
2.69	2.78	0.09	4.52E-01	7.70E-01	FCAR	Fc fragment of IgA, receptor for	chr19q13.2-q13.4	211305_x_at	NM_002000 /// NM_133269 /// NM_133271 /// NM_133272 /// NM_133273 /// NM_133274 /// NM_133277 /// NM_133278 /// NM_133279
5.42	5.56	0.14	4.53E-01	7.70E-01	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	chr11q11-q13	204632_at	NM_001006944 /// NM_003942
2.16	2.26	0.10	4.53E-01	7.70E-01	FLJ37078	Hypothetical protein FLJ37078	chr7q11.23	1558725_at	NM_001110199 /// XM_001713635 /// XM_001713636 /// XM_001713637 /// XM_001713638
3.82	4.12	0.30	4.53E-01	7.71E-01	FEM1C	fem-1 homolog c (C. elegans)	chr5q22	213341_at	NM_020177
2.03	2.15	0.11	4.53E-01	7.71E-01	---	---	---	233707_at	---
2.69	2.85	0.16	4.53E-01	7.71E-01	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	chr2q24	211224_s_at	NM_003742
2.14	2.25	0.11	4.53E-01	7.71E-01	---	---	---	216171_at	---
1.94	2.02	0.08	4.53E-01	7.71E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	214887_at	NM_001079691 /// NM_052818
2.00	2.14	0.14	4.53E-01	7.71E-01	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	chr2q14	215508_at	NM_004336
4.79	4.93	0.14	4.53E-01	7.71E-01	SAV1	salvador homolog 1 (Drosophila)	chr14q13-q23	234491_s_at	NM_021818
2.49	2.62	0.12	4.53E-01	7.71E-01	---	---	---	232126_at	---
2.53	2.65	0.12	4.53E-01	7.71E-01	---	---	---	234261_at	---
3.58	3.77	0.19	4.53E-01	7.71E-01	FOXS1	forkhead box S1	chr20q11.21	229731_at	NM_004118
3.23	3.40	0.17	4.53E-01	7.71E-01	GGT7	gamma-glutamyltransferase 7	chr20q11.22	226471_at	NM_178026
5.53	5.98	0.45	4.53E-01	7.71E-01	---	---	---	235538_at	---
2.68	2.87	0.19	4.53E-01	7.71E-01	S100A10	S100 calcium binding protein A10	chr1q21	238909_at	NM_002966
2.48	2.65	0.17	4.53E-01	7.71E-01	LOC730057	Hypothetical LOC730057	chr3p14.1	233113_at	XM_001132251 /// XM_001132871 /// XM_001716450
3.46	3.63	0.16	4.53E-01	7.71E-01	---	---	---	243157_at	---
2.60	2.71	0.11	4.53E-01	7.71E-01	SOBP	Sine oculis binding protein homolog (Drosophila)	chr6q21	229646_at	NM_018013
6.28	6.45	0.17	4.53E-01	7.71E-01	DAGLB	diacylglycerol lipase, beta	chr7p22.1	225832_s_at	NM_139179
5.76	5.91	0.15	4.53E-01	7.71E-01	RHPN1	rhophilin, Rho GTPase binding protein 1	chr8q24.3	228405_at	NM_052924
3.75	3.89	0.14	4.53E-01	7.71E-01	---	---	---	244544_at	---
2.96	3.08	0.12	4.53E-01	7.71E-01	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D	chr7q22.1	242229_at	NM_001122838 /// NM_198990
2.50	2.59	0.09	4.53E-01	7.71E-01	LYZL1 /// LYZL2	lysozyme-like 1 /// lysozyme-like 2	chr10p11.23	233973_at	NM_032517 /// NM_183058
5.18	5.38	0.21	4.53E-01	7.71E-01	ZDHHC14	zinc finger, DHHC-type containing 14	chr6q25.3	219247_s_at	NM_024630 /// NM_153746
2.43	2.56	0.12	4.54E-01	7.71E-01	WNT8A	wingless-type MMTV integration site family, member 8A	chr5q31	224259_at	NM_058244
3.05	3.20	0.15	4.54E-01	7.71E-01	RG9MTD2	RNA (guanine-9-) methyltransferase domain containing 2	chr4q23	230243_at	NM_001134665 /// NM_001134666 /// NM_152292
1.98	2.08	0.10	4.54E-01	7.71E-01	---	---	---	241194_at	---
2.02	2.11	0.10	4.54E-01	7.71E-01	---	---	---	1559814_at	---
2.31	2.41	0.10	4.54E-01	7.71E-01	TPD52	tumor protein D52	chr8q21	201689_s_at	NM_001025252 /// NM_001025253 /// NM_005079
2.24	2.36	0.11	4.54E-01	7.71E-01	C2orf3	Chromosome 2 open reading frame 3	chr2p11.2-p11.1	237531_at	NM_003203
3.41	3.55	0.14	4.54E-01	7.71E-01	---	---	---	1569501_at	---
3.13	3.25	0.12	4.54E-01	7.71E-01	SYT12	Synaptotagmin XII	chr11q13.1	215860_at	NM_177963
3.57	3.82	0.25	4.54E-01	7.71E-01	KIN	KIN, antigenic determinant of recA protein homolog (mouse)	chr10p15-p14	205664_at	NM_012311
3.54	3.75	0.20	4.54E-01	7.71E-01	---	---	---	235525_at	---
2.40	2.50	0.10	4.54E-01	7.71E-01	---	---	---	243583_at	---

1.92	2.00	0.08	4.54E-01	7.71E-01	---	---	---	1557829_at	---
6.51	6.87	0.36	4.54E-01	7.71E-01	FUSIP1 /// LOC642558	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1	chr1p36.11	210178_x_at	NM_006625 /// NM_054016 /// XM_001713958 /// XM_001713979
2.36	2.50	0.14	4.54E-01	7.71E-01	MGC16385	Hypothetical protein MGC16385	chr16q24.3	229171_at	NM_145039
4.26	4.39	0.13	4.54E-01	7.71E-01	MTMR15	Myotubularin related protein 15	chr15q13.2-q13.3	232016_at	NM_014967
2.66	2.76	0.10	4.54E-01	7.71E-01	MMP15	matrix metallopeptidase 15 (membrane-inserted)	chr16q13-q21	243883_at	NM_002428
2.13	2.21	0.08	4.54E-01	7.71E-01	INTS10	integrator complex subunit 10	chr8p21.3	1560172_at	NM_018142
10.90	11.08	0.18	4.54E-01	7.71E-01	PABPC1	poly(A) binding protein, cytoplasmic 1	chr8q22.2-q23	215157_x_at	NM_002568
2.61	2.77	0.16	4.54E-01	7.72E-01	GPR39	G protein-coupled receptor 39	chr2q21-q22	208600_s_at	NM_001508
2.01	2.09	0.08	4.54E-01	7.72E-01	AKAP14	A kinase (PRKA) anchor protein 14	chrXq24	237281_at	NM_001008534 /// NM_001008535 /// NM_178813
6.19	6.56	0.37	4.54E-01	7.72E-01	SPTBN1	spectrin, beta, non-erythrocytic 1	chr2p21	200671_s_at	NM_003128 /// NM_178313
7.35	7.53	0.18	4.54E-01	7.72E-01	CCBL2	cysteine conjugate-beta lyase 2	chr1p22.2	209472_at	NM_001008661 /// NM_001008662 /// NM_019610
2.81	2.99	0.18	4.54E-01	7.72E-01	---	---	---	235701_at	---
2.10	2.22	0.11	4.54E-01	7.72E-01	ZNF831	zinc finger protein 831	chr20q13.32	1558827_a_at	NM_178457
1.91	2.01	0.10	4.54E-01	7.72E-01	---	---	---	1556081_at	---
2.12	2.21	0.09	4.54E-01	7.72E-01	LOC400768	hypothetical gene supported by BC051808	chr1p13.3	239337_at	XM_378883
2.53	2.61	0.08	4.54E-01	7.72E-01	AK5	adenylate kinase 5	chr1p31	222862_s_at	NM_012093 /// NM_174858
1.90	1.98	0.08	4.54E-01	7.72E-01	---	---	---	1564169_at	---
5.61	5.85	0.24	4.55E-01	7.72E-01	FAM172A	family with sequence similarity 172, member A	chr5q15	212936_at	NM_032042
2.05	2.18	0.14	4.55E-01	7.72E-01	IL7	interleukin 7	chr8q12-q13	206693_at	NM_000880
7.36	7.75	0.39	4.55E-01	7.72E-01	GPBP1	GC-rich promoter binding protein 1	chr5q11.2	223705_s_at	NM_001127235 /// NM_001127236 /// NM_022913
4.75	4.88	0.13	4.55E-01	7.72E-01	FCRL2	Fc receptor-like 2	chr1q21	224194_at	NM_030764 /// NM_138738
1.90	1.99	0.09	4.55E-01	7.72E-01	BRDT	bromodomain, testis-specific	chr1p22.1	206787_at	NM_001726 /// NM_207189
2.33	2.46	0.13	4.55E-01	7.72E-01	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	chr3q13.31	1560695_at	NM_024638
2.54	2.63	0.10	4.55E-01	7.72E-01	FLJ10038	hypothetical protein FLJ10038	chr15q15.3	205511_at	---
2.35	2.44	0.09	4.55E-01	7.72E-01	---	---	---	237976_at	---
3.10	3.20	0.10	4.55E-01	7.72E-01	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2	chr12q24.31	235255_at	NM_012463
1.95	2.04	0.09	4.55E-01	7.72E-01	---	---	---	1556884_a_at	---
2.38	2.47	0.09	4.55E-01	7.72E-01	CD4	CD4 molecule	chr12pter-p12	216424_at	NM_000616
2.01	2.09	0.08	4.55E-01	7.72E-01	---	---	---	1557468_at	---
4.45	4.67	0.22	4.55E-01	7.72E-01	NEK1	NIMA (never in mitosis gene a)-related kinase 1	chr4q33	213331_s_at	NM_012224
3.17	3.39	0.22	4.55E-01	7.72E-01	TMTC3	transmembrane and tetratricopeptide repeat containing 3	chr12q21.32	226600_at	NM_181783
6.10	6.22	0.12	4.55E-01	7.72E-01	C17orf85	chromosome 17 open reading frame 85	chr17p13.2	222779_s_at	NM_001114118 /// NM_018553
2.08	2.20	0.12	4.55E-01	7.72E-01	RP4-621O15.2	hypothetical protein FLJ31401	chr1q42.13	1553299_at	XR_041137
2.03	2.14	0.11	4.55E-01	7.72E-01	---	---	---	236489_at	---
2.04	2.13	0.08	4.55E-01	7.72E-01	---	---	---	1566772_at	---
1.87	1.95	0.08	4.55E-01	7.72E-01	RP1-177G6.2	hypothetical protein LOC286411	chrXq27.1	1557133_at	NM_001126492 /// XM_932619 /// XM_942964
5.91	6.14	0.23	4.55E-01	7.72E-01	---	---	---	229640_x_at	---
4.72	4.86	0.14	4.55E-01	7.72E-01	CRYBB2	crystallin, beta B2	chr22q11.2-q12.1|22q11.23	206778_at	NM_000496
3.67	3.83	0.15	4.55E-01	7.72E-01	PHF20	PHD finger protein 20	chr20q11.22-q11.23	209423_s_at	NM_016436
4.46	4.57	0.10	4.55E-01	7.72E-01	---	---	---	222260_at	---
3.13	3.23	0.10	4.56E-01	7.72E-01	---	---	---	234674_at	---
2.15	2.25	0.10	4.56E-01	7.72E-01	---	---	---	231674_at	---
7.09	7.25	0.16	4.56E-01	7.72E-01	TAGLN2	transgelin 2	chr1q21-q25	210978_s_at	NM_003564
5.14	5.32	0.18	4.56E-01	7.73E-01	FAR1	fatty acyl CoA reductase 1	chr11p15.2	224865_at	NM_032228
4.78	5.07	0.29	4.56E-01	7.73E-01	---	---	---	242143_at	---
2.46	2.56	0.10	4.56E-01	7.73E-01	MTMR6	myotubularin related protein 6	chr13q12	228789_at	NM_004685
6.35	6.72	0.38	4.56E-01	7.73E-01	CNOT2	CCR4-NOT transcription complex, subunit 2	chr12q15	222182_s_at	NM_014515
1.91	2.00	0.09	4.56E-01	7.73E-01	RP3-398D13.1	hypothetical protein FLJ33708	chr6p25.1	1556366_s_at	NM_173675
2.66	2.78	0.12	4.56E-01	7.73E-01	---	---	---	230711_at	---

2.59	2.70	0.11	4.56E-01	7.73E-01	COL19A1	collagen, type XIX, alpha 1	chr6q12-q13	211011_at	NM_001858
2.16	2.24	0.08	4.56E-01	7.73E-01	---	---	---	234330_at	---
7.85	8.21	0.36	4.56E-01	7.73E-01	IFITM1	interferon induced transmembrane protein 1 (9-27)	chr11p15.5	214022_s_at	NM_003641
4.24	4.38	0.15	4.56E-01	7.73E-01	---	---	---	1566432_at	---
2.27	2.38	0.10	4.56E-01	7.73E-01	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	chr2q31.1	222827_s_at	NM_006063
2.28	2.38	0.09	4.56E-01	7.73E-01	---	---	---	239872_at	---
3.46	3.62	0.16	4.56E-01	7.73E-01	---	---	---	226365_at	---
8.73	8.88	0.16	4.56E-01	7.73E-01	DDAH1	dimethylarginine dimethylaminohydrolase 1	chr1p22	209094_at	NM_001134445 /// NM_012137
2.88	3.03	0.15	4.56E-01	7.73E-01	STK32A	serine/threonine kinase 32A	chr5q32	1553938_a_at	NM_001112724 /// NM_145001
2.87	2.98	0.12	4.56E-01	7.73E-01	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	chr1q21.1	214474_at	NM_005399
2.16	2.26	0.10	4.56E-01	7.73E-01	---	---	---	1558354_s_at	---
2.87	2.96	0.09	4.56E-01	7.73E-01	LY6K	lymphocyte antigen 6 complex, locus K	chr8q24.3	223687_s_at	NM_017527
2.16	2.25	0.08	4.56E-01	7.73E-01	LOC388692	hypothetical gene supported by AK123662	chr1q21.1	235185_s_at	XR_039906 /// XR_039907 /// XR_039908
6.15	6.41	0.25	4.56E-01	7.73E-01	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	chr4q12	212855_at	NM_001040402 /// NM_015115
2.80	2.94	0.14	4.57E-01	7.73E-01	---	---	---	1558438_a_at	---
5.30	5.56	0.25	4.57E-01	7.73E-01	---	---	---	229321_s_at	---
3.46	3.70	0.24	4.57E-01	7.73E-01	TRIP11	thyroid hormone receptor interactor 11	chr14q31-q32	209778_at	NM_004239
5.16	5.28	0.11	4.57E-01	7.73E-01	RPL35A	Ribosomal protein L35a	chr3q29-qter	215208_x_at	NM_000996
4.79	5.08	0.29	4.57E-01	7.73E-01	MRPL50	mitochondrial ribosomal protein L50	chr9q31.1	225580_at	NM_019051
3.07	3.18	0.10	4.57E-01	7.74E-01	C9orf130	chromosome 9 open reading frame 130	chr9q22.32	234429_at	NR_023389 /// NR_023390 /// XM_001722853 /// XM_001724349 /// XM_001732875
3.16	3.29	0.14	4.57E-01	7.74E-01	WSCD2	WSC domain containing 2	chr12q23.3	229032_at	NM_014653
2.16	2.26	0.10	4.57E-01	7.74E-01	PTGDR	prostaglandin D2 receptor (DP)	chr14q22.1	215894_at	NM_000953
4.30	4.68	0.38	4.57E-01	7.74E-01	TGFBR1	Transforming growth factor, beta receptor 1	chr9q22	236561_at	NM_001130916 /// NM_004612
2.39	2.50	0.11	4.57E-01	7.74E-01	---	---	---	230858_at	---
2.41	2.50	0.09	4.57E-01	7.74E-01	DNTT	Deoxynucleotidyltransferase, terminal	chr10q23-q24	1566362_at	NM_001017520 /// NM_004088
2.95	3.10	0.15	4.57E-01	7.74E-01	PYGB	Phosphorylase, glycogen; brain	chr20p11.2-p11.1	243238_at	NM_002862
5.70	6.13	0.43	4.57E-01	7.74E-01	---	---	---	229024_at	---
2.80	3.21	0.41	4.57E-01	7.74E-01	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	chr4q12-q13	214146_s_at	NM_002704
3.98	4.14	0.16	4.57E-01	7.74E-01	---	---	---	216658_at	---
2.52	2.66	0.14	4.57E-01	7.74E-01	CAPN9	calpain 9	chr1q42.11-q42.3	208063_s_at	NM_006615 /// NM_016452
2.96	3.10	0.14	4.57E-01	7.74E-01	---	---	---	1565705_x_at	---
4.03	4.16	0.13	4.57E-01	7.74E-01	ACY3	aspartoacylase (aminocyclase) 3	chr11q13.2	230481_at	NM_080658
2.96	3.06	0.10	4.57E-01	7.74E-01	CD36	CD36 molecule (thrombospondin receptor)	chr7q11.2	209554_at	NM_000072 /// NM_001001547 /// NM_001001548 /// NM_001127443 /// NM_001127444
2.46	2.56	0.10	4.57E-01	7.74E-01	---	---	---	1562576_at	---
7.60	7.95	0.35	4.57E-01	7.74E-01	CYFIP2	cytoplasmic FMR1 interacting protein 2	chr5q33.3	215785_s_at	NM_001037332 /// NM_001037333 /// NM_014376
4.26	4.61	0.34	4.57E-01	7.74E-01	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	chr17q23.1	211578_s_at	NM_003161
2.17	2.34	0.18	4.58E-01	7.74E-01	---	---	---	244482_at	---
4.13	4.29	0.16	4.57E-01	7.74E-01	ACVRL1	activin A receptor type II-like 1	chr12q11-q14	210838_s_at	NM_000020 /// NM_001077401
2.33	2.49	0.16	4.57E-01	7.74E-01	---	---	---	235876_at	---

2.92	3.05	0.13	4.57E-01	7.74E-01	A2BP1	ataxin 2-binding protein 1	chr16p13.3	1553422_s_at	NM_018723 /// NM_145891 /// NM_145892 /// NM_145893																					
3.09	3.21	0.12	4.58E-01	7.74E-01	---	---	---	239115_at	---																					
2.49	2.61	0.12	4.58E-01	7.74E-01	---	---	---	230631_s_at	---																					
2.09	2.19	0.10	4.58E-01	7.74E-01	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1	chr4p12	241805_at	NM_173536																					
2.62	2.72	0.10	4.58E-01	7.74E-01	TMC5	Transmembrane channel-like 5	chr16p12.3	240303_at	NM_001105248 /// NM_001105249 /// NM_024780																					
1.98	2.07	0.10	4.58E-01	7.74E-01	PLCH1	phospholipase C, eta 1	chr3q25.31	216634_at	NM_001130960 /// NM_001130961 /// NM_014996																					
1.87	1.95	0.08	4.57E-01	7.74E-01	C10orf107	chromosome 10 open reading frame 107	chr10q21.2	1553630_at	NM_173554																					
6.03	6.21	0.18	4.58E-01	7.74E-01	HDAC8	histone deacetylase 8	chrXq13	223345_at	NM_018486																					
2.17	2.26	0.09	4.58E-01	7.74E-01	SLAIN2	SLAIN motif family, member 2	chr4p12	224843_at	NM_020846																					
1.97	2.08	0.11	4.58E-01	7.74E-01	UBR2	ubiquitin protein ligase E3 component n-recognin 2	chr6p21.1	1569140_at	NM_015255																					
2.07	2.15	0.08	4.58E-01	7.74E-01	LOC644852	hypothetical LOC644852	chr1q44	1554307_at	XR_040314 /// XR_040315 /// XR_040316																					
4.36	4.49	0.13	4.58E-01	7.74E-01	ZNF71	zinc finger protein 71	chr19q13.4	233754_x_at	NM_021216																					
3.98	4.30	0.32	4.58E-01	7.74E-01	ENAH	enabled homolog (Drosophila)	chr1q42.12	222434_at	NM_001008493 /// NM_018212																					
2.24	2.34	0.10	4.58E-01	7.74E-01	---	---	---	238922_at	---																					
1.77	1.88	0.10	4.58E-01	7.74E-01	LOC253573	hypothetical protein LOC253573	chr3q27.3	1557871_at	XM_934672 /// XM_945539																					
2.64	2.77	0.13	4.58E-01	7.74E-01	---	---	---	239191_at	---																					
2.04	2.12	0.08	4.58E-01	7.74E-01	---	---	---	244275_at	---																					
2.59	2.84	0.25	4.58E-01	7.74E-01	RBM34	RNA binding motif protein 34	chr1q42.3	214943_s_at	NM_015014																					
5.41	5.54	0.14	4.58E-01	7.74E-01	CDK5RAP2	CDK5 regulatory subunit associated protein 2	chr9q33.2	220935_s_at	NM_001011649 /// NM_018249																					
2.85	2.97	0.12	4.58E-01	7.74E-01	---	---	---	1566653_at	---																					
2.55	2.65	0.10	4.58E-01	7.74E-01	MOG	myelin oligodendrocyte glycoprotein	chr6p22.1	1555807_a_at	NM_001008228 /// NM_001008229 /// NM_002433 /// NM_206809 /// NM_206810 /// NM_206811 /// NM_206812 /// NM_206813 /// NM_206814																					
2.44	2.52	0.08	4.58E-01	7.74E-01	---	---	---	243989_at	---																					
2.13	2.21	0.08	4.58E-01	7.74E-01	---	---	---	AFFX-r2-Bs-phe-3_at	---																					
7.84	8.01	0.17	4.58E-01	7.74E-01	---	---	---	AFFX-r2-Ec-bioC-5_at	---																					
2.42	2.55	0.13	4.58E-01	7.74E-01	---	---	---	237442_at	---																					
1.99	2.11	0.12	4.58E-01	7.74E-01	MMP21	matrix metallopeptidase 21	chr10q26.2	1552592_at	NM_147191																					
2.19	2.29	0.09	4.58E-01	7.74E-01	---	---	---	233704_at	---																					
2.66	2.76	0.10	4.58E-01	7.74E-01	ULBP1	UL16 binding protein 1	chr6q25	221323_at	NM_025218																					
3.25	3.37	0.12	4.58E-01	7.74E-01	OPN4	opsin 4	chr10q22	234226_at	NM_001030015 /// NM_033282																					
1.88	2.00	0.12	4.58E-01	7.74E-01	---	---	---	1570622_at	---																					
3.04	3.15	0.11	4.58E-01	7.74E-01	---	---	---	241767_at	---																					
2.72	2.84	0.12	4.59E-01	7.74E-01	---	---	---	240763_at	---																					
2.26	2.37	0.11	4.59E-01	7.74E-01	CSNK2A1	Casein kinase 2, alpha 1 polypeptide	chr20p13	229216_s_at	NM_001895 /// NM_177559 /// NM_177560																					
2.54	2.70	0.15	4.59E-01	7.74E-01	---	---	---	1556432_at	---																					
2.37	2.48	0.11	4.59E-01	7.74E-01	MRGPRX2	MAS-related GPR, member X2	chr11p15.1	1553889_at	NM_054030																					
3.91	4.00	0.09	4.59E-01	7.74E-01	CLEC2L	C-type lectin domain family 2, member L	chr7q34	232173_at	NM_001080511																					
4.78	4.92	0.14	4.59E-01	7.74E-01	---	---	---	233315_at	---																					
2.65	2.91	0.26	4.59E-01	7.74E-01	MORF4L2	Mortality factor 4 like 2	chrXq22	243683_at	NM_012286																					
2.94	3.06	0.12	4.59E-01	7.74E-01	---	---	---	234169_at	---																					
3.31	3.43	0.11	4.59E-01	7.74E-01	PELI3	Pellino homolog 3 (Drosophila)	chr11q13.1	244214_at	NM_001098510 /// NM_145065																					

3.33	3.43	0.10	4.59E-01	7.74E-01	IGH@ /// IGHD /// IGHG1 /// LOC100134331 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33	217198_x_at	XM_001724554 /// XM_941465																				
1.91	2.01	0.10	4.59E-01	7.74E-01	LRRC2	leucine rich repeat containing 2	chr3p21.31	219949_at	NM_024512 /// NM_024750																				
2.16	2.25	0.09	4.59E-01	7.74E-01	FBXL13	F-box and leucine-rich repeat protein 13	chr7q22.1	1556770_a_at	NM_001111038 /// NM_145032																				
1.93	2.01	0.08	4.59E-01	7.74E-01	RNF32	ring finger protein 32	chr7q36	220991_s_at	NM_030936																				
2.76	2.86	0.10	4.59E-01	7.74E-01	C9orf148	chromosome 9 open reading frame 148	chr9q33.2	1559340_at	---																				
2.22	2.33	0.10	4.59E-01	7.75E-01	ZNF440	zinc finger protein 440	chr19p13.2	241731_x_at	NM_152357																				
6.63	6.84	0.21	4.59E-01	7.75E-01	PGRMC2	progesterone receptor membrane component 2	chr4q26	213227_at	NM_006320																				
3.04	3.34	0.30	4.59E-01	7.75E-01	---	---	---	243134_at	---																				
4.83	5.01	0.18	4.59E-01	7.75E-01	GYG2	glycogenin 2	chrXp22.3	215695_s_at	NM_001079855 /// NM_003918																				
2.73	2.84	0.12	4.59E-01	7.75E-01	CLDN6	claudin 6	chr16p13.3	237810_at	NM_021195																				
3.17	3.34	0.17	4.59E-01	7.75E-01	---	---	---	234991_at	---																				
2.52	2.65	0.14	4.59E-01	7.75E-01	GUCY2F	guanylate cyclase 2F, retinal	chrXq22	208053_at	NM_001522																				
1.96	2.09	0.13	4.59E-01	7.75E-01	---	---	---	242796_x_at	---																				
2.31	2.43	0.12	4.59E-01	7.75E-01	LOC338864	hypothetical protein LOC338864	chr13q21.33	237980_at	---																				
4.01	4.12	0.12	4.59E-01	7.75E-01	DHX37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	chr12q24.31	223364_s_at	NM_032656																				
1.93	2.04	0.10	4.59E-01	7.75E-01	---	---	---	235892_at	---																				
2.12	2.21	0.10	4.59E-01	7.75E-01	ST18	Suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	chr8q11.23	1570306_at	NM_014682																				
2.31	2.38	0.08	4.59E-01	7.75E-01	ATP1A4	ATPase, Na+/K+ transporting, alpha 4 polypeptide	chr1q21-q23	1558612_a_at	NM_001001734 /// NM_144699																				
1.93	2.04	0.11	4.59E-01	7.75E-01	---	---	---	1564795_at	---																				
2.66	2.78	0.12	4.60E-01	7.75E-01	OR8B8	olfactory receptor, family 8, subfamily B, member 8	chr11q24.2	1555212_at	NM_012378																				
2.59	2.71	0.13	4.60E-01	7.75E-01	MIOX	myo-inositol oxygenase	chr22q13.3	224179_s_at	NM_017584																				
3.87	3.99	0.13	4.60E-01	7.75E-01	PACRG	PARK2 co-regulated	chr6q26	215472_at	NM_001080378 /// NM_001080379 /// NM_152410																				
2.11	2.21	0.10	4.60E-01	7.75E-01	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	chr7q31.2	215702_s_at	NM_000492																				
4.26	4.61	0.35	4.60E-01	7.75E-01	---	---	---	243993_at	---																				
2.65	2.79	0.14	4.60E-01	7.75E-01	---	---	---	1562557_at	---																				
4.06	4.23	0.17	4.60E-01	7.75E-01	---	---	---	232583_at	---																				
2.91	3.02	0.11	4.60E-01	7.75E-01	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	chr5q13	231939_s_at	NM_018429																				
2.09	2.17	0.08	4.60E-01	7.75E-01	LOC400655	hypothetical gene supported by BC013370; BC034583	chr18q22.3	1561514_at	XM_378753 /// XM_932193 /// XM_944987 /// XM_944989																				
2.28	2.37	0.09	4.60E-01	7.75E-01	ST14	suppression of tumorigenicity 14 (colon carcinoma)	chr11q24-q25	216906_at	NM_021978																				
3.46	3.59	0.13	4.60E-01	7.75E-01	LPCAT4	lysophosphatidylcholine acyltransferase 4	chr15q14	215409_at	NM_153613																				
2.14	2.24	0.10	4.60E-01	7.75E-01	MLLT10	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	216480_x_at	NM_001009569 /// NM_004641																				
3.10	3.30	0.20	4.60E-01	7.75E-01	TPM4	tropomyosin 4	chr19p13.1	1567107_s_at	NM_003290																				
3.59	3.72	0.13	4.60E-01	7.75E-01	PBRM1	polybromo 1	chr3p21	223899_at	NM_018165 /// NM_018313 /// NM_181042																				
4.33	4.46	0.13	4.60E-01	7.75E-01	---	---	---	237922_at	---																				
2.03	2.13	0.10	4.60E-01	7.75E-01	---	---	---	242298_x_at	---																				
5.43	5.78	0.35	4.60E-01	7.76E-01	PARP8	poly (ADP-ribose) polymerase family, member 8	chr5q11.1	219033_at	NM_024615																				
2.30	2.41	0.11	4.60E-01	7.76E-01	PHLDB2	Pleckstrin homology-like domain, family B, member 2	chr3q13.2	1557578_at	NM_001134437 /// NM_001134438 /// NM_001134439 /// NM_145753																				
3.11	3.21	0.10	4.60E-01	7.76E-01	CDKL5	cyclin-dependent kinase-like 5	chrXp22	216923_at	NM_001037343 /// NM_003159																				
5.74	5.94	0.20	4.60E-01	7.76E-01	NKIRAS1	NFKB inhibitor interacting Ras-like 1	chr3p24.2	225930_at	NM_020345																				
2.80	2.93	0.12	4.60E-01	7.76E-01	---	---	---	235889_at	---																				
3.65	3.82	0.16	4.61E-01	7.76E-01	---	---	---	1558103_a_at	---																				
4.96	5.09	0.13	4.61E-01	7.76E-01	PKD1	polycystic kidney disease 1 (autosomal dominant)	chr16p13.3	202327_s_at	NM_000296 /// NM_001009944																				

6.34	6.58	0.25	4.61E-01	7.76E-01	SRPK2	SFRS protein kinase 2	chr7q22-q31.1	203182_s_at	NM_182691 /// NM_182692
3.69	3.89	0.20	4.61E-01	7.76E-01	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	chr9q22.33	218885_s_at	NM_024642
1.76	1.90	0.14	4.61E-01	7.76E-01	---	---	---	1563396_x_at	---
3.82	3.93	0.11	4.61E-01	7.76E-01	---	---	---	231324_at	---
2.96	3.07	0.11	4.61E-01	7.76E-01	---	---	---	1560868_s_at	---
2.82	2.91	0.09	4.61E-01	7.76E-01	IFT140	Intraflagellar transport 140 homolog (Chlamydomonas)	chr16p13.3	232844_at	NM_014714
4.00	4.11	0.11	4.61E-01	7.76E-01	---	---	---	231291_at	---
2.23	2.33	0.10	4.61E-01	7.76E-01	---	---	---	1566963_at	---
1.93	2.02	0.09	4.61E-01	7.76E-01	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	chr6p22.3	220039_s_at	NM_017774
2.59	2.68	0.10	4.61E-01	7.76E-01	C22orf30	chromosome 22 open reading frame 30	chr22q12.2-q12.3	216555_at	NM_173566
2.42	2.54	0.12	4.61E-01	7.76E-01	USP49	ubiquitin specific peptidase 49	chr6p21	220667_at	NM_018561
2.26	2.41	0.15	4.61E-01	7.76E-01	CUGBP2	CUG triplet repeat, RNA binding protein 2	chr10p13	242268_at	NM_001025076 /// NM_001025077 /// NM_001083591 /// NM_006561
2.15	2.23	0.08	4.61E-01	7.76E-01	---	---	---	1562502_at	---
3.61	3.88	0.27	4.61E-01	7.76E-01	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	chr9q33-q34.1	201808_s_at	NM_000118 /// NM_001114753
3.54	3.68	0.13	4.61E-01	7.76E-01	BRPF3	bromodomain and PHD finger containing, 3	chr6p21	1565843_s_at	NM_015695
9.10	9.26	0.16	4.61E-01	7.76E-01	COPB1	coatomer protein complex, subunit beta 1	chr11p15.2	201358_s_at	NM_016451
5.14	5.28	0.14	4.61E-01	7.76E-01	ADCY9	Adenylate cyclase 9	chr16p13.3	215400_x_at	NM_001116
2.82	2.95	0.13	4.61E-01	7.76E-01	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	chr5q31.1	219112_at	NM_016340
2.71	2.82	0.12	4.61E-01	7.76E-01	UBR4	ubiquitin protein ligase E3 component n-recognin 4	chr1p36.13	215636_at	NM_020765
5.18	5.37	0.19	4.61E-01	7.76E-01	---	---	---	217142_at	---
2.14	2.26	0.11	4.61E-01	7.76E-01	TTC9C	tetratricopeptide repeat domain 9C	chr11q12.3	1569189_at	NM_173810
2.13	2.25	0.12	4.61E-01	7.76E-01	KLB	klotho beta	chr4p14	244276_at	NM_175737
1.97	2.06	0.09	4.61E-01	7.76E-01	SAMD3	sterile alpha motif domain containing 3	chr6q23.1	1553876_at	NM_001017373 /// NM_152552
3.18	3.27	0.09	4.61E-01	7.76E-01	---	---	---	241613_at	---
3.84	4.03	0.18	4.61E-01	7.76E-01	SCARF2	scavenger receptor class F, member 2	chr22q11.21	227557_at	NM_153334 /// NM_182895
4.52	4.65	0.13	4.61E-01	7.76E-01	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	chr2q36	203191_at	NM_005689
1.87	1.97	0.10	4.61E-01	7.76E-01	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)	chr11q22.3	1566515_at	NM_152434
4.21	4.38	0.17	4.62E-01	7.76E-01	REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	chr19p13.3	244281_at	NM_020695
2.09	2.18	0.10	4.62E-01	7.76E-01	---	---	---	1568648_a_at	---
5.87	6.23	0.35	4.62E-01	7.76E-01	TMEM30A	transmembrane protein 30A	chr6q14.1	217743_s_at	NM_018247
2.38	2.50	0.12	4.62E-01	7.76E-01	THSD4	thrombospondin, type I, domain containing 4	chr15q23	219153_s_at	NM_024817
2.04	2.11	0.08	4.62E-01	7.76E-01	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	chr10p11.2	215878_at	NM_002211 /// NM_033666 /// NM_033667 /// NM_033668 /// NM_033669 /// NM_133376
2.70	2.82	0.12	4.62E-01	7.76E-01	---	---	---	1569499_at	---
2.34	2.44	0.09	4.62E-01	7.76E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	221994_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257
4.66	5.11	0.45	4.62E-01	7.76E-01	PLDN	pallidin homolog (mouse)	chr15q21.1	224883_at	NM_012388
4.26	4.42	0.16	4.62E-01	7.76E-01	LOC727901 /// VWA1	hypothetical LOC727901 /// von Willebrand factor A domain containing 1	chr1p36.33	228651_at	NM_022834 /// NM_199121 /// XR_042309 /// XR_042470
2.27	2.37	0.10	4.62E-01	7.76E-01	CNGA4	cyclic nucleotide gated channel alpha 4	chr11p15.4	1562273_at	NM_001037329
2.22	2.31	0.09	4.62E-01	7.76E-01	---	---	---	237925_at	---
3.37	3.49	0.13	4.62E-01	7.77E-01	FSHB	follicle stimulating hormone, beta polypeptide	chr11p13	214489_at	NM_000510 /// NM_001018080
5.84	6.01	0.16	4.62E-01	7.77E-01	ISYNA1	myo-inositol 1-phosphate synthase A1	chr19p13.11	229324_x_at	NM_016368
4.06	4.21	0.15	4.62E-01	7.77E-01	PCSK9	proprotein convertase subtilisin/kexin type 9	chr1p32.3	227759_at	NM_174936
2.23	2.35	0.12	4.62E-01	7.77E-01	FGF16	fibroblast growth factor 16	chrXq13	221374_at	NM_003868
2.15	2.25	0.10	4.62E-01	7.77E-01	SRD5A3	steroid 5 alpha-reductase 3	chr4q12	218800_at	NM_024592

1.96	2.04	0.08	4.62E-01	7.77E-01	TRPM8	transient receptor potential cation channel, subfamily M, member 8	chr2q37.1	243483_at	NM_024080
2.10	2.18	0.08	4.62E-01	7.77E-01	---	---	---	242724_x_at	---
4.04	4.21	0.17	4.62E-01	7.77E-01	LOC92659	hypothetical LOC92659	chr17q25.3	1559352_a_at	---
4.75	5.13	0.38	4.63E-01	7.77E-01	SLC46A3	solute carrier family 46, member 3	chr13q12.3	214719_at	NM_181785
9.16	9.45	0.29	4.63E-01	7.77E-01	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	chr17q23-q24	200605_s_at	NM_002734 /// NM_212471 /// NM_212472
7.97	8.18	0.21	4.63E-01	7.77E-01	CD99	CD99 molecule	chrXp22.32; Yp11.3	201028_s_at	NM_001122898 /// NM_002414
4.27	4.43	0.16	4.63E-01	7.77E-01	MED28	mediator complex subunit 28	chr4p16	222636_at	NM_025205
2.84	2.98	0.14	4.63E-01	7.77E-01	LOC283788	hypothetical protein LOC283788	---	1558109_x_at	XM_001721615 /// XM_001723582 /// XM_001723589
4.50	4.62	0.13	4.63E-01	7.77E-01	EVPL	envoplakin	chr17q25	204503_at	NM_001988
2.48	2.60	0.11	4.63E-01	7.77E-01	---	---	---	236963_at	---
2.24	2.35	0.11	4.63E-01	7.77E-01	LOC728173	hypothetical LOC728173	chr12q24.32	243485_at	XM_001129061 /// XM_001134385 /// XM_001721489
2.50	2.60	0.11	4.63E-01	7.77E-01	PARP11	poly (ADP-ribose) polymerase family, member 11	chr12p13.3	1554116_s_at	NM_020367
3.18	3.28	0.10	4.63E-01	7.77E-01	C4orf29	chromosome 4 open reading frame 29	chr4q28.2	219980_at	NM_001039717
2.03	2.12	0.09	4.63E-01	7.77E-01	---	---	---	207881_at	---
2.89	3.06	0.16	4.63E-01	7.77E-01	---	---	---	1561155_at	---
2.09	2.21	0.12	4.63E-01	7.77E-01	---	---	---	1563392_at	---
4.36	4.48	0.12	4.63E-01	7.77E-01	HPCAL4	hippocalcin like 4	chr1p34.2	222091_at	NM_016257
7.51	7.68	0.17	4.63E-01	7.77E-01	GLRX3	glutaredoxin 3	chr10q26	209080_x_at	NM_006541
3.89	4.02	0.14	4.63E-01	7.77E-01	HNRPDL	Heterogeneous nuclear ribonucleoprotein D-like	chr4q13-q21	214379_at	NM_031372 /// NR_003249
2.22	2.33	0.11	4.63E-01	7.77E-01	---	---	---	231626_at	---
3.48	3.59	0.10	4.63E-01	7.77E-01	IL1R1	interleukin 1 receptor, type I	chr2q12	215561_s_at	NM_000877
2.12	2.24	0.12	4.63E-01	7.77E-01	IGFBP1	Insulin-like growth factor binding protein 1	chr7p13-p12	237989_at	NM_000596
5.38	5.83	0.45	4.63E-01	7.77E-01	CAPN7	calpain 7	chr3p24	203357_s_at	NM_014296
2.25	2.39	0.14	4.63E-01	7.78E-01	RDHE2	epidermal retinal dehydrogenase 2	chr8q12.1	238017_at	NM_138969
2.71	2.83	0.12	4.63E-01	7.78E-01	WWC1	WW and C2 domain containing 1	chr5q35.1	216074_x_at	NM_015238
5.53	5.66	0.13	4.63E-01	7.78E-01	PTBP1	Polypyrimidine tract binding protein 1	chr19p13.3	226491_x_at	NM_002819 /// NM_031990 /// NM_031991 /// NM_175847
4.26	4.39	0.13	4.63E-01	7.78E-01	NSL1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	chr1q41	235799_at	NM_001042549 /// NM_015471
2.15	2.26	0.12	4.63E-01	7.78E-01	---	---	---	1570566_at	---
2.24	2.36	0.12	4.63E-01	7.78E-01	---	---	---	1566126_at	---
2.04	2.14	0.10	4.63E-01	7.78E-01	WDR17	WD repeat domain 17	chr4q34	1557132_at	NM_170710 /// NM_181265
7.93	8.16	0.23	4.64E-01	7.78E-01	DENR	density-regulated protein	chr12q24.31	231896_s_at	NM_003677
4.66	4.88	0.22	4.64E-01	7.78E-01	IPO8	importin 8	chr12p11.21	205701_at	NM_006390
9.37	9.57	0.20	4.64E-01	7.78E-01	KARS	lysyl-tRNA synthetase	chr16q23-q24	200840_at	NM_001130089 /// NM_005548
2.72	2.84	0.13	4.63E-01	7.78E-01	BMP7	bone morphogenetic protein 7	chr20q13	209590_at	NM_001719
2.21	2.32	0.12	4.64E-01	7.78E-01	---	---	---	242719_at	---
3.44	3.54	0.10	4.63E-01	7.78E-01	RBMS2	RNA binding motif, single stranded interacting protein 2	chr12q13.3	34187_at	NM_002898
2.09	2.19	0.10	4.64E-01	7.78E-01	---	---	---	235171_at	---
2.31	2.45	0.14	4.64E-01	7.78E-01	---	---	---	241113_at	---
2.14	2.26	0.12	4.64E-01	7.78E-01	---	---	---	1559374_at	---
4.96	5.07	0.11	4.64E-01	7.78E-01	---	---	---	242151_at	---
8.38	8.59	0.21	4.64E-01	7.78E-01	SHFM1	split hand/foot malformation (ectrodactyly) type 1	chr7q21.3-q22.1	202276_at	NM_006304
3.86	3.95	0.09	4.64E-01	7.78E-01	CYHR1	Hypothetical protein LOC100132129	chr8q24.3	229945_at	NM_001129888 /// NM_032687 /// NM_138496
9.45	9.59	0.14	4.64E-01	7.78E-01	TMED2	transmembrane emp24 domain trafficking protein 2	chr12q24.31	200087_s_at	NM_006815
2.37	2.50	0.13	4.64E-01	7.78E-01	LOC221946	hypothetical protein LOC221946	chr7p22.2	1569739_at	---
5.10	5.33	0.23	4.64E-01	7.78E-01	ZNF131	zinc finger protein 131	chr5p12-p11	221842_s_at	NM_003432
5.81	6.04	0.22	4.64E-01	7.78E-01	EFNA1	ephrin-A1	chr1q21-q22	202023_at	NM_004428 /// NM_182685
2.95	3.11	0.16	4.64E-01	7.78E-01	PRKRA /// PRKRAP1	protein kinase, interferon-inducible double stranded RNA dependent activator /// protein kinase, interferon-inducible double stranded RNA dependent activator pseudogene 1	chr2q31.2	237107_at	NM_003690 /// XR_038302

2.77	2.90	0.13	4.64E-01	7.78E-01	CCDC82	coiled-coil domain containing 82	chr11q21	220693_at	NM_024725
2.59	2.72	0.13	4.64E-01	7.78E-01	---	---	---	236057_at	---
2.32	2.43	0.11	4.64E-01	7.78E-01	ARL4D	ADP-ribosylation factor-like 4D	chr17q12-q21	203587_at	NM_001661
2.94	3.04	0.10	4.64E-01	7.78E-01	---	---	---	233624_at	---
2.00	2.09	0.09	4.64E-01	7.78E-01	---	---	---	239065_at	---
2.30	2.39	0.09	4.64E-01	7.78E-01	C6orf58	Chromosome 6 open reading frame 58	chr6q22.33	238385_at	NM_001010905
2.19	2.27	0.08	4.64E-01	7.78E-01	MAP4	microtubule-associated protein 4	chr3p21	235066_at	NM_001134364 /// NM_001134365 /// NM_002375 /// NM_030884 /// NM_030885
5.04	5.18	0.14	4.64E-01	7.78E-01	TOM1L2	target of myb1-like 2 (chicken)	chr17p11.2	237109_at	NM_001033551 /// NM_001082968
3.13	3.24	0.12	4.64E-01	7.78E-01	GJA5	gap junction protein, alpha 5, 40kDa	chr1q21.1	226701_at	NM_005266 /// NM_181703
2.16	2.24	0.08	4.64E-01	7.78E-01	GCET2	germinal center expressed transcript 2	chr3q13.2	235310_at	NM_001008756 /// NM_152785
2.62	2.74	0.11	4.65E-01	7.78E-01	ENO1	enolase 1, (alpha)	chr1p36.3-p36.2	240258_at	NM_001428
2.87	2.98	0.11	4.65E-01	7.78E-01	GNL1	guanine nucleotide binding protein-like 1	chr6p21.3	239068_at	NM_005275
1.84	1.95	0.10	4.64E-01	7.78E-01	LOC339260	Hypothetical gene supported by BC072410	chr17p11.2	1560099_at	---
1.98	2.07	0.09	4.65E-01	7.78E-01	---	---	---	236650_at	---
6.46	6.63	0.17	4.65E-01	7.78E-01	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	chr12p13	206031_s_at	NM_001098536 /// NM_003481
4.19	4.36	0.17	4.65E-01	7.78E-01	---	---	---	222366_at	---
2.21	2.30	0.09	4.65E-01	7.78E-01	---	---	---	1562116_at	---
3.13	3.22	0.09	4.65E-01	7.78E-01	LRRN4	leucine rich repeat neuronal 4	chr20p12.3	1553169_at	NM_152611
1.85	1.93	0.08	4.65E-01	7.78E-01	---	---	---	241868_at	---
2.24	2.34	0.10	4.65E-01	7.78E-01	USP42	Ubiquitin specific peptidase 42	chr7p22.1	228982_s_at	NM_032172
5.59	5.94	0.35	4.65E-01	7.79E-01	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	chr10q21	208152_s_at	NM_004728
2.03	2.11	0.08	4.65E-01	7.79E-01	FLJ43944	FLJ43944 protein	chr17q12	1563750_at	XR_042035 /// XR_042036 /// XR_042037
6.82	7.08	0.26	4.65E-01	7.79E-01	ZC3H15	zinc finger CCCH-type containing 15	chr2q32.1	201595_s_at	NM_018471
4.33	4.52	0.19	4.65E-01	7.79E-01	TRAC	T cell receptor alpha constant	chr14q11	209670_at	---
2.78	2.93	0.15	4.65E-01	7.79E-01	---	---	---	236379_at	---
2.86	3.00	0.15	4.65E-01	7.79E-01	---	---	---	232203_at	---
5.15	5.27	0.11	4.65E-01	7.79E-01	---	---	---	234795_at	---
2.30	2.44	0.14	4.65E-01	7.79E-01	---	---	---	215864_at	---
2.18	2.28	0.10	4.65E-01	7.79E-01	FLJ25037	hypothetical protein FLJ25037	chr7q11.21	1563887_at	XR_041315 /// XR_041316
4.11	4.30	0.19	4.65E-01	7.79E-01	---	---	---	236494_x_at	---
3.93	4.07	0.14	4.65E-01	7.79E-01	GLI2	GLI-Kruppel family member GLI2	chr2q14	228537_at	NM_005270
2.80	2.94	0.14	4.65E-01	7.79E-01	---	---	---	237065_s_at	---
3.05	3.18	0.13	4.65E-01	7.79E-01	---	---	---	242933_at	---
2.42	2.54	0.12	4.65E-01	7.79E-01	FLJ10489	hypothetical protein FLJ10489	chr8q22.3	1562433_at	XM_001723905 /// XM_001723926 /// XM_001723986
4.06	4.18	0.12	4.65E-01	7.79E-01	C14orf73	chromosome 14 open reading frame 73	chr14q32.32	230677_at	NM_001077594
2.37	2.45	0.09	4.65E-01	7.79E-01	JRK	jerky homolog (mouse)	chr8q24.3	217146_at	NM_001077527 /// NM_003724
6.16	6.41	0.25	4.65E-01	7.79E-01	ADNP2	ADNP homeobox 2	chr18q23	203321_s_at	NM_014913
3.98	4.26	0.28	4.66E-01	7.79E-01	RECQL	RecQ protein-like (DNA helicase Q1-like)	chr12p12	205091_x_at	NM_002907 /// NM_032941
4.89	5.11	0.22	4.66E-01	7.79E-01	CISH	cytokine inducible SH2-containing protein	chr3p21.3	221223_x_at	NM_013324 /// NM_145071
2.95	3.14	0.19	4.66E-01	7.79E-01	SFRS18	splicing factor, arginine/serine-rich 18	chr6q16.3	230375_at	NM_015491 /// NM_032870
5.36	5.50	0.14	4.66E-01	7.79E-01	FLJ27365	FLJ27365 protein	chr22q13.31	232480_at	XR_041674 /// XR_041675 /// XR_041676
3.21	3.35	0.14	4.66E-01	7.79E-01	C22orf28	chromosome 22 open reading frame 28	chr22q12	234283_at	NM_014306
3.20	3.34	0.14	4.66E-01	7.79E-01	---	---	---	241429_at	---
2.89	3.02	0.14	4.66E-01	7.79E-01	CA13	carbonic anhydrase XIII	chr8q21.2	235899_at	NM_198584

3.34	3.47	0.13	4.65E-01	7.79E-01	AKT1S1	AKT1 substrate 1 (proline-rich)	chr19q13.33	1555821_a_at	NM_001098632 /// NM_001098633 /// NM_032375																				
2.28	2.41	0.13	4.66E-01	7.79E-01	FBXL17	F-box and leucine-rich repeat protein 17	chr5q21.3	242034_at	NM_022824																				
2.97	3.09	0.12	4.66E-01	7.79E-01	---	---	---	230553_at	---																				
2.16	2.27	0.11	4.66E-01	7.79E-01	---	---	---	244670_at	---																				
5.99	6.09	0.11	4.66E-01	7.79E-01	KIAA0427	KIAA0427	chr18q21.1	204302_s_at	NM_014772																				
2.35	2.45	0.10	4.66E-01	7.79E-01	---	---	---	229288_at	---																				
2.23	2.33	0.10	4.66E-01	7.79E-01	ANKRD33	ankyrin repeat domain 33	chr12q13.13	242209_at	NM_001130015 /// NM_182608																				
2.28	2.38	0.10	4.66E-01	7.79E-01	MAGOHB	mago-nashi homolog B (Drosophila)	chr12p13.2	222776_at	NM_018048																				
4.02	4.12	0.10	4.66E-01	7.79E-01	AMBP	alpha-1-microglobulin/bikunin precursor	chr9q32-q33	205477_s_at	NM_001633																				
1.84	1.94	0.09	4.66E-01	7.79E-01	ZNF780B	zinc finger protein 780B	chr19q13.2	214899_at	NM_001005851																				
3.04	3.13	0.09	4.66E-01	7.79E-01	C9orf62	chromosome 9 open reading frame 62	chr9q34.3	1553919_at	XR_041823 /// XR_041824 /// XR_041825																				
2.32	2.41	0.08	4.65E-01	7.79E-01	HNMT	histamine N-methyltransferase	chr2q22.1	204111_at	NM_001024074 /// NM_001024075 /// NM_006895																				
4.17	4.35	0.18	4.66E-01	7.79E-01	---	---	---	231346_s_at	---																				
2.53	2.65	0.12	4.66E-01	7.79E-01	ATP11A	ATPase, class VI, type 11A	chr13q34	213582_at	NM_015205 /// NM_032189																				
2.87	2.98	0.11	4.66E-01	7.79E-01	PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	chr7p21-p11.2	232212_at	NM_032639																				
4.09	4.20	0.11	4.66E-01	7.79E-01	MTG1	Mitochondrial GTPase 1 homolog (S. cerevisiae)	chr10q26.3	238334_at	NM_138384																				
3.79	3.96	0.18	4.66E-01	7.79E-01	PDE7B	phosphodiesterase 7B	chr6q23-q24	230109_at	NM_018945																				
3.00	3.17	0.17	4.66E-01	7.79E-01	C9orf71	chromosome 9 open reading frame 71	chr9q13	1553809_a_at	NM_153237																				
2.50	2.61	0.11	4.66E-01	7.79E-01	KIAA1755	KIAA1755	chr20q11.23	231893_at	NM_001029864																				
2.64	2.72	0.09	4.66E-01	7.79E-01	C1S	Complement component 1, s subcomponent	chr12p13	233042_at	NM_001734 /// NM_201442																				
2.01	2.09	0.08	4.66E-01	7.79E-01	BCL2L14	BCL2-like 14 (apoptosis facilitator)	chr12p13-p12	1552841_s_at	NM_030766 /// NM_138722 /// NM_138723 /// NM_138724																				
1.84	1.94	0.10	4.66E-01	7.79E-01	C20orf74	Chromosome 20 open reading frame 74	chr20p11.22	1559699_at	NM_020343																				
2.23	2.32	0.09	4.66E-01	7.79E-01	---	---	---	237942_at	---																				
1.92	2.03	0.11	4.66E-01	7.79E-01	EDA	ectodysplasin A	chrXq12-q13.1|Xq12	211131_s_at	NM_001005609 /// NM_001005610 /// NM_001005611 /// NM_001005612 /// NM_001005615 /// NM_001399																				
2.24	2.31	0.08	4.67E-01	7.79E-01	---	---	---	1569731_at	---																				
7.41	7.59	0.18	4.67E-01	7.79E-01	RAB2A	RAB2A, member RAS oncogene family	chr8q12.1	208734_x_at	NM_002865																				
2.18	2.29	0.11	4.67E-01	7.79E-01	---	---	---	1566294_at	---																				
2.30	2.40	0.10	4.67E-01	7.79E-01	OR6B1	olfactory receptor, family 6, subfamily B, member 1	chr7q35	234363_at	NM_001005281																				
5.98	6.35	0.37	4.67E-01	7.79E-01	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	chr15q25.1-q25.2	202069_s_at	NM_005530																				
5.42	5.68	0.26	4.67E-01	7.79E-01	NICN1	nicolin 1	chr3p21.31	223442_at	NM_032316																				
5.10	5.21	0.11	4.67E-01	7.79E-01	DPYSL4	Dihydropyrimidinase-like 4	chr10q26	214301_s_at	NM_006426																				
2.39	2.49	0.11	4.67E-01	7.79E-01	C2	complement component 2	chr6p21.3	1554533_at	NM_000063																				
5.15	5.44	0.29	4.67E-01	7.79E-01	CRIP2	cysteine-rich protein 2	chr14q32.3	208978_at	NM_001312																				
4.13	4.25	0.13	4.67E-01	7.79E-01	FAM125B	family with sequence similarity 125, member B	chr9q33.3	222241_at	NM_001011703 /// NM_033446																				
5.05	5.44	0.39	4.67E-01	7.79E-01	ARMC1	armadillo repeat containing 1	chr8q13.1	218185_s_at	NM_018120																				
2.14	2.30	0.16	4.67E-01	7.79E-01	EYA4	eyes absent homolog 4 (Drosophila)	chr6q23	238877_at	NM_004100 /// NM_172103 /// NM_172105																				
4.24	4.40	0.15	4.67E-01	7.79E-01	---	---	---	236388_at	---																				
3.41	3.53	0.12	4.67E-01	7.79E-01	NOS1	nitric oxide synthase 1 (neuronal)	chr12q24.2-q24.31	207310_s_at	NM_000620																				
2.40	2.52	0.12	4.67E-01	7.79E-01	---	---	---	1562412_at	---																				
10.56	10.67	0.11	4.67E-01	7.79E-01	RHOA	ras homolog gene family, member A	chr3p21.3	200059_s_at	NM_001664																				
2.22	2.31	0.09	4.67E-01	7.79E-01	---	---	---	216290_x_at	---																				
1.97	2.05	0.08	4.67E-01	7.79E-01	---	---	---	234622_at	---																				

2.42	2.50	0.08	4.67E-01	7.79E-01	KRT18P44	keratin 18 pseudogene 44	chrXq25	217333_at	XM_001715438 /// XM_001719134 /// XM_001720462
1.89	1.96	0.08	4.67E-01	7.79E-01	DKFZp686O1327	Similar to hCG2041586	chr2q22.3	216874_at	XM_379141
2.04	2.14	0.11	4.67E-01	7.79E-01	---	---	---	240762_at	---
3.03	3.81	0.78	4.67E-01	7.79E-01	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	chr9q22.1-q22.3	209990_s_at	NM_005458
4.89	5.35	0.46	4.67E-01	7.79E-01	PICALM	phosphatidylinositol binding clathrin assembly protein	chr11q14	215236_s_at	NM_001008660 /// NM_007166
5.88	6.20	0.32	4.67E-01	7.79E-01	GTPBP4	GTP binding protein 4	chr10p15-p14	218239_s_at	NM_012341
5.00	5.25	0.26	4.67E-01	7.79E-01	MYNN	myoneurin	chr3q26.2	224206_x_at	NM_018657
2.79	2.89	0.10	4.67E-01	7.79E-01	KLHL29	kelch-like 29 (Drosophila)	chr2p24.1	1554261_at	XM_001717454 /// XM_001717533 /// XM_940375
1.98	2.07	0.09	4.67E-01	7.79E-01	---	---	---	233926_at	---
1.98	2.06	0.08	4.67E-01	7.79E-01	MIA2	melanoma inhibitory activity 2	chr14q13.2	221177_at	NM_054024
4.25	4.47	0.22	4.67E-01	7.80E-01	YIPF6	Yip1 domain family, member 6	chrXq12	212342_at	NM_173834
5.80	6.05	0.25	4.67E-01	7.80E-01	FAM98B	Family with sequence similarity 98, member B	chr15q14	225086_at	NM_001042429 /// NM_173611
2.56	2.72	0.16	4.67E-01	7.80E-01	NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	chr8p22	206797_at	NM_000015
2.24	2.37	0.13	4.67E-01	7.80E-01	---	---	---	1562111_at	---
2.82	2.94	0.12	4.67E-01	7.80E-01	GPX2	glutathione peroxidase 2 (gastrointestinal)	chr14q24.1	202831_at	NM_002083
2.03	2.12	0.10	4.67E-01	7.80E-01	LOC646627	phospholipase inhibitor	chr1q44	1568933_at	NM_001085474
9.01	9.29	0.28	4.68E-01	7.80E-01	RPL22	ribosomal protein L22	chr1p36.3-p36.2	221726_at	NM_000983
3.53	3.67	0.14	4.68E-01	7.80E-01	CCDC36	coiled-coil domain containing 36	chr3p21.31	1564600_a_at	NM_178173
2.59	2.69	0.10	4.68E-01	7.80E-01	BBS7	Bardet-Biedl syndrome 7	chr4q27	219688_at	NM_018190 /// NM_176824
5.37	5.59	0.22	4.68E-01	7.80E-01	GIMAP1	GTPase, IMAP family member 1	chr7q36.1	1552315_at	NM_130759
4.49	4.88	0.39	4.68E-01	7.80E-01	---	---	---	240046_at	---
2.01	2.11	0.11	4.68E-01	7.80E-01	C6orf162	Chromosome 6 open reading frame 162	chr6q15-q16.1	233438_at	NM_001042493 /// NM_020425
2.71	3.02	0.31	4.68E-01	7.80E-01	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	chr14q12-q13	205229_s_at	NM_004086
6.53	6.70	0.17	4.68E-01	7.80E-01	NTAN1	N-terminal asparagine amidase	chr16p13.11	213062_at	NM_173474
3.23	3.39	0.16	4.68E-01	7.80E-01	KIAA0564	KIAA0564	chr13q14.11	214231_s_at	NM_001009814 /// NM_015058
4.91	5.12	0.21	4.68E-01	7.80E-01	PTEN	phosphatase and tensin homolog	chr10q23.3	211711_s_at	NM_000314
3.03	3.23	0.20	4.68E-01	7.80E-01	C1orf58	chromosome 1 open reading frame 58	chr1q41	239078_at	NM_144695
4.10	4.29	0.20	4.68E-01	7.80E-01	CCDC126	coiled-coil domain containing 126	chr7p15.3	228061_at	NM_138771
3.13	3.27	0.14	4.68E-01	7.80E-01	IL6R	interleukin 6 receptor	chr1q21	205945_at	NM_000565 /// NM_181359
2.30	2.41	0.11	4.68E-01	7.80E-01	---	---	---	236164_at	---
2.78	2.89	0.11	4.68E-01	7.80E-01	PDE7A	Phosphodiesterase 7A	chr8q13	230500_at	NM_002603 /// NM_002604
2.13	2.23	0.11	4.68E-01	7.80E-01	---	---	---	240503_at	---
5.64	5.82	0.19	4.68E-01	7.80E-01	UBXN2B	UBX domain protein 2B	chr8q12.1	212934_at	NM_001077619
2.28	2.46	0.18	4.68E-01	7.80E-01	RNF6	ring finger protein (C3H2C3 type) 6	chr13q12.2	210932_s_at	NM_005977 /// NM_183043 /// NM_183044
3.35	3.48	0.13	4.68E-01	7.80E-01	HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	chr7p14.1-p13	215584_at	NM_015052
2.03	2.15	0.13	4.68E-01	7.80E-01	LOC613126	hypothetical protein LOC613126	chr7q21.2	233942_at	---
2.39	2.51	0.12	4.68E-01	7.80E-01	SEC24D	SEC24 related gene family, member D (S. cerevisiae)	chr4q26	215641_at	NM_014822
2.45	2.57	0.12	4.68E-01	7.80E-01	---	---	---	229815_at	---
2.15	2.25	0.10	4.68E-01	7.80E-01	---	---	---	1557403_s_at	---
2.71	2.79	0.08	4.68E-01	7.80E-01	CNTNAP4	contactin associated protein-like 4	chr16q23.1	1554377_a_at	NM_033401 /// NM_138994
6.77	6.97	0.20	4.68E-01	7.80E-01	UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)	chr2q31.1	230029_x_at	NM_172070
2.00	2.10	0.09	4.68E-01	7.80E-01	---	---	---	1555489_at	---
4.02	4.19	0.16	4.68E-01	7.80E-01	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	chr19q13.2	217612_at	NM_001001563
6.07	6.24	0.17	4.68E-01	7.80E-01	FAM59A	family with sequence similarity 59, member A	chr18q12.1	219377_at	NM_022751
2.65	2.81	0.17	4.68E-01	7.80E-01	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	chr5q21	206925_at	NM_005668 /// NM_175052

6.31	6.43	0.12	4.68E-01	7.80E-01	ACAD9	acyl-Coenzyme A dehydrogenase family, member 9	chr3q21.3	224160_s_at	NM_014049
2.17	2.25	0.08	4.68E-01	7.80E-01	C14orf166B	chromosome 14 open reading frame 166B	chr14q24.3	234454_at	NM_001081002 /// NM_194287
4.50	4.79	0.29	4.69E-01	7.80E-01	SDCCAG1	serologically defined colon cancer antigen 1	chr14q22	1558675_s_at	NM_004713
4.12	4.32	0.20	4.69E-01	7.80E-01	ST7L	suppression of tumorigenicity 7 like	chr1p13.2	219964_at	NM_017744 /// NM_138727 /// NM_138728 /// NM_138729
4.82	4.99	0.17	4.68E-01	7.80E-01	FLJ37798	hypothetical gene supported by AK095117	chr6p12.3	227298_at	---
3.83	3.96	0.13	4.69E-01	7.80E-01	CCDC105	coiled-coil domain containing 105	chr19p13.12	1553893_at	NM_173482
2.60	2.71	0.11	4.69E-01	7.80E-01	---	---	---	233901_at	---
1.92	2.03	0.10	4.69E-01	7.80E-01	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	chr2p14	234212_at	NM_001005386 /// NM_005722
6.03	6.13	0.11	4.69E-01	7.80E-01	SPEG	SPEG complex locus	chr2q35	232153_at	NM_005876
2.56	2.68	0.12	4.69E-01	7.80E-01	---	---	---	238727_at	---
2.66	2.76	0.10	4.69E-01	7.80E-01	CLEC7A	C-type lectin domain family 7, member A	chr12p13.2	1555214_a_at	NM_022570 /// NM_197947 /// NM_197948 /// NM_197949 /// NM_197950 /// NM_197954
2.75	2.85	0.10	4.69E-01	7.80E-01	LOC400960	Hypothetical gene supported by BC040598	chr2p14	235909_at	XM_934552 /// XM_945536
2.23	2.32	0.10	4.69E-01	7.80E-01	GUCA1C	guanylate cyclase activator 1C	chr3q13.1	223928_s_at	NM_005459
4.16	4.25	0.09	4.69E-01	7.80E-01	---	---	---	232471_at	---
2.09	2.17	0.09	4.69E-01	7.80E-01	---	---	---	1562011_at	---
2.10	2.19	0.08	4.69E-01	7.80E-01	---	---	---	1558977_at	---
3.68	3.83	0.15	4.69E-01	7.80E-01	---	---	---	234099_at	---
2.86	3.01	0.15	4.69E-01	7.81E-01	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	chr1p33-p32	1554481_a_at	NM_004437 /// NM_203342 /// NM_203343
5.30	5.63	0.33	4.69E-01	7.81E-01	NES	nestin	chr1q23.1	218678_at	NM_006617
2.29	2.42	0.13	4.69E-01	7.81E-01	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	chr13q12	210287_s_at	NM_002019
3.75	3.91	0.16	4.69E-01	7.81E-01	MYO1G	myosin IG	chr7p13-p11.2	227799_at	NM_033054
2.48	2.57	0.09	4.69E-01	7.81E-01	ACRV1	acrosomal vesicle protein 1	chr11q23-q24	206776_x_at	NM_001612 /// NM_020069 /// NM_020107 /// NM_020108 /// NM_020109 /// NM_020110 /// NM_020111 /// NM_020113 /// NM_020115
2.12	2.20	0.08	4.69E-01	7.81E-01	PAPOLB	poly(A) polymerase beta (testis specific)	chr7p22.1	242158_at	NM_020144
3.10	3.26	0.16	4.69E-01	7.81E-01	NT5M	5',3'-nucleotidase, mitochondrial	chr17p11.2	219708_at	NM_020201
2.29	2.42	0.13	4.69E-01	7.81E-01	MAPK4	mitogen-activated protein kinase 4	chr18q12-q21	204708_at	NM_002747
2.28	2.38	0.11	4.69E-01	7.81E-01	---	---	---	234028_at	---
3.63	3.96	0.33	4.69E-01	7.81E-01	GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	chr11p15.3	1554079_at	NM_198516
2.22	2.32	0.11	4.70E-01	7.81E-01	LOC100129562	hypothetical protein LOC100129562	chr7q22.1	240366_at	XM_001714915 /// XM_001716050 /// XM_001718238
2.52	2.76	0.24	4.70E-01	7.81E-01	ANGPT2	angiopoietin 2	chr8p23.1	236034_at	NM_001118887 /// NM_001118888 /// NM_001147
5.57	5.76	0.19	4.70E-01	7.81E-01	ZNF529	zinc finger protein 529	chr19q13.13	231940_at	NM_020951
7.35	7.52	0.18	4.70E-01	7.81E-01	ZNF160	zinc finger protein 160	chr19q13.41	214715_x_at	NM_001102603 /// NM_033288 /// NM_198893
3.03	3.18	0.15	4.70E-01	7.81E-01	CTTNBP2NL	CTTNBP2 N-terminal like	chr1p13.2	239525_at	NM_018704
2.45	2.57	0.12	4.70E-01	7.81E-01	C15orf28	chromosome 15 open reading frame 28	chr15q23	220710_at	XR_040962 /// XR_040963 /// XR_040964
3.13	3.24	0.11	4.70E-01	7.81E-01	CHRDL2	chordin-like 2	chr11q14	223987_at	NM_015424
2.33	2.41	0.08	4.70E-01	7.81E-01	BIVM	Basic, immunoglobulin-like variable motif containing	chr13q32-q33.1	1569289_at	NM_017693
2.09	2.20	0.11	4.70E-01	7.81E-01	RNF32	ring finger protein 32	chr7q36	232830_at	NM_030936

3.73	3.91	0.19	4.70E-01	7.81E-01	NF1	neurofibromin 1	chr17q11.2	216115_at	NM_000267 /// NM_001042492 /// NM_001128147
4.24	4.41	0.17	4.70E-01	7.81E-01	NCOR2	nuclear receptor co-repressor 2	chr12q24	208888_s_at	NM_001077261 /// NM_006312
2.49	2.60	0.11	4.70E-01	7.81E-01	LOC400238	hypothetical gene supported by AK093266	chr14q32.12	1557657_a_at	---
1.95	2.04	0.09	4.70E-01	7.81E-01	SCNN1G	sodium channel, nonvoltage-gated 1, gamma	chr16p12	241436_at	NM_001039
1.99	2.06	0.07	4.70E-01	7.81E-01	---	---	---	233722_at	---
3.09	3.30	0.21	4.70E-01	7.81E-01	---	---	---	1556836_at	---
2.46	2.58	0.12	4.70E-01	7.81E-01	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	chr4q28-q32	207528_s_at	NM_014331
6.28	6.66	0.38	4.70E-01	7.81E-01	ANK2	ankyrin 2, neuronal	chr4q25-q27	202920_at	NM_001127493 /// NM_001148 /// NM_020977
3.75	3.97	0.22	4.70E-01	7.81E-01	---	---	---	216538_at	---
3.10	3.23	0.14	4.70E-01	7.81E-01	SPAG9	sperm associated antigen 9	chr17q21.33	1554543_at	NM_001130528 /// NM_003971
2.93	3.04	0.11	4.70E-01	7.81E-01	TNRC18	Trinucleotide repeat containing 18	chr7p22.1	235755_at	NM_001080495
5.87	6.06	0.19	4.70E-01	7.81E-01	BTN3A3	butyrophilin, subfamily 3, member A3	chr6p21.3	38241_at	NM_006994 /// NM_197974
2.03	2.13	0.09	4.70E-01	7.81E-01	---	---	---	240751_at	---
2.40	2.53	0.14	4.70E-01	7.82E-01	---	---	---	244003_at	---
2.38	2.54	0.16	4.70E-01	7.82E-01	---	---	---	232651_at	---
5.97	6.18	0.21	4.70E-01	7.82E-01	UVRAG	UV radiation resistance associated gene	chr11q13.5	203241_at	NM_003369
2.11	2.22	0.12	4.70E-01	7.82E-01	---	---	---	236861_at	---
3.01	3.14	0.13	4.70E-01	7.82E-01	ADCY1	adenylate cyclase 1 (brain)	chr7p13-p12	232062_at	NM_021116
2.13	2.25	0.12	4.70E-01	7.82E-01	C19orf30	chromosome 19 open reading frame 30	chr19p13.3	223973_at	XR_040340 /// XR_040341 /// XR_040342
1.87	1.94	0.08	4.70E-01	7.82E-01	CMTM6	CKLF-like MARVEL transmembrane domain containing 6	chr3p22.3	1565657_at	NM_017801
5.72	5.97	0.24	4.71E-01	7.82E-01	STYXL1	serine/threonine/tyrosine interacting-like 1	chr7q11.23	230370_x_at	NM_016086
6.39	6.53	0.14	4.70E-01	7.82E-01	MUC8	mucin 8	chr12q24.3	216671_x_at	---
2.97	3.10	0.14	4.71E-01	7.82E-01	---	---	---	1569417_at	---
2.68	2.78	0.10	4.71E-01	7.82E-01	---	---	---	235246_at	---
2.38	2.56	0.18	4.71E-01	7.82E-01	---	---	---	215774_s_at	---
4.34	4.73	0.39	4.71E-01	7.82E-01	GSPT1	G1 to S phase transition 1	chr16p13.1	234975_at	NM_001130006 /// NM_001130007 /// NM_002094
2.83	2.93	0.10	4.71E-01	7.82E-01	C3orf43	chromosome 3 open reading frame 43	chr3q29	1559429_a_at	NM_001077657
3.11	3.22	0.10	4.71E-01	7.82E-01	ZFP41	zinc finger protein 41 homolog (mouse)	chr8q24.3	227902_at	NM_173832
4.32	4.47	0.15	4.71E-01	7.82E-01	AQP5	aquaporin 5	chr12q13	213611_at	NM_001651
2.49	2.63	0.14	4.71E-01	7.82E-01	PCSK6	proprotein convertase subtilisin/kexin type 6	chr15q26.3	210553_x_at	NM_002570 /// NM_138319 /// NM_138320 /// NM_138321 /// NM_138322 /// NM_138323 /// NM_138324 /// NM_138325
9.41	9.51	0.10	4.71E-01	7.82E-01	VDAC2	voltage-dependent anion channel 2	chr10q22	211662_s_at	NM_003375
2.53	2.62	0.09	4.71E-01	7.82E-01	---	---	---	233956_at	---
3.63	3.76	0.13	4.71E-01	7.82E-01	CTSLL3	cathepsin L-like 3	chr9q22.1	1563445_x_at	---
3.22	3.34	0.12	4.71E-01	7.82E-01	RHBDD1	Rhomboid domain containing 1	chr2q36.3	236690_at	NM_032276
2.67	2.85	0.18	4.71E-01	7.82E-01	---	---	---	1556338_at	---
2.42	2.51	0.09	4.71E-01	7.82E-01	C6orf58	chromosome 6 open reading frame 58	chr6q22.33	238383_at	NM_001010905
5.21	5.36	0.15	4.71E-01	7.82E-01	GGT1	gamma-glutamyltransferase 1	chr22q11.23	208284_x_at	NM_001032364 /// NM_001032365 /// NM_005265 /// NM_013430
5.44	5.71	0.27	4.71E-01	7.82E-01	C10orf84	chromosome 10 open reading frame 84	chr10q26.11	222617_s_at	NM_001134672 /// NM_022063
4.00	4.14	0.14	4.71E-01	7.82E-01	TUBD1	tubulin, delta 1	chr17q23.1	210389_x_at	NM_016261
5.46	5.79	0.33	4.71E-01	7.82E-01	C1orf115	chromosome 1 open reading frame 115	chr1q41	218546_at	NM_024709
2.03	2.14	0.11	4.71E-01	7.82E-01	---	---	---	240081_at	---
2.42	2.51	0.09	4.71E-01	7.82E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	233780_at	NM_018151

6.77	6.92	0.15	4.71E-01	7.82E-01	SPOP	speckle-type POZ protein	chr17q21.33	204640_s_at	NM_001007226 /// NM_001007227 /// NM_001007228 /// NM_001007229 /// NM_001007230 /// NM_003563																				
3.52	3.73	0.21	4.72E-01	7.82E-01	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	chr14q31-q32.1	204633_s_at	NM_004755 /// NM_182398																				
2.69	2.83	0.15	4.72E-01	7.82E-01	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	chr6q13	210799_at	NM_000863																				
5.68	5.80	0.13	4.72E-01	7.82E-01	PDPK1	3-phosphoinositide dependent protein kinase-1	chr16p13.3	32029_at	NM_002613 /// NM_031268																				
1.99	2.09	0.10	4.72E-01	7.82E-01	41340	Membrane-associated ring finger (C3HC4) 7	chr2q24.2	1557703_at	NM_022826																				
2.05	2.14	0.09	4.72E-01	7.82E-01	---	---	---	1562035_at	---																				
5.40	5.61	0.21	4.72E-01	7.83E-01	AHCYL2	S-adenosylhomocysteine hydrolase-like 2	chr7q32.1	212814_at	NM_001130720 /// NM_001130722 /// NM_001130723 /// NM_015328																				
2.20	2.32	0.12	4.72E-01	7.83E-01	CASS4	Cas scaffolding protein family member 4	chr20q13.31	1554786_at	NM_020356																				
2.79	2.90	0.11	4.72E-01	7.83E-01	ZNF396	zinc finger protein 396	chr18q12	1554231_a_at	NM_145756																				
2.09	2.19	0.10	4.72E-01	7.83E-01	---	---	---	237446_at	---																				
6.25	6.57	0.32	4.72E-01	7.83E-01	---	---	---	231467_at	---																				
2.16	2.26	0.10	4.72E-01	7.83E-01	---	---	---	1557638_at	---																				
1.95	2.06	0.11	4.72E-01	7.83E-01	LOC401098	hypothetical LOC401098	chr3q26.1	1556609_at	XR_017816 /// XR_017824 /// XR_041584																				
2.11	2.20	0.10	4.72E-01	7.83E-01	IL1F7	interleukin 1 family, member 7 (zeta)	chr2q12-q14.1	221470_s_at	NM_014439 /// NM_173202 /// NM_173203 /// NM_173204 /// NM_173205																				
5.83	5.97	0.14	4.72E-01	7.83E-01	PSEN1	presenilin 1	chr14q24.3	226577_at	NM_000021 /// NM_007318																				
4.88	5.22	0.34	4.72E-01	7.83E-01	AHCTF1	AT hook containing transcription factor 1	chr1q44	214766_s_at	NM_015446																				
8.58	8.75	0.18	4.72E-01	7.83E-01	STRAP	serine/threonine kinase receptor associated protein	chr12p12.3	200870_at	NM_007178																				
2.02	2.17	0.15	4.72E-01	7.83E-01	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1	chr8q21.11	223475_at	NM_031461																				
5.29	5.42	0.13	4.72E-01	7.83E-01	BATF	basic leucine zipper transcription factor, ATF-like	chr14q24.3	205965_at	NM_006399																				
2.82	2.94	0.12	4.72E-01	7.83E-01	---	---	---	1559631_at	---																				
2.09	2.20	0.10	4.72E-01	7.83E-01	---	---	---	205772_s_at	---																				
2.41	2.50	0.08	4.72E-01	7.83E-01	LOC100128988	similar to hCG2018847	chr20q12	232849_at	XM_001721060 /// XM_001721091 /// XM_001721587																				
6.59	7.23	0.64	4.72E-01	7.83E-01	C4orf18	chromosome 4 open reading frame 18	chr4q32.1	219872_at	NM_001031700 /// NM_001128424 /// NM_016613																				
6.60	7.01	0.42	4.72E-01	7.83E-01	LARS	leucyl-tRNA synthetase	chr5q32	222427_s_at	NM_020117																				
6.85	7.18	0.33	4.73E-01	7.83E-01	PTEN /// PTENP1	phosphatase and tensin homolog /// phosphatase and tensin homolog pseudogene 1	chr10q23.3 /// chr9p21	217492_s_at	NM_000314 /// NR_023917																				
3.69	3.86	0.16	4.73E-01	7.83E-01	TNIP1	TNFAIP3 interacting protein 1	chr5q32-q33.1	243423_at	NM_006058																				
3.24	3.40	0.16	4.72E-01	7.83E-01	---	---	---	243827_at	---																				
2.62	2.76	0.14	4.72E-01	7.83E-01	---	---	---	1566823_a_at	---																				
2.54	2.64	0.10	4.72E-01	7.83E-01	CYP2A7	cytochrome P450, family 2, subfamily A, polypeptide 7	chr19q13.2	207718_x_at	NM_000764 /// NM_030589																				
1.96	2.05	0.09	4.73E-01	7.83E-01	---	---	---	1557646_at	---																				
4.48	4.59	0.11	4.73E-01	7.83E-01	FBXO9	F-box protein 9	chr6p12.3-p11.2	238472_at	NM_012347 /// NM_033480 /// NM_033481																				
5.33	5.42	0.10	4.73E-01	7.83E-01	LOC100130544	Hypothetical protein LOC100130544	chr6q25.3	215200_x_at	XM_001716277 /// XM_001716352 /// XM_001726880																				

6.69	7.16	0.47	4.73E-01	7.83E-01	GPR116	G protein-coupled receptor 116	chr6p12.3	212950_at	NM_001098518 /// NM_015234
2.49	2.58	0.09	4.73E-01	7.83E-01	LY9	lymphocyte antigen 9	chr1q21.3-q22	231124_x_at	NM_001033667 /// NM_002348
5.47	5.75	0.29	4.73E-01	7.83E-01	ANGPTL2	angiopoietin-like 2	chr9q34	213001_at	NM_012098
2.28	2.40	0.12	4.73E-01	7.83E-01	---	---	---	1563169_at	---
2.35	2.44	0.09	4.73E-01	7.83E-01	EHF	ets homologous factor	chr11p12	232361_s_at	NM_012153
3.02	3.18	0.16	4.73E-01	7.83E-01	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	chr1q21-q23	203295_s_at	NM_000702
2.56	2.67	0.10	4.73E-01	7.83E-01	GANC	glucosidase, alpha; neutral C	chr15q15.2	235714_at	NM_198141
2.10	2.18	0.08	4.73E-01	7.83E-01	TYR	tyrosinase (oculocutaneous albinism IA)	chr11q14-q21	1555505_a_at	NM_000372
4.76	5.13	0.37	4.73E-01	7.83E-01	WBP4	WW domain binding protein 4 (formin binding protein 21)	chr13q14.11	203597_s_at	NM_007187
3.70	3.91	0.20	4.73E-01	7.83E-01	ZNF24	Zinc finger protein 24	chr18q12	242210_at	NM_006965
3.84	4.02	0.18	4.73E-01	7.83E-01	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	chr3p23-p21	201072_s_at	NM_003074
11.57	11.75	0.18	4.73E-01	7.83E-01	NACA	nascent polypeptide-associated complex alpha subunit	chr12q23-q24.1	200735_x_at	NM_001113201 /// NM_001113202 /// NM_001113203 /// NM_005594
2.95	3.05	0.10	4.73E-01	7.83E-01	---	---	---	1560511_at	---
1.94	2.01	0.07	4.73E-01	7.83E-01	OR51E2	olfactory receptor, family 51, subfamily E, member 2	chr11p15	232482_at	NM_030774
7.00	7.26	0.27	4.73E-01	7.83E-01	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	chr1p31.1-p22.1	203284_s_at	NM_001134492 /// NM_012262
4.52	4.74	0.22	4.73E-01	7.83E-01	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	chr13q32.1	218801_at	NM_020121
3.63	3.76	0.13	4.73E-01	7.83E-01	CHRNE	cholinergic receptor, nicotinic, epsilon	chr17p13-p12	215916_at	NM_000080
6.79	7.00	0.21	4.73E-01	7.83E-01	GPN1	GPN-loop GTPase 1	chr2p23.3	209313_at	NM_007266
2.30	2.40	0.09	4.73E-01	7.83E-01	C20orf112	Hypothetical protein LOC284804	chr20q11.1-q11.23	241830_at	NM_080616
4.71	4.92	0.21	4.73E-01	7.83E-01	---	---	---	243634_at	---
2.98	3.09	0.11	4.73E-01	7.84E-01	RRBP1	Ribosome binding protein 1 homolog 180kDa (dog)	chr20p12	227888_at	NM_001042576 /// NM_004587
3.37	3.52	0.15	4.74E-01	7.84E-01	---	---	---	240943_at	---
3.70	3.82	0.12	4.74E-01	7.84E-01	CREBL1	cAMP responsive element binding protein-like 1	chr6p21.3	216208_s_at	NM_004381
2.48	2.59	0.11	4.74E-01	7.84E-01	MGC5590	hypothetical protein MGC5590	chr13q14.11	220931_at	XM_930060 /// XM_941452
4.84	5.19	0.35	4.74E-01	7.84E-01	SLC39A6	solute carrier family 39 (zinc transporter), member 6	chr18q12.2	1556551_s_at	NM_001099406 /// NM_012319
4.91	5.24	0.32	4.74E-01	7.84E-01	CSNK1G3	casein kinase 1, gamma 3	chr5q23	220768_s_at	NM_001031812 /// NM_001044722 /// NM_001044723 /// NM_004384
6.71	6.95	0.24	4.74E-01	7.84E-01	AP3M1	adaptor-related protein complex 3, mu 1 subunit	chr10q22.2	222516_at	NM_012095 /// NM_207012
6.60	6.76	0.15	4.74E-01	7.84E-01	---	---	---	226902_at	---
2.53	2.68	0.15	4.74E-01	7.84E-01	---	---	---	1563341_at	---
2.70	2.82	0.12	4.74E-01	7.84E-01	ZNF518B	zinc finger protein 518B	chr4p16.1	230715_at	NM_053042
2.18	2.30	0.12	4.74E-01	7.84E-01	ZNF214	zinc finger protein 214	chr11p15.4	243456_at	NM_013249
2.16	2.27	0.12	4.74E-01	7.84E-01	PGLYRP3	peptidoglycan recognition protein 3	chr1q21	1553059_at	NM_052891
2.43	2.53	0.11	4.74E-01	7.84E-01	HDAC6	histone deacetylase 6	chrXp11.23	211722_s_at	NM_006044
3.29	3.39	0.10	4.74E-01	7.84E-01	GNRHR2	gonadotropin-releasing hormone (type 2) receptor 2	chr1q12	1553067_a_at	NR_002328
2.27	2.37	0.10	4.74E-01	7.84E-01	---	---	---	1560634_a_at	---
2.18	2.28	0.10	4.74E-01	7.84E-01	---	---	---	1556713_at	---
2.07	2.17	0.10	4.74E-01	7.84E-01	C13orf26	chromosome 13 open reading frame 26	chr13q12.3	243884_at	NM_152325
2.04	2.12	0.08	4.74E-01	7.84E-01	LRRC19	leucine rich repeat containing 19	chr9p21.2	220376_at	NM_022901
2.24	2.39	0.15	4.74E-01	7.84E-01	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	chr6q27	229775_s_at	NM_001040000 /// NM_001040001 /// NM_005936
2.30	2.41	0.11	4.74E-01	7.84E-01	LOC100131413	pRbBP-39	chr16p13.2	1555456_at	XM_001722266 /// XM_001722423 /// XM_001724929
2.80	2.89	0.09	4.74E-01	7.84E-01	AMELY	amelogenin, Y-linked	chrYp11.2	208220_x_at	NM_001143
2.60	2.72	0.13	4.74E-01	7.84E-01	---	---	---	240866_at	---

1.89	1.97	0.08	4.74E-01	7.84E-01	LOC440061	Hypothetical LOC440061	chr11q14.3	1561997_at	XR_016187 /// XR_037839
5.76	6.08	0.32	4.74E-01	7.84E-01	STX7	syntaxin 7	chr6q23.1	212632_at	NM_003569
5.55	5.70	0.14	4.74E-01	7.84E-01	POU2F2	POU class 2 homeobox 2	chr19q13.2	229750_at	NM_002698
1.97	2.07	0.10	4.74E-01	7.84E-01	---	---	---	237492_at	---
2.50	2.59	0.09	4.74E-01	7.84E-01	---	---	---	240621_at	---
2.77	2.89	0.12	4.74E-01	7.84E-01	---	---	---	240940_at	---
2.01	2.11	0.11	4.74E-01	7.84E-01	C10orf44	chromosome 10 open reading frame 44	---	1557881_at	---
2.33	2.43	0.10	4.74E-01	7.84E-01	LOC646626	hypothetical LOC646626	chr1p22.3	244619_at	XM_001715407 /// XM_933781 /// XM_942822
2.34	2.44	0.10	4.74E-01	7.84E-01	---	---	---	1566455_at	---
2.36	2.45	0.09	4.74E-01	7.84E-01	---	---	---	224349_at	---
2.15	2.25	0.11	4.74E-01	7.84E-01	C11orf47	chromosome 11 open reading frame 47	chr11p15.4	242540_at	NM_173589
2.36	2.44	0.08	4.74E-01	7.84E-01	---	---	---	241041_at	---
2.11	2.21	0.10	4.74E-01	7.84E-01	PCSK1	proprotein convertase subtilisin/kexin type 1	chr5q15-q21	205825_at	NM_000439
3.77	4.01	0.24	4.75E-01	7.84E-01	ATG4C /// CTR9	ATG4 autophagy related 4 homolog C (S. cerevisiae) /// Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr11p15.3 /// chr1p31.3	228190_at	NM_014633 /// NM_032852 /// NM_178221
2.47	2.59	0.12	4.75E-01	7.84E-01	SYNJ1	synaptojanin 1	chr21q22.2	207594_s_at	NM_003895 /// NM_203446
2.25	2.34	0.09	4.75E-01	7.84E-01	FEZF2	FEZ family zinc finger 2	chr3p14.2	233897_at	NM_018008
2.07	2.16	0.09	4.75E-01	7.84E-01	ABRA	actin-binding Rho activating protein	chr8q23.1	1552731_at	NM_139166
7.22	7.38	0.16	4.75E-01	7.84E-01	GPBP1L1	GC-rich promoter binding protein 1-like 1	chr1p34.1	217877_s_at	NM_021639
3.15	3.25	0.10	4.75E-01	7.84E-01	FSTL1	Follistatin-like 1	chr3q13.33	240891_at	NM_007085
1.94	2.02	0.08	4.75E-01	7.84E-01	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	chr21q11	1569599_at	NM_022136
2.05	2.12	0.08	4.75E-01	7.84E-01	OXCT1	3-oxoacid CoA transferase 1	chr5p13.1	244134_at	NM_000436
6.84	7.23	0.39	4.75E-01	7.84E-01	HLTF	helicase-like transcription factor	chr3q25.1-q26.1	202983_at	NM_003071 /// NM_139048
5.27	5.44	0.17	4.75E-01	7.84E-01	HFE	hemochromatosis	chr6p21.3	206087_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
7.57	7.72	0.15	4.75E-01	7.84E-01	NFIB	nuclear factor I/B	chr9p24.1	213029_at	NM_005596
2.51	2.62	0.11	4.75E-01	7.84E-01	---	---	---	215284_at	---
3.96	4.31	0.35	4.75E-01	7.85E-01	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	chr1q22-q25	206049_at	NM_003005
6.70	6.93	0.23	4.75E-01	7.85E-01	LOC100131564	hypothetical protein LOC100131564	chr1p22.1	227074_at	XM_001714658 /// XM_001715045 /// XM_001719527
6.46	6.68	0.22	4.75E-01	7.85E-01	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	chr14q31	210740_s_at	NM_014216
5.72	5.94	0.21	4.75E-01	7.85E-01	AKAP12	A kinase (PRKA) anchor protein 12	chr6q24-q25	227530_at	NM_005100 /// NM_144497
9.19	9.39	0.20	4.75E-01	7.85E-01	CD99	CD99 molecule	chrXp22.32; Yp11.3	201029_s_at	NM_001122898 /// NM_002414
3.29	3.42	0.13	4.75E-01	7.85E-01	RAB11FIP4	RAB11 family interacting protein 4 (class II)	chr17q11.2	225739_at	NM_032932
11.99	12.19	0.20	4.75E-01	7.85E-01	LOC653737 /// LOC729402 /// RPL21	hypothetical LOC653737 /// hypothetical LOC729402 /// ribosomal protein L21	chr10q26.12 /// chr13q12.2 /// chr16p13.2	200012_x_at	NM_000982 /// XM_001133535 /// XM_001721328 /// XM_001722740 /// XM_001722741 /// XM_001722742 /// XM_001726209 /// XM_929340
2.34	2.47	0.13	4.75E-01	7.85E-01	ZDHHC20	zinc finger, DHHC-type containing 20	chr13q12.11	243786_at	NM_153251

3.33	3.43	0.10	4.75E-01	7.85E-01	IL9R /// LOC729486	interleukin 9 receptor /// similar to hCG1790853	chr16p13.3 /// chrXq28 and Yq12	214950_at	NM_002186 /// NM_176786 /// NR_024033 /// XR_042290 /// XR_042385 /// XR_042402
1.93	2.03	0.10	4.75E-01	7.85E-01	---	---	---	232410_at	---
6.28	6.75	0.46	4.75E-01	7.85E-01	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	chr10q22.1	218976_at	NM_021800 /// NM_201262
8.52	8.86	0.35	4.75E-01	7.85E-01	PBX1	pre-B-cell leukemia homeobox 1	chr1q23	212151_at	NM_002585
2.30	2.43	0.13	4.75E-01	7.85E-01	---	---	---	237587_at	---
6.25	6.37	0.12	4.76E-01	7.85E-01	LONP2	lon peptidase 2, peroxisomal	chr16q12.1	223099_s_at	NM_031490
1.99	2.09	0.10	4.76E-01	7.85E-01	---	---	---	1563541_at	---
1.89	1.96	0.07	4.75E-01	7.85E-01	LOC157381	hypothetical protein LOC157381	chr8q24.13	236950_s_at	---
5.73	5.98	0.24	4.76E-01	7.85E-01	C11orf57	chromosome 11 open reading frame 57	chr11q23.1	222588_s_at	NM_001082969 /// NM_001082970 /// NM_018195
5.41	5.57	0.16	4.76E-01	7.85E-01	---	---	---	236802_at	---
2.35	2.43	0.08	4.76E-01	7.85E-01	C21orf71	chromosome 21 open reading frame 71	---	1556414_at	NR_024092
2.14	2.21	0.07	4.76E-01	7.85E-01	---	---	---	1562642_at	---
3.13	3.38	0.25	4.76E-01	7.85E-01	LOC100127980 /// LOC100131741	hypothetical protein LOC100127980 /// hypothetical protein LOC100131741	chr19q13.12	243924_at	XM_001720119 /// XM_001720402 /// XM_001722412 /// XM_001722650
4.71	4.84	0.13	4.76E-01	7.85E-01	CAMK2N2	calcium/calmodulin-dependent protein kinase II inhibitor 2	chr3q27.1	1552893_at	NM_033259
4.84	4.92	0.09	4.76E-01	7.85E-01	NPTXR	neuronal pentraxin receptor	chr22q13.1	217041_at	NM_014293
6.50	6.79	0.28	4.76E-01	7.85E-01	GJA4	gap junction protein, alpha 4, 37kDa	chr1p35.1	204904_at	NM_002060
5.86	6.25	0.39	4.76E-01	7.85E-01	RAB5A	RAB5A, member RAS oncogene family	chr3p24-p22	206113_s_at	NM_004162
2.93	3.06	0.13	4.76E-01	7.85E-01	---	---	---	231492_at	---
4.67	4.77	0.11	4.76E-01	7.85E-01	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	chr9p13-p12	216153_x_at	NM_021111
6.17	6.41	0.23	4.76E-01	7.85E-01	PTK2	PTK2 protein tyrosine kinase 2	chr8q24-qter	207821_s_at	NM_005607 /// NM_153831
2.74	2.85	0.12	4.76E-01	7.85E-01	---	---	---	1563840_at	---
2.62	2.73	0.11	4.76E-01	7.85E-01	---	---	---	238927_at	---
2.59	2.70	0.11	4.76E-01	7.85E-01	---	---	---	1570282_at	---
2.33	2.43	0.09	4.76E-01	7.85E-01	KRT73	keratin 73	chr12q13.3	1553537_at	NM_175068
2.68	2.77	0.09	4.76E-01	7.85E-01	FLJ36840	Hypothetical LOC645524	---	231527_at	XR_040530 /// XR_040531 /// XR_040532
6.53	6.86	0.33	4.76E-01	7.85E-01	WAC	WW domain containing adaptor with coiled-coil	---	217742_s_at	NM_016628 /// NM_100264 /// NM_100486
2.11	2.21	0.10	4.76E-01	7.85E-01	---	---	---	1570224_at	---
6.20	6.47	0.27	4.76E-01	7.85E-01	SCOC	short coiled-coil protein	chr4q31.1	224786_at	NM_032547
3.12	3.21	0.08	4.76E-01	7.85E-01	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	chr6p21.3	224360_s_at	NM_020804
2.49	2.60	0.10	4.76E-01	7.85E-01	STXBP6	syntaxin binding protein 6 (amisyn)	chr14q12	220994_s_at	NM_014178
4.10	4.22	0.12	4.76E-01	7.85E-01	SH2D6	SH2 domain containing 6	chr2p11.2	242543_at	NM_198482
5.11	5.32	0.21	4.76E-01	7.85E-01	NCOR1	nuclear receptor co-repressor 1	chr17p11.2	200857_s_at	NM_006311
4.31	4.45	0.14	4.76E-01	7.85E-01	CA7	carbonic anhydrase VII	chr16q22.1	207504_at	NM_001014435 /// NM_005182
3.24	3.38	0.14	4.76E-01	7.85E-01	NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	chr16q23.1	215818_at	NM_001105663
2.75	2.88	0.14	4.76E-01	7.85E-01	MIDN	midnolin	chr19p13.3	231072_at	NM_177401
2.11	2.20	0.09	4.77E-01	7.85E-01	MYLK3	myosin light chain kinase 3	chr16q11.2	217623_at	NM_182493
7.81	8.06	0.25	4.77E-01	7.85E-01	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	224581_s_at	NM_022731
2.37	2.45	0.08	4.77E-01	7.85E-01	---	---	---	234298_at	---
4.13	4.32	0.18	4.77E-01	7.85E-01	DDEF1IT1	DDEF1 intronic transcript 1 (non-protein coding)	chr8q24.21	220694_at	NR_002765
1.89	1.98	0.09	4.77E-01	7.85E-01	PLK4	polo-like kinase 4 (Drosophila)	chr4q28	211088_s_at	NM_014264
7.49	7.64	0.15	4.77E-01	7.85E-01	GAS6 /// LOC100133684	growth arrest-specific 6 /// similar to growth arrest-specific 6	chr13q34	1598_g_at	NM_000820 /// XM_001716774
3.46	3.77	0.32	4.77E-01	7.86E-01	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	chr2p13-p12	206036_s_at	NM_002908

3.85	4.00	0.15	4.77E-01	7.86E-01	ANK1	ankyrin 1, erythrocytic	chr8p11.1	240363_at	NM_000037 /// NM_020475 /// NM_020476 /// NM_020477 /// NM_020478 /// NM_020480
3.46	3.58	0.12	4.77E-01	7.86E-01	ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	chr12q24.12	238655_at	NM_025247
3.33	3.45	0.12	4.77E-01	7.86E-01	MYBPH	myosin binding protein H	chr1q32.1	206304_at	NM_004997
5.53	5.63	0.10	4.77E-01	7.86E-01	---	---	---	242866_x_at	---
2.44	2.54	0.10	4.77E-01	7.86E-01	---	---	---	217327_at	---
1.86	1.95	0.09	4.77E-01	7.86E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1555708_a_at	NM_153003
1.79	1.87	0.08	4.77E-01	7.86E-01	---	---	---	232712_at	---
4.19	4.36	0.17	4.77E-01	7.86E-01	CCNF	cyclin F	chr16p13.3	204826_at	NM_001761
8.67	8.86	0.19	4.77E-01	7.86E-01	TCF4	transcription factor 4	chr18q21.1	213891_s_at	NM_001083962 /// NM_003199
3.41	3.54	0.13	4.77E-01	7.86E-01	HBM	hemoglobin, mu	chr16p13.3	240336_at	NM_001003938
3.46	3.57	0.11	4.77E-01	7.86E-01	CST8	cystatin 8 (cystatin-related epididymal specific)	chr20p11.21	220627_at	NM_005492
5.49	5.75	0.26	4.77E-01	7.86E-01	CIB2	calcium and integrin binding family member 2	chr15q24	205008_s_at	NM_006383
5.98	6.16	0.18	4.77E-01	7.86E-01	SNX24	sorting nexin 24	chr5q23.2	222716_s_at	NM_014035
3.96	4.22	0.26	4.77E-01	7.86E-01	DENR	density-regulated protein	chr12q24.31	234915_s_at	NM_003677
6.03	6.24	0.21	4.77E-01	7.86E-01	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	chr3p21.3	202787_s_at	NM_004635
4.03	4.17	0.15	4.77E-01	7.86E-01	CCDC131	coiled-coil domain containing 131	chr12q21.1	244499_at	NM_144982
2.68	2.79	0.12	4.77E-01	7.86E-01	DCD	dermcidin	chr12q13.1	1553946_at	NM_053283
2.03	2.14	0.11	4.77E-01	7.86E-01	C9orf11	chromosome 9 open reading frame 11	chr9p21	232868_at	NM_020641
1.93	2.02	0.09	4.78E-01	7.86E-01	KDSR	3-ketodihydrosphingosine reductase	chr18q21.3	222359_x_at	NM_002035
3.82	3.94	0.12	4.78E-01	7.86E-01	RTKN	rhotekin	chr2p13.1	225151_at	NM_001015055 /// NM_001015056 /// NM_033046
2.07	2.18	0.10	4.78E-01	7.86E-01	ZNF404	zinc finger protein 404	chr19q13.31	239043_at	NM_001033719
1.97	2.05	0.08	4.78E-01	7.86E-01	---	---	---	241235_at	---
3.76	4.02	0.26	4.78E-01	7.86E-01	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	chr9q21	214785_at	NM_001018037 /// NM_001018038 /// NM_015186 /// NM_033305
7.07	7.31	0.24	4.78E-01	7.86E-01	TSN	translin	chr2q21.1	201515_s_at	NM_004622
2.33	2.43	0.10	4.78E-01	7.86E-01	---	---	---	233388_at	---
2.85	2.94	0.09	4.78E-01	7.86E-01	NAT8L	N-acetyltransferase 8-like	chr4p16.3	235316_at	NM_178557
2.21	2.30	0.09	4.78E-01	7.86E-01	GLIPR1L1	GLI pathogenesis-related 1 like 1	chr12q21.1	238296_at	NM_152779
2.95	3.12	0.17	4.78E-01	7.86E-01	---	---	---	1555616_at	---
5.98	6.25	0.27	4.78E-01	7.87E-01	C3orf26	chromosome 3 open reading frame 26	chr3q12.1	224523_s_at	NM_032359
2.32	2.43	0.11	4.78E-01	7.87E-01	---	---	---	244821_at	---
4.13	4.24	0.11	4.78E-01	7.87E-01	GJD2	gap junction protein, delta 2, 36kDa	chr15q14	221407_at	NM_020660
2.46	2.61	0.15	4.79E-01	7.87E-01	TBL1X	transducin (beta)-like 1X-linked	chrXp22.3	1570293_at	NM_005647
2.70	2.87	0.17	4.79E-01	7.87E-01	MCHR1	melanin-concentrating hormone receptor 1	chr22q13.2	221354_s_at	NM_005297
2.25	2.32	0.07	4.79E-01	7.87E-01	---	---	---	215872_at	---
2.10	2.19	0.09	4.79E-01	7.87E-01	---	---	---	1559221_at	---
3.78	4.00	0.22	4.79E-01	7.87E-01	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	chr3q22.1	209935_at	NM_001001485 /// NM_001001486 /// NM_001001487 /// NM_014382
2.02	2.09	0.07	4.79E-01	7.87E-01	---	---	---	237876_at	---
2.45	2.54	0.08	4.79E-01	7.87E-01	---	---	---	1569741_at	---
2.48	2.59	0.11	4.79E-01	7.87E-01	---	---	---	236438_at	---
2.08	2.19	0.11	4.79E-01	7.87E-01	GNAT3	guanine nucleotide binding protein, alpha transducing 3	chr7q21.11	216590_at	NM_001102386
6.10	6.42	0.32	4.79E-01	7.87E-01	FXYD5	FXYD domain containing ion transport regulator 5	chr19q12-q13.1	224252_s_at	NM_014164 /// NM_144779
6.23	6.48	0.26	4.79E-01	7.87E-01	C4orf27	chromosome 4 open reading frame 27	chr4q33	218646_at	NM_017867
4.98	5.22	0.24	4.79E-01	7.87E-01	LARS	leucyl-tRNA synthetase	chr5q32	223888_s_at	NM_020117
4.99	5.22	0.23	4.79E-01	7.87E-01	LRBA	LPS-responsive vesicle trafficking, beach and anchor containing	chr4q31.3	214109_at	NM_006726
4.95	5.18	0.23	4.79E-01	7.87E-01	---	---	---	240314_at	---
4.35	4.56	0.21	4.79E-01	7.87E-01	---	---	---	226374_at	---

7.06	7.27	0.21	4.80E-01	7.87E-01	PPAP2B	phosphatidic acid phosphatase type 2B	chr1pter-p22.1	209355_s_at	NM_003713 /// NM_177414
2.70	2.88	0.18	4.80E-01	7.87E-01	---	---	---	244217_at	---
5.60	5.78	0.18	4.79E-01	7.87E-01	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	chr2p13.1	201299_s_at	NM_018221
5.83	5.99	0.16	4.79E-01	7.87E-01	CLDN5	claudin 5	chr22q11.21	204482_at	NM_001130861 /// NM_003277
2.18	2.32	0.14	4.79E-01	7.87E-01	C6orf105	chromosome 6 open reading frame 105	chr6p24.1	229070_at	NM_032744
7.01	7.16	0.14	4.79E-01	7.87E-01	C6orf89	chromosome 6 open reading frame 89	chr6p21.2	225729_at	NM_152734
2.46	2.60	0.14	4.79E-01	7.87E-01	SOX17	SRY (sex determining region Y)-box 17	chr8q11.23	230943_at	NM_022454
2.59	2.72	0.14	4.80E-01	7.87E-01	RUNX2	runt-related transcription factor 2	chr6p21	216994_s_at	NM_001015051 /// NM_001024630 /// NM_004348
4.38	4.51	0.13	4.79E-01	7.87E-01	ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	chr16p12.1	230693_at	NM_004320 /// NM_173201
6.45	6.57	0.13	4.79E-01	7.87E-01	RIOK3	RIO kinase 3 (yeast)	chr18q11.2	215588_x_at	NM_003831
2.56	2.67	0.11	4.79E-01	7.87E-01	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	chr1p36.21	1557771_at	NM_052929 /// XM_001714211 /// XM_934889 /// XM_946265
1.97	2.08	0.11	4.79E-01	7.87E-01	TMED5	transmembrane emp24 protein transport domain containing 5	chr1pter-q31.3	1558813_at	NM_016040
2.18	2.29	0.11	4.79E-01	7.87E-01	EMR3	egf-like module containing, mucin-like, hormone receptor-like 3	chr19p13.1	210724_at	NM_032571
1.99	2.10	0.11	4.79E-01	7.87E-01	TRPM6	transient receptor potential cation channel, subfamily M, member 6	chr9q21.13	224412_s_at	NM_017662
9.10	9.21	0.11	4.79E-01	7.87E-01	APLP2	amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	208248_x_at	NM_001642
5.00	5.11	0.11	4.79E-01	7.87E-01	C21orf67	chromosome 21 open reading frame 67	chr21q22.3	1552528_at	XR_039924 /// XR_039925 /// XR_039926
2.54	2.64	0.10	4.80E-01	7.87E-01	---	---	---	1570248_at	---
2.17	2.27	0.09	4.79E-01	7.87E-01	RNF152	ring finger protein 152	chr18q21.33	1553722_s_at	NM_173557
2.63	2.72	0.09	4.79E-01	7.87E-01	LOC283485	hypothetical protein LOC283485	chr13q34	1556477_a_at	---
2.00	2.09	0.09	4.80E-01	7.87E-01	DOCK1	dedicator of cytokinesis 1	chr10q26.13-q26.3	241708_at	NM_001380
2.55	2.64	0.09	4.79E-01	7.87E-01	---	---	---	242504_at	---
2.68	2.77	0.08	4.80E-01	7.87E-01	---	---	---	237051_at	---
1.90	1.97	0.07	4.79E-01	7.87E-01	---	---	---	207471_at	---
2.46	2.67	0.22	4.80E-01	7.87E-01	SUSD4	sushi domain containing 4	chr1q41	223821_s_at	NM_001037175 /// NM_017982
2.00	2.13	0.12	4.80E-01	7.87E-01	MBD2	methyl-CpG binding domain protein 2	chr18q21	214397_at	NM_003927 /// NM_015832
11.57	11.84	0.26	4.80E-01	7.87E-01	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	chr6p21.3	214622_at	NM_000500 /// NM_001128590
3.03	3.11	0.09	4.80E-01	7.87E-01	---	---	---	237270_at	---
5.67	5.89	0.22	4.80E-01	7.87E-01	---	---	---	241965_at	---
3.77	3.97	0.20	4.80E-01	7.87E-01	---	---	---	1566163_at	---
5.32	5.47	0.14	4.80E-01	7.87E-01	ZFYVE1	zinc finger, FYVE domain containing 1	chr14q22-q24	223388_s_at	NM_021260 /// NM_178441
2.99	3.13	0.13	4.80E-01	7.87E-01	DOCK1	dedicator of cytokinesis 1	chr10q26.13-q26.3	241709_s_at	NM_001380
2.70	2.80	0.09	4.80E-01	7.87E-01	BRF1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	chr14q	1552399_a_at	NM_001519 /// NM_145685
2.27	2.35	0.08	4.80E-01	7.87E-01	---	---	---	232875_at	---
2.54	2.62	0.09	4.80E-01	7.87E-01	LOC646982	TTL/TEL fusion protein TTL-T	chr13q14.11	1554927_at	XM_929953 /// XM_941294
1.85	1.94	0.08	4.80E-01	7.87E-01	ASB4	ankyrin repeat and SOCS box-containing 4	chr7q21-q22	217229_at	NM_016116 /// NM_145872
7.62	8.08	0.46	4.80E-01	7.88E-01	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	chr3q26	202688_at	NM_003810
1.84	1.94	0.10	4.80E-01	7.88E-01	---	---	---	233591_at	---
1.89	1.97	0.08	4.80E-01	7.88E-01	---	---	---	1557842_at	---
3.07	3.19	0.12	4.80E-01	7.88E-01	ALPI	alkaline phosphatase, intestinal	chr2q37.1	211618_s_at	NM_001631
3.17	3.34	0.17	4.80E-01	7.88E-01	---	---	---	1560617_at	---
8.15	8.34	0.19	4.80E-01	7.88E-01	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	chr8p22-p21.3	213702_x_at	NM_001127505 /// NM_004315 /// NM_177924
7.23	7.39	0.16	4.80E-01	7.88E-01	ACLY	ATP citrate lyase	chr17q12-q21	201127_s_at	NM_001096 /// NM_198830
2.78	2.89	0.11	4.80E-01	7.88E-01	UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1	chr5p13.2	237572_at	NM_152404
3.39	3.48	0.09	4.80E-01	7.88E-01	---	---	---	234397_at	---

1.80	1.91	0.10	4.81E-01	7.88E-01	SPO11	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)	chr20q13.2-q13.3	222259_s_at	NM_012444 /// NM_198265																					
2.27	2.37	0.10	4.81E-01	7.88E-01	---	---	---	236912_at	---																					
1.95	2.04	0.09	4.81E-01	7.88E-01	ZNF169	zinc finger protein 169	chr9q22.32	1570354_s_at	NM_194320																					
3.76	4.02	0.26	4.81E-01	7.88E-01	SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	chr3q21.2	219874_at	NM_024628																					
2.51	2.63	0.13	4.81E-01	7.88E-01	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17p13.3	221707_s_at	NM_001128159 /// NM_018289																					
1.88	1.96	0.08	4.81E-01	7.88E-01	RBM39	RNA binding motif protein 39	chr20q11.22	238355_at	NM_004902 /// NM_184234																					
5.96	6.24	0.28	4.81E-01	7.88E-01	PSIP1	PC4 and SFRS1 interacting protein 1	chr9p22.3	209337_at	NM_001128217 /// NM_021144 /// NM_033222																					
2.13	2.20	0.07	4.81E-01	7.88E-01	IGF2BP3 /// LOC645468	insulin-like growth factor 2 mRNA binding protein 3 /// similar to putative RNA binding protein KOC	chr6q27 /// chr7p11	216493_s_at	NM_006547 /// XR_017635 /// XR_038251 /// XR_039797																					
4.75	4.95	0.20	4.81E-01	7.88E-01	LOC100129500	hypothetical protein LOC100129500	chr19q13.32	212874_at	XM_001722911 /// XM_001722946 /// XM_001724653 /// XM_001724655																					
6.29	6.43	0.14	4.81E-01	7.88E-01	RRP9	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)	chr3p21.1	204133_at	NM_004704																					
2.62	2.75	0.14	4.81E-01	7.88E-01	VNN1	vanin 1	chr6q23-q24	1558549_s_at	NM_004666																					
2.12	2.23	0.11	4.81E-01	7.88E-01	POF1B	premature ovarian failure, 1B	chrXq21.1-q21.2	1555383_a_at	NM_024921																					
2.17	2.26	0.09	4.81E-01	7.88E-01	C6orf124 /// LOC729439	chromosome 6 open reading frame 124 /// similar to HGC6.4	chr6q27	210409_at	NM_001042508 /// XM_001723745																					
7.31	7.47	0.16	4.81E-01	7.88E-01	SNW1	SNW domain containing 1	chr14q24.3	201575_at	NM_012245																					
8.10	8.26	0.15	4.81E-01	7.88E-01	RAB6A	RAB6A, member RAS oncogene family	chr11q13.3	201047_x_at	NM_002869 /// NM_198896																					
8.31	8.45	0.14	4.81E-01	7.88E-01	NDRG3	NDRG family member 3	chr20q11.21-q11.23	217286_s_at	NM_022477 /// NM_032013																					
2.87	3.00	0.13	4.81E-01	7.88E-01	---	---	---	240323_at	---																					
1.95	2.05	0.10	4.81E-01	7.88E-01	HMGCLL1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	chr6p12.1	232305_at	NM_001042406 /// NM_019036																					
2.14	2.24	0.10	4.81E-01	7.88E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	211265_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719																					
2.48	2.57	0.09	4.81E-01	7.88E-01	HDGFRP3	Hepatoma-derived growth factor, related protein 3	chr15q25.2	221976_s_at	NM_016073																					
2.34	2.43	0.09	4.81E-01	7.88E-01	---	---	---	236125_at	---																					
3.49	3.58	0.09	4.81E-01	7.88E-01	---	---	---	238233_at	---																					
2.07	2.15	0.08	4.81E-01	7.88E-01	---	---	---	234503_at	---																					
2.17	2.25	0.08	4.81E-01	7.88E-01	TNXB	tenascin XB	chr6p21.3	1565242_at	NM_019105 /// NM_032470																					
2.28	2.36	0.08	4.81E-01	7.88E-01	---	---	---	1570082_x_at	---																					
2.49	2.58	0.09	4.81E-01	7.88E-01	---	---	---	1562269_at	---																					
2.51	2.61	0.10	4.81E-01	7.88E-01	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	chr19p13.3	214865_at	NM_032482																					
6.07	6.23	0.16	4.81E-01	7.88E-01	SLC46A1	solute carrier family 46 (folate transporter), member 1	chr17q11.2	1558703_at	NM_080669																					
2.59	2.71	0.12	4.81E-01	7.88E-01	LOC100129969	hypothetical protein LOC100129969	chr9p13.3	237827_at	XM_001721469 /// XM_001723968 /// XM_001725789																					
1.98	2.09	0.11	4.81E-01	7.88E-01	---	---	---	244483_at	---																					
1.90	2.01	0.11	4.81E-01	7.88E-01	ZNF81	zinc finger protein 81	chrXp11.23	215901_at	NM_007137																					
2.06	2.16	0.10	4.82E-01	7.88E-01	PDZK1P1	PDZ domain containing 1 pseudogene 1	chr1q21.1	244468_at	NR_003377																					
5.75	6.17	0.42	4.82E-01	7.89E-01	AGA	aspartylglucosaminidase	chr4q32-q33	216064_s_at	NM_000027																					
4.83	5.20	0.37	4.82E-01	7.89E-01	SCARB2	scavenger receptor class B, member 2	chr4q21.1	201647_s_at	NM_005506																					
3.08	3.27	0.20	4.82E-01	7.89E-01	SH2D3C	SH2 domain containing 3C	chr9q34.11	1552667_a_at	NM_005489 /// NM_170600																					

2.50	2.59	0.10	4.82E-01	7.89E-01	KRTAP11-1	keratin associated protein 11-1	chr21q22.1	1564803_at	NM_175858
4.29	4.42	0.14	4.82E-01	7.89E-01	NKD2	naked cuticle homolog 2 (Drosophila)	chr5p15.3	232201_at	NM_033120
2.87	2.98	0.11	4.82E-01	7.89E-01	---	---	---	229249_at	---
2.99	3.11	0.13	4.82E-01	7.89E-01	C11orf30	chromosome 11 open reading frame 30	chr11q13.5	242847_at	NM_020193
2.03	2.11	0.08	4.82E-01	7.89E-01	C14orf174	chromosome 14 open reading frame 174	chr14q24.3	232316_at	NM_001010860
1.93	2.03	0.11	4.82E-01	7.89E-01	---	---	---	241979_x_at	---
2.47	2.64	0.17	4.82E-01	7.89E-01	CD24	CD24 molecule	chr6q21	208651_x_at	NM_013230 /// XM_001725629
3.51	3.74	0.23	4.82E-01	7.89E-01	---	---	---	1560384_a_at	---
1.96	2.07	0.11	4.82E-01	7.89E-01	---	---	---	1569716_at	---
2.63	2.75	0.13	4.82E-01	7.89E-01	---	---	---	224054_at	---
2.42	2.54	0.12	4.82E-01	7.89E-01	AK7	adenylate kinase 7	chr14q32.2	1569699_at	NM_152327
3.31	3.41	0.10	4.82E-01	7.89E-01	---	---	---	1566954_at	---
3.10	3.21	0.11	4.82E-01	7.89E-01	ZNF391	zinc finger protein 391	chr6p22.1	1562446_at	NM_001076781
1.89	1.98	0.09	4.82E-01	7.89E-01	MGC26356	similar to zinc finger protein 595	chr4p16.3	1569468_at	XR_041102 /// XR_041103 /// XR_041104
5.59	5.71	0.13	4.82E-01	7.89E-01	DEDD	death effector domain containing	chr1q23.3	202480_s_at	NM_001039711 /// NM_001039712 /// NM_032998
2.85	2.98	0.13	4.82E-01	7.89E-01	SLC8A2	solute carrier family 8 (sodium/calcium exchanger), member 2	chr19q13.3	215267_s_at	NM_015063
2.54	2.66	0.13	4.82E-01	7.89E-01	KAAG1	kidney associated antigen 1	chr6p22.1	224157_at	NM_181337
3.22	3.34	0.12	4.82E-01	7.89E-01	---	---	---	1570227_at	---
4.09	4.20	0.12	4.82E-01	7.89E-01	LRRN2	leucine rich repeat neuronal 2	chr1q32.1	216164_at	NM_006338 /// NM_201630
2.42	2.52	0.10	4.82E-01	7.89E-01	C6orf217	chromosome 6 open reading frame 217	chr6q23.3	1561106_at	XM_001717359 /// XM_001717782 /// XM_001719694
2.02	2.11	0.09	4.82E-01	7.89E-01	---	---	---	237408_at	---
2.23	2.32	0.09	4.83E-01	7.89E-01	LOC100129194	hypothetical protein LOC100129194	chr3p22.3	238088_at	XM_001723061 /// XM_001723861 /// XM_001725682
2.36	2.48	0.12	4.83E-01	7.89E-01	---	---	---	238298_at	---
3.87	3.97	0.10	4.83E-01	7.89E-01	EFS	embryonal Fyn-associated substrate	chr14q11.2-q12	210880_s_at	NM_005864 /// NM_032459
2.16	2.24	0.08	4.83E-01	7.90E-01	---	---	---	1560021_at	---
2.07	2.17	0.10	4.83E-01	7.90E-01	ANKRD18A	Ankyrin repeat domain 18A	chr9p13.1	242045_at	XM_001713970 /// XM_001717620 /// XM_001726105
8.04	8.69	0.65	4.83E-01	7.90E-01	RGS2	regulator of G-protein signaling 2, 24kDa	chr1q31	202388_at	NM_002923
3.26	3.40	0.14	4.83E-01	7.90E-01	TAPT1	transmembrane anterior posterior transformation 1	chr4p15.32	238798_at	NM_153365
4.30	4.38	0.08	4.83E-01	7.90E-01	SEBOX	SEBOX homeobox	chr17q11.2	234256_at	NM_001080837 /// NM_001083896
5.11	5.29	0.19	4.83E-01	7.90E-01	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	chr3q22.1	207749_s_at	NM_002718 /// NM_181897
5.03	5.20	0.17	4.83E-01	7.90E-01	ALDH16A1	aldehyde dehydrogenase 16 family, member A1	chr19q13.33	227592_at	NM_153329
2.23	2.33	0.10	4.83E-01	7.90E-01	HIST1H4G	histone cluster 1, H4g	chr6p21.3	208551_at	NM_003547
2.77	2.90	0.12	4.83E-01	7.90E-01	FAM125B	family with sequence similarity 125, member B	chr9q33.3	1554065_at	NM_001011703 /// NM_033446
11.00	11.22	0.22	4.83E-01	7.90E-01	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	chr18q12-q21	213738_s_at	NM_001001937 /// NM_004046
4.22	4.34	0.12	4.83E-01	7.90E-01	---	---	---	230334_at	---
3.02	3.13	0.11	4.83E-01	7.90E-01	SYNJ2	Synaptojanin 2	chr6q25.3	216182_at	NM_003898
1.92	2.01	0.09	4.83E-01	7.90E-01	---	---	---	1561151_a_at	---
2.92	3.02	0.10	4.83E-01	7.90E-01	RSPH1	radial spoke head 1 homolog (Chlamydomonas)	chr21q22.3	230093_at	NM_080860
3.91	4.06	0.15	4.84E-01	7.90E-01	PQLC3	PQ loop repeat containing 3	chr2p25.1	216458_at	NM_152391
1.87	1.94	0.07	4.84E-01	7.90E-01	COL24A1	collagen, type XXIV, alpha 1	chr1p22.3	238732_at	NM_152890
5.51	5.63	0.12	4.84E-01	7.90E-01	OSBPL5	oxysterol binding protein-like 5	chr11p15.4	233734_s_at	NM_020896 /// NM_145638

3.01	3.12	0.11	4.84E-01	7.90E-01	---	---	---	237519_at	---
2.68	2.81	0.13	4.84E-01	7.90E-01	PCNXL2	pecanex-like 2 (Drosophila)	chr1q42.2	205689_at	NM_014801
5.90	6.08	0.18	4.84E-01	7.90E-01	PTPRM	protein tyrosine phosphatase, receptor type, M	chr18p11.2	203329_at	NM_001105244 /// NM_002845
2.71	2.83	0.12	4.84E-01	7.90E-01	ESR1	estrogen receptor 1	chr6q25.1	215552_s_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742
2.52	2.63	0.11	4.84E-01	7.90E-01	LOC338667	hypothetical protein LOC338667	chr11q24.2	1564786_at	XM_001715277 /// XM_001726523 /// XM_294675
2.75	3.10	0.35	4.84E-01	7.90E-01	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	chr3p14.3-p14.2	220287_at	NM_182920
2.98	3.13	0.15	4.84E-01	7.90E-01	ZNF418	zinc finger protein 418	chr19q13.43	243439_at	NM_133460
2.05	2.16	0.11	4.84E-01	7.90E-01	LOC285593	hypothetical protein LOC285593	chr5q35.2	1560260_at	---
1.97	2.08	0.10	4.84E-01	7.90E-01	MTBP	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa	chr8q24.12	1563614_at	NM_022045
1.95	2.03	0.08	4.84E-01	7.90E-01	UTX	ubiquitously transcribed tetratricopeptide repeat, X chromosome	chrXp11.2	238220_at	NM_021140
2.64	2.85	0.21	4.84E-01	7.90E-01	ZNF658	zinc finger protein 658	chr9p12	231950_at	NM_033160
2.75	2.85	0.11	4.84E-01	7.90E-01	---	---	---	216545_at	---
3.61	3.73	0.12	4.84E-01	7.90E-01	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	chr20q11	209144_s_at	NM_001032999 /// NM_001039709 /// NM_005093
2.72	2.84	0.11	4.84E-01	7.90E-01	LHX9	LIM homeobox 9	chr1q31-q32	1565406_a_at	NM_001014434 /// NM_020204
2.36	2.45	0.09	4.84E-01	7.90E-01	---	---	---	243460_at	---
6.38	6.55	0.17	4.84E-01	7.90E-01	APBB1	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	chr11p15	202652_at	NM_001164 /// NM_145689
1.99	2.08	0.09	4.84E-01	7.90E-01	AKR1C2	Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	chr10p15-p14	1560098_at	NM_001354 /// NM_205845
4.57	4.80	0.24	4.84E-01	7.90E-01	WARS2	tryptophanyl tRNA synthetase 2, mitochondrial	chr1p13.3-p13.1	218766_s_at	NM_015836 /// NM_201263
3.68	3.84	0.16	4.84E-01	7.90E-01	TFG	TRK-fused gene	chr3q12.2	221871_s_at	NM_001007565 /// NM_006070
2.36	2.48	0.12	4.84E-01	7.90E-01	---	---	---	1556808_at	---
2.23	2.34	0.11	4.84E-01	7.90E-01	MED13	Mediator complex subunit 13	chr17q22-q23	244611_at	NM_005121
2.03	2.11	0.08	4.84E-01	7.90E-01	MOBP	myelin-associated oligodendrocyte basic protein	chr3p22.1	210193_at	NM_182935 /// NR_003090
1.90	1.98	0.08	4.84E-01	7.90E-01	LOC730051	Similar to hCG2044798	chr19q13.43	1556204_a_at	XM_001725674 /// XM_001725708 /// XM_001726286
1.93	1.99	0.07	4.85E-01	7.91E-01	---	---	---	236619_at	---
3.39	3.56	0.17	4.85E-01	7.91E-01	FAM149B1	family with sequence similarity 149, member B1	chr10q22.2	213463_s_at	NM_173348 /// XM_001721910 /// XM_001722273 /// XM_001723052
4.56	4.73	0.16	4.85E-01	7.91E-01	CLDN7	claudin 7	chr17p13	202790_at	NM_001307
4.29	4.45	0.16	4.85E-01	7.91E-01	KIF7	kinesin family member 7	chr15q26.1	229405_at	NM_198525
3.24	3.39	0.15	4.85E-01	7.91E-01	C10orf91	chromosome 10 open reading frame 91	chr10q26.3	1553880_at	NM_173541
2.19	2.27	0.08	4.85E-01	7.91E-01	MS4A6E	membrane-spanning 4-domains, subfamily A, member 6E	chr11q12.2	231335_at	NM_139249
2.01	2.08	0.08	4.85E-01	7.91E-01	---	---	---	233066_at	---
2.24	2.34	0.10	4.85E-01	7.91E-01	GRM5	Glutamate receptor, metabotropic 5	chr11q14.2-q14.3	214217_at	NM_000842
2.06	2.15	0.09	4.85E-01	7.91E-01	MR1	major histocompatibility complex, class I-related	chr1q25.3	210528_at	NM_001531
3.49	3.65	0.16	4.85E-01	7.91E-01	---	---	---	1557193_at	---
3.47	3.60	0.13	4.85E-01	7.91E-01	FFAR1	free fatty acid receptor 1	chr19q13.1	231761_at	NM_005303
2.82	2.95	0.13	4.85E-01	7.91E-01	---	---	---	228717_at	---
5.01	5.35	0.34	4.85E-01	7.91E-01	LBH	limb bud and heart development homolog (mouse)	chr2p23.1	221011_s_at	NM_030915
2.42	2.51	0.10	4.85E-01	7.91E-01	---	---	---	232917_at	---

3.36	3.46	0.10	4.85E-01	7.91E-01	---	---	---	1562272_at	---
2.04	2.13	0.10	4.85E-01	7.91E-01	---	---	---	240331_at	---
2.02	2.11	0.09	4.85E-01	7.91E-01	LOC100129436	hypothetical protein LOC100129436	chr6q14.1	244635_s_at	XM_001718927 /// XM_001719868 /// XM_001725266
5.11	5.28	0.17	4.85E-01	7.91E-01	IGF2AS	insulin-like growth factor 2 antisense	chr11p15.5	220561_at	NM_016412
5.74	5.99	0.24	4.86E-01	7.91E-01	---	---	---	225159_s_at	---
4.40	4.58	0.18	4.86E-01	7.91E-01	SLC44A1	solute carrier family 44, member 1	chr9q31.2	228486_at	NM_080546
2.89	3.01	0.11	4.85E-01	7.91E-01	C14orf174	chromosome 14 open reading frame 174	chr14q24.3	1557680_at	NM_001010860
2.93	3.04	0.11	4.86E-01	7.91E-01	---	---	---	215445_x_at	---
2.92	3.02	0.10	4.85E-01	7.91E-01	CSNK1A1	Casein kinase 1, alpha 1	chr5q32	226920_at	NM_001025105 /// NM_001892
2.38	2.47	0.09	4.86E-01	7.91E-01	---	---	---	1566165_at	---
1.82	1.90	0.08	4.86E-01	7.91E-01	NLN	neurolysin (metallopeptidase M3 family)	chr5q12.3	224063_at	NM_020726
2.85	2.96	0.11	4.86E-01	7.91E-01	---	---	---	231390_at	---
1.96	2.04	0.08	4.86E-01	7.91E-01	MUC7	mucin 7, secreted	chr4q13-q21	217059_at	NM_152291
2.18	2.26	0.08	4.86E-01	7.91E-01	MYEF2	myelin expression factor 2	chr15q21.1	222153_at	NM_016132
1.97	2.04	0.07	4.86E-01	7.91E-01	---	---	---	AFFX-DapX-5_at	---
1.85	1.93	0.08	4.86E-01	7.91E-01	---	---	---	236735_at	---
2.54	2.63	0.08	4.86E-01	7.91E-01	---	---	---	220874_at	---
2.01	2.09	0.08	4.86E-01	7.91E-01	DIAPH1	diaphanous homolog 1 (Drosophila)	chr5q31	1560080_at	NM_001079812 /// NM_005219
2.58	2.70	0.12	4.86E-01	7.91E-01	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	chr6q12	211204_at	NM_002395
1.99	2.09	0.11	4.86E-01	7.91E-01	NR5A2	nuclear receptor subfamily 5, group A, member 2	chr1q32.1	208343_s_at	NM_003822 /// NM_205860
3.05	3.26	0.21	4.86E-01	7.91E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	211633_x_at	---
10.00	10.18	0.18	4.86E-01	7.91E-01	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	chr11p15	200004_at	NM_001042559 /// NM_001418
3.56	3.68	0.11	4.86E-01	7.91E-01	---	---	---	236903_at	---
4.91	5.11	0.20	4.86E-01	7.91E-01	RAB4B	RAB4B, member RAS oncogene family	chr19q13.2	237257_at	NM_016154
3.04	3.19	0.15	4.86E-01	7.91E-01	---	---	---	240418_at	---
5.96	6.40	0.44	4.86E-01	7.91E-01	LARP7	La ribonucleoprotein domain family, member 7	chr4q25	212785_s_at	NM_015454 /// NM_016648
4.45	4.59	0.13	4.86E-01	7.91E-01	LOC93444	hypothetical protein LOC93444	chr15q22.32	234956_at	---
2.37	2.47	0.10	4.86E-01	7.91E-01	SLC35F3	solute carrier family 35, member F3	chr1q42.2	229065_at	NM_173508
4.30	4.49	0.20	4.86E-01	7.92E-01	IPO5	importin 5	chr13q32.2	211952_at	NM_002271
2.43	2.61	0.18	4.86E-01	7.92E-01	FGD4	FYVE, RhoGEF and PH domain containing 4	chr12p11.21	242445_at	NM_139241
3.12	3.23	0.11	4.86E-01	7.92E-01	---	---	---	236177_s_at	---
3.91	4.01	0.10	4.86E-01	7.92E-01	FAM178B	family with sequence similarity 178, member B	chr2q11.2	223812_at	NM_001122646 /// NM_016490
2.71	2.80	0.08	4.86E-01	7.92E-01	LOC283901	hypothetical protein LOC283901	chr16p12.1	1558525_at	---
2.25	2.37	0.11	4.86E-01	7.92E-01	---	---	---	1561605_at	---
2.13	2.21	0.09	4.86E-01	7.92E-01	IFT80	Intraflagellar transport 80 homolog (Chlamydomonas)	chr3q26.1	240251_at	NM_020800
3.01	3.15	0.14	4.87E-01	7.92E-01	CA5B	carbonic anhydrase VB, mitochondrial	chrXp21.1	207129_at	NM_007220
3.81	3.97	0.15	4.87E-01	7.92E-01	KCNIP3	Kv channel interacting protein 3, calsenilin	chr2q21.1	228269_x_at	NM_001034914 /// NM_013434
4.28	4.41	0.13	4.87E-01	7.92E-01	ZNF34	zinc finger protein 34	chr8q24.3	219801_at	NM_030580
2.22	2.31	0.09	4.87E-01	7.92E-01	---	---	---	237674_at	---
6.25	6.40	0.15	4.87E-01	7.92E-01	TRIM56	tripartite motif-containing 56	chr7q22.1	231876_at	NM_030961
6.58	6.73	0.15	4.87E-01	7.92E-01	C7orf58	chromosome 7 open reading frame 58	chr7q31.31	228728_at	NM_001105533 /// NM_024913
5.98	6.24	0.26	4.87E-01	7.92E-01	TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	chr20p12.3	222768_s_at	NM_015939
4.70	4.83	0.13	4.87E-01	7.92E-01	BCAN	brevican	chr1q31	219107_at	NM_021948 /// NM_198427
2.38	2.47	0.09	4.87E-01	7.92E-01	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	chr10q24	211524_at	NM_001077493 /// NM_001077494 /// NM_002502
2.60	2.75	0.15	4.87E-01	7.92E-01	RBM4	RNA binding motif protein 4	chr11q13	236157_at	NM_002896
4.17	4.42	0.25	4.87E-01	7.92E-01	CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	chr16p13.3	205845_at	NM_001005407 /// NM_021098

1.85	1.93	0.08	4.87E-01	7.92E-01	LOC338739	hypothetical protein LOC338739	chr11p13	1560202_at	XM_001130961 /// XM_001132667 /// XM_001717033																				
2.48	2.59	0.11	4.87E-01	7.92E-01	KIAA1661	KIAA1661 protein	---	215943_at	---																				
4.86	5.36	0.50	4.87E-01	7.92E-01	---	---	---	237305_at	---																				
2.48	2.63	0.15	4.87E-01	7.92E-01	LOC100132726	hypothetical protein LOC100132726	chr15q13.2	243336_at	XM_001724495																				
2.68	2.81	0.13	4.87E-01	7.92E-01	---	---	---	1567139_at	---																				
3.11	3.21	0.10	4.87E-01	7.92E-01	---	---	---	237497_at	---																				
3.72	4.12	0.40	4.87E-01	7.92E-01	---	---	---	232528_at	---																				
3.69	3.90	0.21	4.87E-01	7.92E-01	FHDC1	FH2 domain containing 1	chr4q31.3	226599_at	NM_033393																				
4.78	4.93	0.15	4.87E-01	7.92E-01	WDTC1	WD and tetratricopeptide repeats 1	chr1p36.11	215497_s_at	NM_015023																				
2.93	3.08	0.14	4.87E-01	7.92E-01	---	---	---	236508_at	---																				
1.92	2.03	0.11	4.87E-01	7.92E-01	MYLK3	myosin light chain kinase 3	chr16q11.2	1568925_at	NM_182493																				
2.19	2.28	0.09	4.87E-01	7.92E-01	DEFB124	defensin, beta 124	chr20q11.1	1568375_at	NM_001037500																				
2.25	2.33	0.08	4.87E-01	7.92E-01	---	---	---	234567_at	---																				
4.28	4.59	0.31	4.88E-01	7.92E-01	TJP2	tight junction protein 2 (zona occludens 2)	chr9q13-q21	232017_at	NM_004817 /// NM_201629																				
1.92	2.00	0.08	4.87E-01	7.92E-01	KIAA1702 /// ZNF451	KIAA1702 protein /// zinc finger protein 451	chr6p11 /// chr6p12.1	231885_at	NM_001031623 /// NM_015555 /// XM_001722675 /// XM_001724453 /// XM_001726133																				
3.95	4.09	0.14	4.88E-01	7.92E-01	NLGN3	neuroligin 3	chrXq13.1	234751_s_at	NM_018977																				
2.82	2.95	0.13	4.88E-01	7.93E-01	LOC440934	Hypothetical gene supported by BC008048	chr2q36.1	230844_at	XR_015854 /// XR_016028 /// XR_041304																				
2.81	2.94	0.13	4.88E-01	7.93E-01	---	---	---	238408_at	---																				
2.10	2.23	0.13	4.88E-01	7.93E-01	---	---	---	229201_at	---																				
3.59	3.70	0.11	4.88E-01	7.93E-01	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	chr8p22-p21	206222_at	NM_003841																				
2.42	2.51	0.09	4.88E-01	7.93E-01	---	---	---	237543_at	---																				
2.06	2.13	0.07	4.88E-01	7.93E-01	DNAH6	dynein, axonemal, heavy chain 6	---	1565337_at	NM_001370																				
2.55	2.69	0.14	4.88E-01	7.93E-01	SPATA5	spermatogenesis associated 5	chr4q28.1	242251_at	NM_145207																				
1.98	2.08	0.09	4.88E-01	7.93E-01	KIF21A	kinesin family member 21A	chr12q12	231875_at	NM_017641																				
4.00	4.28	0.28	4.88E-01	7.93E-01	---	---	---	233995_at	---																				
2.96	3.15	0.19	4.88E-01	7.93E-01	DOCK8	dedicator of cytokinesis 8	chr9p24.3	239027_at	NM_203447																				
4.37	4.69	0.32	4.88E-01	7.93E-01	ZFYVE16	zinc finger, FYVE domain containing 16	chr5q14	1554638_at	NM_001105251 /// NM_014733																				
7.28	7.56	0.28	4.88E-01	7.93E-01	HSPA4	heat shock 70kDa protein 4	chr5q31.1-q31.2	208815_x_at	NM_002154																				
4.06	4.32	0.26	4.88E-01	7.93E-01	RTP4	receptor (chemosensory) transporter protein 4	chr3q27.3	219684_at	NM_022147																				
2.96	3.16	0.20	4.88E-01	7.93E-01	---	---	---	236117_at	---																				
3.30	3.45	0.15	4.88E-01	7.93E-01	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	chr11p15.1	229102_at	NM_001098520 /// NM_001098521 /// NM_001098522 /// NM_001098523 /// NM_006410																				
4.59	4.74	0.15	4.88E-01	7.93E-01	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	chr6p21.3	204769_s_at	NM_000544 /// NM_018833																				
3.54	3.68	0.14	4.88E-01	7.93E-01	FLJ23569	BC040926	chr19q13.4	232462_s_at	NR_015380 /// XR_040373 /// XR_040374																				
2.36	2.49	0.13	4.88E-01	7.93E-01	DAPK3	Death-associated protein kinase 3	chr19p13.3	228681_x_at	NM_001348																				
2.89	2.99	0.10	4.88E-01	7.93E-01	HIP1	huntingtin interacting protein 1	chr7q11.23	205426_s_at	NM_005338																				
2.46	2.56	0.10	4.88E-01	7.93E-01	---	---	---	216742_at	---																				
2.97	3.07	0.10	4.88E-01	7.93E-01	---	---	---	232944_at	---																				
1.96	2.06	0.10	4.88E-01	7.93E-01	---	---	---	1563858_at	---																				
1.98	2.07	0.10	4.88E-01	7.93E-01	---	---	---	241099_at	---																				
2.16	2.24	0.08	4.88E-01	7.93E-01	---	---	---	220876_at	---																				
3.84	4.10	0.25	4.88E-01	7.93E-01	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	chr16q13	213461_at	NM_007006																				
2.53	2.75	0.22	4.88E-01	7.93E-01	ACSBG1	acyl-CoA synthetase bubblegum family member 1	chr15q23-q24	206465_at	NM_015162																				
4.40	4.58	0.18	4.88E-01	7.93E-01	ZNF350	zinc finger protein 350	chr19q13.33	219266_at	NM_021632																				

10.03	10.15	0.12	4.89E-01	7.93E-01	HLA-B /// HLA-C /// MICA /// XXbac-BPG181B23.1	major histocompatibility complex, class I, B /// major histocompatibility complex, class I, C /// MHC class I polypeptide-related sequence A /// MHC class I polypeptide-related sequence A	chr6p21.3 /// chr6p21.33	216526_x_at	NM_000247 /// NM_002117 /// NM_005514 /// XM_001713607 /// XM_001715881 /// XM_001717045 /// XM_001719879																				
2.50	2.57	0.08	4.89E-01	7.93E-01	---	---	---	AFFX-ThrX-3_at	---																				
2.72	2.85	0.13	4.89E-01	7.93E-01	---	---	---	216413_at	---																				
4.46	4.73	0.27	4.89E-01	7.93E-01	MFN1	mitofusin 1	chr3q26.32	207098_s_at	NM_033540																				
2.19	2.31	0.12	4.89E-01	7.93E-01	ZNF771	zinc finger protein 771	chr16p11.2	219782_s_at	NM_016643 /// XM_001721231 /// XM_001721234																				
2.20	2.28	0.09	4.89E-01	7.93E-01	---	---	---	233976_at	---																				
3.17	3.28	0.11	4.89E-01	7.93E-01	C7orf20	Chromosome 7 open reading frame 20	chr7p22.3	227588_s_at	NM_015949																				
2.57	2.67	0.10	4.89E-01	7.93E-01	---	---	---	1555158_at	---																				
2.81	2.89	0.09	4.89E-01	7.93E-01	LOC283875	hypothetical protein LOC283875	chr16p13.3	1564122_at	XM_944407																				
2.25	2.33	0.08	4.89E-01	7.93E-01	PFTK1	PFTAIRE protein kinase 1	chr7q21-q22	211502_s_at	NM_012395																				
8.42	8.72	0.30	4.89E-01	7.93E-01	FBLN1	fibulin 1	chr22q13.31	202994_s_at	NM_001996 /// NM_006485 /// NM_006486 /// NM_006487																				
3.18	3.29	0.11	4.89E-01	7.93E-01	CUBN	cubilin (intrinsic factor-cobalamin receptor)	chr10p12.31	206775_at	NM_001081																				
6.03	6.36	0.33	4.89E-01	7.93E-01	GPR89A /// GPR89B /// GPR89C	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	chr1q21.1	220642_x_at	NM_001097612 /// NM_001097613 /// NM_001097616 /// NM_016334																				
2.47	2.58	0.11	4.89E-01	7.93E-01	C22orf15	chromosome 22 open reading frame 15	chr22q11.23	1558333_at	NM_182520																				
2.09	2.18	0.09	4.89E-01	7.93E-01	OXGR1	oxoglutarate (alpha-ketoglutarate) receptor 1	chr13q32.1	1553319_at	NM_080818																				
5.72	5.91	0.19	4.89E-01	7.93E-01	---	---	---	203812_at	---																				
4.67	5.06	0.39	4.89E-01	7.93E-01	LPL	lipoprotein lipase	chr8p22	203549_s_at	NM_000237																				
2.41	2.54	0.13	4.89E-01	7.93E-01	MYCBPAP	MYCBP associated protein	chr17q21.33	1562791_at	NM_032133																				
3.03	3.13	0.10	4.89E-01	7.93E-01	---	---	---	242505_at	---																				
6.76	7.10	0.35	4.89E-01	7.94E-01	PCNP	PEST proteolytic signal containing nuclear protein	chr3q12.3	1554868_s_at	NM_020357																				
6.52	6.77	0.24	4.89E-01	7.94E-01	RFC1	replication factor C (activator 1) 1, 145kDa	chr4p14-p13	208021_s_at	NM_002913																				
2.49	2.59	0.10	4.89E-01	7.94E-01	COG1	Component of oligomeric golgi complex 1	chr17q25.1	230878_s_at	NM_018714																				
2.41	2.51	0.10	4.89E-01	7.94E-01	RP1L1	retinitis pigmentosa 1-like 1	chr8p23	1555245_s_at	NM_178857																				
6.87	7.11	0.24	4.90E-01	7.94E-01	SUZ12	suppressor of zeste 12 homolog (Drosophila)	chr17q11.2	212287_at	NM_015355																				
4.47	4.59	0.12	4.90E-01	7.94E-01	MRPL55	Mitochondrial ribosomal protein L55	chr1q42.13	227024_s_at	NM_181441 /// NM_181454 /// NM_181455 /// NM_181456 /// NM_181462 /// NM_181463 /// NM_181464 /// NM_181465																				
2.11	2.18	0.08	4.90E-01	7.94E-01	WDR40B	WD repeat domain 40B	chrXq25	238205_at	NM_178470																				
6.07	6.40	0.33	4.90E-01	7.94E-01	ZRANB1	zinc finger, RAN-binding domain containing 1	chr10q26.13	225131_at	NM_017580																				
6.12	6.28	0.16	4.90E-01	7.94E-01	ARID5A	AT rich interactive domain 5A (MRF1-like)	chr2q11.2	213138_at	NM_212481																				
2.87	2.97	0.11	4.90E-01	7.94E-01	---	---	---	1564264_at	---																				
1.94	2.03	0.09	4.90E-01	7.94E-01	---	---	---	241160_at	---																				
2.22	2.38	0.17	4.90E-01	7.94E-01	---	---	---	231192_at	---																				
8.37	8.51	0.14	4.90E-01	7.94E-01	HDLBP	high density lipoprotein binding protein	chr2q37.3	200643_at	NM_005336 /// NM_203346																				
2.54	2.66	0.12	4.90E-01	7.94E-01	TSIX	X (inactive)-specific transcript, antisense (non-protein coding)	chrXq13.2	231592_at	NR_003255																				
2.56	2.68	0.12	4.90E-01	7.94E-01	GPR126	G protein-coupled receptor 126	chr6q24.1	233887_at	NM_001032394 /// NM_001032395 /// NM_020455 /// NM_198569																				

5.13	5.29	0.16	4.90E-01	7.94E-01	ARF1	ADP-ribosylation factor 1	chr1q42	232175_at	NM_001024226 /// NM_001024227 /// NM_001024228 /// NM_001658
4.01	4.14	0.12	4.90E-01	7.94E-01	AMH	anti-Mullerian hormone	chr19p13.3	206516_at	NM_000479
2.34	2.44	0.10	4.90E-01	7.94E-01	PSMD5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	chr9q33.2	215546_at	NM_005047
2.18	2.27	0.08	4.90E-01	7.94E-01	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)	chr7q31.3	216989_at	NM_003117 /// NM_153189
2.88	3.21	0.33	4.90E-01	7.94E-01	ZNF280A	zinc finger protein 280A	chr22q11.22	216034_at	NM_080740
7.40	7.67	0.27	4.90E-01	7.94E-01	NAE1	NEDD8 activating enzyme E1 subunit 1	chr16q22	202268_s_at	NM_001018159 /// NM_001018160 /// NM_003905
3.50	3.66	0.16	4.90E-01	7.94E-01	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	chr3p14.1	232859_s_at	NM_001033057 /// NM_004742 /// NM_015520
3.17	3.33	0.16	4.90E-01	7.94E-01	---	---	---	1562834_at	---
4.52	4.66	0.14	4.90E-01	7.94E-01	MTX3	metaxin 3	chr5q14.1	241779_at	NM_001010891
2.10	2.19	0.10	4.90E-01	7.94E-01	STAP1	signal transducing adaptor family member 1	chr4q13.2	1554343_a_at	NM_012108
1.91	2.00	0.09	4.90E-01	7.94E-01	---	---	---	1556328_at	---
5.14	5.33	0.19	4.90E-01	7.94E-01	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	chr2q13	223403_s_at	NM_019014
3.13	3.24	0.11	4.90E-01	7.94E-01	CIITA	class II, major histocompatibility complex, transactivator	chr16p13	210925_at	NM_000246
3.83	4.11	0.28	4.90E-01	7.94E-01	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	chr3q26.32	222634_s_at	NM_024665
4.12	4.33	0.21	4.90E-01	7.94E-01	---	---	---	242868_at	---
4.95	5.10	0.15	4.90E-01	7.94E-01	GK	glycerol kinase	chrXp21.3	214681_at	NM_000167 /// NM_001128127 /// NM_203391
4.52	4.63	0.11	4.90E-01	7.94E-01	FGFR4	fibroblast growth factor receptor 4	chr5q35.1-qter	1554962_a_at	NM_002011 /// NM_022963 /// NM_213647
2.24	2.35	0.11	4.90E-01	7.94E-01	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	chr6p24-p22.3	1560485_at	NM_002114
2.35	2.46	0.11	4.90E-01	7.94E-01	TGM4	transglutaminase 4 (prostate)	chr3p22-p21.33	206260_at	NM_003241
2.53	2.61	0.09	4.90E-01	7.94E-01	BOLL	bol, boule-like (Drosophila)	chr2q33	236954_at	NM_033030 /// NM_197970
2.52	2.60	0.08	4.90E-01	7.94E-01	---	---	---	244339_at	---
2.16	2.24	0.08	4.90E-01	7.94E-01	---	---	---	1559664_at	---
2.36	2.43	0.07	4.90E-01	7.94E-01	---	---	---	234058_at	---
5.04	5.60	0.56	4.90E-01	7.94E-01	BCLAF1	BCL2-associated transcription factor 1	chr6q22-q23	201101_s_at	NM_001077440 /// NM_001077441 /// NM_014739
5.71	6.08	0.37	4.90E-01	7.94E-01	---	---	---	1564424_at	---
3.49	3.62	0.12	4.90E-01	7.94E-01	FIGN	fidgetin	chr2q24.3	222956_at	NM_018086
1.96	2.06	0.10	4.90E-01	7.94E-01	HELLS	helicase, lymphoid-specific	chr10q24.2	234040_at	NM_018063
2.32	2.41	0.09	4.90E-01	7.94E-01	NPBWR2	neuropeptides B/W receptor 2	chr20q13.3	221358_at	NM_005286
4.78	4.93	0.14	4.91E-01	7.94E-01	ERCC6	excision repair cross-complementing rodent repair deficiency, complementation group 6	chr10q11.23	230108_at	NM_000124
2.06	2.15	0.09	4.91E-01	7.94E-01	NBEAL1	neurobeachin-like 1	chr2q33.2	1561589_a_at	NM_001099273 /// NM_198945
3.17	3.27	0.10	4.91E-01	7.94E-01	SALL4	Sal-like 4 (Drosophila)	chr20q13.13-q13.2	236501_at	NM_020436
3.27	3.39	0.13	4.91E-01	7.94E-01	ESR1	estrogen receptor 1	chr6q25.1	211233_x_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742
2.60	2.71	0.11	4.91E-01	7.94E-01	HOXC11	homeobox C11	chr12q13.3	206745_at	NM_014212
1.97	2.07	0.10	4.91E-01	7.94E-01	CATR1	CATR tumorigenicity conversion 1	chr7q32	211601_at	---
7.49	7.74	0.25	4.91E-01	7.94E-01	TMEM126A	transmembrane protein 126A	chr11q14.1	223334_at	NM_032273
4.28	4.51	0.23	4.91E-01	7.94E-01	HTATSF1	HIV-1 Tat specific factor 1	chrXq26.1-q27.2	202601_s_at	NM_014500
3.01	3.09	0.09	4.91E-01	7.94E-01	---	---	---	233747_at	---
5.84	6.19	0.35	4.91E-01	7.94E-01	ZNF397	zinc finger protein 397	chr18q12.2	228927_at	NM_032347
3.81	4.01	0.20	4.91E-01	7.94E-01	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	chr13q12-q14	212290_at	NM_003045
4.24	4.39	0.15	4.91E-01	7.94E-01	POLA2	polymerase (DNA directed), alpha 2 (70kD subunit)	chr11q13.1	204441_s_at	NM_002689

6.25	6.38	0.12	4.91E-01	7.94E-01	CYLD	cylindromatosis (turban tumor syndrome)	chr16q12.1	39582_at	NM_001042355 /// NM_001042412 /// NM_015247																				
2.23	2.33	0.10	4.91E-01	7.94E-01	---	---	---	235957_at	---																				
2.91	3.01	0.10	4.91E-01	7.94E-01	---	---	---	233363_at	---																				
2.68	2.76	0.08	4.91E-01	7.94E-01	LOC100133772 /// SLC16A5	similar to MCT /// solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	chr17q25.1	213590_at	NM_004695 /// XM_001715145																				
1.92	1.99	0.07	4.91E-01	7.94E-01	ESR2	estrogen receptor 2 (ER beta)	chr14q23.2	211119_at	NM_001040275 /// NM_001040276 /// NM_001437																				
2.58	2.73	0.15	4.91E-01	7.94E-01	---	---	---	1569376_s_at	---																				
2.07	2.19	0.12	4.91E-01	7.94E-01	---	---	---	244609_at	---																				
1.94	2.01	0.08	4.91E-01	7.94E-01	ZBTB33	zinc finger and BTB domain containing 33	chrXq23	214631_at	NM_006777																				
2.01	2.09	0.08	4.91E-01	7.94E-01	---	---	---	241592_at	---																				
4.39	4.64	0.26	4.91E-01	7.94E-01	SDCCAG8	Serologically defined colon cancer antigen 8	chr1q43-q44	243963_at	NM_006642																				
2.91	3.05	0.14	4.91E-01	7.94E-01	THSD7A	thrombospondin, type I, domain containing 7A	chr7p21.3	214920_at	NM_015204																				
2.26	2.34	0.08	4.91E-01	7.94E-01	CYBB	Cytochrome b-245, beta polypeptide	chrXp21.1	233538_s_at	NM_000397																				
3.40	3.71	0.31	4.91E-01	7.94E-01	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	chr13q22.1	234660_s_at	NM_001128226 /// NM_014953																				
4.08	4.31	0.23	4.92E-01	7.95E-01	PANK3	pantothenate kinase 3	chr5q34	218433_at	NM_024594																				
2.65	2.76	0.11	4.92E-01	7.95E-01	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	chr10q22.3	228414_at	NM_001014797 /// NM_002247																				
2.33	2.43	0.11	4.92E-01	7.95E-01	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	chr20q13.31	208383_s_at	NM_002591																				
2.20	2.31	0.11	4.92E-01	7.95E-01	NEO1	Neogenin homolog 1 (chicken)	chr15q22.3-q23	229877_at	NM_002499																				
4.94	5.10	0.16	4.92E-01	7.95E-01	DVL3	dishevelled, dsh homolog 3 (Drosophila)	chr3q27	201907_x_at	NM_004423																				
3.64	3.78	0.14	4.92E-01	7.95E-01	IL1F7	interleukin 1 family, member 7 (zeta)	chr2q12-q14.1	224555_x_at	NM_014439 /// NM_173202 /// NM_173203 /// NM_173204 /// NM_173205																				
3.20	3.32	0.13	4.92E-01	7.95E-01	---	---	---	243441_at	---																				
5.99	6.09	0.10	4.92E-01	7.95E-01	CARS	cysteinyl-tRNA synthetase	chr11p15.5	202402_s_at	NM_001014437 /// NM_001014438 /// NM_001751 /// NM_139273																				
2.95	3.06	0.12	4.92E-01	7.95E-01	---	---	---	1561133_at	---																				
2.51	2.60	0.10	4.92E-01	7.95E-01	---	---	---	244781_x_at	---																				
3.11	3.21	0.10	4.92E-01	7.95E-01	H1FNT	H1 histone family, member N, testis-specific	chr12q13.11	236876_at	NM_181788																				
2.81	2.96	0.15	4.92E-01	7.95E-01	---	---	---	1557744_at	---																				
3.12	3.27	0.15	4.92E-01	7.95E-01	IGHA1 /// IGHG1 /// IGHG3 /// IGHM /// IGHV4-31 /// IGHV@ /// LOC100133739	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// immunoglobulin heavy variable group /// similar to hCG2038920	chr14q32.33	216557_x_at	XM_001718220																				
5.16	5.31	0.15	4.92E-01	7.95E-01	GPATCH4	G patch domain containing 4	chr1q22	224632_at	NM_015590 /// NM_182679																				
1.96	2.04	0.09	4.92E-01	7.95E-01	---	---	---	1562800_at	---																				
3.61	3.82	0.21	4.92E-01	7.95E-01	PGGT1B	protein geranylgeranyltransferase type I, beta subunit	chr5q22.3	206288_at	NM_005023																				
4.71	4.86	0.15	4.92E-01	7.95E-01	LAGE3	L antigen family, member 3	chrXq28	221982_x_at	NM_006014																				
3.48	3.58	0.10	4.92E-01	7.95E-01	RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)	chr19q13.42	235249_at	NM_138412																				
2.47	2.58	0.11	4.92E-01	7.95E-01	---	---	---	237128_at	---																				
3.29	3.42	0.13	4.92E-01	7.95E-01	CDH4	Cadherin 4, type 1, R-cadherin (retinal)	chr20q13.3	239485_at	NM_001794																				
5.79	5.96	0.18	4.92E-01	7.95E-01	KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	chr1p36.3	203402_at	NM_003636 /// NM_172130																				
3.62	3.78	0.16	4.92E-01	7.95E-01	ACRBP	acrosin binding protein	chr12p13.31	230833_at	NM_032489																				
2.66	2.79	0.13	4.92E-01	7.95E-01	---	---	---	217376_at	---																				
4.99	5.14	0.15	4.92E-01	7.95E-01	GABPB1 /// RP11-68I18.1	GA binding protein transcription factor, beta subunit 2 /// hypothetical protein MGC29891	chr15q21.2 /// chr1q21.2	204618_s_at	NM_002041 /// NM_005254 /// NM_016654 /// NM_016655 /// NM_144618 /// NM_181427																				
2.07	2.16	0.09	4.92E-01	7.95E-01	C9orf95	chromosome 9 open reading frame 95	chr9q21.13	1562761_at	NM_001127603 /// NM_017881 /// NR_023352																				
2.11	2.20	0.09	4.92E-01	7.95E-01	---	---	---	1568888_at	---																				

2.73	2.98	0.26	4.93E-01	7.95E-01	MPPED2	metallophosphoesterase domain containing 2	chr11p13	205413_at	NM_001584
2.88	3.06	0.17	4.93E-01	7.95E-01	---	---	---	1560108_at	---
3.25	3.37	0.13	4.93E-01	7.95E-01	ATXN3	ataxin 3	chr14q24.3-q32.2	238723_at	NM_001127696 /// NM_001127697 /// NM_004993 /// NM_030660
3.58	3.73	0.15	4.93E-01	7.95E-01	DIO3OS	DIO3 opposite strand (non-protein coding)	chr14q32.31	223757_at	NR_002770
2.73	2.86	0.12	4.93E-01	7.95E-01	LOC400548	hypothetical gene supported by BC040918	chr16q24.1	1562659_at	---
3.08	3.19	0.11	4.93E-01	7.95E-01	SPATA12	spermatogenesis associated 12	chr3p14.3	237807_at	NM_181727
2.38	2.47	0.09	4.93E-01	7.95E-01	NALCN	sodium leak channel, non-selective	chr13q32.3	1554702_at	NM_052867
2.22	2.30	0.08	4.93E-01	7.95E-01	FANCC	Fanconi anemia, complementation group C	chr9q22.3	1559513_a_at	NM_000136
3.14	3.21	0.08	4.93E-01	7.95E-01	---	---	---	234560_at	---
3.76	3.84	0.08	4.93E-01	7.95E-01	SPTBN4	spectrin, beta, non-erythrocytic 4	chr19q13.13	224551_s_at	NM_020971 /// NM_025213
2.78	2.95	0.17	4.93E-01	7.95E-01	RNGTT	RNA guanylyltransferase and 5'-phosphatase	chr6q16	211849_s_at	NM_003800
4.30	4.42	0.12	4.93E-01	7.95E-01	KCNA6	potassium voltage-gated channel, shaker-related subfamily, member 6	chr12p13	205616_at	NM_002235
2.69	2.84	0.16	4.93E-01	7.95E-01	SERPINA2	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 2	chr14q32.13	208531_at	XR_041181 /// XR_041182 /// XR_041183
3.06	3.20	0.14	4.93E-01	7.95E-01	---	---	---	1561421_a_at	---
3.03	3.16	0.13	4.93E-01	7.95E-01	IGLV6-57	immunoglobulin lambda variable 6-57	chr22q11.2	215035_at	---
2.21	2.33	0.12	4.93E-01	7.95E-01	---	---	---	1562670_at	---
2.23	2.34	0.11	4.93E-01	7.95E-01	TDRKH	tudor and KH domain containing	chr1q21	221052_at	NM_001083963 /// NM_001083964 /// NM_001083965 /// NM_006862
2.39	2.50	0.11	4.93E-01	7.95E-01	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	chr7q22.3	206369_s_at	NM_002649
2.83	2.93	0.11	4.93E-01	7.95E-01	PRAMEF12	PRAME family member 12	chr1p36.21	216001_at	NM_001080830
3.63	3.73	0.10	4.93E-01	7.95E-01	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	chr11q24.2	1552804_a_at	NM_001039661 /// NM_148910
3.45	3.54	0.09	4.93E-01	7.95E-01	GPHA2	glycoprotein hormone alpha 2	chr11q13.1	237230_at	NM_130769
2.72	2.81	0.09	4.93E-01	7.95E-01	MAP2K7	mitogen-activated protein kinase kinase 7	chr19p13.3-p13.2	209952_s_at	NM_145185
2.13	2.22	0.09	4.93E-01	7.95E-01	LOC648556	uncharacterized gastric protein ZA43P	---	232696_at	XM_937610
2.14	2.23	0.08	4.93E-01	7.96E-01	FBN2	fibrillin 2	chr5q23-q31	1554737_at	NM_001999
3.41	3.50	0.09	4.93E-01	7.96E-01	---	---	---	243950_at	---
2.79	2.98	0.19	4.94E-01	7.96E-01	---	---	---	216278_at	---
2.19	2.27	0.07	4.94E-01	7.96E-01	---	---	---	243635_at	---
1.80	1.90	0.10	4.94E-01	7.96E-01	DEFB132	defensin, beta 32	chr20p13	243311_at	NM_207469
2.32	2.48	0.16	4.94E-01	7.96E-01	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	chr9q21	214852_x_at	NM_001018037 /// NM_001018038 /// NM_015186 /// NM_033305
3.37	3.52	0.15	4.94E-01	7.96E-01	WNK1	WNK lysine deficient protein kinase 1	chr12p13.3	202940_at	NM_018979
2.89	3.02	0.13	4.94E-01	7.96E-01	---	---	---	213403_at	---
2.14	2.27	0.12	4.94E-01	7.96E-01	RAG1	recombination activating gene 1	chr11p13	1554994_at	NM_000448
3.59	3.82	0.23	4.94E-01	7.96E-01	MXRA7	matrix-remodelling associated 7	chr17q25.1-q25.2	235836_at	NM_001008528 /// NM_001008529 /// NM_198530
1.93	2.01	0.08	4.94E-01	7.96E-01	C17orf57	chromosome 17 open reading frame 57	chr17q21.32	1569876_at	NM_152347
5.37	5.48	0.11	4.94E-01	7.96E-01	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	chr19p13.1	206539_s_at	NM_023944
4.36	4.52	0.16	4.94E-01	7.96E-01	PARVA	parvin, alpha	chr11p15.3	222455_s_at	NM_018222
2.45	2.58	0.13	4.94E-01	7.96E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	1558769_s_at	NM_015512
4.47	4.57	0.10	4.94E-01	7.96E-01	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	chr2q12	214032_at	NM_001079 /// NM_207519
2.00	2.09	0.09	4.94E-01	7.96E-01	---	---	---	242928_at	---
3.43	3.59	0.16	4.94E-01	7.96E-01	NRG2	neuregulin 2	chr5q23-q33	206879_s_at	NM_004883 /// NM_013981 /// NM_013982 /// NM_013983
3.65	3.81	0.16	4.94E-01	7.96E-01	FOXD4	forkhead box D4	chr9p11-q11	1567341_at	NM_207305
3.12	3.23	0.11	4.94E-01	7.96E-01	DNAJC5G	DnaJ (Hsp40) homolog, subfamily C, member 5 gamma	chr2p23.3	1552450_a_at	NM_173650
2.33	2.43	0.09	4.94E-01	7.96E-01	SFXN1	sideroflexin 1	---	232055_at	NM_022754
7.98	8.11	0.14	4.94E-01	7.96E-01	---	---	---	235529_x_at	---

3.61	3.73	0.11	4.94E-01	7.96E-01	---	---	---	1559800_a_at	---
5.30	5.50	0.20	4.94E-01	7.96E-01	ABLIM1	actin binding LIM protein 1	chr10q25	210461_s_at	NM_001003407 /// NM_001003408 /// NM_002313 /// NM_006720
1.82	1.88	0.07	4.94E-01	7.96E-01	TMCO5A	transmembrane and coiled-coil domains 5A	chr15q14	1560184_at	NM_152453
4.05	4.18	0.13	4.94E-01	7.96E-01	---	---	---	231393_x_at	---
5.72	6.01	0.29	4.94E-01	7.96E-01	---	---	---	239955_at	---
5.06	5.23	0.17	4.95E-01	7.96E-01	POU2F1	POU class 2 homeobox 1	chr1q22-q23	206789_s_at	NM_002697
4.28	4.43	0.15	4.95E-01	7.96E-01	ACSL5	acyl-CoA synthetase long-chain family member 5	chr10q25.1-q25.2	222592_s_at	NM_016234 /// NM_203379 /// NM_203380
5.14	5.26	0.12	4.95E-01	7.96E-01	TMCC2	transmembrane and coiled-coil domain family 2	chr1q32.1	213096_at	NM_014858
3.23	3.44	0.21	4.95E-01	7.97E-01	---	---	---	239604_at	---
3.39	3.52	0.13	4.95E-01	7.97E-01	MAML2	mastermind-like 2 (Drosophila)	chr11q21	235106_at	NM_032427
5.30	5.42	0.11	4.95E-01	7.97E-01	WWOX	WW domain containing oxidoreductase	chr16q23.3-q24.1	210695_s_at	NM_016373 /// NM_130791 /// NM_130844
2.31	2.41	0.10	4.95E-01	7.97E-01	ZNF547	zinc finger protein 547	chr19q13.43	1558995_at	NM_173631
5.29	5.39	0.10	4.95E-01	7.97E-01	CDC27	cell division cycle 27 homolog (S. cerevisiae)	chr17q12-q23.2	217880_at	NM_001114091 /// NM_001256
3.34	3.45	0.11	4.95E-01	7.97E-01	---	---	---	233623_at	---
2.13	2.22	0.09	4.95E-01	7.97E-01	---	---	---	238852_at	---
7.34	7.56	0.23	4.95E-01	7.97E-01	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	chr9q22.2	202277_at	NM_006415 /// NM_178324
2.11	2.20	0.09	4.95E-01	7.97E-01	STYK1	serine/threonine/tyrosine kinase 1	chr12p13.2	220030_at	NM_018423
6.00	6.20	0.20	4.95E-01	7.97E-01	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	chr15q22-q24	223279_s_at	NM_001008224 /// NM_018003
4.38	4.54	0.15	4.95E-01	7.97E-01	SAAL1	serum amyloid A-like 1	chr11p15.1	225614_at	NM_138421
2.38	2.49	0.11	4.95E-01	7.97E-01	CCDC124	Coiled-coil domain containing 124	chr19p13.11	225453_x_at	NM_138442
6.08	6.46	0.38	4.95E-01	7.97E-01	USP16	ubiquitin specific peptidase 16	chr21q22.11	218386_x_at	NM_001001992 /// NM_001032410 /// NM_006447
2.48	2.58	0.10	4.95E-01	7.97E-01	CCDC81	coiled-coil domain containing 81	chr11q14.2	220389_at	NM_021827
6.42	6.52	0.09	4.95E-01	7.97E-01	KIAA0894	KIAA0894 protein	chr10q23.33	207436_x_at	---
7.91	8.06	0.15	4.95E-01	7.97E-01	TNS1	tensin 1	chr2q35-q36	221246_x_at	NM_022648
2.13	2.21	0.08	4.95E-01	7.97E-01	---	---	---	238288_at	---
5.86	6.15	0.29	4.96E-01	7.97E-01	NARS2	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	chr11q14.1	219217_at	NM_024678
2.31	2.40	0.09	4.96E-01	7.97E-01	---	---	---	1564765_at	---
2.06	2.16	0.10	4.96E-01	7.97E-01	---	---	---	244016_at	---
4.42	4.60	0.18	4.96E-01	7.97E-01	---	---	---	233431_x_at	---
3.58	3.69	0.11	4.96E-01	7.97E-01	---	---	---	1561411_at	---
2.14	2.25	0.12	4.96E-01	7.97E-01	---	---	---	241311_at	---
4.27	4.42	0.15	4.96E-01	7.97E-01	CTSG	cathepsin G	chr14q11.2	205653_at	NM_001911
3.89	4.48	0.59	4.96E-01	7.97E-01	PPAP2C	phosphatidic acid phosphatase type 2C	chr19p13	209529_at	NM_003712 /// NM_177526 /// NM_177543
6.15	6.41	0.25	4.96E-01	7.97E-01	NANP	N-acetylneuraminic acid phosphatase	chr20p11.1	228073_at	NM_152667
4.66	4.83	0.17	4.96E-01	7.97E-01	GUF1	GUF1 GTPase homolog (S. cerevisiae)	chr4p13	222770_s_at	NM_021927
2.34	2.47	0.13	4.96E-01	7.97E-01	OR1A1	olfactory receptor, family 1, subfamily A, member 1	chr17p13.3	221388_at	NM_014565
2.45	2.56	0.11	4.96E-01	7.97E-01	---	---	---	1563797_at	---
2.55	2.65	0.10	4.96E-01	7.97E-01	---	---	---	222295_x_at	---
2.62	2.71	0.08	4.96E-01	7.98E-01	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	chr5q31	217366_at	NM_001903
1.77	1.84	0.07	4.96E-01	7.98E-01	---	---	---	240463_at	---
2.83	2.97	0.13	4.96E-01	7.98E-01	---	---	---	241679_at	---
2.48	2.59	0.11	4.96E-01	7.98E-01	KIAA1853	KIAA1853	chr12q24.23	230010_at	NM_194286
1.99	2.08	0.09	4.96E-01	7.98E-01	SCN9A	sodium channel, voltage-gated, type IX, alpha subunit	chr2q24	206950_at	NM_002977
2.67	2.80	0.13	4.96E-01	7.98E-01	FGFR3	fibroblast growth factor receptor 3	chr4p16.3	204379_s_at	NM_000142 /// NM_022965
2.25	2.33	0.08	4.96E-01	7.98E-01	NEUROD1	neurogenic differentiation 1	chr2q32	1556057_s_at	NM_002500
6.23	7.36	1.13	4.96E-01	7.98E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	214677_x_at	---
8.10	8.31	0.21	4.96E-01	7.98E-01	PDIA6	protein disulfide isomerase family A, member 6	chr2p25.1	208639_x_at	NM_005742
3.88	4.08	0.20	4.96E-01	7.98E-01	---	---	---	235107_at	---
3.97	4.08	0.10	4.97E-01	7.98E-01	FRAP1	FK506 binding protein 12-rapamycin associated protein 1	chr1p36.2	215381_at	NM_004958
6.01	6.19	0.18	4.97E-01	7.98E-01	RNF145	ring finger protein 145	chr5q33.3	238949_at	NM_144726
2.24	2.33	0.08	4.97E-01	7.98E-01	NPFFR2	neuropeptide FF receptor 2	chr4q21	224169_at	NM_004885 /// NM_053036
2.86	2.99	0.13	4.97E-01	7.98E-01	ECEL1	endothelin converting enzyme-like 1	chr2q36-q37	219914_at	NM_004826
2.70	2.80	0.10	4.97E-01	7.98E-01	---	---	---	1560246_at	---

4.91	5.19	0.28	4.97E-01	7.98E-01	PICALM	phosphatidylinositol binding clathrin assembly protein	chr11q14	215832_x_at	NM_001008660 /// NM_007166
3.96	4.16	0.19	4.97E-01	7.98E-01	VAMP4	vesicle-associated membrane protein 4	chr1q24-q25	207350_s_at	NM_003762
2.03	2.11	0.08	4.97E-01	7.98E-01	---	---	---	1561581_at	---
2.31	2.39	0.08	4.97E-01	7.98E-01	---	---	---	238598_s_at	---
3.23	3.42	0.18	4.97E-01	7.98E-01	ZNF224	zinc finger protein 224	chr19q13.2	244462_at	NM_013398
2.00	2.11	0.11	4.97E-01	7.98E-01	LOC152274	hypothetical protein LOC152274	chr3p25.1	1563572_at	---
2.30	2.40	0.11	4.97E-01	7.98E-01	ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	chr12q24.12	237481_at	NM_025247
2.23	2.35	0.13	4.97E-01	7.98E-01	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	chr12q21.31	1558295_a_at	NM_003625
2.31	2.40	0.09	4.97E-01	7.98E-01	---	---	---	220861_at	---
4.50	4.63	0.13	4.97E-01	7.98E-01	---	---	---	228240_at	---
3.75	3.88	0.12	4.97E-01	7.98E-01	HIST1H2AD /// HIST1H2BN /// HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	histone cluster 1, H2ad /// histone cluster 1, H2bn /// histone cluster 1, H3a /// histone cluster 1, H3b /// histone cluster 1, H3c /// histone cluster 1, H3d /// histone cluster 1, H3e /// histone cluster 1, H3f /// histone cluster 1, H3g /// histone cluster 1, H3h /// histone cluster 1, H3i /// histone cluster 1, H3j	chr6p21.3 /// chr6p22-p21.3 /// chr6p22.1	208496_x_at	NM_003520 /// NM_003529 /// NM_003530 /// NM_003531 /// NM_003532 /// NM_003533 /// NM_003534 /// NM_003535 /// NM_003536 /// NM_003537 /// NM_021018 /// NM_021065
2.14	2.26	0.12	4.97E-01	7.98E-01	LOC150051	hypothetical LOC150051	chr21q22.11	1556344_at	XR_040909 /// XR_040910 /// XR_040911
2.18	2.28	0.10	4.97E-01	7.98E-01	ZKSCAN3	zinc finger with KRAB and SCAN domains 3	chr6p22.1	1562305_x_at	NM_024493
2.22	2.32	0.10	4.97E-01	7.98E-01	---	---	---	1562572_at	---
1.91	1.99	0.08	4.97E-01	7.98E-01	---	---	---	1569596_at	---
5.26	5.57	0.31	4.97E-01	7.99E-01	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	chr13q32	235341_at	NM_006260
3.33	3.47	0.14	4.97E-01	7.99E-01	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	chr10q24-q25.2	210053_at	NM_006951
2.36	2.46	0.10	4.97E-01	7.99E-01	TBC1D2B	TBC1 domain family, member 2B	chr15q24.3-q25.1	230377_s_at	NM_015079 /// NM_144572
2.48	2.56	0.08	4.97E-01	7.99E-01	---	---	---	1557517_a_at	---
4.94	5.21	0.26	4.98E-01	7.99E-01	LOC654342	similar to lymphocyte-specific protein 1	chr2p11.1	214110_s_at	XR_041236
5.81	6.16	0.35	4.98E-01	7.99E-01	DNM1L	dynamin 1-like	chr12p11.21	226154_at	NM_005690 /// NM_012062 /// NM_012063
2.51	2.62	0.11	4.98E-01	7.99E-01	CACNG8	calcium channel, voltage-dependent, gamma subunit 8	chr19q13.4	234756_at	NM_031895
3.13	3.22	0.09	4.98E-01	7.99E-01	---	---	---	242556_at	---
2.35	2.44	0.09	4.98E-01	7.99E-01	HIST1H2BJ	histone cluster 1, H2bj	chr6p22.1	214502_at	NM_021058
1.99	2.07	0.07	4.98E-01	7.99E-01	---	---	---	231470_at	---
3.57	3.68	0.11	4.98E-01	7.99E-01	LOC253724	hypothetical LOC253724	chr12q23.3	1570212_a_at	XR_015316 /// XR_041116 /// XR_041117
3.39	3.55	0.16	4.98E-01	7.99E-01	LPP	LIM domain containing preferred translocation partner in lipoma	chr3q28	1558469_at	NM_005578
2.14	2.25	0.11	4.98E-01	7.99E-01	C4orf16	Chromosome 4 open reading frame 16	chr4q25	231010_at	NM_001128426 /// NM_018569
3.13	3.22	0.10	4.98E-01	7.99E-01	ACTL7B	actin-like 7B	chr9q31	220498_at	NM_006686
3.77	3.95	0.18	4.98E-01	7.99E-01	CD40	CD40 molecule, TNF receptor superfamily member 5	chr20q12-q13.2	205153_s_at	NM_001250 /// NM_152854
2.64	2.74	0.10	4.98E-01	7.99E-01	TXNDC8	thioredoxin domain containing 8 (spermatozoa)	chr9q31.3	1564386_at	NM_001003936
2.48	2.58	0.09	4.98E-01	7.99E-01	HNRNPM	heterogeneous nuclear ribonucleoprotein M	chr19p13.3-p13.2	1556084_at	NM_005968 /// NM_031203
2.05	2.12	0.07	4.98E-01	7.99E-01	---	---	---	1565616_at	---
2.47	2.58	0.12	4.98E-01	7.99E-01	TRPA1	transient receptor potential cation channel, subfamily A, member 1	chr8q13	217590_s_at	NM_007332
3.02	3.13	0.11	4.98E-01	7.99E-01	LOC727901	hypothetical LOC727901	---	222723_at	XR_042309 /// XR_042470
3.14	3.26	0.11	4.98E-01	7.99E-01	RNF31	ring finger protein 31	chr14q11.2	225122_at	NM_017999
2.05	2.15	0.10	4.98E-01	7.99E-01	KRT6A	keratin 6A	chr12q12-q13	209125_at	NM_005554
3.07	3.31	0.24	4.98E-01	7.99E-01	FAM29A	family with sequence similarity 29, member A	chr9p22.1	233655_s_at	NM_017645
5.48	5.64	0.16	4.98E-01	7.99E-01	BEST1	bestrophin 1	chr11q13	1554442_at	NM_004183
5.19	5.29	0.10	4.98E-01	7.99E-01	THRAP3	thyroid hormone receptor associated protein 3	chr1p34.3	217847_s_at	NM_005119
2.45	2.54	0.09	4.98E-01	7.99E-01	---	---	---	1558430_at	---

3.61	3.79	0.18	4.98E-01	7.99E-01	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	chr12q13	209530_at	NM_000725																					
2.64	2.75	0.11	4.99E-01	7.99E-01	TRO	trophinin	chrXp11.22-p11.21	205028_at	NM_001039705 /// NM_016157 /// NM_177556																					
8.56	8.73	0.17	4.99E-01	7.99E-01	---	---	---	227853_at	---																					
2.46	2.54	0.08	4.99E-01	7.99E-01	---	---	---	1556082_a_at	---																					
2.34	2.48	0.14	4.99E-01	7.99E-01	---	---	---	1562925_at	---																					
3.14	3.28	0.13	4.99E-01	7.99E-01	---	---	---	231699_at	---																					
3.28	3.41	0.13	4.99E-01	7.99E-01	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	chr17p13.3	210448_s_at	NM_002561 /// NM_175080 /// NM_175081																					
7.94	8.06	0.12	4.99E-01	7.99E-01	FLJ45803	FLJ45803 protein	chr11q23.1	238701_x_at	NM_207429																					
2.40	2.50	0.10	4.99E-01	7.99E-01	FCRL3	Fc receptor-like 3	chr1q21-q22	1553196_a_at	NM_052939																					
2.41	2.50	0.09	4.99E-01	7.99E-01	COL12A1	collagen, type XII, alpha 1	chr6q12-q13	234951_s_at	NM_004370 /// NM_080645																					
2.70	2.79	0.09	4.99E-01	7.99E-01	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	chr10p11.23	237495_at	NM_173496																					
1.95	2.03	0.08	4.99E-01	7.99E-01	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	chr9q31	205123_s_at	NM_003692																					
5.76	5.93	0.17	4.99E-01	7.99E-01	AGRN	agrin	chr1p36.33	212285_s_at	NM_198576																					
7.11	7.24	0.13	4.99E-01	7.99E-01	CEP27	centrosomal protein 27kDa	chr15q15.1	220071_x_at	NM_001130447 /// NM_018097																					
2.61	2.69	0.08	4.99E-01	7.99E-01	CES7	carboxylesterase 7	chr16q12.2	1553465_a_at	NM_145024																					
3.33	3.42	0.09	4.99E-01	7.99E-01	FOXK1	forkhead box K1	chr7p22.1	236011_at	NM_001037165																					
2.06	2.15	0.10	4.99E-01	7.99E-01	CPXCR1	CPX chromosome region, candidate 1	chrXq21.3	1560493_a_at	NM_033048																					
6.22	6.45	0.23	4.99E-01	8.00E-01	FAM20B	family with sequence similarity 20, member B	chr1q25	202915_s_at	NM_014864																					
3.64	3.71	0.08	4.99E-01	8.00E-01	GJA8	gap junction protein, alpha 8, 50kDa	chr1q21.1	208489_at	NM_005267																					
2.10	2.20	0.10	4.99E-01	8.00E-01	FLJ30375	hypothetical gene supported by AK054937	chr3q24	241440_at	XM_001724993 /// XM_001725199 /// XM_001725628																					
2.42	2.52	0.10	4.99E-01	8.00E-01	C7orf16	chromosome 7 open reading frame 16	chr7p15	220231_at	NM_006658																					
2.72	2.81	0.09	4.99E-01	8.00E-01	RUFY3	RUN and FYVE domain containing 3	chr4q13.3	213430_at	NM_001037442 /// NM_001130709 /// NM_014961																					
5.26	5.44	0.19	4.99E-01	8.00E-01	AZI2	5-azacytidine induced 2	chr3p24.1	222498_at	NM_001134432 /// NM_001134433 /// NM_022461																					
7.15	7.38	0.23	4.99E-01	8.00E-01	SLC39A9	solute carrier family 39 (zinc transporter), member 9	chr14q24.1	222445_at	NM_018375																					
6.02	6.16	0.13	4.99E-01	8.00E-01	SIRT6	sirtuin (silent mating type information regulation 2 homolog) 6 (S. cerevisiae)	chr19p13.3	233179_x_at	NM_016539																					
9.62	9.75	0.14	4.99E-01	8.00E-01	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	chr19q13.2-q13.3	211047_x_at	NM_004069 /// NM_021575																					
5.30	5.67	0.37	5.00E-01	8.00E-01	ASPH	aspartate beta-hydroxylase	chr8q12.1	205808_at	NM_004318 /// NM_020164 /// NM_032466 /// NM_032467 /// NM_032468																					
4.22	4.52	0.30	5.00E-01	8.00E-01	EFHD1	EF-hand domain family, member D1	chr2q37.1	209343_at	NM_025202																					
2.93	3.04	0.11	5.00E-01	8.00E-01	---	---	---	215398_at	---																					
2.29	2.40	0.11	4.99E-01	8.00E-01	CXADR	coxsackie virus and adenovirus receptor	chr21q21.1	1555716_a_at	NM_001338																					
2.16	2.25	0.09	5.00E-01	8.00E-01	---	---	---	1555692_at	---																					
2.00	2.09	0.09	5.00E-01	8.00E-01	---	---	---	1557779_at	---																					
2.17	2.25	0.08	5.00E-01	8.00E-01	C9orf84	chromosome 9 open reading frame 84	chr9q31.3	1553920_at	NM_001080551 /// NM_173521																					
1.81	1.89	0.08	5.00E-01	8.00E-01	---	---	---	1569218_at	---																					
2.30	2.41	0.11	5.00E-01	8.00E-01	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	chr10q25.3	217380_s_at	NM_020383																					
2.53	2.61	0.09	5.00E-01	8.00E-01	NSAP11	nervous system abundant protein 11	chr8p22	1555366_at	XM_001721705 /// XM_001722355 /// XM_001722999																					

5.51	5.66	0.15	5.00E-01	8.00E-01	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	chr15q25.1	225061_at	NM_001130182 /// NM_001130183 /// NM_018602
2.63	2.75	0.12	5.00E-01	8.00E-01	---	---	---	214947_at	---
4.07	4.15	0.08	5.00E-01	8.00E-01	PHC3	polyhomeotic homolog 3 (Drosophila)	chr3q26.2	215521_at	NM_024947
4.41	4.59	0.17	5.00E-01	8.00E-01	ADAM15	ADAM metallopeptidase domain 15	chr1q21.3	217007_s_at	NM_003815 /// NM_207191 /// NM_207194 /// NM_207195 /// NM_207196 /// NM_207197
2.29	2.39	0.10	5.00E-01	8.00E-01	SPINK7	serine peptidase inhibitor, Kazal type 7 (putative)	chr5q33.1	223720_at	NM_032566
2.31	2.40	0.09	5.00E-01	8.00E-01	---	---	---	237511_at	---
2.84	2.93	0.09	5.00E-01	8.00E-01	---	---	---	236464_at	---
2.35	2.43	0.08	5.00E-01	8.00E-01	LOC284757	hypothetical protein LOC284757	chr20q13.33	1562051_at	XR_041615 /// XR_041616 /// XR_041617
3.56	3.68	0.11	5.00E-01	8.01E-01	---	---	---	234505_at	---
4.76	4.99	0.24	5.00E-01	8.01E-01	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	chr8q22.3	202872_at	NM_001695
2.30	2.40	0.10	5.00E-01	8.01E-01	---	---	---	224515_at	---
4.11	4.30	0.19	5.00E-01	8.01E-01	---	---	---	243511_at	---
2.11	2.20	0.09	5.00E-01	8.01E-01	MAGEA12	melanoma antigen family A, 12	chrXq28	210467_x_at	NM_005367
6.71	6.93	0.21	5.01E-01	8.01E-01	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	chr5q11.2-q13.1	203893_at	NM_001015891 /// NM_001015892 /// NM_003187 /// NM_016283
3.85	4.00	0.15	5.01E-01	8.01E-01	TTC13	tetratricopeptide repeat domain 13	chr1q42.2	219481_at	NM_001122835 /// NM_024525
2.70	2.85	0.15	5.01E-01	8.01E-01	---	---	---	229359_at	---
3.18	3.30	0.12	5.01E-01	8.01E-01	SLC32A1	solute carrier family 32 (GABA vesicular transporter), member 1	chr20q11.23	240532_at	NM_080552
2.45	2.57	0.12	5.01E-01	8.01E-01	---	---	---	222254_at	---
3.20	3.31	0.11	5.01E-01	8.01E-01	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	chr19p13.12-p13.11	211407_at	NM_004146
3.17	3.28	0.10	5.01E-01	8.01E-01	PGLYRP2	peptidoglycan recognition protein 2	chr19p13.12	242817_at	NM_052890
2.30	2.39	0.09	5.01E-01	8.01E-01	LOC284561	hypothetical protein LOC284561	chr1q21.3	233737_s_at	---
2.47	2.56	0.09	5.01E-01	8.01E-01	---	---	---	216857_at	---
1.82	1.91	0.09	5.01E-01	8.01E-01	---	---	---	1556889_s_at	---
1.96	2.05	0.09	5.01E-01	8.01E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1553075_a_at	NM_153003
9.25	9.40	0.15	5.01E-01	8.01E-01	TKT	transketolase	chr3p14.3	208700_s_at	NM_001064
2.55	2.65	0.10	5.01E-01	8.01E-01	ZNF154	zinc finger protein 154	chr19q13.4	217242_at	NM_001085384
1.88	1.96	0.08	5.01E-01	8.01E-01	---	---	---	224296_x_at	---
6.08	6.34	0.26	5.01E-01	8.01E-01	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	chr12q12	227176_at	NM_052885
3.96	4.08	0.12	5.01E-01	8.01E-01	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	chr2q24.3	202786_at	NM_013233
2.45	2.54	0.09	5.01E-01	8.01E-01	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	chr2q12	1555613_a_at	NM_001079 /// NM_207519
2.76	2.84	0.09	5.01E-01	8.01E-01	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	chr8p11.2	221248_s_at	NM_017778 /// NM_023034
2.07	2.13	0.07	5.01E-01	8.01E-01	SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	chr2p16.3	239667_at	NM_000341
2.38	2.61	0.23	5.01E-01	8.01E-01	CYorf14	chromosome Y open reading frame 14	chrYq11.222	207063_at	NR_001544
3.36	3.48	0.12	5.01E-01	8.01E-01	---	---	---	236960_at	---
3.00	3.11	0.11	5.01E-01	8.01E-01	---	---	---	233484_at	---
3.19	3.28	0.09	5.01E-01	8.01E-01	---	---	---	1570372_at	---
5.96	6.26	0.30	5.01E-01	8.01E-01	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	chr18q12.1	201724_s_at	NM_020474
2.64	2.77	0.13	5.01E-01	8.01E-01	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	chr1q32	208488_s_at	NM_000573 /// NM_000651
5.45	5.74	0.29	5.01E-01	8.01E-01	SORBS2	sorbin and SH3 domain containing 2	chr4q35.1	1558815_at	NM_003603 /// NM_021069
2.21	2.30	0.09	5.01E-01	8.01E-01	---	---	---	1554214_at	---
4.95	5.24	0.29	5.01E-01	8.01E-01	CISH	cytokine inducible SH2-containing protein	chr3p21.3	223377_x_at	NM_013324 /// NM_145071
5.09	5.27	0.18	5.01E-01	8.01E-01	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	chr22q12.3-q13.1|22q13.1	204200_s_at	NM_002608 /// NM_033016
3.07	3.22	0.15	5.01E-01	8.01E-01	SPIRE1	spire homolog 1 (Drosophila)	chr18p11.21	1559517_a_at	NM_001128626 /// NM_001128627 /// NM_020148

3.88	4.01	0.13	5.01E-01	8.01E-01	TRPM3	transient receptor potential cation channel, subfamily M, member 3	chr9q21.11-q21.12	233022_at	NM_001007470 /// NM_001007471 /// NM_020952 /// NM_024971 /// NM_206944 /// NM_206945 /// NM_206946 /// NM_206947 /// NM_206948
3.64	3.75	0.11	5.01E-01	8.01E-01	---	---	---	244711_at	---
2.03	2.13	0.10	5.01E-01	8.01E-01	---	---	---	1557214_at	---
2.59	2.67	0.08	5.01E-01	8.01E-01	---	---	---	222213_x_at	---
2.06	2.15	0.09	5.02E-01	8.01E-01	RAD18	RAD18 homolog (S. cerevisiae)	chr3p25-p24	224200_s_at	NM_020165
1.98	2.07	0.08	5.02E-01	8.01E-01	---	---	---	235445_at	---
2.47	2.54	0.08	5.02E-01	8.01E-01	---	---	---	1563224_at	---
2.85	2.98	0.13	5.02E-01	8.01E-01	MAPRE3	microtubule-associated protein, RP/EB family, member 3	chr2p23.3-p23.1	203841_x_at	NM_012326
1.92	2.01	0.09	5.02E-01	8.01E-01	---	---	---	1561328_at	---
4.33	4.42	0.09	5.02E-01	8.01E-01	CRYGC	crystallin, gamma C	chr2q33-q35	207531_at	NM_020989
9.43	9.57	0.14	5.02E-01	8.01E-01	LOC341315 /// LOC652607 /// PABPC1 /// PABPC3	similar to FAP protein /// similar to Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) /// poly(A) binding protein, cytoplasmic 1 /// poly(A) binding protein, cytoplasmic 3	chr12q14.2 /// chr13q12-q13 /// chr8q22.2-q23	215823_x_at	NM_002568 /// NM_030979 /// XR_017616 /// XR_019485 /// XR_038197 /// XR_039180
7.14	7.38	0.25	5.02E-01	8.01E-01	FLJ20160	FLJ20160 protein	chr2q32.2	225325_at	NM_017694
3.67	3.83	0.16	5.02E-01	8.01E-01	---	---	---	1566185_at	---
4.69	4.81	0.12	5.02E-01	8.01E-01	COL13A1	collagen, type XIII, alpha 1	chr10q22	208535_x_at	NM_001130103 /// NM_005203 /// NM_080798 /// NM_080799 /// NM_080800 /// NM_080801 /// NM_080802 /// NM_080803 /// NM_080804 /// NM_080805 /// NM_080806 /// NM_080807 /// NM_080808 /// NM_080809 /// NM_080810 /// NM_080811 /// NM_080812 /// NM_080813 /// NM_080814 /// NM_080815
2.09	2.21	0.12	5.02E-01	8.01E-01	C12orf50	chromosome 12 open reading frame 50	chr12q21.32	238219_at	NM_152589
3.09	3.21	0.12	5.02E-01	8.01E-01	---	---	---	235800_at	---
3.84	3.96	0.12	5.02E-01	8.01E-01	MTMR15	myotubularin related protein 15	chr15q13.2-q13.3	239289_x_at	NM_014967
2.77	2.86	0.09	5.02E-01	8.01E-01	---	---	---	1570297_at	---
2.10	2.20	0.10	5.02E-01	8.01E-01	---	---	---	236851_x_at	---
3.24	3.32	0.09	5.02E-01	8.01E-01	---	---	---	241442_at	---
4.61	4.71	0.11	5.02E-01	8.01E-01	IDUA	Iduronidase, alpha-L-	chr4p16.3	213723_s_at	NM_000203

2.40	2.50	0.10	5.02E-01	8.01E-01	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	chr3p25-p24	205921_s_at	NM_001134367 /// NM_001134368 /// NM_003043
2.10	2.22	0.12	5.02E-01	8.01E-01	---	---	---	238372_s_at	---
3.87	4.00	0.13	5.02E-01	8.01E-01	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	chr9q34	234916_at	NM_000787
2.38	2.45	0.07	5.02E-01	8.01E-01	PMCH	pro-melanin-concentrating hormone	chr12q23-q24	206942_s_at	NM_002674
2.67	2.76	0.10	5.02E-01	8.01E-01	ARG1	Arginase, liver	chr6q23	231663_s_at	NM_000045
1.86	1.92	0.07	5.02E-01	8.01E-01	---	---	---	1557849_at	---
2.10	2.23	0.12	5.02E-01	8.02E-01	DOPEY2	dopey family member 2	chr21q22.2	215219_at	NM_005128
8.65	8.93	0.29	5.03E-01	8.02E-01	RBM47	RNA binding motif protein 47	chr4p13-p12	218035_s_at	NM_001098634 /// NM_019027
1.97	2.06	0.08	5.03E-01	8.02E-01	---	---	---	237664_at	---
2.26	2.34	0.08	5.03E-01	8.02E-01	KCNIP4	Kv channel interacting protein 4	chr4p15.31	240591_at	NM_001035003 /// NM_001035004 /// NM_025221 /// NM_147181 /// NM_147182 /// NM_147183
7.94	8.07	0.13	5.03E-01	8.02E-01	TMBIM4	transmembrane BAX inhibitor motif containing 4	chr12q14.1|12q14.1-q15	219206_x_at	NM_016056
2.33	2.41	0.08	5.03E-01	8.02E-01	PRDM7	PR domain containing 7	chr16q24.3	224228_s_at	NM_001098173 /// NM_052996
3.66	3.88	0.22	5.03E-01	8.02E-01	---	---	---	1556818_at	---
2.19	2.29	0.10	5.03E-01	8.02E-01	---	---	---	234564_at	---
2.45	2.55	0.10	5.03E-01	8.02E-01	TMEM19	transmembrane protein 19	chr12q21.1	219941_at	NM_018279
1.94	2.02	0.08	5.03E-01	8.02E-01	LOC727867 /// LOC729501 /// LOC729863 /// ZNF834	similar to PRED65 /// Putative zinc finger protein ENSP00000344568 /// similar to PRED65 /// zinc finger protein 834	chr13q11 /// chr18p11.21 /// chr21q11.2	216469_at	XR_015683 /// XR_036978 /// XR_037080 /// XR_037864 /// XR_037909
3.24	3.34	0.10	5.03E-01	8.02E-01	DNAH3	dynein, axonemal, heavy chain 3	chr16p12.2	215266_at	NM_017539
10.53	10.82	0.29	5.03E-01	8.02E-01	GPX3	glutathione peroxidase 3 (plasma)	chr5q23	201348_at	NM_002084
3.26	3.38	0.12	5.03E-01	8.02E-01	HSPA12B	heat shock 70kD protein 12B	chr20p13	234610_at	NM_052970
2.32	2.42	0.09	5.03E-01	8.02E-01	NXF3	nuclear RNA export factor 3	chrXq22-q23	220110_s_at	NM_022052
5.29	5.57	0.27	5.03E-01	8.02E-01	C3orf14	chromosome 3 open reading frame 14	chr3p14.2	219288_at	NM_020685
3.62	3.77	0.14	5.03E-01	8.02E-01	---	---	---	215845_x_at	---
2.11	2.21	0.10	5.03E-01	8.02E-01	NHEDC1	Na+/H+ exchanger domain containing 1	chr4q24	1555142_at	NM_001100874 /// NM_139173
3.21	3.38	0.17	5.03E-01	8.02E-01	---	---	---	234089_at	---
7.77	7.98	0.21	5.03E-01	8.02E-01	COX3 /// LOC440552	cytochrome c oxidase III /// OK/SW-cl.16	chr1p36.33	238199_x_at	---
4.35	4.51	0.16	5.03E-01	8.02E-01	C21orf81	chromosome 21 open reading frame 81	chr21q11.2	241233_x_at	XR_040134 /// XR_040135
2.01	2.10	0.09	5.04E-01	8.03E-01	TMEM132B	transmembrane protein 132B	chr12q24.31-q24.32	236824_at	NM_052907
6.19	6.31	0.12	5.04E-01	8.03E-01	TMEM165	transmembrane protein 165	chr4q12	222515_x_at	NM_018475
3.38	3.59	0.21	5.04E-01	8.03E-01	HEY1	hairy/enhancer-of-split related with YRPW motif 1	chr8q21	218839_at	NM_001040708 /// NM_012258
3.64	3.83	0.18	5.04E-01	8.03E-01	DMRTA1	DMRT-like family A1	chr9p21.2	244725_at	NM_022160
6.08	6.24	0.16	5.04E-01	8.03E-01	ZFHX3	zinc finger homeobox 3	chr16q22.3-q23.1	242738_s_at	NM_006885
7.15	7.30	0.15	5.04E-01	8.03E-01	TMEM141	transmembrane protein 141	chr9q34.3	225568_at	NM_032928
3.69	3.79	0.10	5.04E-01	8.03E-01	---	---	---	234084_x_at	---
6.11	6.39	0.28	5.04E-01	8.03E-01	ACSS3	acyl-CoA synthetase short-chain family member 3	chr12q21.31	219616_at	NM_024560
6.82	7.03	0.21	5.04E-01	8.03E-01	NAT13	N-acetyltransferase 13	chr3q13.2	217745_s_at	NM_025146
4.67	4.88	0.21	5.04E-01	8.03E-01	RHOF	ras homolog gene family, member F (in filopodia)	chr12q24.31	1554539_a_at	NM_019034
4.34	4.47	0.13	5.04E-01	8.03E-01	POU6F1	POU class 6 homeobox 1	chr12q13.13	216332_at	NM_002702
5.06	5.19	0.13	5.04E-01	8.03E-01	C1orf176	chromosome 1 open reading frame 176	chr1p34.2	222902_s_at	NM_022774
3.49	3.62	0.13	5.04E-01	8.03E-01	RGS14	regulator of G-protein signaling 14	chr5q35.3	204280_at	NM_006480
5.00	5.12	0.12	5.04E-01	8.03E-01	---	---	---	243121_x_at	---
2.28	2.38	0.11	5.04E-01	8.03E-01	---	---	---	1557745_at	---
4.25	4.34	0.09	5.04E-01	8.03E-01	---	---	---	237695_at	---
2.45	2.54	0.09	5.04E-01	8.03E-01	LOC647081 /// SDHD	hypothetical LOC647081 /// succinate dehydrogenase complex, subunit D, integral membrane protein	chr11q23 /// chr7q33	215652_at	NM_003002 /// XR_017490 /// XR_018838 /// XR_039162
1.99	2.07	0.08	5.04E-01	8.03E-01	---	---	---	231628_s_at	---
2.10	2.18	0.08	5.04E-01	8.03E-01	---	---	---	241266_at	---

1.80	1.88	0.08	5.04E-01	8.03E-01	SIAE	sialic acid acetylesterase	chr11q24	1554354_at	NM_170601
2.29	2.36	0.08	5.04E-01	8.03E-01	MMP27	matrix metallopeptidase 27	chr11q24	220783_at	NM_022122
4.02	4.19	0.17	5.05E-01	8.03E-01	NUB1	negative regulator of ubiquitin-like proteins 1	chr7q36	1557071_s_at	NM_016118
2.71	2.85	0.15	5.05E-01	8.03E-01	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	chr19q13.2	217209_at	NM_001815
3.24	3.38	0.14	5.05E-01	8.03E-01	RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	chr14q11	206608_s_at	NM_020366
9.61	9.74	0.12	5.04E-01	8.03E-01	MRLC2	myosin regulatory light chain MRLC2	chr18p11.31	221474_at	NM_033546
7.62	7.71	0.09	5.04E-01	8.03E-01	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	chr9q33-q34	215235_at	NM_001130438 /// NM_003127
2.71	2.80	0.09	5.04E-01	8.03E-01	NUDCD2	NudC domain containing 2	chr5q34	1558124_at	NM_145266
2.04	2.13	0.09	5.05E-01	8.03E-01	---	---	---	238251_at	---
4.45	4.79	0.34	5.05E-01	8.03E-01	MED23	mediator complex subunit 23	chr6q22.33-q24.1	242706_s_at	NM_004830 /// NM_015979
7.28	7.56	0.28	5.05E-01	8.03E-01	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	chr17q11.2	202416_at	NM_003315
4.95	5.19	0.24	5.05E-01	8.03E-01	SLIT3	slit homolog 3 (Drosophila)	chr5q35	203813_s_at	NM_003062
6.95	7.18	0.23	5.05E-01	8.03E-01	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	chr4q24	209043_at	NM_005443
4.08	4.31	0.22	5.05E-01	8.03E-01	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	chr18q22.3	227978_s_at	NM_175907
3.98	4.12	0.14	5.05E-01	8.03E-01	SHB	Src homology 2 domain containing adaptor protein B	chr9p13.2-p13.1	243595_at	NM_003028
4.06	4.19	0.13	5.05E-01	8.03E-01	BCAN	brevican	chr1q31	223633_s_at	NM_021948 /// NM_198427
3.59	3.70	0.11	5.05E-01	8.03E-01	---	---	---	241411_at	---
3.10	3.20	0.10	5.05E-01	8.03E-01	LOC284630	hypothetical protein LOC284630	chr1p36.32	1565728_at	---
2.36	2.46	0.10	5.05E-01	8.03E-01	SPOCK3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	chr4q32.3	206433_s_at	NM_001040159 /// NM_016950
2.17	2.25	0.08	5.05E-01	8.03E-01	SPAG1	sperm associated antigen 1	chr8q22.2	210117_at	NM_003114 /// NM_172218
2.56	2.63	0.07	5.05E-01	8.03E-01	---	---	---	229184_at	---
2.00	2.07	0.07	5.05E-01	8.03E-01	---	---	---	1563128_at	---
3.20	3.30	0.11	5.05E-01	8.03E-01	LOC149684	hypothetical protein LOC149684	chr20q12	244231_at	---
1.93	2.02	0.09	5.05E-01	8.03E-01	---	---	---	1563110_at	---
5.89	6.15	0.26	5.05E-01	8.03E-01	RAD23B	RAD23 homolog B (S. cerevisiae)	chr9q31.2	223598_at	NM_002874
3.16	3.28	0.13	5.05E-01	8.03E-01	ACVR1B	activin A receptor, type IB	chr12q13	208222_at	NM_004302 /// NM_020327 /// NM_020328
4.55	4.67	0.11	5.05E-01	8.03E-01	---	---	---	230401_at	---
2.13	2.24	0.11	5.05E-01	8.03E-01	---	---	---	221043_at	---
2.46	2.54	0.09	5.05E-01	8.03E-01	ZNF625	zinc finger protein 625	chr19p13.2	1552769_at	NM_145233
2.37	2.48	0.11	5.05E-01	8.03E-01	---	---	---	241988_x_at	---
3.98	4.12	0.15	5.05E-01	8.03E-01	PRDM2	PR domain containing 2, with ZNF domain	chr1p36.21	203056_s_at	NM_001007257 /// NM_012231 /// NM_015866
3.74	3.87	0.13	5.05E-01	8.03E-01	LOC283738	hypothetical protein LOC283738	chr15q25.3	231469_at	---
3.36	3.48	0.12	5.05E-01	8.03E-01	LOC643008	PP12104	chr17q25.1	229740_at	XR_041570 /// XR_041571 /// XR_041572
2.73	2.83	0.10	5.05E-01	8.03E-01	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	chrXq13.1	216955_at	NM_004606 /// NM_138923
1.98	2.07	0.09	5.05E-01	8.03E-01	C13orf39	chromosome 13 open reading frame 39	chr13q33.1	230331_at	NM_001010977
1.98	2.06	0.07	5.05E-01	8.03E-01	---	---	---	216758_at	---
2.01	2.10	0.09	5.06E-01	8.03E-01	SLC25A27	solute carrier family 25, member 27	chr6p11.2-q12	1554161_at	NM_004277
7.06	7.29	0.23	5.06E-01	8.03E-01	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	chr4q31.1-q31.2	213251_at	NM_003601
6.74	6.91	0.17	5.06E-01	8.03E-01	TBK1	TANK-binding kinase 1	chr12q14.1	218520_at	NM_013254
2.17	2.29	0.12	5.06E-01	8.03E-01	PNLIPRP2	pancreatic lipase-related protein 2	chr10q25.3	211766_s_at	NM_005396
2.38	2.50	0.12	5.06E-01	8.03E-01	CYLD	cylindromatosis (turban tumor syndrome)	chr16q12.1	222142_at	NM_001042355 /// NM_001042412 /// NM_015247
2.07	2.18	0.11	5.06E-01	8.03E-01	TRDN	triadin	chr6q22-q23	222919_at	NM_006073
2.83	2.92	0.09	5.06E-01	8.03E-01	PKNOX1	PBX/knotted 1 homeobox 1	chr21q22.3	54051_at	NM_004571
1.98	2.06	0.08	5.06E-01	8.03E-01	---	---	---	234794_at	---
2.15	2.25	0.10	5.06E-01	8.03E-01	DKFZp434K191	hypothetical locus DKFZp434K191	chr22q11.2	1557633_at	XR_040035
2.81	2.94	0.13	5.06E-01	8.03E-01	LOC100131601	similar to hCG1980470	chr16q23.1	232442_at	XM_001724890 /// XM_001724913 /// XM_001726807
5.32	5.46	0.13	5.06E-01	8.03E-01	---	---	---	234644_x_at	---
3.93	4.46	0.53	5.06E-01	8.03E-01	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	chr5q11	204864_s_at	NM_002184 /// NM_175767

3.08	3.26	0.17	5.06E-01	8.03E-01	FUT6	Fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	1565660_at	NM_000150 /// NM_001040701
2.90	2.99	0.09	5.06E-01	8.03E-01	ZDHHC18	zinc finger, DHHC-type containing 18	chr1p36.11	231908_at	NM_032283
5.01	5.19	0.17	5.06E-01	8.03E-01	SCUBE3	signal peptide, CUB domain, EGF-like 3	chr6p21.3	230290_at	NM_152753
5.55	5.79	0.24	5.06E-01	8.03E-01	---	---	---	225902_at	---
2.77	2.88	0.11	5.06E-01	8.03E-01	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	chr15q11.2-q12	227830_at	NM_000814 /// NM_021912
2.05	2.13	0.08	5.06E-01	8.03E-01	---	---	---	216124_at	---
2.35	2.44	0.08	5.06E-01	8.03E-01	FAM92A1	Family with sequence similarity 92, member A1	chr8q22.1	237910_x_at	NM_145269
4.06	4.31	0.25	5.06E-01	8.03E-01	SNX13	sorting nexin 13	chr7p21.1	1553148_a_at	NM_015132
2.34	2.46	0.12	5.06E-01	8.04E-01	IL12RB2	interleukin 12 receptor, beta 2	chr1p31.3-p31.2	206999_at	NM_001559
4.24	4.65	0.41	5.06E-01	8.04E-01	TRBC1 /// TRBC2 /// TRBV19	T cell receptor beta constant 1 /// T cell receptor beta constant 2 /// T cell receptor beta variable 19	chr7q34	211796_s_at	---
3.52	3.79	0.27	5.06E-01	8.04E-01	---	---	---	239832_at	---
3.43	3.64	0.21	5.06E-01	8.04E-01	GPR124	G protein-coupled receptor 124	chr8p12	65718_at	NM_032777
5.97	6.17	0.20	5.06E-01	8.04E-01	PDLIM2	PDZ and LIM domain 2 (mystique)	chr8p21.2	219165_at	NM_021630 /// NM_176871 /// NM_198042
5.38	5.52	0.14	5.06E-01	8.04E-01	---	---	---	1558837_a_at	---
2.58	2.69	0.11	5.06E-01	8.04E-01	SLAMF7	SLAM family member 7	chr1q23.1-q24.1	222838_at	NM_021181
2.37	2.48	0.11	5.06E-01	8.04E-01	ZMYM6	zinc finger, MYM-type 6	chr1p34.2	1552969_a_at	NM_007167
2.91	3.02	0.11	5.06E-01	8.04E-01	DSCR10	Down syndrome critical region gene 10	chr21q22.13	1552468_a_at	NM_148676
2.19	2.29	0.10	5.06E-01	8.04E-01	LOC283352	hypothetical protein LOC283352	chr12q24.33	1561757_a_at	---
3.56	3.66	0.10	5.06E-01	8.04E-01	---	---	---	236788_at	---
3.39	3.49	0.10	5.06E-01	8.04E-01	ANAPC10 /// ANAPC10P	anaphase promoting complex subunit 10 /// anaphase promoting complex subunit 10 pseudogene	chr1p32.3 /// chr4q31	241959_at	NM_014885 /// XR_015956 /// XR_016035 /// XR_039726
2.18	2.26	0.09	5.06E-01	8.04E-01	PP14571	similar to hCG1777210	chr2q37.3	214858_at	NR_024014 /// XM_001719668 /// XM_001722120 /// XM_001724543
3.22	3.38	0.17	5.06E-01	8.04E-01	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	chr11p15.5	217187_at	NM_017511 /// XM_001134429 /// XM_001714104 /// XM_001714774
2.28	2.36	0.09	5.06E-01	8.04E-01	LOC728806	Similar to Vesicle-fusing ATPase (Vesicular-fusion protein NSF) (N-ethylmaleimide sensitive fusion protein) (NEM-sensitive fusion protein)	chr17q21.31-q21.32	1566784_at	XM_001128535
6.44	6.73	0.29	5.07E-01	8.04E-01	PCCA	propionyl Coenzyme A carboxylase, alpha polypeptide	chr13q32	203860_at	NM_000282 /// NM_001127692
3.87	4.09	0.23	5.07E-01	8.04E-01	ZCCHC10	zinc finger, CCHC domain containing 10	chr5q31.1	221193_s_at	NM_017665
5.32	5.49	0.17	5.07E-01	8.04E-01	ERGIC2	ERGIC and golgi 2	chr12p11.22	226422_at	NM_016570
2.42	2.54	0.12	5.07E-01	8.04E-01	HOXB8	homeobox B8	chr17q21.3	221278_at	NM_024016
2.10	2.22	0.12	5.07E-01	8.04E-01	---	---	---	1556813_at	---
2.41	2.52	0.11	5.07E-01	8.04E-01	---	---	---	237175_at	---
1.84	1.94	0.11	5.07E-01	8.04E-01	HMGA2	high mobility group AT-hook 2	chr12q15	1561633_at	NM_003483 /// NM_003484
3.69	3.79	0.10	5.07E-01	8.04E-01	---	---	---	242953_at	---
2.46	2.56	0.10	5.07E-01	8.04E-01	FAM171B	Family with sequence similarity 171, member B	chr2q32.1	238564_at	NM_177454
2.15	2.24	0.09	5.07E-01	8.04E-01	---	---	---	234259_at	---
1.90	1.99	0.09	5.07E-01	8.04E-01	---	---	---	224354_at	---
2.08	2.15	0.08	5.07E-01	8.04E-01	---	---	---	224136_at	---
6.33	6.91	0.58	5.07E-01	8.04E-01	TMEM176A	transmembrane protein 176A	chr7q36.1	218345_at	NM_018487
4.52	4.80	0.28	5.07E-01	8.04E-01	LARP4	La ribonucleoprotein domain family, member 4	chr12q13.13	238959_at	NM_052879 /// NM_199188 /// NM_199190
3.81	3.94	0.13	5.07E-01	8.04E-01	ESR1	estrogen receptor 1	chr6q25.1	211235_s_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742
5.04	5.15	0.12	5.07E-01	8.04E-01	FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	chr9q34.3	208439_s_at	NM_004108 /// NM_015837
5.06	5.17	0.11	5.07E-01	8.04E-01	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	chr4q25-q27	219290_x_at	NM_014395

1.90	2.01	0.11	5.07E-01	8.04E-01	MAP2K5	Mitogen-activated protein kinase kinase 5	chr15q23	216435_at	NM_002757 /// NM_145160
2.51	2.60	0.09	5.07E-01	8.04E-01	---	---	---	241950_at	---
1.79	1.87	0.08	5.07E-01	8.04E-01	MSTN	myostatin	chr2q32.2	207145_at	NM_005259
2.08	2.16	0.08	5.07E-01	8.04E-01	---	---	---	242529_x_at	---
4.34	4.46	0.12	5.07E-01	8.04E-01	CEP78	centrosomal protein 78kDa	chr9q21.2	228774_at	NM_001098802 /// NM_032171
8.98	9.27	0.28	5.07E-01	8.04E-01	NDRG2	NDRG family member 2	chr14q11.2	206453_s_at	NM_016250 /// NM_201535 /// NM_201536 /// NM_201537 /// NM_201538 /// NM_201539 /// NM_201540 /// NM_201541
9.23	9.37	0.14	5.07E-01	8.04E-01	SSR1	signal sequence receptor, alpha	chr6p24.3	200891_s_at	NM_003144
4.54	4.70	0.16	5.07E-01	8.04E-01	PXK	PX domain containing serine/threonine kinase	chr3p14.3	1552275_s_at	NM_017771
4.78	4.89	0.11	5.07E-01	8.04E-01	BAT3	HLA-B associated transcript 3	chr6p21.3	230513_at	NM_001098534 /// NM_004639 /// NM_080702 /// NM_080703
2.30	2.40	0.10	5.07E-01	8.04E-01	---	---	---	244210_at	---
2.02	2.11	0.09	5.07E-01	8.04E-01	KRT20	keratin 20	chr17q21.2	213953_at	NM_019010
2.29	2.38	0.09	5.07E-01	8.04E-01	DKFZp547E087 /// LOC440354	hypothetical gene LOC283846 /// PI-3-kinase-related kinase SMG-1 pseudogene	chr16p11.2 /// chr18p11.21	1558534_at	NR_002473 /// XM_496136 /// XM_931802 /// XM_931808 /// XM_931814 /// XM_931818 /// XM_931827 /// XM_931837 /// XM_931840 /// XR_042165
5.98	6.12	0.14	5.08E-01	8.04E-01	RPRD2	regulation of nuclear pre-mRNA domain containing 2	chr1q21.2	226527_at	NM_015203
2.49	2.59	0.10	5.08E-01	8.04E-01	FLJ37543	hypothetical protein FLJ37543	chr5q12.1	1553426_at	NM_173667 /// XM_001719936 /// XM_001719943 /// XM_001722926
5.41	5.72	0.30	5.08E-01	8.04E-01	LAMB1	laminin, beta 1	chr7q22	201505_at	NM_002291
3.75	3.99	0.24	5.08E-01	8.04E-01	---	---	---	233257_at	---
2.39	2.51	0.11	5.08E-01	8.04E-01	FCAR	Fc fragment of IgA, receptor for	chr19q13.2-q13.4	211306_s_at	NM_002000 /// NM_133269 /// NM_133271 /// NM_133272 /// NM_133273 /// NM_133274 /// NM_133277 /// NM_133278 /// NM_133279
2.39	2.48	0.09	5.08E-01	8.04E-01	---	---	---	1569100_a_at	---
2.03	2.12	0.09	5.08E-01	8.04E-01	---	---	---	242101_at	---
3.74	3.86	0.12	5.08E-01	8.04E-01	---	---	---	236891_at	---
2.63	2.72	0.09	5.08E-01	8.04E-01	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	chr6p21.3	215669_at	NM_021983 /// XM_001723414 /// XM_001723417 /// XM_001723419
2.05	2.13	0.08	5.08E-01	8.04E-01	KRT37	Keratin 37	chr17q12-q21	1557068_at	NM_003770
4.04	4.17	0.13	5.08E-01	8.04E-01	LOC100134287	hypothetical protein LOC100134287	---	1565772_at	XM_001723937
3.03	3.18	0.15	5.08E-01	8.04E-01	TBC1D22B	TBC1 domain family, member 22B	chr6p21.2	233430_at	NM_017772
5.64	5.81	0.16	5.08E-01	8.04E-01	CNNM2	cyclin M2	chr10q24.32	209874_x_at	NM_017649 /// NM_199076 /// NM_199077
2.79	2.92	0.13	5.08E-01	8.04E-01	---	---	---	239800_at	---
2.63	2.74	0.11	5.08E-01	8.05E-01	---	---	---	1561249_a_at	---
2.39	2.49	0.10	5.08E-01	8.05E-01	FOXO1	Forkhead box O1	chr13q14.1	228484_s_at	NM_002015
4.50	4.59	0.09	5.08E-01	8.05E-01	KNDC1	Kinase non-catalytic C-lobe domain (KIND) containing 1	chr10q26.3	230558_at	NM_152643

1.84	1.93	0.09	5.08E-01	8.05E-01	---	---	---	242063_s_at	---
2.45	2.56	0.11	5.08E-01	8.05E-01	OLAH	oleoyl-ACP hydrolase	chr10p13	222945_x_at	NM_001039702 /// NM_018324
1.96	2.04	0.09	5.08E-01	8.05E-01	FAM161A	family with sequence similarity 161, member A	chr2p15	239090_at	NM_032180
2.38	2.47	0.09	5.08E-01	8.05E-01	TDP1	Tyrosyl-DNA phosphodiesterase 1	chr14q32.11	240822_at	NM_001008744 /// NM_018319
5.01	5.34	0.33	5.08E-01	8.05E-01	CBWD1 /// CBWD2 /// CBWD3 /// CBWD5 /// CBWD6 /// CBWD7 /// LOC100132072 /// LOC100133216	COBW domain containing 1 /// COBW domain containing 2 /// COBW domain containing 3 /// COBW domain containing 5 /// COBW domain containing 6 /// COBW domain containing 7 /// hypothetical protein LOC100132072 /// hypothetical protein LOC100133216	chr2q14.1 /// chr9p11.2 /// chr9p12 /// chr9p24.3 /// chr9q12 /// chr9q13	220175_s_at	NM_001024916 /// NM_001085457 /// NM_018491 /// NM_172003 /// NM_201453 /// XM_001716392 /// XM_001717050 /// XM_001717183 /// XM_001721390
2.86	2.99	0.12	5.08E-01	8.05E-01	FAM115C	family with sequence similarity 115, member C	chr7q35	239315_at	NM_001130025 /// NM_001130026 /// NM_173678
2.78	2.89	0.10	5.09E-01	8.05E-01	LOC100129907	hypothetical protein LOC100129907	chr16p11.2	244497_at	XM_001720756 /// XM_001720899 /// XM_001725722
2.38	2.47	0.09	5.09E-01	8.05E-01	ZFP28	zinc finger protein 28 homolog (mouse)	---	240565_at	NM_020828
2.07	2.16	0.09	5.09E-01	8.05E-01	NUB1	Negative regulator of ubiquitin-like proteins 1	chr7q36	1559732_at	NM_016118
2.10	2.17	0.07	5.09E-01	8.05E-01	C3orf67	chromosome 3 open reading frame 67	chr3p14.2	239697_x_at	NM_198463
4.61	5.08	0.48	5.09E-01	8.05E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	224941_at	NM_002581
3.98	4.15	0.18	5.09E-01	8.05E-01	FRS2	fibroblast growth factor receptor substrate 2	chr12q15	221308_at	NM_001042555 /// NM_006654
4.23	4.39	0.16	5.09E-01	8.05E-01	---	---	---	238568_s_at	---
3.74	3.87	0.13	5.09E-01	8.05E-01	C20orf142	chromosome 20 open reading frame 142	chr20q13.12	233061_at	NM_001080472
2.81	2.91	0.10	5.09E-01	8.05E-01	SLC35C2	solute carrier family 35, member C2	chr20q13.12	238814_at	NM_015945 /// NM_173073 /// NM_173179 /// XM_001722057 /// XM_001722102 /// XM_001722502
1.90	1.98	0.08	5.09E-01	8.05E-01	LOC149773	Hypothetical protein LOC149773	chr20q13.32	1559433_at	XR_042084 /// XR_042085 /// XR_042086
9.25	9.44	0.18	5.09E-01	8.05E-01	41519	septin 2	chr2q37	200015_s_at	NM_001008491 /// NM_001008492 /// NM_004404 /// NM_006155
6.26	6.37	0.11	5.09E-01	8.05E-01	ATF7IP	activating transcription factor 7 interacting protein	chr12p13.1	231825_x_at	NM_018179
2.08	2.17	0.09	5.09E-01	8.05E-01	SERGEF	Secretion regulating guanine nucleotide exchange factor	chr11p14.3	239114_at	NM_012139
2.40	2.48	0.08	5.09E-01	8.05E-01	---	---	---	243034_at	---
2.29	2.40	0.11	5.09E-01	8.05E-01	LOC100129662	hypothetical protein LOC100129662	chrXq26.3	1560537_at	XM_001715624 /// XM_001716152
2.39	2.47	0.08	5.09E-01	8.05E-01	C1QTNF7	C1q and tumor necrosis factor related protein 7	chr4p16-p15	223877_at	NM_031911
2.05	2.13	0.07	5.09E-01	8.05E-01	CLEC2D	C-type lectin domain family 2, member D	chr12p13	228426_at	NM_001004419 /// NM_013269
6.61	6.77	0.16	5.09E-01	8.05E-01	RBMS1	RNA binding motif, single stranded interacting protein 1	chr2q24.2	215127_s_at	NM_002897 /// NM_016836 /// NM_016839
3.99	4.09	0.10	5.09E-01	8.05E-01	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	chr13q14	205134_s_at	NM_012345

5.31	5.61	0.30	5.09E-01	8.05E-01	ZNF770	zinc finger protein 770	chr15q14	225517_at	NM_014106
4.43	4.57	0.13	5.09E-01	8.05E-01	---	---	---	232290_at	---
6.07	6.31	0.24	5.09E-01	8.05E-01	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	chr5q31.3	216321_s_at	NM_000176 /// NM_001018074 /// NM_001018075 /// NM_001018076 /// NM_001018077 /// NM_001020825 /// NM_001024094
1.96	2.04	0.08	5.09E-01	8.05E-01	THRAP3	thyroid hormone receptor associated protein 3	chr1p34.3	242163_at	NM_005119
2.93	3.02	0.10	5.09E-01	8.05E-01	AUTS2	autism susceptibility candidate 2	chr7q11.22	243364_at	NM_001127231 /// NM_001127232 /// NM_015570
2.27	2.36	0.10	5.09E-01	8.05E-01	NTNG1	netrin G1	chr1p13.3	236088_at	NM_001113226 /// NM_001113228 /// NM_014917
2.10	2.19	0.09	5.09E-01	8.05E-01	NCAPG	non-SMC condensin I complex, subunit G	chr4p15.33	218663_at	NM_022346
2.65	2.79	0.14	5.09E-01	8.05E-01	LOC283270	hypothetical protein LOC283270	chr11p13	1556319_at	---
3.18	3.33	0.15	5.10E-01	8.05E-01	---	---	---	244298_at	---
4.13	4.27	0.14	5.10E-01	8.05E-01	CDH23	cadherin-like 23	chr10q21-q22	1552436_a_at	NM_022124 /// NM_052836
2.07	2.13	0.07	5.10E-01	8.05E-01	INADL	InaD-like (Drosophila)	chr1p31.3	240570_at	NM_176877
3.00	3.17	0.17	5.10E-01	8.05E-01	FERD3L	Fer3-like (Drosophila)	chr7p21.1	1553517_at	NM_152898
2.57	2.68	0.10	5.10E-01	8.05E-01	SFRP1	secreted frizzled-related protein 1	chr8p12-p11.1	202035_s_at	NM_003012
1.99	2.08	0.10	5.10E-01	8.05E-01	SALL1	sal-like 1 (Drosophila)	chr16q12.1	206893_at	NM_001127892 /// NM_002968
6.62	6.78	0.15	5.10E-01	8.05E-01	LOC729013	hypothetical protein LOC729013	chr11p15.3	235010_at	XR_042023 /// XR_042024 /// XR_042025
2.27	2.40	0.14	5.10E-01	8.05E-01	ZIC1	Zic family member 1 (odd-paired homolog, Drosophila)	chr3q24	206373_at	NM_003412
6.59	6.76	0.18	5.10E-01	8.05E-01	TATDN1	TatD DNase domain containing 1	chr8q24.13	223231_at	NM_032026
2.24	2.34	0.10	5.10E-01	8.05E-01	LOC222159	hypothetical protein LOC222159	chr7p15.1	1558859_at	---
2.89	2.98	0.09	5.10E-01	8.05E-01	OFCC1	orofacial cleft 1 candidate 1	chr6p24.3	1564783_x_at	NM_153003
5.32	5.52	0.20	5.10E-01	8.05E-01	SCAMP4	secretory carrier membrane protein 4	chr19p13.3	213244_at	NM_079834
2.08	2.17	0.10	5.10E-01	8.05E-01	CCDC148	coiled-coil domain containing 148	chr2q24.1	1564757_a_at	NM_138803
2.65	2.77	0.12	5.10E-01	8.05E-01	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	chr8q21.13	227354_at	NM_018440
1.97	2.07	0.10	5.10E-01	8.05E-01	---	---	---	1565923_at	---
2.96	3.05	0.10	5.10E-01	8.05E-01	OR4D1	olfactory receptor, family 4, subfamily D, member 1	chr17q23.2	1567069_at	NM_012374
8.74	8.82	0.09	5.10E-01	8.05E-01	PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	chr3q27.1	200830_at	NM_002808
1.99	2.07	0.08	5.10E-01	8.05E-01	---	---	---	231614_at	---
4.77	4.95	0.18	5.10E-01	8.05E-01	THSD4	thrombospondin, type I, domain containing 4	chr15q23	222835_at	NM_024817
2.09	2.19	0.10	5.10E-01	8.06E-01	LOC647946	hypothetical protein LOC647946	---	240365_at	XM_943589
8.09	8.40	0.32	5.10E-01	8.06E-01	PON2	paraoxonase 2	chr7q21.3	210830_s_at	NM_000305 /// NM_001018161
5.52	5.83	0.32	5.10E-01	8.06E-01	---	---	---	242551_at	---
1.97	2.05	0.08	5.10E-01	8.06E-01	LRRC34	leucine rich repeat containing 34	chr3q26.2	236917_at	NM_153353
2.26	2.36	0.10	5.10E-01	8.06E-01	---	---	---	1555978_s_at	---
5.15	5.48	0.34	5.11E-01	8.06E-01	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	chr7q21	227692_at	NM_002069
6.51	6.82	0.30	5.11E-01	8.06E-01	USP48	ubiquitin specific peptidase 48	chr1p36.12	225925_s_at	NM_001032730 /// NM_032236
7.79	8.00	0.21	5.11E-01	8.06E-01	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	chr4q12	201803_at	NM_000938
1.95	2.04	0.09	5.11E-01	8.06E-01	---	---	---	233413_at	---

4.24	4.32	0.08	5.11E-01	8.06E-01	SCAND2	SCAN domain containing 2 pseudogene	chr15q25-q26	222211_x_at	NM_022050 /// NM_033633 /// NM_033634 /// NM_033635 /// NM_033636 /// NM_033640 /// NR_003654 /// NR_004859
2.10	2.18	0.08	5.11E-01	8.06E-01	ZNF93	zinc finger protein 93	chr19p12	1569240_at	NM_031218
6.46	6.53	0.07	5.11E-01	8.06E-01	HABP4	hyaluronan binding protein 4	chr9q22.3-q31	209818_s_at	NM_014282
2.32	2.42	0.09	5.11E-01	8.06E-01	SLC17A3	solute carrier family 17 (sodium phosphate), member 3	chr6p21.3	207298_at	NM_001098486 /// NM_006632
2.59	2.74	0.14	5.11E-01	8.06E-01	---	---	---	229715_at	---
2.94	3.07	0.13	5.11E-01	8.06E-01	RAD51L1	RAD51-like 1 (S. cerevisiae)	chr14q23-q24.2	1561122_a_at	NM_002877 /// NM_133509 /// NM_133510
2.29	2.38	0.09	5.11E-01	8.06E-01	---	---	---	1566276_at	---
2.51	2.59	0.08	5.11E-01	8.06E-01	SYN3	synapsin III	chr22q12.3	206322_at	NM_003490 /// NM_133633
5.39	5.67	0.27	5.11E-01	8.06E-01	LRRC8C	leucine rich repeat containing 8 family, member C	chr1p22.2	223533_at	NM_032270
7.90	8.08	0.19	5.11E-01	8.06E-01	KIF5B	kinesin family member 5B	chr10pter-q22.1	224662_at	NM_004521
4.18	4.32	0.14	5.11E-01	8.06E-01	ADCY1	adenylate cyclase 1 (brain)	chr7p13-p12	215348_at	NM_021116
2.09	2.21	0.11	5.11E-01	8.06E-01	---	---	---	241913_at	---
2.10	2.19	0.09	5.11E-01	8.06E-01	C1orf176	chromosome 1 open reading frame 176	chr1p34.2	219567_s_at	NM_022774
2.21	2.30	0.09	5.11E-01	8.06E-01	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	chr1p21	210743_s_at	NM_003672 /// NM_033312 /// NM_033313
2.11	2.20	0.09	5.11E-01	8.06E-01	CHAF1A	Chromatin assembly factor 1, subunit A (p150)	chr19p13.3	229808_at	NM_005483
2.36	2.44	0.08	5.11E-01	8.06E-01	FAM24A	family with sequence similarity 24, member A	chr10q26.13	243143_at	NM_001029888
1.85	1.91	0.07	5.11E-01	8.06E-01	DNAJB7	DnaJ (Hsp40) homolog, subfamily B, member 7	chr22q13.2	1552675_at	NM_145174
2.48	2.56	0.08	5.11E-01	8.06E-01	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	chrXq13.1	219650_at	NM_017669
3.10	3.21	0.11	5.11E-01	8.06E-01	MAL	mal, T-cell differentiation protein	chr2cen-q13	204777_s_at	NM_002371 /// NM_022438 /// NM_022439 /// NM_022440
5.61	5.90	0.29	5.11E-01	8.06E-01	SNX14	sorting nexin 14	chr6q14.3	225101_s_at	NM_020468 /// NM_153816
1.90	1.97	0.07	5.11E-01	8.06E-01	---	---	---	232958_at	---
1.97	2.06	0.09	5.11E-01	8.06E-01	DSG1	desmoglein 1	chr18q12.1	206642_at	NM_001942
6.65	6.81	0.16	5.11E-01	8.06E-01	CYB561D1	cytochrome b-561 domain containing 1	chr1p13.3	227981_at	NM_001134400 /// NM_001134402 /// NM_001134403 /// NM_001134404 /// NM_182580
4.24	4.36	0.12	5.11E-01	8.06E-01	HEL308	DNA helicase HEL308	chr4q21.23	243809_at	NM_133636
2.78	2.88	0.10	5.11E-01	8.06E-01	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	chr6q22.31	213561_at	NM_014034
2.46	2.55	0.09	5.11E-01	8.06E-01	LMO7	LIM domain 7	chr13q22.2	202674_s_at	NM_005358
2.08	2.15	0.07	5.11E-01	8.06E-01	---	---	---	1562755_at	---
5.55	5.75	0.20	5.12E-01	8.06E-01	LOC100132134 /// LOC100134401 /// LOC653188	similar to LOC653391 protein /// hypothetical protein LOC100134401 /// similar to Beta-glucuronidase-like protein SMA3	chr5q13.2	213089_at	XM_001717368 /// XM_001719459 /// XM_001719462 /// XM_001719469 /// XM_001721330 /// XM_001721429
2.21	2.30	0.09	5.12E-01	8.06E-01	---	---	---	234142_at	---
3.11	3.28	0.17	5.12E-01	8.06E-01	---	---	---	216284_at	---
2.80	2.93	0.13	5.12E-01	8.06E-01	GLIS1	GLIS family zinc finger 1	chr1p32.3	244128_x_at	NM_147193

2.55	2.65	0.10	5.12E-01	8.06E-01	S100A7	S100 calcium binding protein A7	chr1q21	205916_at	NM_002963
2.88	2.99	0.11	5.12E-01	8.06E-01	CAPN11	calpain 11	chr6p12	207962_at	NM_007058
2.77	2.87	0.10	5.12E-01	8.06E-01	LOC100130598	hypothetical protein LOC100130598	chr13q32.2	1570409_x_at	XM_001719254 /// XM_001720068 /// XM_001721180
2.35	2.45	0.10	5.12E-01	8.06E-01	MEOX1	mesenchyme homeobox 1	chr17q21	205619_s_at	NM_001040002 /// NM_004527 /// NM_013999
1.87	1.95	0.08	5.12E-01	8.06E-01	---	---	---	1570561_at	---
2.29	2.39	0.10	5.12E-01	8.07E-01	---	---	---	234215_at	---
4.42	4.61	0.19	5.12E-01	8.07E-01	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	chr7q36.1	218292_s_at	NM_001040633 /// NM_016203 /// NM_024429
2.48	2.56	0.08	5.12E-01	8.07E-01	CCR3	chemokine (C-C motif) receptor 3	chr3p21.3	208304_at	NM_001837 /// NM_178329
5.45	5.72	0.26	5.12E-01	8.07E-01	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	chr12q23.3	219459_at	NM_018082
3.39	3.61	0.22	5.12E-01	8.07E-01	C1orf25	chromosome 1 open reading frame 25	chr1q25.2	233750_s_at	NM_030934
2.67	2.81	0.14	5.12E-01	8.07E-01	LOC646778	Hypothetical LOC646778	chr18q12.1	231342_at	XR_041105 /// XR_041106
4.71	4.86	0.14	5.12E-01	8.07E-01	GTPBP5	GTP binding protein 5 (putative)	chr20q13.33	226598_s_at	NM_015666
3.28	3.41	0.13	5.12E-01	8.07E-01	---	---	---	1565879_at	---
2.25	2.38	0.13	5.12E-01	8.07E-01	---	---	---	242254_at	---
3.65	3.77	0.12	5.12E-01	8.07E-01	PLK1	polo-like kinase 1 (Drosophila)	chr16p12.1	202240_at	NM_005030
3.22	3.34	0.12	5.12E-01	8.07E-01	WDR42A	WD repeat domain 42A	chr1q22-q23	233637_at	NM_015726
2.58	2.69	0.12	5.12E-01	8.07E-01	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	chrXq13	214225_at	NM_006223
2.01	2.13	0.11	5.12E-01	8.07E-01	SOX6	SRY (sex determining region Y)-box 6	chr11p15.3	1563454_at	NM_017508 /// NM_033326
2.18	2.28	0.10	5.12E-01	8.07E-01	MFAP3L	microfibrillar-associated protein 3-like	chr4q32.3	210492_at	NM_001009554 /// NM_021647
2.50	2.61	0.10	5.12E-01	8.07E-01	HELLS	helicase, lymphoid-specific	chr10q24.2	223556_at	NM_018063
1.95	2.05	0.10	5.12E-01	8.07E-01	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	chr4q31.22	237831_x_at	NM_172250
2.93	3.03	0.10	5.12E-01	8.07E-01	SH2D1A	SH2 domain protein 1A	chrXq25-q26	211211_x_at	NM_001114937 /// NM_002351
2.37	2.46	0.09	5.12E-01	8.07E-01	---	---	---	236398_s_at	---
2.37	2.46	0.09	5.12E-01	8.07E-01	RP11-589B3.4 /// SFTPA1 /// SFTPA1B /// SFTPA2B	surfactant, pulmonary-associated protein A2 /// surfactant protein A1 /// surfactant protein A1B /// surfactant protein A2B	chr10q22.3	223678_s_at	NM_001093770 /// NM_001098668 /// NM_005411 /// NM_006926
2.77	2.84	0.07	5.12E-01	8.07E-01	FAM155A	family with sequence similarity 155, member A	chr13q33.3	214825_at	NM_001080396
2.09	2.16	0.07	5.12E-01	8.07E-01	---	---	---	216793_x_at	---
1.99	2.06	0.06	5.12E-01	8.07E-01	ZNF720	zinc finger protein 720	chr16p11.2	242091_at	NM_001004300 /// NM_001130913
2.43	2.54	0.11	5.12E-01	8.07E-01	ZNF645	zinc finger protein 645	chrXp22.11	1552967_at	NM_152577
5.89	6.14	0.26	5.12E-01	8.07E-01	RBM18	RNA binding motif protein 18	chr9q33.2	225236_at	NM_033117
1.85	1.91	0.07	5.12E-01	8.07E-01	C11orf64	chromosome 11 open reading frame 64	chr11q12.2	1554764_a_at	XR_039987 /// XR_039988 /// XR_039989
2.20	2.28	0.08	5.12E-01	8.07E-01	---	---	---	244888_at	---
4.37	4.53	0.16	5.13E-01	8.07E-01	KIAA1219	KIAA1219	chr20q11.23	221738_at	NM_020336
2.30	2.40	0.10	5.13E-01	8.07E-01	ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	chr7q33-q34	220197_at	NM_020632 /// NM_130840 /// NM_130841
5.60	5.78	0.18	5.13E-01	8.07E-01	OSGEPL1	O-sialoglycoprotein endopeptidase-like 1	chr2q32.2	220631_at	NM_022353
2.45	2.55	0.10	5.13E-01	8.07E-01	---	---	---	1563127_at	---
2.02	2.10	0.08	5.13E-01	8.07E-01	NUDT16P	nudix (nucleoside diphosphate linked moiety X)-type motif 16 pseudogene	chr3q22.1	232251_at	NR_002949
3.01	3.11	0.10	5.13E-01	8.07E-01	---	---	---	1570249_x_at	---

2.41	2.49	0.08	5.13E-01	8.07E-01	LOC340239	hypothetical protein LOC340239	chr7q11.21	1557664_at	XM_001719418 /// XM_001719419 /// XM_001719577 /// XM_001719578 /// XM_001720342 /// XM_001720344
3.15	3.28	0.13	5.13E-01	8.07E-01	AFF1	AF4/FMR2 family, member 1	chr4q21	215451_s_at	NM_005935
2.95	3.07	0.12	5.13E-01	8.07E-01	ZNF721	zinc finger protein 721	chr4p16.3	228029_at	NM_133474
2.70	2.83	0.13	5.13E-01	8.07E-01	S100A3	S100 calcium binding protein A3	chr1q21	206027_at	NM_002960
3.23	3.39	0.16	5.13E-01	8.07E-01	NOS3	nitric oxide synthase 3 (endothelial cell)	chr7q36	205581_s_at	NM_000603
1.90	2.01	0.11	5.13E-01	8.07E-01	---	---	---	237825_x_at	---
5.37	5.52	0.15	5.13E-01	8.07E-01	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	chr6p22.3-p22.1	218536_at	NM_020662
1.82	1.89	0.07	5.13E-01	8.07E-01	---	---	---	1561156_at	---
2.14	2.25	0.11	5.13E-01	8.07E-01	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	chr8p11	1559142_at	NM_001099412 /// NM_001099413 /// NM_006766
1.91	1.98	0.07	5.13E-01	8.07E-01	---	---	---	1560918_at	---
2.75	2.82	0.07	5.13E-01	8.07E-01	ACTL7A	actin-like 7A	chr9q31	220501_at	NM_006687
2.69	2.79	0.11	5.13E-01	8.07E-01	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	chr9q33-q34	214926_at	NM_001130438 /// NM_003127
2.05	2.12	0.07	5.13E-01	8.07E-01	GIT2	G protein-coupled receptor kinase interactor 2	chr12q24.1	1556913_a_at	NM_014776 /// NM_057169 /// NM_057170 /// NM_139201
4.32	4.47	0.15	5.13E-01	8.07E-01	N4BP2L1	NEDD4 binding protein 2-like 1	chr13q12-q13	214906_x_at	NM_001079691 /// NM_052818
5.13	5.26	0.13	5.13E-01	8.07E-01	HTT	huntingtin	chr4p16.3	202390_s_at	NM_002111
5.76	5.87	0.12	5.13E-01	8.07E-01	USP40	ubiquitin specific peptidase 40	chr2q37.1	225089_at	NM_018218
3.19	3.28	0.09	5.13E-01	8.07E-01	IL16	interleukin 16 (lymphocyte chemoattractant factor)	chr15q26.3	1555016_at	NM_004513 /// NM_172217
3.20	3.40	0.19	5.13E-01	8.07E-01	---	---	---	232659_at	---
9.26	9.42	0.17	5.13E-01	8.07E-01	HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	chr2p23	201007_at	NM_000183
2.32	2.41	0.09	5.14E-01	8.08E-01	---	---	---	1565495_at	---
2.45	2.55	0.10	5.14E-01	8.08E-01	---	---	---	229635_at	---
2.26	2.34	0.08	5.14E-01	8.08E-01	C6orf224	chromosome 6 open reading frame 224	chr6q21	239828_at	NM_173559
2.31	2.39	0.08	5.14E-01	8.08E-01	ZSCAN20	zinc finger and SCAN domain containing 20	chr1p34.3	1552499_a_at	NM_145238
7.57	7.69	0.12	5.14E-01	8.08E-01	HRASLS3	HRAS-like suppressor 3	chr11q12.3-q13.1	209581_at	NM_001128203 /// NM_007069
5.47	5.94	0.47	5.14E-01	8.08E-01	TMEM30A	transmembrane protein 30A	chr6q14.1	232591_s_at	NM_018247
5.70	5.99	0.29	5.14E-01	8.08E-01	LOC729082	Hypothetical protein LOC729082	chr15q15.1	225332_at	XR_040992 /// XR_040993 /// XR_040994
5.12	5.31	0.19	5.14E-01	8.08E-01	CTPS2	CTP synthase II	chrXp22	222819_at	NM_019857 /// NM_175859
6.68	6.84	0.16	5.14E-01	8.08E-01	P76	mannose-6-phosphate protein p76	chr12q24.13	228845_at	NM_173542
5.42	5.56	0.14	5.14E-01	8.08E-01	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	chr6p21	232237_at	NM_153487
3.04	3.17	0.14	5.14E-01	8.08E-01	---	---	---	241867_at	---
2.50	2.63	0.12	5.14E-01	8.08E-01	---	---	---	243870_at	---
2.04	2.15	0.11	5.14E-01	8.08E-01	---	---	---	244645_at	---
6.70	6.79	0.09	5.14E-01	8.08E-01	PDCD5	programmed cell death 5	chr19q12-q13.1	219275_at	NM_004708
2.38	2.47	0.09	5.14E-01	8.08E-01	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	chr10q24.1	1554508_at	NM_152309
3.67	3.75	0.08	5.14E-01	8.08E-01	DTX3	Deltex 3 homolog (Drosophila)	chr12q13.3	222022_at	NM_178502
2.05	2.13	0.08	5.14E-01	8.08E-01	PER4	period 4 pseudogene	chr7p21.3	1566843_at	NR_002790
1.93	2.01	0.07	5.14E-01	8.08E-01	---	---	---	234606_at	---
2.13	2.19	0.07	5.14E-01	8.08E-01	ASB10	ankyrin repeat and SOCS box-containing 10	chr7q36.1	1564536_at	NM_080871
3.20	3.29	0.09	5.14E-01	8.08E-01	DGCR12	DiGeorge syndrome critical region gene 12	chr22q11.21	1566236_at	---
4.67	4.82	0.15	5.14E-01	8.08E-01	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	chr1p31.1-p22.1	203283_s_at	NM_001134492 /// NM_012262
2.16	2.24	0.08	5.15E-01	8.08E-01	SLC26A7	solute carrier family 26, member 7	chr8q23	1552827_s_at	NM_052832 /// NM_134266

2.45	2.72	0.28	5.15E-01	8.08E-01	ANGPT2	angiopoietin 2	chr8p23.1	205572_at	NM_001118887 /// NM_001118888 /// NM_001147
4.91	5.14	0.23	5.15E-01	8.08E-01	DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	chr14q23.1	219179_at	NM_001079520 /// NM_016651
2.13	2.23	0.11	5.15E-01	8.08E-01	FRAS1	Fraser syndrome 1	chr4q21.21	226145_s_at	NM_025074
11.48	11.58	0.11	5.15E-01	8.08E-01	CFL1	cofilin 1 (non-muscle)	chr11q13	200021_at	NM_005507
7.13	7.52	0.40	5.15E-01	8.08E-01	CFD	complement factor D (adipsin)	chr19p13.3	205382_s_at	NM_001928
2.52	2.64	0.12	5.15E-01	8.08E-01	MED14	mediator complex subunit 14	chrXp11.4-p11.2	217120_s_at	NM_004229
2.52	2.63	0.11	5.15E-01	8.08E-01	DLX5	distal-less homeobox 5	chr7q22	213707_s_at	NM_005221
2.62	2.70	0.08	5.15E-01	8.08E-01	WTAP	Wilms tumor 1 associated protein	chr6q25-q27	214759_at	NM_004906 /// NM_152857 /// NM_152858
2.64	2.79	0.16	5.15E-01	8.08E-01	DSPP	dentin sialophosphoprotein	chr4q21.3	221681_s_at	NM_014208
1.98	2.05	0.07	5.15E-01	8.08E-01	LOC133874	hypothetical gene LOC133874	chr5q35.1	237956_s_at	NM_001102609
4.82	5.16	0.34	5.15E-01	8.08E-01	KPNA1	karyopherin alpha 1 (importin alpha 5)	chr3q21	202058_s_at	NM_002264
2.29	2.39	0.10	5.15E-01	8.08E-01	---	---	---	216214_at	---
2.15	2.24	0.09	5.15E-01	8.08E-01	NADSYN1	NAD synthetase 1	chr11q13.4	1565906_at	NM_018161
2.37	2.47	0.10	5.15E-01	8.08E-01	ZNF792	zinc finger protein 792	chr19q13.11	235052_at	NM_175872
1.90	1.97	0.07	5.15E-01	8.09E-01	---	---	---	1570469_at	---
3.02	3.23	0.21	5.15E-01	8.09E-01	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	chr1p12	202234_s_at	NM_003051
2.90	3.02	0.13	5.15E-01	8.09E-01	---	---	---	232525_at	---
2.26	2.36	0.11	5.15E-01	8.09E-01	OR8G2	olfactory receptor, family 8, subfamily G, member 2	chr11q24.2	1567056_at	NM_001007249
2.02	2.09	0.08	5.15E-01	8.09E-01	---	---	---	220878_at	---
2.64	2.70	0.07	5.15E-01	8.09E-01	C6orf163	chromosome 6 open reading frame 163	chr6q15	242446_at	XM_001720089 /// XM_001720635 /// XM_001725542
4.04	4.12	0.08	5.16E-01	8.09E-01	LOC100129514	hypothetical protein LOC100129514	chr7q34	231143_at	XM_001716072 /// XM_001723883 /// XM_001724518
2.24	2.35	0.11	5.16E-01	8.09E-01	---	---	---	1555727_at	---
1.86	1.93	0.07	5.16E-01	8.09E-01	INADL	InaD-like (Drosophila)	chr1p31.3	214705_at	NM_176877
6.18	6.47	0.29	5.16E-01	8.09E-01	FBXO8	F-box protein 8	chr4q34.1	1554806_a_at	NM_012180
3.75	3.95	0.20	5.16E-01	8.09E-01	EML1	echinoderm microtubule associated protein like 1	chr14q32	204797_s_at	NM_001008707 /// NM_004434
4.15	4.32	0.17	5.16E-01	8.09E-01	THEX1	three prime histone mRNA exonuclease 1	chr8p23.1	226416_at	NM_153332
5.09	5.26	0.16	5.16E-01	8.09E-01	FLJ37078	hypothetical protein FLJ37078	chr7q11.23	235880_at	NM_001110199 /// XM_001713635 /// XM_001713636 /// XM_001713637 /// XM_001713638
3.70	3.85	0.16	5.16E-01	8.09E-01	LOC100144597	hypothetical transcript	---	1557892_at	---
2.95	3.06	0.12	5.16E-01	8.09E-01	FGF3	fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog)	chr11q13	214571_at	NM_005247
3.97	4.08	0.10	5.16E-01	8.09E-01	---	---	---	215662_at	---
4.44	4.54	0.10	5.16E-01	8.09E-01	---	---	---	220743_at	---
3.50	3.69	0.19	5.16E-01	8.09E-01	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	chr20p13	219090_at	NM_020689
4.03	4.20	0.17	5.16E-01	8.09E-01	C4orf10	chromosome 4 open reading frame 10	chr4p16.3	215141_at	NR_015453
2.24	2.33	0.10	5.16E-01	8.09E-01	---	---	---	1556021_at	---
2.20	2.28	0.09	5.16E-01	8.09E-01	BET3L	BET3 like (S. cerevisiae)	chr6q22.31	232368_at	XM_001723259 /// XM_001725041 /// XM_001726393
7.09	7.23	0.14	5.16E-01	8.09E-01	CACYBP	calcyclin binding protein	chr1q24-q25	201381_x_at	NM_001007214 /// NM_014412
2.23	2.33	0.10	5.16E-01	8.09E-01	CLMN	calmin (calponin-like, transmembrane)	chr14q32.13	225759_x_at	NM_024734

4.94	5.10	0.15	5.16E-01	8.09E-01	MAPK9	mitogen-activated protein kinase 9	chr5q35	210570_x_at	NM_002752 /// NM_139068 /// NM_139069 /// NM_139070																				
7.05	7.17	0.12	5.16E-01	8.09E-01	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	chr22q13	224319_s_at	NM_019008																				
3.51	3.65	0.14	5.16E-01	8.09E-01	LOC100134937	hypothetical LOC100134937	---	229685_at	---																				
2.38	2.45	0.07	5.16E-01	8.09E-01	NSMCE4A	Non-SMC element 4 homolog A (S. cerevisiae)	chr10q26.13	227387_at	NM_017615																				
9.56	9.90	0.34	5.16E-01	8.09E-01	AOX1	aldehyde oxidase 1	chr2q33	205083_at	NM_001159																				
6.41	6.68	0.27	5.17E-01	8.09E-01	RCHY1	ring finger and CHY zinc finger domain containing 1	chr4q21.1	212749_s_at	NM_001008925 /// NM_001009922 /// NM_015436																				
6.32	6.59	0.27	5.16E-01	8.09E-01	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	chr2q14.1	208897_s_at	NM_006773																				
3.81	3.96	0.15	5.16E-01	8.09E-01	---	---	---	233244_at	---																				
2.61	2.75	0.14	5.17E-01	8.09E-01	DPH5	DPH5 homolog (S. cerevisiae)	chr1p21.2	222360_at	NM_001077394 /// NM_001077395 /// NM_015958																				
1.97	2.08	0.11	5.16E-01	8.09E-01	---	---	---	1570194_x_at	---																				
3.56	3.66	0.10	5.17E-01	8.09E-01	GFRA3	GDNF family receptor alpha 3	chr5q31.1-q31.3	214479_at	NM_001496																				
2.99	3.09	0.09	5.17E-01	8.09E-01	---	---	---	1560095_s_at	---																				
2.01	2.10	0.09	5.16E-01	8.09E-01	NAT12	N-acetyltransferase 12	chr14q23.1	228321_s_at	NM_001011713																				
2.87	2.96	0.09	5.17E-01	8.09E-01	---	---	---	1557538_at	---																				
2.33	2.41	0.08	5.16E-01	8.09E-01	---	---	---	1563027_at	---																				
2.02	2.10	0.08	5.16E-01	8.09E-01	---	---	---	222964_at	---																				
1.78	1.85	0.07	5.16E-01	8.09E-01	---	---	---	1562992_at	---																				
4.56	4.71	0.15	5.17E-01	8.09E-01	CERCAM	cerebral endothelial cell adhesion molecule	chr9q34.11	224794_s_at	NM_016174																				
2.76	2.86	0.10	5.17E-01	8.09E-01	TRIM3	tripartite motif-containing 3	chr11p15.5	204910_s_at	NM_006458 /// NM_033278																				
2.25	2.36	0.11	5.17E-01	8.09E-01	---	---	---	1559723_s_at	---																				
2.14	2.22	0.08	5.17E-01	8.09E-01	---	---	---	1566517_at	---																				
3.40	3.57	0.18	5.17E-01	8.09E-01	TNNI1	troponin I type 1 (skeletal, slow)	chr1q31.3	205177_at	NM_003281																				
3.47	3.60	0.13	5.17E-01	8.09E-01	EFR3B	EFR3 homolog B (S. cerevisiae)	chr2p23.3	215328_at	NM_014971 /// XM_001717587 /// XM_039733 /// XM_940464																				
2.78	2.90	0.13	5.17E-01	8.09E-01	LOC257396	hypothetical protein LOC257396	chr5q11.2	236076_at	XM_001715389 /// XM_001715402 /// XM_001715431 /// XM_001715443 /// XM_001721313 /// XM_001721316																				
2.48	2.60	0.12	5.17E-01	8.09E-01	AHI1	Abelson helper integration site 1	chr6q23.3	220842_at	NM_017651																				
3.49	3.57	0.08	5.17E-01	8.09E-01	---	---	---	243493_at	---																				
1.75	1.83	0.08	5.17E-01	8.09E-01	GYPA	glycophorin A (MNS blood group)	chr4q28.2-q31.1	205837_s_at	NM_002099																				
3.43	3.55	0.12	5.17E-01	8.09E-01	LOC646870	hypothetical protein LOC646870	chr1q25.1	229364_at	XR_040282 /// XR_040283 /// XR_042128																				
2.12	2.19	0.07	5.17E-01	8.09E-01	HEXDC	Hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	chr17q25.3	238033_at	NM_173620																				
2.31	2.40	0.09	5.17E-01	8.09E-01	SERPINE2	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	chr2q33-q35	227487_s_at	NM_006216																				
3.01	3.13	0.13	5.17E-01	8.09E-01	---	---	---	215217_at	---																				
5.07	5.19	0.12	5.17E-01	8.09E-01	GDF5	growth differentiation factor 5	chr20q11.2	206614_at	NM_000557																				
4.53	4.68	0.14	5.17E-01	8.09E-01	ARHGAP25	Rho GTPase activating protein 25	chr2p14	204882_at	NM_001007231 /// NM_014882																				
5.01	5.40	0.39	5.18E-01	8.09E-01	SNX13	sorting nexin 13	chr7p21.1	213292_s_at	NM_015132																				
3.99	4.26	0.27	5.18E-01	8.09E-01	---	---	---	1554771_at	---																				
3.73	3.95	0.22	5.18E-01	8.09E-01	PTEN	phosphatase and tensin homolog	chr10q23.3	204054_at	NM_000314																				
3.54	3.71	0.17	5.18E-01	8.09E-01	ARL4C	ADP-ribosylation factor-like 4C	chr2q37.1	202206_at	NM_005737																				
6.86	7.02	0.16	5.17E-01	8.09E-01	HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	chr19q13.33	219113_x_at	NM_016246																				

3.66	3.79	0.13	5.18E-01	8.09E-01	DGKA	diacylglycerol kinase, alpha 80kDa	chr12q13.3	211272_s_at	NM_001345 /// NM_201444 /// NM_201445 /// NM_201554
3.35	3.47	0.12	5.18E-01	8.09E-01	SH2D2A	SH2 domain protein 2A	chr1q21	207351_s_at	NM_003975
3.01	3.12	0.11	5.17E-01	8.09E-01	CAMK1D	calcium/calmodulin-dependent protein kinase ID	chr10p13	220246_at	NM_020397 /// NM_153498
2.24	2.35	0.11	5.17E-01	8.09E-01	DMGDH	dimethylglycine dehydrogenase	chr5q14.1	231790_at	NM_013391
2.64	2.74	0.10	5.18E-01	8.09E-01	KRT23	keratin 23 (histone deacetylase inducible)	chr17q21.2	218963_s_at	NM_015515
3.27	3.37	0.10	5.18E-01	8.09E-01	RBM7	RNA binding motif protein 7	chr11q23.1-q23.2	235045_at	NM_016090
3.94	4.03	0.10	5.18E-01	8.09E-01	---	---	---	215595_x_at	---
2.08	2.15	0.07	5.18E-01	8.09E-01	LOC401022	hypothetical LOC401022	chr2q31.2	239182_at	---
1.99	2.06	0.07	5.17E-01	8.09E-01	KCNJ15 /// LOC100131955	potassium inwardly-rectifying channel, subfamily J, member 15 /// similar to potassium inwardly-rectifying channel, subfamily J, member 15	chr21q22.13-q22.2 /// chr21q22.2	238428_at	NM_002243 /// NM_170736 /// NM_170737 /// XM_001713900 /// XM_001715532 /// XM_001718954
2.63	2.72	0.09	5.18E-01	8.09E-01	---	---	---	237279_at	---
7.51	7.73	0.22	5.18E-01	8.09E-01	C2orf30	chromosome 2 open reading frame 30	chr2p16.2	224630_at	NM_001127397 /// NM_001127398 /// NM_015701
3.01	3.13	0.13	5.18E-01	8.09E-01	TSGA13	testis specific, 13	chr7q32	1553641_a_at	NM_052933
3.74	3.85	0.11	5.18E-01	8.09E-01	HRNBP3 /// LOC100130312 /// LOC100133332	hexaribonucleotide binding protein 3 /// hypothetical protein LOC100130312 /// hypothetical protein LOC100133332	chr17q25.3	240975_x_at	NM_001082575 /// XM_001713646 /// XM_001713647
2.52	2.60	0.09	5.18E-01	8.09E-01	LOC652637 /// WHDC1 /// WHDC1L1 /// WHDC1L2	similar to junction-mediating and regulatory protein /// WAS protein homology region 2 domain containing 1 /// WAS protein homology region 2 domain containing 1-like 1 /// WAS protein homology region 2 domain containing 1-like 2	chr15q11.2 /// chr15q13.1 /// chr15q25.2	222367_at	NM_001080435 /// NR_003521 /// XM_926785 /// XM_942188 /// XR_042166
2.56	2.65	0.08	5.18E-01	8.09E-01	CENPA	centromere protein A	chr2p24-p21	204962_s_at	NM_001042426 /// NM_001809
3.53	3.80	0.26	5.18E-01	8.10E-01	LOX	lysyl oxidase	chr5q23.2	215446_s_at	NM_002317
6.16	6.33	0.16	5.18E-01	8.10E-01	CLIP1	CAP-GLY domain containing linker protein 1	chr12q24.3	201975_at	NM_002956 /// NM_198240
2.48	2.57	0.09	5.18E-01	8.10E-01	BRD7	Bromodomain containing 7	chr16q12	238545_at	NM_013263
3.37	3.49	0.13	5.18E-01	8.10E-01	SNAP23	Synaptosomal-associated protein, 23kDa	chr15q15.1	229773_at	NM_003825 /// NM_130798
2.30	2.39	0.09	5.18E-01	8.10E-01	CXorf22	chromosome X open reading frame 22	chrXp21.1	1553905_at	NM_152632
4.04	4.14	0.10	5.18E-01	8.10E-01	---	---	---	244054_at	---
2.47	2.57	0.10	5.18E-01	8.10E-01	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	chr10q24	206155_at	NM_000392
2.67	2.76	0.09	5.18E-01	8.10E-01	---	---	---	232405_at	---
3.71	3.98	0.27	5.18E-01	8.10E-01	---	---	---	243176_at	---
4.85	4.96	0.11	5.18E-01	8.10E-01	C16orf59	chromosome 16 open reading frame 59	chr16p13.3	219556_at	NM_025108
6.73	6.97	0.24	5.18E-01	8.10E-01	GOLGA5	golgi autoantigen, golgin subfamily a, 5	chr14q32.12-q32.13	218241_at	NM_005113
1.98	2.04	0.07	5.18E-01	8.10E-01	C20orf26	chromosome 20 open reading frame 26	chr20p11.23	240453_at	NM_015585
2.04	2.11	0.07	5.18E-01	8.10E-01	LOC100130104	PNAS-17	chr11p13	224295_at	XM_001722524 /// XM_001723899 /// XM_001724101
7.59	7.78	0.18	5.18E-01	8.10E-01	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	chr2q23.3	218053_at	NM_017892
1.96	2.05	0.09	5.18E-01	8.10E-01	---	---	---	1559655_at	---
6.55	6.80	0.25	5.18E-01	8.10E-01	TLN1	talin 1	chr9p13	203254_s_at	NM_006289
5.55	5.69	0.14	5.18E-01	8.10E-01	PCDH1	protocadherin 1	chr5q32-q33	203918_at	NM_002587 /// NM_032420
1.98	2.08	0.10	5.18E-01	8.10E-01	---	---	---	207588_at	---
2.19	2.26	0.07	5.18E-01	8.10E-01	---	---	---	1565700_at	---
1.87	1.94	0.07	5.18E-01	8.10E-01	---	---	---	1567386_at	---
2.95	3.09	0.14	5.18E-01	8.10E-01	CCNK	cyclin K	chr14q32	219273_at	NM_001099402 /// NM_003858
2.43	2.56	0.13	5.18E-01	8.10E-01	---	---	---	235736_at	---

3.44	3.66	0.22	5.18E-01	8.10E-01	ORC4L	origin recognition complex, subunit 4-like (yeast)	chr2q22-q23	203352_at	NM_002552 /// NM_181741 /// NM_181742																				
3.55	3.66	0.11	5.19E-01	8.10E-01	SPATA8	spermatogenesis associated 8	chr15q26.2	231006_at	NM_173499																				
6.36	6.55	0.19	5.19E-01	8.10E-01	C6orf225	chromosome 6 open reading frame 225	chr6q21	225812_at	NM_001033564																				
4.78	4.93	0.15	5.19E-01	8.10E-01	SCRN2	secernin 2	chr17q21.32	225513_at	NM_138355																				
7.99	8.13	0.14	5.19E-01	8.10E-01	CARHSP1	calcium regulated heat stable protein 1, 24kDa	chr16p13.2	218384_at	NM_001042476 /// NM_014316																				
3.98	4.09	0.11	5.19E-01	8.10E-01	ELMO3	engulfment and cell motility 3	chr16q22.1	219411_at	NM_024712																				
2.15	2.24	0.08	5.19E-01	8.10E-01	DKFZP564C196	DKFZP564C196 protein	chr1q25.3	222384_at	XM_001134212 /// XM_001134393																				
2.24	2.32	0.08	5.19E-01	8.10E-01	C8orf79	chromosome 8 open reading frame 79	chr8p22	1558541_at	NM_001099677 /// NM_020844																				
2.19	2.30	0.11	5.19E-01	8.10E-01	LOC727818	similar to PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	chr2p25.3	1561169_at	XR_041979																				
3.53	3.65	0.13	5.19E-01	8.10E-01	---	---	---	222198_at	---																				
5.30	5.49	0.20	5.19E-01	8.10E-01	ELP4	elongation protein 4 homolog (S. cerevisiae)	chr11p13	203829_at	NM_019040																				
2.85	2.94	0.09	5.19E-01	8.10E-01	KRT75	keratin 75	chr12q13	207065_at	NM_004693																				
2.38	2.47	0.09	5.19E-01	8.10E-01	LOC340602	similar to CG32656-PA	chrXp11.22	1555396_s_at	NM_203407																				
2.51	2.62	0.11	5.19E-01	8.10E-01	LCE1B	late cornified envelope 1B	chr1q21.3	1560531_at	NM_178349																				
2.54	2.63	0.09	5.19E-01	8.10E-01	DCST2	DC-STAMP domain containing 2	chr1q21.3	242988_at	NM_144622																				
2.29	2.36	0.07	5.19E-01	8.10E-01	SMYD1	SET and MYND domain containing 1	chr2p11.2	228406_at	NM_198274																				
4.05	4.21	0.15	5.19E-01	8.10E-01	AZI2	5-azacytidine induced 2	chr3p24.1	227905_s_at	NM_001134432 /// NM_001134433 /// NM_022461																				
2.09	2.18	0.10	5.19E-01	8.10E-01	NMNAT2	nicotinamide nucleotide adenylyltransferase 2	chr1q25	1556029_s_at	NM_015039 /// NM_170706																				
2.90	2.99	0.09	5.19E-01	8.10E-01	---	---	---	244529_at	---																				
2.31	2.39	0.09	5.19E-01	8.10E-01	SYCE1	synaptonemal complex central element protein 1	chr10q26.3	1554675_a_at	NM_130784 /// NM_201564																				
2.79	2.91	0.12	5.20E-01	8.11E-01	LRRC68	leucine rich repeat containing 68	chr19q13.32	213781_at	XM_001722969 /// XM_001723010 /// XM_001724714																				
2.91	3.02	0.11	5.20E-01	8.11E-01	CCNJ	cyclin J	chr10pter-q26.12	222888_at	NM_001134375 /// NM_001134376 /// NM_019084																				
2.29	2.38	0.09	5.20E-01	8.11E-01	ZNF474	zinc finger protein 474	chr5q23.1-q23.2	1556907_at	NM_207317																				
2.20	2.28	0.08	5.20E-01	8.11E-01	MOG	myelin oligodendrocyte glycoprotein	chr6p22.1	214650_x_at	NM_001008228 /// NM_001008229 /// NM_002433 /// NM_206809 /// NM_206810 /// NM_206811 /// NM_206812 /// NM_206813 /// NM_206814																				
1.89	1.97	0.08	5.20E-01	8.11E-01	---	---	---	1562301_at	---																				
5.42	5.58	0.15	5.20E-01	8.11E-01	PLEC1	plectin 1, intermediate filament binding protein 500kDa	chr8q24	216971_s_at	NM_000445 /// NM_201378 /// NM_201379 /// NM_201380 /// NM_201381 /// NM_201382 /// NM_201383 /// NM_201384																				
2.02	2.11	0.08	5.20E-01	8.11E-01	---	---	---	214645_at	---																				
2.64	2.77	0.13	5.20E-01	8.11E-01	DNAJC30	DnaJ (Hsp40) homolog, subfamily C, member 30	chr7q11.23	239194_at	NM_032317																				
4.52	4.63	0.10	5.20E-01	8.11E-01	MYH14	myosin, heavy chain 14	chr19q13.33	219946_x_at	NM_001077186 /// NM_024729																				
1.93	2.01	0.08	5.20E-01	8.11E-01	LOC285026	hypothetical protein LOC285026	chr2q31.2	1563456_at	---																				

5.98	6.16	0.19	5.20E-01	8.11E-01	ATRN	attractin	chr20p13	212517_at	NM_139321 /// NM_139322																					
4.05	4.17	0.13	5.20E-01	8.11E-01	LOC390940	similar to R28379_1	chr19q13.31	213556_at	XM_001129773 /// XM_001131816 /// XM_001724340																					
1.94	2.01	0.07	5.20E-01	8.11E-01	---	---	---	234602_x_at	---																					
4.71	4.99	0.28	5.20E-01	8.11E-01	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	chr14q23.1	227653_at	NM_020810																					
4.62	4.75	0.13	5.20E-01	8.11E-01	AP1GBP1	AP1 gamma subunit binding protein 1	chr17q12	232981_s_at	NM_007247 /// NM_080550																					
2.51	2.60	0.09	5.20E-01	8.11E-01	UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	chr11q13	207349_s_at	NM_003356 /// NM_022803																					
5.41	5.65	0.24	5.20E-01	8.11E-01	RP1-21O18.1	kazrin	chr1p36.21	215138_s_at	NM_001017999 /// NM_001018000 /// NM_001018001 /// NM_015209 /// NM_201628																					
5.37	5.59	0.23	5.20E-01	8.11E-01	SLC25A46	Solute carrier family 25, member 46	chr5q22.1	226831_at	NM_138773																					
6.64	6.81	0.18	5.20E-01	8.11E-01	ANXA4	annexin A4	chr2p13	201301_s_at	NM_001153																					
3.03	3.14	0.12	5.20E-01	8.11E-01	STXBP4	syntaxin binding protein 4	chr17q22	244404_at	NM_178509																					
2.34	2.45	0.11	5.20E-01	8.11E-01	FAM44C	family with sequence similarity 44, member C	chr18q21.31	231368_at	---																					
5.88	6.01	0.13	5.20E-01	8.11E-01	PRRC1	proline-rich coiled-coil 1	chr5q23.2	221734_at	NM_130809																					
3.79	3.94	0.15	5.20E-01	8.11E-01	OTOP2	otopetrin 2	chr17q25.1	234271_at	NM_178160																					
3.52	3.64	0.12	5.20E-01	8.11E-01	---	---	---	230118_at	---																					
6.62	7.81	1.20	5.21E-01	8.11E-01	IGH@ /// IGHG1 /// IGHG2 /// IGHM /// IGHV4-31	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31	chr14q32.33	211430_s_at	---																					
3.65	3.82	0.17	5.21E-01	8.11E-01	---	---	---	239716_at	---																					
4.29	4.44	0.15	5.21E-01	8.11E-01	FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	chr8p12	235472_at	NM_032664																					
1.96	2.05	0.09	5.21E-01	8.11E-01	---	---	---	1561577_at	---																					
7.34	7.53	0.19	5.21E-01	8.11E-01	WRB	tryptophan rich basic protein	chr21q22.3	202749_at	NM_004627																					
2.27	2.35	0.08	5.21E-01	8.11E-01	---	---	---	1559925_s_at	---																					
1.81	1.89	0.07	5.21E-01	8.11E-01	---	---	---	217132_at	---																					
3.21	3.31	0.10	5.21E-01	8.11E-01	FCRL2	Fc receptor-like 2	chr1q21	224193_s_at	NM_030764 /// NM_138738																					
2.06	2.14	0.08	5.21E-01	8.11E-01	---	---	---	234765_at	---																					
3.05	3.16	0.11	5.21E-01	8.11E-01	---	---	---	1556078_at	---																					
2.54	2.62	0.09	5.21E-01	8.11E-01	KLHL11	kelch-like 11 (Drosophila)	chr17q21.2	220657_at	NM_018143																					
2.85	2.96	0.11	5.21E-01	8.11E-01	BCLAF1	BCL2-associated transcription factor 1	chr6q22-q23	239897_at	NM_001077440 /// NM_001077441 /// NM_014739																					
7.23	7.39	0.16	5.21E-01	8.11E-01	PDK2	pyruvate dehydrogenase kinase, isozyme 2	chr17q21.33	202590_s_at	NM_002611																					
3.74	3.86	0.12	5.21E-01	8.11E-01	EDN2	endothelin 2	chr1p34	206758_at	NM_001956																					
2.37	2.44	0.08	5.21E-01	8.11E-01	GHRHR	growth hormone releasing hormone receptor	chr7p14	211544_s_at	NM_000823 /// NM_001009824																					
3.86	3.97	0.11	5.21E-01	8.12E-01	HR	hairless homolog (mouse)	chr8p21.2	220163_s_at	NM_005144 /// NM_018411																					
2.49	2.60	0.10	5.21E-01	8.12E-01	KRT77	keratin 77	chr12q13.13	237120_at	NM_175078																					
4.79	5.05	0.26	5.22E-01	8.12E-01	PTCD3	Pentatricopeptide repeat domain 3	chr2p11.2	228590_at	NM_017952																					
2.59	2.77	0.18	5.21E-01	8.12E-01	PLA1A	phospholipase A1 member A	chr3q13.13-q13.2	219584_at	NM_015900																					
3.77	3.86	0.10	5.21E-01	8.12E-01	COL17A1	collagen, type XVII, alpha 1	chr10q24.3	204636_at	NM_000494																					
2.15	2.24	0.09	5.22E-01	8.12E-01	NFKBIZ	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	chr3p12-q12	1556153_s_at	NM_001005474 /// NM_031419																					
2.25	2.32	0.07	5.21E-01	8.12E-01	PDE4DIP	phosphodiesterase 4D interacting protein	chr1q12	215575_at	NM_001002810 /// NM_001002811 /// NM_001002812 /// NM_014644 /// NM_022359																					

4.41	4.61	0.19	5.22E-01	8.12E-01	CASP8	caspase 8, apoptosis-related cysteine peptidase	chr2q33-q34	207686_s_at	NM_001080124 /// NM_001080125 /// NM_001228 /// NM_033355 /// NM_033356 /// NM_033358																					
2.14	2.23	0.08	5.22E-01	8.12E-01	---	---	---	232429_at	---																					
3.28	3.43	0.15	5.22E-01	8.12E-01	MAGIX	MAGI family member, X-linked	chrXp11.23	1565559_at	NM_001099680 /// NM_001099681 /// NM_001099682 /// NM_024859																					
2.83	2.96	0.13	5.22E-01	8.12E-01	SH2D3C	SH2 domain containing 3C	chr9q34.11	215639_at	NM_005489 /// NM_170600																					
2.28	2.36	0.08	5.22E-01	8.12E-01	CDRT1	CMT1A duplicated region transcript 1	chr17p12	215999_at	NM_006382																					
5.28	5.50	0.21	5.22E-01	8.12E-01	---	---	---	243030_at	---																					
7.25	7.55	0.31	5.22E-01	8.12E-01	TMEM126B	transmembrane protein 126B	chr11q14.1	221622_s_at	NM_018480																					
5.21	5.45	0.23	5.22E-01	8.12E-01	MEF2C	myocyte enhancer factor 2C	chr5q14	207968_s_at	NM_001131005 /// NM_002397																					
7.14	7.36	0.22	5.22E-01	8.12E-01	TRIM16	tripartite motif-containing 16	chr17p11.2	204341_at	NM_006470																					
2.49	2.60	0.12	5.22E-01	8.12E-01	---	---	---	1563008_at	---																					
4.30	4.40	0.10	5.22E-01	8.12E-01	RPS6KA4	Ribosomal protein S6 kinase, 90kDa, polypeptide 4	chr11q11-q13	230544_at	NM_001006944 /// NM_003942																					
2.71	2.79	0.08	5.22E-01	8.12E-01	ADH6	alcohol dehydrogenase 6 (class V)	chr4q23	214261_s_at	NM_000672 /// NM_001102470																					
3.38	3.53	0.15	5.22E-01	8.12E-01	---	---	---	231107_at	---																					
3.89	4.03	0.14	5.22E-01	8.12E-01	SSBP3	single stranded DNA binding protein 3	chr1p32.3	223635_s_at	NM_001009955 /// NM_018070 /// NM_145716																					
3.15	3.25	0.10	5.22E-01	8.12E-01	ZXDC	ZXD family zinc finger C	chr3q21.2	230106_at	NM_001040653 /// NM_025112																					
2.14	2.23	0.10	5.22E-01	8.12E-01	---	---	---	244213_at	---																					
3.27	3.36	0.09	5.22E-01	8.12E-01	---	---	---	240910_at	---																					
3.81	3.94	0.12	5.22E-01	8.12E-01	RAB15	RAB15, member RAS onocogene family	chr14q23.3	221810_at	NM_198686																					
2.36	2.45	0.09	5.22E-01	8.12E-01	KIAA1333	KIAA1333	chr14q12	223257_at	NM_017769																					
2.49	2.58	0.09	5.22E-01	8.12E-01	---	---	---	234887_at	---																					
2.42	2.51	0.09	5.22E-01	8.12E-01	---	---	---	243525_at	---																					
5.36	5.60	0.24	5.22E-01	8.12E-01	PTPRB	protein tyrosine phosphatase, receptor type, B	chr12q15-q21	230250_at	NM_001109754 /// NM_002837																					
2.86	2.96	0.10	5.22E-01	8.12E-01	UBASH3A	ubiquitin associated and SH3 domain containing, A	chr21q22.3	220418_at	NM_001001895 /// NM_018961																					
5.66	5.90	0.23	5.23E-01	8.12E-01	RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	chr2p11.2	212482_at	NM_022780																					
3.35	3.45	0.10	5.23E-01	8.12E-01	GPR78	G protein-coupled receptor 78	chr4p16.1	1553063_at	NM_080819																					
2.48	2.57	0.09	5.23E-01	8.12E-01	NRAP	nebulin-related anchoring protein	chr10q24-q26	235313_at	NM_006175 /// NM_198060																					
2.49	2.58	0.09	5.23E-01	8.12E-01	---	---	---	239906_at	---																					
2.58	2.67	0.08	5.23E-01	8.12E-01	LOC401321	hypothetical LOC401321	chr7p14.3	1560371_at	XM_001723040 /// XM_379483 /// XM_380099 /// XM_939915																					
3.79	4.08	0.29	5.23E-01	8.12E-01	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	chr18p11.32	212577_at	NM_015295																					
2.34	2.50	0.17	5.23E-01	8.12E-01	RPAP3	RNA polymerase II associated protein 3	chr12q13.11	1557984_s_at	NM_024604																					
4.56	4.69	0.13	5.23E-01	8.12E-01	---	---	---	231516_at	---																					
4.77	4.89	0.13	5.23E-01	8.12E-01	CENTB1	Centaurin, beta 1	chr17p13.1	242081_at	NM_014716																					
3.17	3.29	0.12	5.23E-01	8.12E-01	COL9A1	collagen, type IX, alpha 1	chr6q12-q14	222008_at	NM_001851 /// NM_078485																					
2.79	2.89	0.11	5.23E-01	8.12E-01	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	chr8q13	219810_at	NM_025054																					
2.24	2.34	0.10	5.23E-01	8.12E-01	---	---	---	1558963_at	---																					
2.18	2.26	0.09	5.23E-01	8.12E-01	---	---	---	236466_at	---																					

2.15	2.22	0.07	5.23E-01	8.12E-01	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	chr1p33	207407_x_at	NM_000778
3.32	3.45	0.13	5.23E-01	8.12E-01	LOC283403	hypothetical protein LOC283403	chr12q13.13	1560277_a_at	---
3.58	3.68	0.10	5.23E-01	8.12E-01	LOC285191	hypothetical protein LOC285191	chr2q37.3	1562632_at	XM_001128475
1.88	1.96	0.08	5.23E-01	8.12E-01	LOC339260	Hypothetical gene supported by BC072410	chr17p11.2	1564359_a_at	---
2.12	2.19	0.07	5.23E-01	8.12E-01	---	---	---	217401_at	---
5.38	5.60	0.21	5.23E-01	8.12E-01	PPARA	peroxisome proliferator-activated receptor alpha	chr22q12-q13.1|22q13.31	226978_at	NM_001001928 /// NM_005036
3.93	4.06	0.13	5.23E-01	8.12E-01	KCNH3	potassium voltage-gated channel, subfamily H (eag-related), member 3	chr12q13	223726_at	NM_012284
2.74	2.87	0.12	5.23E-01	8.12E-01	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	chr4q25-q27	222859_s_at	NM_014395
5.46	5.58	0.12	5.23E-01	8.12E-01	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	chr1p36.12	201936_s_at	NM_003760
4.61	4.74	0.13	5.23E-01	8.12E-01	SPATS2	spermatogenesis associated, serine-rich 2	chr12q13.12	218324_s_at	NM_023071
2.83	2.92	0.09	5.23E-01	8.12E-01	---	---	---	1569597_at	---
5.15	5.40	0.25	5.23E-01	8.13E-01	EXOSC9	exosome component 9	chr4q27	205061_s_at	NM_001034194 /// NM_005033
2.44	2.58	0.14	5.24E-01	8.13E-01	PCDH9	protocadherin 9	chr13q14.3-q21.1	219738_s_at	NM_020403 /// NM_203487
2.38	2.49	0.10	5.23E-01	8.13E-01	---	---	---	215650_at	---
2.98	3.08	0.10	5.23E-01	8.13E-01	CATSPER1	cation channel, sperm associated 1	chr11q12.1	1552335_at	NM_053054
2.54	2.63	0.09	5.23E-01	8.13E-01	DLX6	distal-less homeobox 6	chr7q22	221289_at	NM_005222
2.84	2.92	0.08	5.23E-01	8.13E-01	---	---	---	1560901_at	---
2.28	2.43	0.14	5.24E-01	8.13E-01	---	---	---	236312_at	---
3.69	3.80	0.11	5.24E-01	8.13E-01	HIST1H2BH	histone cluster 1, H2bh	chr6p21.3	208546_x_at	NM_003524
1.93	2.00	0.07	5.24E-01	8.13E-01	LOC100127998 /// SNTG1	hypothetical protein LOC100127998 /// syntrophin, gamma 1	chr8q11-q12 /// chr8q11.22	220405_at	NM_018967 /// XM_001714550 /// XM_001714644 /// XM_001714676
3.50	3.66	0.15	5.24E-01	8.13E-01	TRDMT1	tRNA aspartic acid methyltransferase 1	chr10p15.1	206308_at	NM_004412 /// NM_176081 /// NM_176083
3.08	3.22	0.14	5.24E-01	8.13E-01	LOC440836	similar to MGC52679 protein	chr22q13.33	238327_at	NM_001014440
2.37	2.50	0.13	5.24E-01	8.13E-01	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	chr4p14	1568713_a_at	NM_015173
2.57	2.69	0.12	5.24E-01	8.13E-01	---	---	---	240782_at	---
4.55	4.67	0.12	5.24E-01	8.13E-01	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	chr20q13.3	211486_s_at	NM_004518 /// NM_172106 /// NM_172107 /// NM_172108 /// NM_172109
4.33	4.48	0.16	5.24E-01	8.13E-01	PANK1	pantothenate kinase 1	chr10q23.31	226649_at	NM_138316 /// NM_148977 /// NM_148978
3.91	4.04	0.13	5.24E-01	8.13E-01	CNNM4	cyclin M4	chr2p12-p11.2	218900_at	NM_020184
2.72	2.83	0.11	5.24E-01	8.13E-01	---	---	---	240795_at	---
3.56	3.65	0.08	5.24E-01	8.13E-01	FLJ41649	Hypothetical LOC401260	chr6p21.2	1562219_at	XR_040731 /// XR_040732 /// XR_040733
2.22	2.35	0.14	5.24E-01	8.13E-01	POLQ	polymerase (DNA directed), theta	chr3q13.33	207746_at	NM_199420
4.13	4.24	0.11	5.24E-01	8.13E-01	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	chr3p22-p21	206246_at	NM_004567
5.72	5.98	0.26	5.24E-01	8.13E-01	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	chr7p13	201316_at	NM_002787
2.37	2.48	0.10	5.24E-01	8.13E-01	LARP5	La ribonucleoprotein domain family, member 5	chr10p15.3	214215_s_at	NM_015155
2.01	2.10	0.09	5.24E-01	8.13E-01	---	---	---	1563039_at	---
5.33	5.55	0.22	5.24E-01	8.13E-01	C11orf57	chromosome 11 open reading frame 57	chr11q23.1	218314_s_at	NM_001082969 /// NM_001082970 /// NM_018195
4.85	5.01	0.15	5.24E-01	8.13E-01	ZNF224	zinc finger protein 224	chr19q13.2	216983_s_at	NM_013398
5.29	5.41	0.13	5.24E-01	8.13E-01	ETV4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	chr17q21	211603_s_at	NM_001079675 /// NM_001986
2.23	2.34	0.10	5.24E-01	8.13E-01	TM7SF4	transmembrane 7 superfamily member 4	chr8q23	221266_s_at	NM_030788
7.44	7.72	0.28	5.24E-01	8.13E-01	COL6A1	collagen, type VI, alpha 1	chr21q22.3	213428_s_at	NM_001848
2.06	2.15	0.09	5.24E-01	8.13E-01	FGFR3	fibroblast growth factor receptor 3	chr4p16.3	204380_s_at	NM_000142 /// NM_022965
2.41	2.51	0.10	5.25E-01	8.13E-01	UPK2	uroplakin 2	chr11q23	207862_at	NM_006760
5.79	6.01	0.22	5.25E-01	8.13E-01	KIAA0947	KIAA0947 protein	chr5p15.32	209654_at	NM_015325
3.94	4.12	0.18	5.25E-01	8.13E-01	KIAA1627	KIAA1627 protein	chr4q26	235552_at	NM_020961
3.22	3.33	0.11	5.25E-01	8.13E-01	TMEM45B	transmembrane protein 45B	chr11q24.3	226226_at	NM_138788
2.40	2.50	0.10	5.25E-01	8.13E-01	---	---	---	243353_at	---

2.00	2.09	0.09	5.25E-01	8.13E-01	FLJ30594	hypothetical locus FLJ30594	chr2p25.2	1553797_a_at	XR_041760 /// XR_041761 /// XR_041762
2.00	2.07	0.08	5.25E-01	8.13E-01	C18orf54	Chromosome 18 open reading frame 54	chr18q21.2	241733_at	NM_173529
2.33	2.43	0.10	5.25E-01	8.13E-01	---	---	---	1562945_at	---
1.95	2.03	0.08	5.25E-01	8.13E-01	---	---	---	243632_at	---
3.16	3.39	0.23	5.25E-01	8.13E-01	JMJD1C	jumonji domain containing 1C	chr10q21.2-q21.3	228793_at	NM_004241 /// NM_032776
3.86	4.06	0.19	5.25E-01	8.14E-01	FAM108B1	family with sequence similarity 108, member B1	chr9q21.13	220285_at	NM_001025780 /// NM_016014
2.04	2.12	0.08	5.25E-01	8.14E-01	E2F7	E2F transcription factor 7	chr12q21.2	228033_at	NM_203394
2.42	2.53	0.10	5.25E-01	8.14E-01	---	---	---	243499_at	---
1.97	2.05	0.07	5.25E-01	8.14E-01	CACNA1E	Calcium channel, voltage-dependent, R type, alpha 1E subunit	chr1q25-q31	244256_at	NM_000721
7.94	8.14	0.20	5.25E-01	8.14E-01	RYBP	RING1 and YY1 binding protein	chr3p13	201844_s_at	NM_012234
2.14	2.25	0.11	5.25E-01	8.14E-01	LOC729307	hypothetical protein LOC729307	chr4q28.3	1569811_at	XR_041495 /// XR_041496 /// XR_041497
2.16	2.23	0.08	5.25E-01	8.14E-01	---	---	---	233740_at	---
2.57	2.67	0.11	5.25E-01	8.14E-01	---	---	---	1560978_at	---
6.33	6.67	0.34	5.25E-01	8.14E-01	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	chr9p22.3	206544_x_at	NM_003070 /// NM_139045
2.53	2.66	0.12	5.25E-01	8.14E-01	RANBP9	RAN binding protein 9	chr6p23	243108_at	NM_005493
2.41	2.53	0.11	5.25E-01	8.14E-01	---	---	---	1559936_at	---
7.48	7.71	0.23	5.26E-01	8.14E-01	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	chr12p12.3	1555812_a_at	NM_001175
6.14	6.38	0.24	5.26E-01	8.14E-01	AQR	aquarius homolog (mouse)	chr15q14	212584_at	NM_014691
2.13	2.22	0.09	5.26E-01	8.14E-01	BAZ1B	Bromodomain adjacent to zinc finger domain, 1B	chr7q11.23	229658_at	NM_032408
6.72	6.98	0.26	5.26E-01	8.14E-01	ZBTB44	zinc finger and BTB domain containing 44	chr11q24.3	226148_at	NM_014155
6.15	6.26	0.11	5.26E-01	8.14E-01	LOC220906	hypothetical protein LOC220906	chr10p11.23	233013_x_at	XM_001716346 /// XM_001716412
2.01	2.10	0.08	5.26E-01	8.14E-01	FLJ14213	Protor-2	chr11p13-p12	233379_at	NM_024841
6.05	6.35	0.31	5.26E-01	8.14E-01	RP1-21O18.1	kazrin	chr1p36.21	229144_at	NM_001017999 /// NM_001018000 /// NM_001018001 /// NM_015209 /// NM_201628
6.65	6.94	0.29	5.26E-01	8.14E-01	EIF5	eukaryotic translation initiation factor 5	chr14q32.32	208706_s_at	NM_001969 /// NM_183004
7.03	7.20	0.17	5.26E-01	8.14E-01	BECN1	beclin 1, autophagy related	chr17q21	208945_s_at	NM_003766
3.17	3.32	0.15	5.26E-01	8.14E-01	C10orf78	chromosome 10 open reading frame 78	chr10q25.1	238794_at	NM_001002759 /// NM_145247
2.59	2.74	0.14	5.26E-01	8.14E-01	---	---	---	1566693_at	---
3.12	3.22	0.10	5.26E-01	8.14E-01	---	---	---	238201_at	---
3.16	3.26	0.10	5.26E-01	8.14E-01	---	---	---	207476_at	---
1.87	1.96	0.09	5.26E-01	8.14E-01	INTS4	integrator complex subunit 4	chr11q14.1	1569254_s_at	NM_033547
4.25	4.34	0.09	5.26E-01	8.14E-01	C16orf88	chromosome 16 open reading frame 88	chr16p12.3	213237_at	NM_001012991
2.03	2.10	0.08	5.26E-01	8.14E-01	SNX24	Sorting nexin 24	chr5q23.2	239693_at	NM_014035
2.11	2.17	0.06	5.26E-01	8.14E-01	IL17A	interleukin 17A	chr6p12	208402_at	NM_002190
9.08	9.32	0.24	5.26E-01	8.14E-01	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	chr2p23.2	205550_s_at	NM_004899 /// NM_199191 /// NM_199192 /// NM_199193 /// NM_199194
4.52	4.67	0.15	5.26E-01	8.14E-01	PBRM1	polybromo 1	chr3p21	232613_at	NM_018165 /// NM_018313 /// NM_181042
3.55	3.69	0.14	5.26E-01	8.14E-01	SELI	Selenoprotein I	chr2p23.3	1570371_a_at	NM_033505
3.49	3.62	0.13	5.26E-01	8.14E-01	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	chr17q23.3	224952_at	NM_025185
3.16	3.28	0.12	5.26E-01	8.14E-01	---	---	---	229315_at	---
2.85	2.97	0.12	5.26E-01	8.14E-01	CRYGN	crystallin, gamma N	chr7q36.1	1553082_at	NM_144727
2.17	2.25	0.08	5.26E-01	8.14E-01	SDHALP2	Succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	chr3q29	235575_at	NR_003265 /// XR_015171
7.24	7.36	0.12	5.26E-01	8.14E-01	GSTZ1	glutathione transferase zeta 1	chr14q24.3	209531_at	NM_001513 /// NM_145870 /// NM_145871
9.37	9.56	0.19	5.26E-01	8.14E-01	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	chr12q24.1-q24.2	200726_at	NM_002710
4.24	4.39	0.14	5.26E-01	8.14E-01	---	---	---	1556449_at	---
3.43	3.54	0.11	5.26E-01	8.14E-01	RAB42	RAB42, member RAS oncogene family	chr1p35.3	1552846_s_at	NM_152304
2.93	3.01	0.08	5.26E-01	8.14E-01	C2CD3	C2 calcium-dependent domain containing 3	chr11q13.4	231708_at	NM_015531
6.57	6.79	0.22	5.27E-01	8.14E-01	EFR3A	EFR3 homolog A (S. cerevisiae)	chr8q24.22	212150_at	NM_015137

2.07	2.15	0.08	5.27E-01	8.14E-01	---	---	---	1561879_at	---
3.83	3.96	0.13	5.27E-01	8.14E-01	C1orf88	chromosome 1 open reading frame 88	chr1p13.2	228100_at	NM_181643
3.23	3.34	0.11	5.27E-01	8.14E-01	---	---	---	1568625_at	---
3.11	3.21	0.09	5.27E-01	8.14E-01	KLK3	kallikrein-related peptidase 3	chr19q13.41	204583_x_at	NM_001030047 /// NM_001030048 /// NM_001030049 /// NM_001030050 /// NM_001648
2.76	2.86	0.10	5.27E-01	8.14E-01	LOC284017	hypothetical protein LOC284017	chr17p13.3	233840_at	---
2.21	2.31	0.10	5.27E-01	8.14E-01	TTC21B	tetratricopeptide repeat domain 21B	chr2q24.3	220064_at	NM_024753
2.70	2.88	0.18	5.27E-01	8.14E-01	---	---	---	1560383_at	---
2.44	2.55	0.11	5.27E-01	8.14E-01	RARB	retinoic acid receptor, beta	chr3p24	217020_at	NM_000965 /// NM_016152
5.25	5.46	0.21	5.27E-01	8.14E-01	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	chr12q15	202969_at	NM_003583 /// NM_006482
4.24	4.36	0.13	5.27E-01	8.14E-01	---	---	---	216500_at	---
4.01	4.24	0.23	5.27E-01	8.14E-01	---	---	---	242086_at	---
3.48	3.57	0.10	5.27E-01	8.14E-01	UBE3C	Ubiquitin protein ligase E3C	chr7q36.3	243519_at	NM_014671
2.11	2.18	0.07	5.27E-01	8.14E-01	---	---	---	1568826_at	---
4.82	5.09	0.27	5.27E-01	8.15E-01	TRBC1	T cell receptor beta constant 1	chr7q34	213193_x_at	---
1.99	2.07	0.08	5.27E-01	8.15E-01	PCDH7	protocadherin 7	chr4p15	210941_at	NM_002589 /// NM_032456 /// NM_032457
4.36	4.64	0.28	5.28E-01	8.15E-01	STAT1	signal transducer and activator of transcription 1, 91kDa	chr2q32.2	AFFX-HUMISGF3A/M97935_MB_at	NM_007315 /// NM_139266
3.83	4.01	0.17	5.28E-01	8.15E-01	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	chr10q24	212594_at	NM_014456 /// NM_145341
6.82	6.98	0.16	5.28E-01	8.15E-01	POLR1D	polymerase (RNA) I polypeptide D, 16kDa	chr13q12.2	224857_s_at	NM_015972 /// NM_152705
2.63	2.73	0.11	5.28E-01	8.15E-01	TTC39A	tetratricopeptide repeat domain 39A	chr1p32.3	215562_at	NM_001080494
2.66	2.76	0.10	5.28E-01	8.15E-01	BCAP29	B-cell receptor-associated protein 29	chr7q22-q31	217657_at	NM_001008405 /// NM_001008406 /// NM_001008407 /// NM_018844
6.81	6.91	0.10	5.28E-01	8.15E-01	GDF2	growth differentiation factor 2	chr10q11.22	221136_at	NM_016204
2.06	2.15	0.09	5.27E-01	8.15E-01	INTS4	integrator complex subunit 4	chr11q14.1	1569253_at	NM_033547
4.42	4.54	0.12	5.28E-01	8.15E-01	---	---	---	1556718_s_at	---
2.16	2.27	0.11	5.28E-01	8.15E-01	SULT1C4	sulfotransferase family, cytosolic, 1C, member 4	chr2q11.1-q11.2	1553321_a_at	NM_006588
2.23	2.32	0.09	5.28E-01	8.15E-01	XGPY2	Xg pseudogene, Y-linked 2	chrYp11.31	1563420_at	NR_003254 /// XM_001713803
3.13	3.24	0.11	5.28E-01	8.15E-01	MAPT	microtubule-associated protein tau	chr17q21.1	203928_x_at	NM_001123066 /// NM_001123067 /// NM_005910 /// NM_016834 /// NM_016835 /// NM_016841
4.13	4.23	0.10	5.28E-01	8.15E-01	ABBA-1	actin-bundling protein with BAIAP2 homology	chr16q22.1	213978_at	NM_138383
3.26	3.36	0.10	5.28E-01	8.15E-01	ADAM19	ADAM metallopeptidase domain 19 (meltrin beta)	chr5q32-q33	221128_at	NM_023038 /// NM_033274
2.18	2.26	0.09	5.28E-01	8.15E-01	---	---	---	1555940_a_at	---
4.26	4.39	0.13	5.28E-01	8.15E-01	HPX	hemopexin	chr11p15.5-p15.4	39763_at	NM_000613
3.35	3.42	0.07	5.28E-01	8.15E-01	TRIM10	tripartite motif-containing 10	chr6p21.3	210579_s_at	NM_006778 /// NM_052828
2.00	2.08	0.08	5.28E-01	8.15E-01	LMTK2	lemur tyrosine kinase 2	chr7q21.3	235307_at	NM_014916
1.98	2.05	0.08	5.28E-01	8.15E-01	FAM54A	family with sequence similarity 54, member A	chr6q23.3	234945_at	NM_001099286 /// NM_138419
2.00	2.06	0.06	5.28E-01	8.15E-01	RACGAP1 /// RACGAP1P	Rac GTPase activating protein 1 /// Rac GTPase activating protein 1 pseudogene	chr12q12 /// chr12q13.13	224272_at	NM_001126103 /// NM_001126104 /// NM_013277

3.28	3.37	0.09	5.28E-01	8.15E-01	TJP3	tight junction protein 3 (zona occludens 3)	chr19p13.3	35148_at	NM_014428
3.82	3.96	0.14	5.28E-01	8.15E-01	EGLN3	egl nine homolog 3 (C. elegans)	chr14q13.1	222847_s_at	NM_022073
2.04	2.14	0.10	5.28E-01	8.15E-01	---	---	---	236928_at	---
2.74	2.87	0.13	5.28E-01	8.15E-01	TOP2A	topoisomerase (DNA) II alpha 170kDa	chr17q21-q22	201292_at	NM_001067
2.93	3.04	0.11	5.28E-01	8.15E-01	---	---	---	224031_at	---
3.18	3.33	0.15	5.28E-01	8.15E-01	TIGD7	tigger transposable element derived 7	chr16p13.3	224365_s_at	NM_033208
4.57	4.70	0.14	5.29E-01	8.15E-01	FAM148C	family with sequence similarity 148, member C	chr19p13.3	230819_at	XM_001718840 /// XM_065166 /// XM_939576
2.90	3.03	0.13	5.29E-01	8.15E-01	KCTD9	Potassium channel tetramerisation domain containing 9	chr8p21.1	224316_at	NM_017634
3.47	3.60	0.13	5.29E-01	8.15E-01	PIWIL2	piwi-like 2 (Drosophila)	chr8p21.3	220686_s_at	NM_018068
2.01	2.08	0.08	5.29E-01	8.15E-01	---	---	---	244412_at	---
2.32	2.44	0.12	5.29E-01	8.16E-01	---	---	---	1556983_a_at	---
6.09	6.28	0.19	5.29E-01	8.16E-01	MRPL30	mitochondrial ribosomal protein L30	chr2q11.2	223996_s_at	NM_145212 /// NM_145213
4.72	4.88	0.16	5.29E-01	8.16E-01	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	chr21q22.1|21q22.11	212378_at	NM_000819 /// NM_175085
4.07	4.22	0.15	5.29E-01	8.16E-01	PDE8A	Phosphodiesterase 8A	chr15q25.3	239874_at	NM_002605 /// NM_173454
5.21	5.36	0.15	5.29E-01	8.16E-01	COMMD8	COMM domain containing 8	chr4p12	218351_at	NM_017845
2.51	2.64	0.13	5.29E-01	8.16E-01	APOA1	Apolipoprotein A-I	chr11q23-q24	231694_at	NM_000039
2.59	2.72	0.13	5.29E-01	8.16E-01	CARD14	caspase recruitment domain family, member 14	chr17q25	1555309_a_at	NM_024110 /// NM_052819
3.73	3.84	0.12	5.29E-01	8.16E-01	CDKL3	cyclin-dependent kinase-like 3	chr5q31	219831_at	NM_001113575 /// NM_016508
2.40	2.51	0.12	5.29E-01	8.16E-01	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	chr7q36.3	1555829_at	NM_020728
3.24	3.35	0.11	5.29E-01	8.16E-01	hCG_2020170	hCG2020170	chr13q12.3	1555188_at	XM_001129114
2.68	2.79	0.11	5.29E-01	8.16E-01	---	---	---	237237_at	---
2.58	2.67	0.09	5.29E-01	8.16E-01	RXRG	retinoid X receptor, gamma	chr1q22-q23	205954_at	NM_001009598 /// NM_006917
2.05	2.13	0.08	5.29E-01	8.16E-01	---	---	---	233697_at	---
2.75	2.83	0.09	5.29E-01	8.16E-01	---	---	---	1557693_at	---
5.71	6.14	0.43	5.29E-01	8.16E-01	EIF5	eukaryotic translation initiation factor 5	chr14q32.32	208290_s_at	NM_001969 /// NM_183004
2.12	2.18	0.06	5.29E-01	8.16E-01	BAGE	B melanoma antigen	chr21p11.1	1555605_x_at	NM_001187
1.87	1.93	0.07	5.29E-01	8.16E-01	LOC643749	Hypothetical LOC643749	chr6q21	1562566_at	XR_041901 /// XR_041902 /// XR_041903
2.04	2.15	0.11	5.29E-01	8.16E-01	---	---	---	233400_at	---
4.60	4.89	0.29	5.30E-01	8.16E-01	ARL4C	ADP-ribosylation factor-like 4C	chr2q37.1	202207_at	NM_005737
2.36	2.47	0.11	5.30E-01	8.16E-01	HEATR5B	HEAT repeat containing 5B	chr2p22.2	1569503_at	NM_019024
2.41	2.52	0.11	5.29E-01	8.16E-01	CYTH3	cytohesin 3	chr7p22.1	243752_s_at	NM_004227
2.26	2.36	0.10	5.30E-01	8.16E-01	GPSN2	Glycoprotein, synaptic 2	chr19p13.12	231556_at	NM_138501
3.77	3.87	0.10	5.30E-01	8.16E-01	ERICH1 /// FLJ00290	glutamate-rich 1 /// FLJ00290 protein	chr8p23.3	236467_at	NM_207332
2.44	2.52	0.08	5.30E-01	8.16E-01	---	---	---	242142_at	---
2.04	2.11	0.08	5.30E-01	8.16E-01	---	---	---	230825_at	---
2.10	2.17	0.07	5.30E-01	8.16E-01	---	---	---	1568903_at	---
11.47	11.54	0.07	5.30E-01	8.16E-01	PEBP1	phosphatidylethanolamine binding protein 1	chr12q24.23	210825_s_at	NM_002567
6.86	7.15	0.29	5.30E-01	8.16E-01	USP9X	ubiquitin specific peptidase 9, X-linked	chrXp11.4	201099_at	NM_001039590 /// NM_001039591
2.46	2.55	0.10	5.30E-01	8.16E-01	LOC148696	hypothetical LOC148696	chr1q32.2	232430_at	XR_040948 /// XR_040949 /// XR_040950
2.74	2.90	0.15	5.30E-01	8.16E-01	KCNK12	potassium channel, subfamily K, member 12	chr2p22-p21	220448_at	NM_022055
3.17	3.33	0.15	5.30E-01	8.16E-01	CC2D2B /// LOC100131720	coiled-coil and C2 domain containing 2B /// hypothetical protein LOC100131720	chr10q23.33	243534_at	NM_001001732 /// XM_001714363 /// XM_001717910 /// XM_001718132
2.55	2.67	0.12	5.30E-01	8.16E-01	---	---	---	243246_at	---
3.74	3.85	0.10	5.30E-01	8.16E-01	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	chr11q13	223372_at	NM_005528
2.59	2.69	0.09	5.30E-01	8.16E-01	---	---	---	239848_at	---
6.41	6.50	0.09	5.30E-01	8.16E-01	---	---	---	1560296_at	---
1.88	1.96	0.08	5.30E-01	8.16E-01	IFNA8	interferon, alpha 8	chr9p22	207932_at	NM_002170
2.56	2.68	0.12	5.30E-01	8.16E-01	CCDC7	coiled-coil domain containing 7	chr10p11.22	1553215_s_at	NM_001026383 /// NM_145023
3.62	3.71	0.09	5.30E-01	8.16E-01	WNT10A	wingless-type MMTV integration site family, member 10A	chr2q35	223709_s_at	NM_025216

2.25	2.33	0.08	5.30E-01	8.16E-01	---	---	---	241641_at	---
2.86	2.97	0.11	5.30E-01	8.16E-01	---	---	---	1563706_at	---
4.40	4.48	0.09	5.30E-01	8.16E-01	TECTB	tectorin beta	chr10q25-q26	1553656_at	NM_058222
3.55	3.66	0.11	5.30E-01	8.16E-01	LY6G6C	lymphocyte antigen 6 complex, locus G6C	chr6p21.33	207114_at	NM_025261
6.33	6.45	0.12	5.30E-01	8.16E-01	MAN2B2	mannosidase, alpha, class 2B, member 2	chr4p16.1	214703_s_at	NM_015274
2.08	2.18	0.10	5.31E-01	8.16E-01	---	---	---	234839_at	---
2.08	2.18	0.10	5.30E-01	8.16E-01	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3	chr15q12	1555517_at	NM_033223
4.79	4.88	0.09	5.31E-01	8.16E-01	ETV6	ets variant gene 6 (TEL oncogene)	chr12p13	205585_at	NM_001987
2.19	2.27	0.08	5.31E-01	8.16E-01	---	---	---	1560154_a_at	---
1.81	1.89	0.08	5.30E-01	8.16E-01	GYPE	glycophorin E	chr4q31.1	1561137_s_at	NM_002102 /// NM_198682
3.63	3.71	0.08	5.30E-01	8.16E-01	---	---	---	216562_at	---
6.74	7.09	0.35	5.31E-01	8.16E-01	PREPL	prolyl endopeptidase-like	chr2p21	212217_at	NM_001042385 /// NM_001042386 /// NM_006036
4.73	4.89	0.16	5.31E-01	8.16E-01	KIAA0494	KIAA0494	chr1pter-p22.1	201777_s_at	NM_014774
6.17	6.32	0.16	5.31E-01	8.16E-01	41527	septin 10	chr2q13	212698_s_at	NM_144710 /// NM_178584
6.77	6.91	0.13	5.31E-01	8.16E-01	SREBF2	sterol regulatory element binding transcription factor 2	chr22q13	201247_at	NM_004599
2.32	2.42	0.10	5.31E-01	8.16E-01	LOC100130278	hypothetical protein LOC100130278	chr3p21.31	1563793_at	XM_001724635 /// XM_001724773 /// XM_001725296
2.07	2.15	0.07	5.31E-01	8.16E-01	MFAP3L	microfibrillar-associated protein 3-like	chr4q32.3	210843_s_at	NM_001009554 /// NM_021647
3.73	3.86	0.13	5.31E-01	8.17E-01	SEC14L2	SEC14-like 2 (S. cerevisiae)	chr22q12.2	232400_at	NM_012429
1.80	1.86	0.07	5.31E-01	8.17E-01	SRD5A2L2	steroid 5 alpha-reductase 2-like 2	chr4q13.1	241961_at	NM_001010874
4.31	4.43	0.13	5.31E-01	8.17E-01	PKLR	pyruvate kinase, liver and RBC	chr1q21	222078_at	NM_000298 /// NM_181871
3.00	3.12	0.12	5.31E-01	8.17E-01	---	---	---	237409_at	---
2.48	2.59	0.11	5.31E-01	8.17E-01	C7orf53	chromosome 7 open reading frame 53	chr7q31.1	239203_at	NM_001134468 /// NM_182597
3.62	3.71	0.09	5.31E-01	8.17E-01	---	---	---	239021_at	---
2.32	2.40	0.08	5.31E-01	8.17E-01	---	---	---	1568892_at	---
2.33	2.42	0.09	5.31E-01	8.17E-01	OR7E19P	olfactory receptor, family 7, subfamily E, member 19 pseudogene	chr19p13.2	216536_at	---
3.44	3.52	0.08	5.31E-01	8.17E-01	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	chr9q34.13	235436_at	NM_022779 /// NM_138620
6.89	7.07	0.18	5.31E-01	8.17E-01	GABARAPL1	GABA(A) receptor-associated protein like 1	chr12p13.2	208869_s_at	NM_031412
4.25	4.35	0.10	5.31E-01	8.17E-01	ANKRD11	ankyrin repeat domain 11	chr16q24.3	234701_at	NM_013275
8.68	8.96	0.27	5.31E-01	8.17E-01	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	chr7p13	201317_s_at	NM_002787
2.97	3.22	0.24	5.31E-01	8.17E-01	FAIM3	Fas apoptotic inhibitory molecule 3	chr1q32.1	221601_s_at	NM_005449
3.20	3.33	0.12	5.31E-01	8.17E-01	---	---	---	232343_at	---
2.36	2.47	0.11	5.31E-01	8.17E-01	C10orf30	chromosome 10 open reading frame 30	chr10p13	1553327_a_at	NM_001100912 /// NM_152751
2.37	2.44	0.08	5.31E-01	8.17E-01	LOC90246	hypothetical protein LOC90246	chr3q21.3	233835_at	---
7.45	7.79	0.34	5.32E-01	8.17E-01	MATR3	matrin 3	chr5q31.2	200624_s_at	NM_018834 /// NM_199189
6.21	6.50	0.29	5.32E-01	8.17E-01	ZRANB1	zinc finger, RAN-binding domain containing 1	chr10q26.13	225138_at	NM_017580
3.41	3.61	0.21	5.32E-01	8.17E-01	---	---	---	240721_at	---
4.00	4.19	0.18	5.32E-01	8.17E-01	ZNF329	zinc finger protein 329	chr19q13.43	219765_at	NM_024620
9.56	9.71	0.15	5.32E-01	8.17E-01	---	---	---	AFFX-M27830_M_at	---
2.54	2.67	0.13	5.32E-01	8.17E-01	TMEM174	transmembrane protein 174	chr5q13.2	231623_at	NM_153217
2.48	2.57	0.10	5.32E-01	8.17E-01	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	chr5p12	214917_at	NM_006251 /// NM_206907
2.14	2.22	0.09	5.32E-01	8.17E-01	---	---	---	235188_at	---
3.35	3.46	0.11	5.32E-01	8.17E-01	GDAP1	ganglioside-induced differentiation-associated protein 1	chr8q21.11	221279_at	NM_001040875 /// NM_018972
4.86	5.24	0.38	5.32E-01	8.17E-01	CEP57	centrosomal protein 57kDa	chr11q21	203492_x_at	NM_014679
6.24	6.46	0.22	5.32E-01	8.17E-01	CTTNBP2NL	CTTNBP2 N-terminal like	chr1p13.2	226000_at	NM_018704
5.34	5.51	0.17	5.32E-01	8.17E-01	ZNF775	zinc finger protein 775	chr7q36.1	228226_s_at	NM_173680
4.09	4.25	0.16	5.32E-01	8.17E-01	HPS1	Hermansky-Pudlak syndrome 1	chr10q23.1-q23.3	217354_s_at	NM_000195 /// NM_182639

3.29	3.42	0.13	5.32E-01	8.17E-01	SLC12A3	solute carrier family 12 (sodium/chloride transporters), member 3	chr16q13	215274_at	NM_000339 /// NM_001126107 /// NM_001126108
11.27	11.34	0.08	5.32E-01	8.17E-01	MYL6 /// MYL6B	myosin, light chain 6, alkali, smooth muscle and non-muscle /// myosin, light chain 6B, alkali, smooth muscle and non-muscle	chr12q13.13 /// chr12q13.2	212082_s_at	NM_002475 /// NM_021019 /// NM_079423
2.73	2.81	0.08	5.32E-01	8.17E-01	PARVA	parvin, alpha	chr11p15.3	1563458_at	NM_018222
2.05	2.13	0.08	5.32E-01	8.17E-01	---	---	---	1570050_at	---
2.38	2.48	0.09	5.32E-01	8.17E-01	PTPN11	protein tyrosine phosphatase, non-receptor type 11	chr12q24	1552637_at	NM_002834
3.04	3.14	0.09	5.32E-01	8.17E-01	DNAH1	dynein, axonemal, heavy chain 1	chr3p21.1	239059_at	NM_015512
5.18	5.29	0.12	5.32E-01	8.17E-01	PCSK4	proprotein convertase subtilisin/kexin type 4	chr19p13.3	230901_x_at	NM_017573
6.31	6.58	0.28	5.32E-01	8.17E-01	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	chr3q26.3	218583_s_at	NM_020640
4.19	4.35	0.16	5.32E-01	8.17E-01	CD300LB	CD300 molecule-like family member b	chr17q25.1	1554173_at	NM_174892
2.10	2.22	0.12	5.32E-01	8.17E-01	---	---	---	241951_at	---
7.29	7.41	0.12	5.32E-01	8.17E-01	RAP1A	RAP1A, member of RAS oncogene family	chr1p13.3	202362_at	NM_001010935 /// NM_002884
3.09	3.19	0.10	5.32E-01	8.17E-01	DPF3	D4, zinc and double PHD fingers, family 3	chr14q24.3-q31.1	238532_at	NM_012074
2.14	2.22	0.07	5.32E-01	8.17E-01	GTF2A1L /// STON1	general transcription factor IIA, 1-like /// stonin 1	chr2p16.3	1552585_s_at	NM_006872 /// NM_006873 /// NM_172196
1.96	2.03	0.07	5.32E-01	8.17E-01	---	---	---	1566862_at	---
2.10	2.17	0.07	5.32E-01	8.17E-01	---	---	---	231636_s_at	---
7.07	7.30	0.23	5.32E-01	8.17E-01	LOC144871	hypothetical protein LOC144871	chr13q32.1	225284_at	---
5.48	5.62	0.13	5.32E-01	8.17E-01	ZMIZ2	zinc finger, MIZ-type containing 2	chr7p13	221525_at	NM_031449 /// NM_174929
4.94	5.20	0.26	5.32E-01	8.17E-01	CLCC1	chloride channel CLIC-like 1	chr1p13.3	1555543_a_at	NM_001048210 /// NM_015127
3.27	3.36	0.09	5.33E-01	8.17E-01	---	---	---	233991_at	---
3.26	3.39	0.12	5.33E-01	8.18E-01	---	---	---	240404_at	---
3.93	4.06	0.13	5.33E-01	8.18E-01	RADIL	Rap GTPase interactor	chr7p22.1	223693_s_at	NM_018059
5.31	5.42	0.11	5.33E-01	8.18E-01	RAD54L2	RAD54-like 2 (S. cerevisiae)	chr3p21.2	213205_s_at	NM_015106
2.49	2.58	0.09	5.33E-01	8.18E-01	---	---	---	237985_at	---
3.42	3.59	0.17	5.33E-01	8.18E-01	---	---	---	1557632_at	---
2.64	2.79	0.15	5.33E-01	8.18E-01	FAM71B	family with sequence similarity 71, member B	chr5q33.3	1555586_at	NM_130899
2.37	2.45	0.08	5.33E-01	8.18E-01	CACNG4	calcium channel, voltage-dependent, gamma subunit 4	chr17q24	231737_at	NM_014405
2.62	2.77	0.15	5.33E-01	8.18E-01	SYT11	synaptotagmin XI	chr1q21.2	209198_s_at	NM_152280
2.40	2.54	0.14	5.33E-01	8.18E-01	---	---	---	240807_at	---
2.07	2.15	0.07	5.33E-01	8.18E-01	LRMP	Lymphoid-restricted membrane protein	chr12p12.1	240718_at	NM_006152
2.99	3.08	0.10	5.33E-01	8.18E-01	LOC100132369	Hypothetical protein LOC100132369	chr12p13.33	240500_at	XM_001714404 /// XM_001715452 /// XM_001716240
2.09	2.17	0.08	5.33E-01	8.18E-01	---	---	---	236975_at	---
3.71	3.84	0.13	5.33E-01	8.18E-01	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	chr6p21.1-p12.1	215082_at	NM_021814
2.75	2.88	0.13	5.33E-01	8.18E-01	---	---	---	240105_at	---
2.08	2.19	0.11	5.33E-01	8.18E-01	KIF14	kinesin family member 14	chr1q32.1	236641_at	NM_014875
2.36	2.43	0.08	5.33E-01	8.18E-01	---	---	---	244333_at	---
2.03	2.10	0.07	5.33E-01	8.18E-01	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	chr17q11.1-q12	242009_at	NM_001045
6.49	6.71	0.22	5.33E-01	8.18E-01	UTP3	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)	chr4q13.3	209486_at	NM_020368
3.32	3.52	0.20	5.33E-01	8.18E-01	TMEM139	transmembrane protein 139	chr7q34	227753_at	NM_153345
2.32	2.43	0.11	5.33E-01	8.18E-01	LOC219690	hypothetical protein LOC219690	chr10q22.2	1564314_at	---
2.74	2.88	0.14	5.33E-01	8.18E-01	---	---	---	243588_at	---
2.54	2.66	0.12	5.33E-01	8.18E-01	---	---	---	240997_at	---
3.33	3.43	0.11	5.34E-01	8.18E-01	---	---	---	237084_at	---
2.79	2.88	0.09	5.34E-01	8.18E-01	PPARGC1B	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	chr5q33.1	1563943_at	NM_133263
2.12	2.20	0.08	5.34E-01	8.18E-01	---	---	---	1563115_at	---
3.28	3.41	0.13	5.34E-01	8.18E-01	FLJ23356	hypothetical protein FLJ23356	chr8p11.21	1553246_a_at	NM_032237
1.99	2.09	0.10	5.34E-01	8.18E-01	---	---	---	1553462_at	---
3.85	4.00	0.16	5.34E-01	8.18E-01	IER3IP1	immediate early response 3 interacting protein 1	chr18q12	211406_at	NM_016097
2.26	2.33	0.08	5.34E-01	8.18E-01	---	---	---	237758_at	---

2.21	2.30	0.09	5.34E-01	8.18E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	208076_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054																			
4.50	4.85	0.36	5.34E-01	8.18E-01	IFI44L	interferon-induced protein 44-like	chr1p31.1	204439_at	NM_006820 /// XM_001725615 /// XM_001726761 /// XM_001726800																				
3.16	3.31	0.15	5.34E-01	8.18E-01	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	chr3p22.1	236268_at	NM_004206 /// NM_032970																				
3.39	3.52	0.14	5.34E-01	8.18E-01	---	---	---	222276_at	---																				
2.92	3.05	0.13	5.34E-01	8.18E-01	---	---	---	239023_at	---																				
2.66	2.79	0.13	5.34E-01	8.18E-01	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	chr19q13.43	232774_x_at	NM_001010879																				
3.30	3.43	0.13	5.34E-01	8.18E-01	NRG1	neuregulin 1	chr8p12	206237_s_at	NM_004495 /// NM_013956 /// NM_013957 /// NM_013958 /// NM_013959 /// NM_013960 /// NM_013961 /// NM_013962 /// NM_013964																				
3.54	3.66	0.12	5.34E-01	8.18E-01	---	---	---	1567166_at	---																				
2.45	2.55	0.11	5.34E-01	8.18E-01	---	---	---	232947_at	---																				
2.17	2.27	0.10	5.34E-01	8.18E-01	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	chr4q13.3	233083_at	NM_001004346																				
11.59	11.67	0.08	5.34E-01	8.18E-01	EIF1	eukaryotic translation initiation factor 1	chr17q21.2	211956_s_at	NM_005801																				
3.22	3.35	0.13	5.34E-01	8.18E-01	---	---	---	216635_at	---																				
5.09	5.21	0.13	5.34E-01	8.18E-01	AKR1CL2	aldo-keto reductase family 1, member C-like 2	chr10p15.1	223856_at	NM_001040177																				
2.05	2.17	0.12	5.34E-01	8.18E-01	---	---	---	1562110_at	---																				
2.45	2.54	0.09	5.34E-01	8.18E-01	RIMBP2	RIMS binding protein 2	chr12q24.33	241771_at	NM_015347																				
2.11	2.22	0.11	5.34E-01	8.18E-01	---	---	---	1558757_at	---																				
4.70	4.91	0.21	5.34E-01	8.18E-01	RAMP2	receptor (G protein-coupled) activity modifying protein 2	chr17q12-q21.1	205779_at	NM_005854																				
2.31	2.39	0.08	5.34E-01	8.18E-01	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	chr8p23	215139_at	NM_014629																				
1.91	1.98	0.08	5.34E-01	8.18E-01	---	---	---	233460_at	---																				
2.30	2.39	0.09	5.34E-01	8.18E-01	---	---	---	1570350_at	---																				
1.70	1.76	0.06	5.35E-01	8.19E-01	---	---	---	1559722_at	---																				
2.41	2.49	0.08	5.35E-01	8.19E-01	---	---	---	231712_at	---																				
7.11	7.62	0.51	5.35E-01	8.19E-01	THBS2	thrombospondin 2	chr6q27	203083_at	NM_003247																				
3.90	4.11	0.21	5.35E-01	8.19E-01	CDCA3	cell division cycle associated 3	chr12p13	223307_at	NM_031299																				
3.94	4.09	0.15	5.35E-01	8.19E-01	LOC158301	hypothetical protein LOC158301	chr9q34.11	239193_at	XM_001721521																				
7.18	7.39	0.21	5.35E-01	8.19E-01	ECHDC1	enoyl Coenzyme A hydratase domain containing 1	chr6q22.33	223087_at	NM_001002030 /// NM_001105544 /// NM_001105545 /// NM_018479																				
4.84	5.02	0.18	5.35E-01	8.19E-01	BICD2	bicaudal D homolog 2 (Drosophila)	chr9q22.31	212702_s_at	NM_001003800 /// NM_015250																				
2.59	2.72	0.12	5.35E-01	8.19E-01	C4orf31	chromosome 4 open reading frame 31	chr4q27	219747_at	NM_024574																				

3.44	3.56	0.12	5.35E-01	8.19E-01	IL18BP	interleukin 18 binding protein	chr11q13	224283_x_at	NM_001039659 /// NM_001039660 /// NM_173042
1.93	2.02	0.09	5.35E-01	8.19E-01	---	---	---	1556759_at	---
7.31	7.57	0.27	5.35E-01	8.19E-01	IPO7	importin 7	chr11p15.4	200993_at	NM_006391
7.98	8.08	0.09	5.35E-01	8.19E-01	OCIAD1	OCIA domain containing 1	chr4p11	239748_x_at	NM_001079839 /// NM_001079840 /// NM_001079841 /// NM_001079842 /// NM_017830
2.56	2.65	0.09	5.35E-01	8.19E-01	TREML4	triggering receptor expressed on myeloid cells-like 4	chr6p21.1	1567558_at	NM_198153
2.23	2.32	0.09	5.35E-01	8.19E-01	ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13	chr21q11.2	1552582_at	NR_003087 /// NR_003088
2.92	3.01	0.09	5.35E-01	8.19E-01	---	---	---	1562947_x_at	---
2.18	2.28	0.10	5.35E-01	8.19E-01	FBXW2	F-box and WD repeat domain containing 2	chr9q34	1560752_at	NM_012164
1.97	2.04	0.07	5.35E-01	8.19E-01	---	---	---	1564007_at	---
3.22	3.39	0.17	5.35E-01	8.19E-01	C8orf44 /// SGK3	chromosome 8 open reading frame 44 /// serum/glucocorticoid regulated kinase family, member 3	chr8q12.3-q13.1 /// chr8q13.1	220038_at	NM_001033578 /// NM_013257 /// NM_019607 /// NM_170709
2.15	2.23	0.08	5.35E-01	8.19E-01	---	---	---	233672_s_at	---
5.99	6.16	0.17	5.35E-01	8.19E-01	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	chr2q14.3	224713_at	NM_032390
4.32	4.48	0.16	5.35E-01	8.19E-01	METTL8	methyltransferase like 8	chr2q31.1	220007_at	NM_024770
4.07	4.21	0.14	5.35E-01	8.19E-01	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	chr3p24.3	236361_at	NM_054110
3.36	3.50	0.14	5.35E-01	8.19E-01	GRK4	G protein-coupled receptor kinase 4	chr4p16.3	241989_at	NM_001004056 /// NM_001004057 /// NM_182982
2.05	2.14	0.09	5.35E-01	8.19E-01	LOC100130642	hypothetical LOC100130642	chr2p21	243970_at	XM_001724411 /// XM_001725413 /// XM_001726916
2.26	2.34	0.09	5.35E-01	8.19E-01	---	---	---	236432_at	---
2.05	2.13	0.08	5.35E-01	8.19E-01	---	---	---	1563107_at	---
8.41	8.71	0.30	5.35E-01	8.19E-01	IFITM1	interferon induced transmembrane protein 1 (9-27)	chr11p15.5	201601_x_at	NM_003641
2.75	2.87	0.12	5.36E-01	8.19E-01	C14orf118	chromosome 14 open reading frame 118	chr14q22.1-q24.3	219720_s_at	NM_017926 /// NM_017972
3.26	3.41	0.15	5.36E-01	8.19E-01	---	---	---	244650_at	---
2.67	2.77	0.10	5.36E-01	8.19E-01	---	---	---	216410_at	---
3.65	3.76	0.10	5.36E-01	8.19E-01	---	---	---	239804_at	---
7.90	8.06	0.16	5.36E-01	8.19E-01	FAM45A /// FAM45B	family with sequence similarity 45, member A /// family with sequence similarity 45, member B	chr10q25 /// chrXq25	221804_s_at	NM_018472 /// NM_207009
2.15	2.24	0.09	5.36E-01	8.19E-01	ZNF599	zinc finger protein 599	chr19q13.11	1558391_s_at	NM_001007248
1.95	2.04	0.09	5.36E-01	8.19E-01	RTP1	receptor (chemosensory) transporter protein 1	chr3q27.3	1553822_at	NM_153708
6.83	7.10	0.27	5.36E-01	8.20E-01	---	---	---	224996_at	---
1.98	2.07	0.09	5.36E-01	8.20E-01	SLC6A14	solute carrier family 6 (amino acid transporter), member 14	chrXq23-q24	219795_at	NM_007231
6.88	7.10	0.22	5.36E-01	8.20E-01	CD93	CD93 molecule	chr20p11.21	202878_s_at	NM_012072
2.31	2.41	0.09	5.36E-01	8.20E-01	---	---	---	244423_at	---
3.91	4.07	0.16	5.36E-01	8.20E-01	---	---	---	1560443_at	---
3.44	3.60	0.16	5.36E-01	8.20E-01	GPATCH2	G patch domain containing 2	chr1q41	219078_at	NM_018040
2.63	2.75	0.12	5.36E-01	8.20E-01	SHC4	SHC (Src homology 2 domain containing) family, member 4	chr15q21.1-q21.2	235238_at	NM_203349
3.07	3.19	0.12	5.36E-01	8.20E-01	---	---	---	1570257_x_at	---
2.39	2.48	0.09	5.37E-01	8.20E-01	---	---	---	237958_at	---
2.13	2.20	0.08	5.37E-01	8.20E-01	PNPLA1	patatin-like phospholipase domain containing 1	chr6p21.31	1553364_at	NM_173676
2.58	2.70	0.13	5.37E-01	8.20E-01	---	---	---	239134_at	---
2.49	2.60	0.11	5.37E-01	8.20E-01	---	---	---	215362_at	---
2.32	2.43	0.11	5.37E-01	8.20E-01	---	---	---	1559526_at	---
2.17	2.24	0.08	5.37E-01	8.20E-01	---	---	---	240308_at	---
1.89	1.97	0.07	5.37E-01	8.20E-01	PNLIPRP2	pancreatic lipase-related protein 2	chr10q25.3	217343_at	NM_005396
5.13	5.25	0.13	5.37E-01	8.20E-01	---	---	---	230945_at	---
5.04	5.12	0.08	5.37E-01	8.20E-01	RAD52	RAD52 homolog (S. cerevisiae)	chr12p13-p12.2	236880_at	NM_134424
2.80	2.88	0.08	5.37E-01	8.20E-01	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	chr1p13.3	205234_at	NM_004696
2.03	2.09	0.07	5.37E-01	8.20E-01	---	---	---	240112_at	---

7.57	7.75	0.18	5.37E-01	8.20E-01	CAPRIN1	cell cycle associated protein 1	chr11p13	225340_s_at	NM_005898 /// NM_203364
4.85	4.95	0.10	5.37E-01	8.20E-01	---	---	---	229615_at	---
3.31	3.75	0.44	5.37E-01	8.20E-01	FRZB	frizzled-related protein	chr2qter	203698_s_at	NM_001463
4.04	4.19	0.15	5.37E-01	8.20E-01	LIAS	lipoic acid synthetase	chr4p14	214045_at	NM_006859 /// NM_194451
6.74	6.97	0.24	5.37E-01	8.20E-01	XRN2	5'-3' exoribonuclease 2	chr20p11.2-p11.1	223002_s_at	NM_012255
7.59	7.79	0.20	5.37E-01	8.20E-01	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	chr3p25-p24	228754_at	NM_001134367 /// NM_001134368 /// NM_003043
2.05	2.15	0.11	5.37E-01	8.21E-01	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	chr1q23	1565673_at	NM_021642
4.02	4.14	0.12	5.37E-01	8.21E-01	---	---	---	216600_x_at	---
3.95	4.06	0.11	5.37E-01	8.21E-01	KREMEN1	kringle containing transmembrane protein 1	chr22q12.1	235370_at	NM_001039570 /// NM_001039571
4.42	4.71	0.29	5.37E-01	8.21E-01	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	chr9p13	238987_at	NM_001497
2.25	2.36	0.11	5.37E-01	8.21E-01	---	---	---	238907_at	---
6.63	6.88	0.25	5.37E-01	8.21E-01	EXOC1	exocyst complex component 1	chr4q12	222127_s_at	NM_001024924 /// NM_018261 /// NM_178237
5.12	5.28	0.16	5.37E-01	8.21E-01	TTLL1	tubulin tyrosine ligase-like family, member 1	chr22q13.1	205652_s_at	NM_001008572 /// NM_012263
5.95	6.07	0.12	5.37E-01	8.21E-01	MMP11	matrix metallopeptidase 11 (stromelysin 3)	chr22q11.2|22q11.23	235908_at	NM_005940
2.02	2.09	0.07	5.37E-01	8.21E-01	---	---	---	1556263_s_at	---
2.75	2.86	0.11	5.38E-01	8.21E-01	LOC642131	Similar to hCG1812074	chr15q11.2	217222_at	XM_001716198 /// XM_001716834 /// XM_001717736
2.54	2.66	0.12	5.38E-01	8.21E-01	---	---	---	1558797_at	---
2.25	2.32	0.08	5.38E-01	8.21E-01	---	---	---	222373_at	---
2.14	2.23	0.09	5.38E-01	8.21E-01	---	---	---	239229_at	---
4.93	5.14	0.21	5.38E-01	8.21E-01	F3	coagulation factor III (thromboplastin, tissue factor)	chr1p22-p21	204363_at	NM_001993
3.55	3.65	0.10	5.38E-01	8.21E-01	PAPLN	papilin, proteoglycan-like sulfated glycoprotein	chr14q24.2	233896_s_at	NM_173462
4.28	4.65	0.36	5.38E-01	8.21E-01	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	chr16q12	222387_s_at	NM_018206
4.13	4.45	0.32	5.38E-01	8.21E-01	DLG1	Discs, large homolog 1 (Drosophila)	chr3q29	230229_at	NM_001098424 /// NM_004087
2.42	2.51	0.09	5.38E-01	8.21E-01	PRDM16	PR domain containing 16	chr1p36.23-p33	232424_at	NM_022114 /// NM_199454 /// XM_936932
2.34	2.43	0.09	5.38E-01	8.21E-01	FLJ31356	hypothetical protein FLJ31356	chr2p23.3	1560932_at	---
2.14	2.22	0.08	5.38E-01	8.21E-01	SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	chr1q21	206937_at	NM_003126
2.49	2.57	0.07	5.38E-01	8.21E-01	BRCA1	breast cancer 1, early onset	chr17q21	204531_s_at	NM_007294 /// NM_007295 /// NM_007296 /// NM_007297 /// NM_007298 /// NM_007299 /// NM_007300 /// NM_007302 /// NM_007303 /// NM_007304 /// NM_007305
2.37	2.46	0.09	5.38E-01	8.21E-01	BANF2	barrier to autointegration factor 2	chr20p12.1	232766_at	NM_001014977 /// NM_178477
2.01	2.09	0.08	5.38E-01	8.21E-01	LOC100131298	PRO1095	chr22q13.2	211436_at	XM_001724044 /// XM_001725577 /// XM_001726814

2.33	2.42	0.09	5.38E-01	8.21E-01	BBS9	Bardet-Biedl syndrome 9	chr7p14	37547_at	NM_001033604 /// NM_001033605 /// NM_014451 /// NM_198428
6.37	6.49	0.12	5.38E-01	8.21E-01	RNF121	ring finger protein 121	chr11q13.4	219021_at	NM_018320 /// NM_194452 /// NM_194453
5.39	5.49	0.09	5.38E-01	8.21E-01	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	chr14q12	210952_at	NM_001128126 /// NM_007077
6.10	6.18	0.08	5.38E-01	8.21E-01	CUX1	cut-like homeobox 1	chr7q22.1	214743_at	NM_001913 /// NM_181500 /// NM_181552
5.90	6.07	0.17	5.38E-01	8.21E-01	HIF1AN	hypoxia-inducible factor 1, alpha subunit inhibitor	chr10q24	218525_s_at	NM_017902
2.78	2.86	0.08	5.38E-01	8.21E-01	---	---	---	1563036_at	---
2.29	2.37	0.09	5.38E-01	8.21E-01	---	---	---	1564996_at	---
2.01	2.07	0.07	5.38E-01	8.21E-01	---	---	---	1566805_at	---
2.22	2.32	0.10	5.38E-01	8.21E-01	---	---	---	1564949_at	---
2.44	2.53	0.09	5.38E-01	8.21E-01	IQCA1	IQ motif containing with AAA domain 1	chr2q37.2-q37.3	220274_at	NM_024726
3.20	3.28	0.08	5.38E-01	8.21E-01	---	---	---	234549_at	---
5.63	5.87	0.24	5.39E-01	8.21E-01	TXNDC9	thioredoxin domain containing 9	chr2q11.2	203008_x_at	NM_005783
2.52	2.64	0.13	5.39E-01	8.21E-01	---	---	---	244239_at	---
3.10	3.20	0.10	5.39E-01	8.21E-01	DEFB103A /// DEFB103B	defensin, beta 103A /// defensin, beta 103B	chr8p23	224239_at	NM_001081551 /// NM_018661
2.08	2.18	0.09	5.39E-01	8.21E-01	---	---	---	1560510_at	---
3.00	3.10	0.10	5.39E-01	8.21E-01	ZNF701	zinc finger protein 701	chr19q13.41	220242_x_at	NM_018260
2.14	2.21	0.08	5.39E-01	8.21E-01	---	---	---	241649_at	---
1.94	2.02	0.08	5.39E-01	8.21E-01	---	---	---	239895_at	---
7.99	8.18	0.19	5.39E-01	8.21E-01	C20orf199	chromosome 20 open reading frame 199	chr20q13.13	226835_s_at	NR_003604 /// NR_003605 /// NR_003606
1.96	2.05	0.09	5.39E-01	8.21E-01	C1orf110	chromosome 1 open reading frame 110	chr1q23.3	1554960_at	NM_178550
2.22	2.30	0.08	5.39E-01	8.21E-01	UTP18	UTP18, small subunit (SSU) processome component, homolog (yeast)	chr17q21.33	222038_s_at	NM_016001
2.52	2.64	0.12	5.39E-01	8.21E-01	PDE7A	phosphodiesterase 7A	chr8q13	1552343_s_at	NM_002603 /// NM_002604
1.86	1.92	0.07	5.39E-01	8.21E-01	TFEC	transcription factor EC	chr7q31.2	236995_x_at	NM_001018058 /// NM_012252
2.63	2.72	0.10	5.39E-01	8.21E-01	GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	chr19q13.1-qter	229883_at	NM_000836
2.18	2.28	0.10	5.39E-01	8.21E-01	---	---	---	243230_at	---
6.69	6.96	0.27	5.39E-01	8.21E-01	FER1L3	fer-1-like 3, myoferlin (C. elegans)	chr10q24	201798_s_at	NM_013451 /// NM_133337
4.25	4.34	0.09	5.39E-01	8.22E-01	PSMG4	proteasome (prosome, macropain) assembly chaperone 4	chr6p25.2	233443_at	NM_001128591 /// NM_001128592 /// XR_017743 /// XR_017905 /// XR_041314
3.70	3.79	0.10	5.39E-01	8.22E-01	---	---	---	1556824_at	---
3.64	3.96	0.32	5.39E-01	8.22E-01	PHACTR2	phosphatase and actin regulator 2	chr6q24.2	244774_at	NM_001100164 /// NM_001100165 /// NM_001100166 /// NM_014721
2.47	2.57	0.10	5.39E-01	8.22E-01	---	---	---	1563114_at	---
2.63	2.72	0.08	5.39E-01	8.22E-01	---	---	---	215805_at	---
2.42	2.58	0.16	5.39E-01	8.22E-01	ATP8B4	ATPase, class I, type 8B, member 4	chr15q21.2	220416_at	NM_024837
2.12	2.20	0.08	5.39E-01	8.22E-01	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	chr6q22-q23	205065_at	NM_006208
5.76	6.06	0.30	5.39E-01	8.22E-01	GRK5	G protein-coupled receptor kinase 5	chr10q24-qter	204396_s_at	NM_005308
8.44	8.61	0.17	5.39E-01	8.22E-01	HEXB	hexosaminidase B (beta polypeptide)	chr5q13	201944_at	NM_000521
3.28	3.43	0.14	5.39E-01	8.22E-01	LAMA4	laminin, alpha 4	chr6q21	210990_s_at	NM_001105206 /// NM_001105207 /// NM_001105208 /// NM_001105209 /// NM_002290
2.73	2.84	0.11	5.39E-01	8.22E-01	FBXO15	F-box protein 15	chr18q22.3	231472_at	NM_152676
2.24	2.30	0.06	5.39E-01	8.22E-01	TXNDC6	thioredoxin domain containing 6	chr3q22.3	1562619_at	NM_178130

3.73	3.87	0.14	5.39E-01	8.22E-01	KIR2DL1	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1	chr19q13.4	210890_x_at	NM_014218
3.11	3.23	0.11	5.39E-01	8.22E-01	EXOC7	exocyst complex component 7	chr17q25.1	215413_at	NM_001013839 /// NM_015219
4.44	4.71	0.27	5.40E-01	8.22E-01	SOS1	son of sevenless homolog 1 (Drosophila)	chr2p22-p21	212777_at	NM_005633
6.02	6.24	0.22	5.40E-01	8.22E-01	RRAS2	related RAS viral (r-ras) oncogene homolog 2	chr11p15.2	212589_at	NM_001102669 /// NM_012250
3.95	4.14	0.19	5.40E-01	8.22E-01	UEVLD	UEV and lactate/malate dehyrogenase domains	chr11p15.1	220775_s_at	NM_001040697 /// NM_018314
2.46	2.56	0.10	5.40E-01	8.22E-01	LOC285819	hypothetical protein LOC285819	chr6p22.1	1562388_at	---
2.34	2.43	0.09	5.40E-01	8.22E-01	GPR64	G protein-coupled receptor 64	chrXp22.13	206002_at	NM_001079858 /// NM_001079859 /// NM_001079860 /// NM_005756
2.33	2.42	0.09	5.40E-01	8.22E-01	---	---	---	244282_at	---
3.97	4.04	0.07	5.40E-01	8.22E-01	BTBD7	BTB (POZ) domain containing 7	chr14q32.12-q32.13	217141_at	NM_001002860 /// NM_018167
4.33	4.58	0.25	5.40E-01	8.22E-01	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	chr4p14-p13	212985_at	NM_173075
4.07	4.18	0.12	5.40E-01	8.22E-01	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	chr9q31.1	208957_at	NM_015051
2.69	2.76	0.07	5.40E-01	8.22E-01	C3orf49	chromosome 3 open reading frame 49	chr3p14.1	1553805_at	XR_039937 /// XR_039938 /// XR_039939
3.23	3.74	0.51	5.40E-01	8.22E-01	CALCRL	calcitonin receptor-like	chr2q32.1	210815_s_at	NM_005795
8.54	8.67	0.12	5.40E-01	8.22E-01	HLA-A /// HLA-A29.1 /// HLA-B /// HLA-G /// HLA-H /// HLA-J	major histocompatibility complex, class I, A /// major histocompatibility complex class I HLA-A29.1 /// major histocompatibility complex, class I, B /// major histocompatibility complex, class I, G /// major histocompatibility complex, class I, H (pseudogene) /// major histocompatibility complex, class I, J (pseudogene)	chr6p21.3 /// chr6p21.31	217436_x_at	NM_001080840 /// NM_002116 /// NM_002127 /// NM_005514 /// NR_001434 /// XM_001713645 /// XM_001716873
2.37	2.53	0.16	5.40E-01	8.22E-01	---	---	---	1570285_at	---
1.85	1.93	0.08	5.40E-01	8.22E-01	---	---	---	240053_x_at	---
2.58	2.68	0.11	5.40E-01	8.22E-01	LOC653110	hypothetical LOC653110	chr10q11.22	1570140_at	XR_015244 /// XR_041080
3.31	3.47	0.16	5.40E-01	8.22E-01	TMEM48	transmembrane protein 48	chr1p32.3	218073_s_at	NM_018087
2.15	2.24	0.08	5.40E-01	8.22E-01	---	---	---	1556945_a_at	---
5.62	5.73	0.11	5.40E-01	8.22E-01	TP53RK	TP53 regulating kinase	chr20q13.2	235192_at	NM_033550
2.01	2.08	0.07	5.40E-01	8.22E-01	ALDOB	aldolase B, fructose-bisphosphate	chr9q21.3-q22.2	243901_at	NM_000035
3.31	3.57	0.26	5.40E-01	8.22E-01	---	---	---	1556054_at	---
3.07	3.15	0.09	5.40E-01	8.22E-01	LDB3	LIM domain binding 3	chr10q22.3-q23.2	216887_s_at	NM_001080114 /// NM_001080115 /// NM_001080116 /// NM_007078
3.14	3.25	0.11	5.40E-01	8.22E-01	LOC729234	fumarylacetoacetate hydrolase domain containing 2 pseudogene	chr2q11.2	228199_at	NR_003698
6.52	6.76	0.24	5.41E-01	8.22E-01	GCLC	glutamate-cysteine ligase, catalytic subunit	chr6p12	202923_s_at	NM_001498
4.70	5.03	0.33	5.41E-01	8.22E-01	PSIP1	PC4 and SFRS1 interacting protein 1	chr9p22.3	205961_s_at	NM_001128217 /// NM_021144 /// NM_033222
5.21	5.41	0.20	5.41E-01	8.22E-01	BIN2	bridging integrator 2	chr12q13	219191_s_at	NM_016293
4.10	4.25	0.15	5.41E-01	8.22E-01	DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	chr20q11.23	219512_at	NM_024918
2.48	2.62	0.14	5.41E-01	8.22E-01	RBMY3AP	RNA binding motif protein, Y-linked, family 3, member A pseudogene	chrYp11.2	1565320_at	NR_001573
4.50	4.60	0.10	5.41E-01	8.22E-01	C1orf69	chromosome 1 open reading frame 69	chr1q42.13	215490_at	NM_001010867
1.98	2.06	0.08	5.41E-01	8.22E-01	LOC441108	hypothetical gene supported by AK128882	chr5q31.1	1564276_at	NM_001013717
1.90	1.98	0.08	5.41E-01	8.22E-01	C15orf43	chromosome 15 open reading frame 43	chr15q21.1	240876_x_at	NM_152448
2.80	2.87	0.07	5.41E-01	8.22E-01	NCLN	nicalin homolog (zebrafish)	chr19p13.3	215859_at	NM_020170
2.74	2.86	0.12	5.41E-01	8.22E-01	EIF3J	eukaryotic translation initiation factor 3, subunit J	chr15q15.3	217364_x_at	NM_003758
2.03	2.14	0.10	5.41E-01	8.22E-01	CTXN3	cortexin 3	chr5q23.2	231391_at	NM_001048252 /// NM_001127385

3.36	3.46	0.10	5.41E-01	8.22E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	211551_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284																				
6.04	6.33	0.29	5.41E-01	8.22E-01	GRB10	growth factor receptor-bound protein 10	chr7p12-p11.2	209409_at	NM_001001549 /// NM_001001550 /// NM_001001555 /// NM_005311																				
2.09	2.19	0.10	5.41E-01	8.22E-01	CALCA	calcitonin-related polypeptide alpha	chr11p15.2-p15.1	217561_at	NM_001033952 /// NM_001033953 /// NM_001741																				
1.76	1.83	0.06	5.41E-01	8.22E-01	---	---	---	233616_at	---																				
2.06	2.15	0.08	5.41E-01	8.22E-01	C10orf99	chromosome 10 open reading frame 99	chr10q23.1	227736_at	NM_207373																				
5.96	6.15	0.20	5.41E-01	8.23E-01	SP100	SP100 nuclear antigen	chr2q37.1	202863_at	NM_001080391 /// NM_003113																				
2.17	2.25	0.08	5.41E-01	8.23E-01	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	chr3q13.2	220237_at	NM_022488																				
2.42	2.50	0.08	5.41E-01	8.23E-01	---	---	---	1559333_at	---																				
2.15	2.22	0.07	5.41E-01	8.23E-01	---	---	---	1564212_at	---																				
4.30	4.40	0.10	5.41E-01	8.23E-01	LOC390688	CDC37-like	chr16p11.2	217314_at	NM_001080829																				
2.63	2.71	0.08	5.41E-01	8.23E-01	---	---	---	220913_at	---																				
2.82	2.98	0.16	5.41E-01	8.23E-01	NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1	chr11q12	207895_at	NM_005468																				
2.42	2.51	0.09	5.41E-01	8.23E-01	CACNA1E	calcium channel, voltage-dependent, R type, alpha 1E subunit	chr1q25-q31	236013_at	NM_000721																				
2.26	2.35	0.09	5.41E-01	8.23E-01	FLJ32214	hypothetical LOC147664	chr19q13.41	1553255_at	NM_152473																				
1.80	1.87	0.07	5.41E-01	8.23E-01	---	---	---	242802_x_at	---																				
2.34	2.42	0.09	5.41E-01	8.23E-01	LOC643037	similar to hCG1730248	chr11q21	243803_at	XM_926406 /// XM_936787																				
4.90	4.97	0.07	5.41E-01	8.23E-01	TMEM72	transmembrane protein 72	chr10q11.21	1558323_at	NM_001123376 /// XM_001717287 /// XM_926597 /// XM_937160																				
7.70	7.97	0.27	5.41E-01	8.23E-01	FH	fumarate hydratase	chr1q42.1	203033_x_at	NM_000143																				
2.47	2.67	0.20	5.41E-01	8.23E-01	RAB3B	RAB3B, member RAS oncogene family	chr1p32-p31	227123_at	NM_002867																				
3.64	3.75	0.11	5.42E-01	8.23E-01	ABLIM2	Actin binding LIM protein family, member 2	chr4p16-p15	1567622_at	NM_001130083 /// NM_001130084 /// NM_001130085 /// NM_001130086 /// NM_001130087 /// NM_001130088 /// NM_032432																				
2.55	2.66	0.11	5.42E-01	8.23E-01	---	---	---	220879_at	---																				
2.29	2.38	0.09	5.41E-01	8.23E-01	FNIP1	Folliculin interacting protein 1	chr5q23.3	1559060_a_at	NM_001008738 /// NM_133372																				
2.81	2.90	0.09	5.42E-01	8.23E-01	DNTT	deoxynucleotidyltransferase, terminal	chr10q23-q24	210487_at	NM_001017520 /// NM_004088																				
4.66	4.75	0.09	5.42E-01	8.23E-01	LOC100133864 /// NOMO1 /// NOMO2 /// NOMO3	similar to pM5 (3 partial) /// NODAL modulator 1 /// NODAL modulator 2 /// NODAL modulator 3	chr16p12.3 /// chr16p13 /// chr16p13.11	242922_at	NM_001004060 /// NM_001004067 /// NM_014287 /// NM_173614 /// XM_001716489 /// XM_001716493 /// XM_001720597																				
2.46	2.54	0.09	5.42E-01	8.23E-01	---	---	---	1560678_at	---																				
2.39	2.48	0.08	5.42E-01	8.23E-01	RGS22	regulator of G-protein signaling 22	chr8q22.2	223691_at	NM_015668																				
2.50	2.58	0.08	5.41E-01	8.23E-01	ETV5	Ets variant gene 5 (ets-related molecule)	chr3q28	231083_at	NM_004454																				

2.11	2.17	0.06	5.42E-01	8.23E-01	RMST	rhabdomyosarcoma 2 associated transcript (non-protein coding)	chr12q23.1|12q21	1562633_at	NR_024037 /// XR_000219 /// XR_001330																				
8.22	8.42	0.20	5.42E-01	8.23E-01	---	---	---	226377_at	---																				
2.65	2.77	0.13	5.42E-01	8.23E-01	ABTB1	Ankyrin repeat and BTB (POZ) domain containing 1	chr3q21	229162_s_at	NM_032548 /// NM_172027 /// NM_172028																				
2.68	2.80	0.12	5.42E-01	8.23E-01	LOC401220 /// LOC401222	hypothetical gene supported by BC036933 /// hypothetical gene supported by BC036933	chr5q35.3	1566039_a_at	XM_379378 /// XM_379380 /// XM_945580																				
2.35	2.46	0.11	5.42E-01	8.23E-01	---	---	---	216211_at	---																				
2.43	2.54	0.11	5.42E-01	8.23E-01	---	---	---	234249_at	---																				
2.16	2.24	0.08	5.42E-01	8.23E-01	---	---	---	240431_at	---																				
5.21	5.40	0.19	5.42E-01	8.23E-01	---	---	---	216813_at	---																				
5.60	5.73	0.13	5.42E-01	8.23E-01	SNX15	sorting nexin 15	chr11q12	205482_x_at	NM_013306 /// NM_147777																				
2.41	2.53	0.12	5.42E-01	8.23E-01	---	---	---	238787_at	---																				
3.27	3.38	0.11	5.42E-01	8.23E-01	POFUT2	protein O-fucosyltransferase 2	chr21q22.3	1555546_a_at	NM_015227 /// NM_133634 /// NM_133635 /// NR_004858																				
2.50	2.61	0.11	5.42E-01	8.23E-01	---	---	---	1562699_at	---																				
2.21	2.29	0.09	5.42E-01	8.23E-01	MYO10	myosin X	chr5p15.1-p14.3	244350_at	NM_012334																				
2.76	2.84	0.08	5.42E-01	8.23E-01	---	---	---	243830_at	---																				
2.31	2.40	0.09	5.42E-01	8.23E-01	KIAA2018	KIAA2018	chr3q13.2	1559601_at	NM_001009899																				
3.68	3.80	0.12	5.42E-01	8.23E-01	DSCR9	Down syndrome critical region gene 9 (non-protein coding)	chr21q22.13	230470_at	NM_148675																				
2.96	3.05	0.09	5.42E-01	8.23E-01	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	chr12p13.3	242973_at	NM_000719 /// NM_001129827 /// NM_001129829 /// NM_001129830 /// NM_001129831 /// NM_001129832 /// NM_001129833 /// NM_001129834 /// NM_001129835 /// NM_001129836 /// NM_001129837 /// NM_001129838 /// NM_001129839 /// NM_001129840 /// NM_001129841 /// NM_001129842 /// NM_001129843 /// NM_001129844 /// NM_001129846 /// NM_199460																				
2.45	2.57	0.12	5.42E-01	8.23E-01	TCF12	transcription factor 12	chr15q21	215611_at	NM_003205 /// NM_207036 /// NM_207037 /// NM_207038 /// NM_207040																				
2.76	2.87	0.11	5.42E-01	8.23E-01	ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	chr16q24.1	206043_s_at	NM_014861																				

2.46	2.56	0.10	5.42E-01	8.23E-01	LOC255480	hypothetical protein LOC255480	chr12q24.21	239919_at	XM_001134335 /// XM_001719855 /// XM_001723369
2.39	2.46	0.07	5.42E-01	8.23E-01	---	---	---	234651_at	---
4.93	5.13	0.20	5.42E-01	8.23E-01	NID1	nidogen 1	chr1q43	202008_s_at	NM_002508
2.27	2.37	0.09	5.42E-01	8.23E-01	---	---	---	234186_at	---
4.59	4.75	0.16	5.42E-01	8.23E-01	FGFR1OP	FGFR1 oncogene partner	chr6q27	1568678_s_at	NM_007045 /// NM_194429
2.25	2.36	0.11	5.42E-01	8.23E-01	UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)	chr17q11.2	241025_at	NM_018428
3.31	3.50	0.19	5.43E-01	8.23E-01	AHNAK	AHNAK nucleoprotein	chr11q12.2	235281_x_at	NM_001620 /// NM_024060
5.57	5.74	0.17	5.43E-01	8.23E-01	THUMPD1	THUMP domain containing 1	chr16p12.2	213025_at	NM_017736
3.94	4.07	0.13	5.43E-01	8.23E-01	SLC41A2	solute carrier family 41, member 2	chr12q23.3	223798_at	NM_032148
2.13	2.24	0.12	5.42E-01	8.23E-01	ZNF567	zinc finger protein 567	chr19q13.12	242429_at	NM_152603
2.09	2.20	0.11	5.42E-01	8.23E-01	TOP2A	Topoisomerase (DNA) II alpha 170kDa	chr17q21-q22	237469_at	NM_001067
2.20	2.28	0.08	5.42E-01	8.23E-01	---	---	---	233738_at	---
4.21	4.29	0.08	5.43E-01	8.23E-01	---	---	---	216363_at	---
2.43	2.52	0.08	5.42E-01	8.23E-01	---	---	---	237816_at	---
2.34	2.41	0.07	5.43E-01	8.23E-01	---	---	---	240869_at	---
2.03	2.10	0.07	5.43E-01	8.23E-01	---	---	---	1558496_at	---
1.95	2.02	0.07	5.43E-01	8.23E-01	---	---	---	242672_at	---
4.23	4.52	0.29	5.43E-01	8.23E-01	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	chr6p12.3	204160_s_at	NM_014936
2.83	2.93	0.10	5.43E-01	8.23E-01	NUDT14	Nudix (nucleoside diphosphate linked moiety X)-type motif 14	chr14q32.33	231910_at	NM_177533
6.17	6.69	0.52	5.43E-01	8.23E-01	CFI	complement factor I	chr4q25	1555564_a_at	NM_000204
2.52	2.67	0.15	5.43E-01	8.23E-01	---	---	---	215555_at	---
4.03	4.17	0.14	5.43E-01	8.23E-01	PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta	chr4p16.3	238153_at	NM_000283
9.22	9.35	0.13	5.43E-01	8.23E-01	SURF1	surfeit 1	chr9q34.2	204295_at	NM_003172
2.04	2.14	0.11	5.43E-01	8.23E-01	---	---	---	215768_at	---
2.28	2.38	0.10	5.43E-01	8.23E-01	---	---	---	1557898_at	---
2.35	2.49	0.14	5.43E-01	8.23E-01	CDCA7	cell division cycle associated 7	chr2q31	224428_s_at	NM_031942 /// NM_145810
2.86	3.00	0.14	5.43E-01	8.23E-01	---	---	---	239677_at	---
2.05	2.16	0.11	5.43E-01	8.23E-01	C8orf47	chromosome 8 open reading frame 47	chr8q22.2	1552389_at	NM_173549
5.40	5.49	0.10	5.43E-01	8.23E-01	C16orf13	Chromosome 16 open reading frame 13	chr16p13.3	230851_x_at	NM_001040160 /// NM_001040161 /// NM_001040162 /// NM_001040165 /// NM_032366
4.51	4.70	0.19	5.43E-01	8.23E-01	HERC6	hect domain and RLD 6	chr4q22.1	219352_at	NM_017912
6.63	6.80	0.17	5.43E-01	8.23E-01	STARD3	StAR-related lipid transfer (START) domain containing 3	chr17q11-q12	202991_at	NM_006804
2.02	2.12	0.10	5.43E-01	8.23E-01	---	---	---	1558606_s_at	---
2.38	2.44	0.07	5.43E-01	8.23E-01	ZNF850P	zinc finger protein 850 pseudogene	chr19q13.12	244640_at	XM_001720220 /// XM_001720258 /// XM_001722534
3.39	3.51	0.12	5.43E-01	8.23E-01	FAM22A /// FAM22C /// FAM22D /// FAM22E	family with sequence similarity 22, member A /// family with sequence similarity 22, member C /// family with sequence similarity 22, member D /// family with sequence similarity 22, member E	chr10q22.3 /// chr10q23.2	235332_at	NM_001009610 /// NM_001099338 /// XM_001125950 /// XM_925903
5.48	5.79	0.31	5.43E-01	8.23E-01	---	---	---	239331_at	---
2.10	2.20	0.10	5.43E-01	8.23E-01	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	chr10p13	242927_at	NM_001033855 /// NM_001033857 /// NM_001033858 /// NM_022487
2.07	2.15	0.08	5.43E-01	8.23E-01	OR5K1	olfactory receptor, family 5, subfamily K, member 1	chr3q11.2	1567288_at	NM_001004736
2.07	2.14	0.08	5.43E-01	8.23E-01	---	---	---	242483_at	---
3.06	3.20	0.15	5.43E-01	8.23E-01	OTUB2	OTU domain, ubiquitin aldehyde binding 2	chr14q32.13	219369_s_at	NM_023112
2.71	2.86	0.15	5.44E-01	8.23E-01	S100B	S100 calcium binding protein B	chr21q22.3	209686_at	NM_006272

2.47	2.60	0.14	5.44E-01	8.23E-01	---	---	---	213808_at	---
2.27	2.37	0.11	5.44E-01	8.23E-01	---	---	---	242537_at	---
10.08	10.18	0.10	5.44E-01	8.23E-01	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	chr11q23.1-q23.2	218357_s_at	NM_012459
4.12	4.22	0.10	5.44E-01	8.23E-01	CXorf21	chromosome X open reading frame 21	chrXp21.2	220252_x_at	NM_025159
3.50	3.72	0.23	5.44E-01	8.23E-01	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	chr5q11-q12	205488_at	NM_006144
3.04	3.16	0.12	5.44E-01	8.23E-01	LOC254057	hypothetical protein LOC254057	chr3q21.3	232370_at	---
3.18	3.29	0.12	5.44E-01	8.23E-01	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	chr19p13.1	211109_at	NM_000215
2.19	2.28	0.09	5.44E-01	8.23E-01	TMTC2	transmembrane and tetratricopeptide repeat containing 2	chr12q21.31	235775_at	NM_152588
3.00	3.10	0.11	5.44E-01	8.24E-01	GTSE1	G-2 and S-phase expressed 1	chr22q13.2-q13.3	204317_at	NM_016426
5.93	6.24	0.30	5.44E-01	8.24E-01	TMEM77	transmembrane protein 77	chr1p13.3	225230_at	NM_178454
3.76	3.91	0.15	5.44E-01	8.24E-01	---	---	---	243537_at	---
1.76	1.84	0.08	5.44E-01	8.24E-01	---	---	---	1562480_at	---
2.79	2.87	0.09	5.44E-01	8.24E-01	---	---	---	243926_at	---
2.81	2.88	0.07	5.44E-01	8.24E-01	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	chr10q24-q25.2	1553528_a_at	NM_006951
2.25	2.39	0.13	5.44E-01	8.24E-01	XRN1	5'-3' exoribonuclease 1	chr3q23	1555785_a_at	NM_001042604 /// NM_019001
3.94	4.10	0.15	5.44E-01	8.24E-01	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	chr20q13.3-qter	204849_at	NM_006602
3.54	3.64	0.09	5.44E-01	8.24E-01	EMX2OS	EMX2 opposite strand (non-protein coding)	chr10q26.1	230963_at	NR_002791
3.51	3.57	0.06	5.44E-01	8.24E-01	LRP6	low density lipoprotein receptor-related protein 6	chr12p11-p13	34697_at	NM_002336
4.08	4.25	0.17	5.44E-01	8.24E-01	---	---	---	237262_at	---
2.05	2.13	0.08	5.44E-01	8.24E-01	C8orf46	chromosome 8 open reading frame 46	chr8q13.1	228695_at	NM_152765
2.45	2.52	0.07	5.44E-01	8.24E-01	LMO7	LIM domain 7	chr13q22.2	241140_at	NM_005358
3.60	3.74	0.14	5.44E-01	8.24E-01	C13orf18 /// LOC728970	chromosome 13 open reading frame 18 /// hypothetical LOC728970	chr13q14.12 /// chr13q14.13	219471_at	NM_025113 /// XM_001132115 /// XM_001133896 /// XM_001720155
7.34	7.47	0.12	5.44E-01	8.24E-01	CBARA1	calcium binding atopy-related autoantigen 1	chr10q22.1	216903_s_at	NM_006077
6.49	6.61	0.12	5.44E-01	8.24E-01	PREX1	phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1	chr20q13.13	224909_s_at	NM_020820
3.71	3.81	0.10	5.44E-01	8.24E-01	---	---	---	1562409_s_at	---
5.70	5.88	0.18	5.44E-01	8.24E-01	CFL2	cofilin 2 (muscle)	chr14q12	233496_s_at	NM_021914 /// NM_138638
3.06	3.18	0.12	5.44E-01	8.24E-01	C10orf90	chromosome 10 open reading frame 90	chr10q26.2	1562657_a_at	NM_001004298
3.39	3.50	0.11	5.44E-01	8.24E-01	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	chr2p24.1	209757_s_at	NM_005378
4.42	4.53	0.11	5.44E-01	8.24E-01	NKX2-8	NK2 homeobox 8	chr14q13.3	207451_at	NM_014360
1.90	1.97	0.07	5.44E-01	8.24E-01	---	---	---	217440_at	---
3.49	3.57	0.07	5.44E-01	8.24E-01	PALM3	Paralemmin-3	chr19p13.12	231018_at	XM_001726585 /// XM_292820 /// XM_937298
1.85	1.91	0.06	5.44E-01	8.24E-01	---	---	---	242910_x_at	---
2.61	2.80	0.19	5.44E-01	8.24E-01	NRXN3	neurexin 3	chr14q31	229649_at	NM_001105250 /// NM_004796 /// NM_138970
2.44	2.53	0.09	5.45E-01	8.24E-01	---	---	---	235808_at	---
5.78	6.04	0.25	5.45E-01	8.24E-01	GOLT1B	golgi transport 1 homolog B (S. cerevisiae)	chr12p12.1	218193_s_at	NM_016072
4.79	5.05	0.26	5.45E-01	8.24E-01	SCOC	short coiled-coil protein	chr4q31.1	223341_s_at	NM_032547
6.52	6.70	0.18	5.45E-01	8.24E-01	CBX1	chromobox homolog 1 (HP1 beta homolog Drosophila)	chr17q21.32	201518_at	NM_001127228 /// NM_006807
5.32	5.42	0.10	5.45E-01	8.24E-01	---	---	---	239364_at	---
2.17	2.26	0.09	5.45E-01	8.24E-01	ZNRF1	zinc and ring finger 1	chr16q23.1	225960_at	NM_032268
2.34	2.42	0.08	5.45E-01	8.24E-01	MYNN	Myoneurin	chr3q26.2	1566108_at	NM_018657
2.81	2.89	0.08	5.45E-01	8.24E-01	---	---	---	244628_at	---
1.68	1.75	0.07	5.45E-01	8.24E-01	CADPS	Ca++-dependent secretion activator	chr3p14.2	1568603_at	NM_003716 /// NM_183393 /// NM_183394
3.24	3.30	0.06	5.45E-01	8.24E-01	---	---	---	1560102_at	---
4.67	4.79	0.12	5.45E-01	8.24E-01	HNF1B	HNF1 homeobox B	chr17cen-q21.3	205313_at	NM_000458
2.55	2.65	0.10	5.45E-01	8.24E-01	FLJ40142	FLJ40142 protein	chr12q24.11	1556299_s_at	NM_207435
1.92	1.98	0.07	5.45E-01	8.24E-01	---	---	---	1561864_at	---
2.98	3.09	0.11	5.45E-01	8.24E-01	TMEM174	Transmembrane protein 174	chr5q13.2	243569_at	NM_153217
6.68	6.97	0.29	5.45E-01	8.24E-01	KIDINS220	kinase D-interacting substrate of 220 kDa	chr2p24	212163_at	NM_020738
3.41	3.52	0.11	5.45E-01	8.24E-01	---	---	---	232177_at	---
3.35	3.44	0.10	5.45E-01	8.24E-01	SPIRE2	spire homolog 2 (Drosophila)	chr16q24	227706_at	NM_032451

2.06	2.13	0.07	5.45E-01	8.24E-01	---	---	---	243236_at	---
3.97	4.14	0.17	5.45E-01	8.24E-01	FAM85A	family with sequence similarity 85, member A	chr8p23.1	238716_at	---
2.82	2.93	0.11	5.45E-01	8.24E-01	ALKBH1	alkB, alkylation repair homolog 1 (E. coli)	chr14q24.3	236721_at	NM_006020
2.58	2.67	0.08	5.45E-01	8.24E-01	---	---	---	231137_at	---
2.09	2.17	0.08	5.45E-01	8.24E-01	---	---	---	1562046_at	---
2.32	2.40	0.08	5.45E-01	8.24E-01	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	chr19q13.3	204816_s_at	NM_014681
2.14	2.22	0.08	5.45E-01	8.24E-01	C3orf63	Chromosome 3 open reading frame 63	chr3p14.3	227460_at	NM_001112736 /// NM_015224
2.23	2.31	0.07	5.45E-01	8.24E-01	LAMA3	laminin, alpha 3	chr18q11.2	234719_at	NM_000227 /// NM_001127717 /// NM_001127718 /// NM_198129
1.92	1.99	0.07	5.45E-01	8.24E-01	PXDNL	peroxidasin homolog (Drosophila)-like	chr8q11.22-q11.23	241942_at	NM_144651
1.90	1.97	0.07	5.45E-01	8.24E-01	DOPEY1	dopey family member 1	chr6q15	1564387_at	NM_015018
1.86	1.93	0.07	5.46E-01	8.24E-01	---	---	---	236138_at	---
4.21	4.34	0.13	5.46E-01	8.24E-01	CCDC60	coiled-coil domain containing 60	chr12q24.23	1554117_at	NM_178499
4.98	5.09	0.11	5.46E-01	8.24E-01	C20orf57 /// DUSP15	chromosome 20 open reading frame 57 /// dual specificity phosphatase 15	chr20q11.21	230402_at	NM_001012644 /// NM_080611 /// NM_177991
1.98	2.09	0.11	5.46E-01	8.24E-01	FLJ43390	hypothetical LOC646113	chr14q23.2	236902_at	NR_015358 /// XR_041177 /// XR_041178 /// XR_041179
2.17	2.25	0.08	5.46E-01	8.24E-01	FANCC	Fanconi anemia, complementation group C	chr9q22.3	242654_at	NM_000136
3.84	4.05	0.21	5.46E-01	8.24E-01	ZNF423	zinc finger protein 423	chr16q12	214761_at	NM_015069
2.44	2.54	0.10	5.46E-01	8.24E-01	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	chr4q28.1	219427_at	NM_024582
2.55	2.75	0.20	5.46E-01	8.24E-01	AHNAK2	AHNAK nucleoprotein 2	chr14q32.33	212992_at	NM_138420
3.81	3.94	0.12	5.46E-01	8.24E-01	CCDC114	coiled-coil domain containing 114	chr19q13.32	233157_x_at	NM_144577
2.62	2.73	0.10	5.46E-01	8.24E-01	IL1A	interleukin 1, alpha	chr2q14	208200_at	NM_000575
2.50	2.58	0.08	5.46E-01	8.24E-01	C6orf105	chromosome 6 open reading frame 105	chr6p24.1	215100_at	NM_032744
2.07	2.14	0.07	5.46E-01	8.24E-01	---	---	---	207888_at	---
5.68	5.88	0.20	5.46E-01	8.25E-01	NF1	neurofibromin 1	chr17q11.2	212678_at	NM_000267 /// NM_001042492 /// NM_001128147
2.20	2.28	0.08	5.46E-01	8.25E-01	---	---	---	1564227_at	---
3.06	3.18	0.12	5.46E-01	8.25E-01	TUBB4Q	tubulin, beta polypeptide 4, member Q	chr4q35	211915_s_at	NM_020040 /// XM_001713864
2.17	2.25	0.08	5.46E-01	8.25E-01	SFXN5	sideroflexin 5	---	232691_at	NM_144579
6.32	6.56	0.24	5.46E-01	8.25E-01	PWP1	PWP1 homolog (S. cerevisiae)	chr12q23.3	201608_s_at	NM_007062
3.66	3.90	0.24	5.46E-01	8.25E-01	NARG1	NMDA receptor regulated 1	chr4q31.1	222837_s_at	NM_057175
2.15	2.23	0.08	5.46E-01	8.25E-01	---	---	---	1561121_at	---
2.36	2.43	0.07	5.46E-01	8.25E-01	---	---	---	1562052_at	---
3.35	3.47	0.12	5.46E-01	8.25E-01	SGSM1	small G protein signaling modulator 1	chr22q11.23	242921_at	NM_001039948 /// NM_001098497 /// NM_001098498 /// NM_133454
4.95	5.15	0.21	5.46E-01	8.25E-01	TSN	translin	chr2q21.1	201513_at	NM_004622
2.20	2.27	0.08	5.46E-01	8.25E-01	C11orf63	chromosome 11 open reading frame 63	chr11q24.1	220141_at	NM_024806 /// NM_199124
2.63	2.76	0.13	5.46E-01	8.25E-01	DCHS2	dachsous 2 (Drosophila)	chr4q32.1	220373_at	NM_017639
4.36	4.57	0.22	5.46E-01	8.25E-01	SPAG4	sperm associated antigen 4	chr20q11.21	219888_at	NM_003116
6.10	6.31	0.21	5.47E-01	8.25E-01	FLJ11506	hypothetical protein FLJ11506	chr15q22.33-q23	202852_s_at	NM_024666
5.71	5.91	0.19	5.47E-01	8.25E-01	CANX	calnexin	chr5q35	238034_at	NM_001024649 /// NM_001746
3.81	3.99	0.18	5.47E-01	8.25E-01	C7orf58	chromosome 7 open reading frame 58	chr7q31.31	220032_at	NM_001105533 /// NM_024913
4.76	4.92	0.16	5.47E-01	8.25E-01	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	chr9q22.3	206101_at	NM_001393
3.34	3.45	0.11	5.47E-01	8.25E-01	EYA3	eyes absent homolog 3 (Drosophila)	chr1p36	206379_at	NM_001990
4.61	4.71	0.10	5.47E-01	8.25E-01	SNX22	sorting nexin 22	chr15q22.31	230509_at	NM_024798

5.34	5.56	0.22	5.47E-01	8.25E-01	RBM27	RNA binding motif protein 27	chr5q32	225326_at	NM_018989 /// XM_001720239 /// XM_001723796 /// XM_001723897
2.46	2.55	0.09	5.47E-01	8.25E-01	---	---	---	1566880_at	---
2.98	3.09	0.11	5.47E-01	8.25E-01	LMTK2	lemur tyrosine kinase 2	chr7q21.3	206223_at	NM_014916
2.07	2.15	0.08	5.47E-01	8.25E-01	MAGIX	MAGI family member, X-linked	chrXp11.23	219965_s_at	NM_001099680 /// NM_001099681 /// NM_001099682 /// NM_024859
2.37	2.47	0.10	5.47E-01	8.25E-01	LOC401176	hypothetical gene supported by BC043001	chr5p15.1	1562645_at	---
2.75	2.86	0.11	5.47E-01	8.25E-01	COL22A1	collagen, type XXII, alpha 1	chr8q24.23	228873_at	NM_152888
3.58	3.67	0.09	5.47E-01	8.25E-01	---	---	---	1558821_s_at	---
2.60	2.69	0.09	5.47E-01	8.25E-01	ADAM20	ADAM metallopeptidase domain 20	chr14q24.1	207422_at	NM_003814
2.50	2.64	0.14	5.47E-01	8.25E-01	UHRF1BP1	UHRF1 binding protein 1	chr6p21	1568789_at	NM_017754
2.60	2.71	0.11	5.47E-01	8.25E-01	LDB3	LIM domain binding 3	chr10q22.3-q23.2	213371_at	NM_001080114 /// NM_001080115 /// NM_001080116 /// NM_007078
4.24	4.34	0.11	5.47E-01	8.25E-01	---	---	---	1563243_at	---
2.31	2.41	0.10	5.47E-01	8.25E-01	NCAM1	neural cell adhesion molecule 1	chr11q23.1	217359_s_at	NM_000615 /// NM_001076682 /// NM_181351
2.71	2.80	0.09	5.47E-01	8.25E-01	FAM135B	family with sequence similarity 135, member B	chr8q24.23	224001_at	NM_015912
5.61	5.94	0.33	5.47E-01	8.25E-01	ZNF559	zinc finger protein 559	chr19p13.2	224518_s_at	NM_032497
3.60	3.70	0.10	5.47E-01	8.25E-01	LOC440345 /// LOC440354 /// LOC595101 /// LOC641298 /// LOC728423 /// LOC729513 /// SMG1	hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1 /// hypothetical LOC728423 /// similar to PI-3-kinase-related kinase SMG-1 /// PI-3-kinase-related kinase SMG-1	chr16p11.2 /// chr16p12.1 /// chr16p12.2 /// chr16p12.3 /// chr16q22.1	244766_at	NM_015092 /// NR_002453 /// NR_002473 /// XR_015571 /// XR_015617 /// XR_015786 /// XR_039881 /// XR_041850 /// XR_042165
2.31	2.41	0.10	5.47E-01	8.25E-01	PLLP	plasma membrane proteolipid (plasmolipin)	chr16q13	217265_at	NM_015993
2.88	2.95	0.08	5.47E-01	8.25E-01	hCG_2039148	hypothetical protein LOC100132356	chr5p13.1	1558310_s_at	XM_001715035 /// XM_001717477
2.91	2.99	0.08	5.47E-01	8.25E-01	---	---	---	215204_at	---
2.31	2.38	0.07	5.47E-01	8.25E-01	---	---	---	1563656_at	---
1.91	2.01	0.09	5.47E-01	8.25E-01	TAS2R48	taste receptor, type 2, member 48	chr12p13.2	1570384_at	NM_176888
2.63	2.72	0.09	5.47E-01	8.25E-01	---	---	---	240629_at	---
2.24	2.33	0.08	5.47E-01	8.25E-01	SOX5	SRY (sex determining region Y)-box 5	chr12p12.1	207336_at	NM_006940 /// NM_152989 /// NM_178010
5.56	5.80	0.25	5.47E-01	8.25E-01	DLAT	dihydrolipoamide S-acetyltransferase	chr11q23.1	212568_s_at	NM_001931
6.14	6.30	0.15	5.47E-01	8.25E-01	CCDC28B	coiled-coil domain containing 28B	chr1p35.1	221912_s_at	NM_024296
2.12	2.21	0.09	5.47E-01	8.25E-01	PSMAL	growth-inhibiting protein 26	chr11q14.3	211303_x_at	NM_153696
2.69	2.89	0.20	5.48E-01	8.25E-01	CCR2 /// FLJ78302	chemokine (C-C motif) receptor 2 /// chemokine (C-C motif) receptor 2-like	chr3p21.31	206978_at	NM_000647 /// NM_000648 /// NM_001123041 /// NM_001123396 /// XM_001133430 /// XM_001133431
3.22	3.35	0.13	5.48E-01	8.25E-01	ANKRD13C	ankyrin repeat domain 13C	chr1p32.3-p31.3	227375_at	NM_030816
2.12	2.21	0.08	5.48E-01	8.25E-01	ZNF396	zinc finger protein 396	chr18q12	1555166_a_at	NM_145756
2.09	2.17	0.08	5.48E-01	8.25E-01	---	---	---	241244_at	---
4.57	4.70	0.13	5.48E-01	8.25E-01	GM2A	GM2 ganglioside activator	chr5q31.3-q33.1	235678_at	NM_000405
3.83	3.95	0.11	5.48E-01	8.25E-01	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	chr13q34	237555_at	NM_024537
2.23	2.31	0.08	5.48E-01	8.26E-01	---	---	---	1566181_at	---

1.94	2.01	0.07	5.48E-01	8.26E-01	ARPP-21	cyclic AMP-regulated phosphoprotein, 21 kD	chr3p22.3	1560018_at	NM_001025068 /// NM_001025069 /// NM_016300 /// NM_198399
3.87	3.98	0.11	5.48E-01	8.26E-01	BCL2L11	BCL2-like 11 (apoptosis facilitator)	chr2q13	1553088_a_at	NM_006538 /// NM_138621 /// NM_207002
3.41	3.49	0.09	5.48E-01	8.26E-01	RUNX2	runt-related transcription factor 2	chr6p21	236858_s_at	NM_001015051 /// NM_001024630 /// NM_004348
3.15	3.25	0.10	5.48E-01	8.26E-01	AURKC	aurora kinase C	chr19q13.43	211107_s_at	NM_001015878 /// NM_001015879 /// NM_003160
2.18	2.27	0.09	5.48E-01	8.26E-01	---	---	---	1562777_at	---
4.81	5.01	0.20	5.48E-01	8.26E-01	---	---	---	242652_at	---
2.31	2.39	0.08	5.48E-01	8.26E-01	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B	chr12q23.1	219989_s_at	NM_020140 /// NM_152788 /// NM_181670
2.05	2.15	0.10	5.48E-01	8.26E-01	---	---	---	233260_at	---
6.33	6.55	0.22	5.48E-01	8.26E-01	ELP2	elongation protein 2 homolog (S. cerevisiae)	chr18q12.2	231713_s_at	NM_018255
3.54	3.78	0.24	5.48E-01	8.26E-01	SYNJ2	synaptojanin 2	chr6q25.3	210612_s_at	NM_003898
4.80	4.94	0.14	5.48E-01	8.26E-01	---	---	---	239050_s_at	---
5.10	5.27	0.17	5.49E-01	8.26E-01	COX16	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr14q24.2	217645_at	NM_016468
6.69	6.83	0.14	5.49E-01	8.26E-01	FAM45A /// FAM45B	family with sequence similarity 45, member A /// family with sequence similarity 45, member B	chr10q25 /// chrXq25	225351_at	NM_018472 /// NM_207009
2.14	2.22	0.08	5.49E-01	8.26E-01	MANEA	mannosidase, endo-alpha	chr6q16.1	1555227_a_at	NM_024641
4.31	4.41	0.09	5.49E-01	8.26E-01	NPAS1	neuronal PAS domain protein 1	chr19q13.2-q13.3	216975_x_at	NM_002517
1.98	2.05	0.07	5.49E-01	8.26E-01	---	---	---	237458_at	---
3.77	3.90	0.13	5.49E-01	8.26E-01	---	---	---	1560579_s_at	---
5.12	5.22	0.11	5.49E-01	8.26E-01	ROM1	retinal outer segment membrane protein 1	chr11q13	205806_at	NM_000327
2.95	3.05	0.11	5.49E-01	8.26E-01	TNFRSF4	tumor necrosis factor receptor superfamily, member 4	chr1p36	208023_at	NM_003327
2.07	2.14	0.07	5.49E-01	8.26E-01	---	---	---	231138_at	---
3.33	3.45	0.12	5.49E-01	8.27E-01	C20orf195	chromosome 20 open reading frame 195	chr20q13.33	220426_at	NM_024059
2.72	2.82	0.10	5.49E-01	8.27E-01	---	---	---	1561314_at	---
3.75	3.83	0.08	5.49E-01	8.27E-01	PCDHGA3	protocadherin gamma subfamily A, 3	chr5q31	211879_x_at	NM_018916 /// NM_032011
2.05	2.20	0.16	5.49E-01	8.27E-01	EPHA3	EPH receptor A3	chr3p11.2	206070_s_at	NM_005233 /// NM_182644
2.51	2.63	0.12	5.49E-01	8.27E-01	RIMBP2	RIMS binding protein 2	chr12q24.33	238817_at	NM_015347
5.42	5.54	0.12	5.49E-01	8.27E-01	C9orf142	chromosome 9 open reading frame 142	chr9q34.3	226070_at	NM_183241
2.58	2.68	0.10	5.49E-01	8.27E-01	---	---	---	216416_at	---
2.85	2.95	0.10	5.49E-01	8.27E-01	C14orf105	chromosome 14 open reading frame 105	chr14q23.1	1569434_at	NM_018168
2.10	2.19	0.09	5.49E-01	8.27E-01	CD28	CD28 molecule	chr2q33	211861_x_at	NM_006139
2.06	2.13	0.07	5.49E-01	8.27E-01	C3orf56	chromosome 3 open reading frame 56	chr3q21.3	1562762_at	NM_001007534
4.31	4.67	0.36	5.49E-01	8.27E-01	CD58	CD58 molecule	chr1p13	216942_s_at	NM_001779
6.88	7.22	0.34	5.49E-01	8.27E-01	SBDS /// SBDSP	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	chr7q11.21 /// chr7q11.23	1554089_s_at	NM_016038 /// NR_001588 /// NR_024109 /// NR_024110 /// NR_024111
4.17	4.50	0.33	5.49E-01	8.27E-01	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	chr5p12	209799_at	NM_006251 /// NM_206907
2.96	3.21	0.25	5.49E-01	8.27E-01	THSD7A	thrombospondin, type I, domain containing 7A	chr7p21.3	213894_at	NM_015204
2.53	2.64	0.11	5.49E-01	8.27E-01	ARTN	artemin	chr1p33-p32	216052_x_at	NM_003976 /// NM_057090 /// NM_057091 /// NM_057160
8.41	8.77	0.36	5.50E-01	8.27E-01	GSTM3	glutathione S-transferase M3 (brain)	chr1p13.3	202554_s_at	NM_000849
8.55	8.75	0.21	5.50E-01	8.27E-01	GNA13	guanine nucleotide binding protein (G protein), alpha 13	chr17q24.3	224761_at	NM_006572
3.19	3.32	0.13	5.50E-01	8.27E-01	---	---	---	235801_at	---
2.72	2.83	0.11	5.50E-01	8.27E-01	CLMN	calmin (calponin-like, transmembrane)	chr14q32.13	213839_at	NM_024734
2.49	2.60	0.10	5.50E-01	8.27E-01	TREML2P	triggering receptor expressed on myeloid cells-like 2 pseudogene	chr6p21.1	1567624_at	NR_002794
3.05	3.14	0.09	5.50E-01	8.27E-01	---	---	---	239599_at	---
2.45	2.54	0.09	5.50E-01	8.27E-01	CTAG1A /// CTAG1B	cancer/testis antigen 1A /// cancer/testis antigen 1B	chrXq28	217339_x_at	NM_001327 /// NM_139250 /// XM_001719185

3.44	3.52	0.09	5.50E-01	8.27E-01	KIR2DL2 /// KIR2DS1 /// KIR2DS5	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 /// killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5	chr19q13.4	208198_x_at	NM_014219 /// NM_014512 /// NM_014513
6.95	7.15	0.19	5.50E-01	8.27E-01	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	chr7q32	201304_at	NM_005000
2.02	2.11	0.10	5.50E-01	8.27E-01	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	chr4p14-p12	1569773_at	NM_001105529 /// NM_006095
3.29	3.40	0.11	5.50E-01	8.27E-01	TMEM65	transmembrane protein 65	chr8q24.13	241342_at	NM_194291
3.62	3.76	0.13	5.50E-01	8.27E-01	---	---	---	229920_at	---
5.29	5.46	0.17	5.50E-01	8.27E-01	---	---	---	242725_at	---
3.15	3.23	0.09	5.50E-01	8.27E-01	---	---	---	233376_at	---
2.16	2.26	0.10	5.50E-01	8.27E-01	---	---	---	1569824_at	---
3.26	3.35	0.09	5.50E-01	8.27E-01	---	---	---	1562549_at	---
3.35	3.44	0.08	5.50E-01	8.27E-01	APOBEC3D	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D	chr22q13.1-q13.2	1553831_at	NM_152426
2.10	2.19	0.08	5.50E-01	8.27E-01	ZNF230	zinc finger protein 230	chr19q13.31	1557322_at	NM_006300
8.74	8.83	0.08	5.50E-01	8.27E-01	NACAP1	nascent-polypeptide-associated complex alpha polypeptide pseudogene 1	chr8q22.3	211445_x_at	NR_002182
2.65	2.83	0.18	5.50E-01	8.27E-01	---	---	---	239360_at	---
4.50	4.62	0.11	5.50E-01	8.27E-01	ALKBH5	alkB, alkylation repair homolog 5 (E. coli)	chr17p11.2	228034_x_at	NM_017758
2.79	2.88	0.09	5.50E-01	8.27E-01	AGTPBP1	ATP/GTP binding protein 1	chr9q21.33	204499_at	NM_015239
8.41	8.67	0.25	5.50E-01	8.27E-01	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	chr2q35	208642_s_at	NM_021141
6.23	6.43	0.20	5.50E-01	8.27E-01	---	---	---	1560622_at	---
5.27	5.42	0.15	5.50E-01	8.27E-01	---	---	---	237044_s_at	---
2.40	2.47	0.07	5.50E-01	8.27E-01	---	---	---	1558950_at	---
2.86	3.01	0.15	5.50E-01	8.27E-01	XDH	xanthine dehydrogenase	chr2p23.1	210301_at	NM_000379
5.69	6.07	0.39	5.50E-01	8.27E-01	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	chr10q25.2	225424_at	NM_020918
2.49	2.59	0.10	5.50E-01	8.27E-01	---	---	---	242559_at	---
4.55	4.75	0.20	5.51E-01	8.27E-01	IL18BP	interleukin 18 binding protein	chr11q13	222868_s_at	NM_001039659 /// NM_001039660 /// NM_173042
4.77	4.93	0.16	5.51E-01	8.27E-01	FLT1	Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	chr13q12	232809_s_at	NM_002019
2.75	2.89	0.13	5.51E-01	8.27E-01	FAM132B	family with sequence similarity 132, member B	chr2q37.3	229622_at	XM_001130886 /// XM_001714385 /// XM_001715780
2.93	3.06	0.13	5.51E-01	8.27E-01	LOC100130938	hypothetical protein LOC100130938	chr18q21.33	230574_at	XM_001720237 /// XM_001720247 /// XM_001722558
2.43	2.55	0.12	5.51E-01	8.27E-01	---	---	---	241007_at	---
4.34	4.43	0.09	5.51E-01	8.27E-01	FAIM2	Fas apoptotic inhibitory molecule 2	chr12q13	203618_at	NM_012306
3.03	3.11	0.07	5.51E-01	8.27E-01	---	---	---	234234_at	---
4.32	4.39	0.07	5.50E-01	8.27E-01	KCNK7	potassium channel, subfamily K, member 7	chr11q13	224008_s_at	NM_005714 /// NM_033347 /// NM_033348 /// NM_033455
2.10	2.16	0.06	5.50E-01	8.27E-01	---	---	---	229687_s_at	---
2.07	2.13	0.06	5.51E-01	8.27E-01	FLJ32955	hypothetical protein FLJ32955	chr2q23.3	242295_at	NM_153041
1.98	2.05	0.07	5.51E-01	8.27E-01	---	---	---	1560637_at	---
7.50	7.69	0.20	5.51E-01	8.27E-01	C4orf34	chromosome 4 open reading frame 34	chr4p14	224990_at	NM_174921
1.98	2.05	0.07	5.51E-01	8.27E-01	LOC100133205	hypothetical protein LOC100133205	chr6p22.1	1568854_at	XM_001717665
4.05	4.23	0.19	5.51E-01	8.27E-01	NCOA3	nuclear receptor coactivator 3	chr20q12	211352_s_at	NM_006534 /// NM_181659
1.76	1.83	0.07	5.51E-01	8.28E-01	---	---	---	222299_x_at	---
6.35	6.56	0.21	5.51E-01	8.28E-01	LARS	leucyl-tRNA synthetase	chr5q32	222428_s_at	NM_020117
4.32	4.59	0.27	5.51E-01	8.28E-01	CAND2	cullin-associated and neddylation-dissociated 2 (putative)	chr3p25.1	213547_at	NM_012298
2.77	2.88	0.12	5.51E-01	8.28E-01	PAK7	p21 protein (Cdc42/Rac)-activated kinase 7	chr20p12	210721_s_at	NM_020341 /// NM_177990
2.70	2.81	0.11	5.51E-01	8.28E-01	SBF2	SET binding factor 2	chr11p15.4	233914_s_at	NM_030962
5.72	5.93	0.21	5.51E-01	8.28E-01	LYRM7	Lyrm7 homolog (mouse)	chr5q31.1	228841_at	NM_181705
2.03	2.11	0.08	5.51E-01	8.28E-01	---	---	---	1556904_at	---
6.44	6.74	0.30	5.51E-01	8.28E-01	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	chr6q14.1	227708_at	NM_001402
2.82	2.93	0.10	5.52E-01	8.28E-01	PLA2G2D	phospholipase A2, group IID	chr1p36.12	220423_at	NM_012400
2.22	2.30	0.08	5.52E-01	8.28E-01	---	---	---	1568858_at	---

2.60	2.73	0.13	5.52E-01	8.28E-01	KIAA1217	KIAA1217	chr10p12.2-p12.1	1562966_at	NM_001098500 /// NM_001098501 /// NM_019590
3.77	3.89	0.12	5.52E-01	8.28E-01	FADS2	fatty acid desaturase 2	chr11q12-q13.1	243953_at	NM_004265
3.54	3.64	0.10	5.52E-01	8.28E-01	---	---	---	240870_at	---
6.72	6.88	0.16	5.52E-01	8.28E-01	RNF146	ring finger protein 146	chr6q22.1-q22.33	223886_s_at	NM_030963
2.31	2.41	0.10	5.52E-01	8.28E-01	HBE1	Hemoglobin, epsilon 1	chr11p15.5	217683_at	NM_005330
2.02	2.11	0.09	5.52E-01	8.28E-01	OR5H1	olfactory receptor, family 5, subfamily H, member 1	chr3q11.2	1567247_at	NM_001005338
2.95	3.13	0.18	5.52E-01	8.28E-01	GLMN	glomulin, FKBP associated protein	chr1p22.1	236924_at	NM_053274
3.16	3.25	0.09	5.52E-01	8.28E-01	C17orf45	chromosome 17 open reading frame 45	chr17p11.2	239754_at	NM_152350
2.17	2.25	0.08	5.52E-01	8.28E-01	---	---	---	1563298_at	---
3.21	3.29	0.07	5.52E-01	8.28E-01	---	---	---	239803_at	---
2.24	2.31	0.07	5.52E-01	8.28E-01	KIAA1430	KIAA1430	chr4q35.1	230569_at	NM_020827
2.06	2.12	0.06	5.52E-01	8.28E-01	UNC93A	unc-93 homolog A (C. elegans)	chr6q27	214382_at	NM_018974
8.20	8.45	0.25	5.52E-01	8.28E-01	RHOBTB3	Rho-related BTB domain containing 3	chr5q15	202975_s_at	NM_014899
2.09	2.19	0.09	5.52E-01	8.28E-01	---	---	---	215634_at	---
2.00	2.07	0.07	5.52E-01	8.28E-01	FLJ30594	Hypothetical locus FLJ30594	chr2p25.2	236739_at	XR_041760 /// XR_041761 /// XR_041762
3.02	3.14	0.12	5.52E-01	8.28E-01	SNCB	synuclein, beta	chr5q35	207853_s_at	NM_001001502 /// NM_003085
2.37	2.48	0.11	5.52E-01	8.28E-01	RP1-127L4.6	hypothetical protein LOC150297	chr22q12.3	1555990_at	NM_001010859
2.06	2.13	0.06	5.52E-01	8.28E-01	---	---	---	213662_at	---
3.04	3.15	0.11	5.52E-01	8.28E-01	RSU1	Ras suppressor protein 1	chr10p13	230490_x_at	NM_012425 /// NM_152724
2.04	2.12	0.08	5.52E-01	8.28E-01	FLJ36644	hypothetical gene supported by AK093963	chr17q24.3	1558234_at	XM_001126095 /// XM_001131577 /// XM_001718237
2.34	2.41	0.07	5.52E-01	8.28E-01	DUS3L	Dihydrouridine synthase 3-like (S. cerevisiae)	chr19p13.3	230145_at	NM_020175
5.66	5.80	0.14	5.52E-01	8.28E-01	LRP3	low density lipoprotein receptor-related protein 3	chr19q13.11	228525_at	NM_002333
2.46	2.53	0.07	5.52E-01	8.28E-01	LOC283089	hypothetical protein LOC283089	chr10q26.13	1563916_at	---
5.19	5.33	0.14	5.52E-01	8.28E-01	GPSM3	G-protein signaling modulator 3 (AGS3-like, C. elegans)	chr6p21.3	214847_s_at	NM_022107
1.99	2.06	0.08	5.52E-01	8.28E-01	---	---	---	1564323_at	---
1.92	1.98	0.07	5.52E-01	8.28E-01	GBP6	guanylate binding protein family, member 6	chr1p22.2	1559606_at	NM_198460
2.18	2.25	0.07	5.52E-01	8.28E-01	RASAL2	RAS protein activator like 2	chr1q24	217201_at	NM_004841 /// NM_170692
4.56	4.69	0.13	5.52E-01	8.28E-01	NCR2	natural cytotoxicity triggering receptor 2	chr6p21.1	217493_x_at	NM_004828
2.07	2.15	0.08	5.52E-01	8.28E-01	CATSPERB	cation channel, sperm-associated, beta	chr14q32.12	220293_at	NM_024764
2.21	2.30	0.09	5.53E-01	8.28E-01	MGC16291	hypothetical protein MGC16291	chr10q11.21	233566_at	XR_017865 /// XR_017966 /// XR_040081
2.49	2.57	0.08	5.53E-01	8.28E-01	---	---	---	1568878_at	---
2.37	2.44	0.07	5.53E-01	8.28E-01	---	---	---	1562316_at	---
1.74	1.80	0.06	5.53E-01	8.28E-01	---	---	---	237984_x_at	---
7.74	8.05	0.31	5.53E-01	8.29E-01	41519	septin 2	chr2q37	200778_s_at	NM_001008491 /// NM_001008492 /// NM_004404 /// NM_006155
3.66	3.80	0.14	5.53E-01	8.29E-01	HMG4L	high-mobility group (nonhistone chromosomal) protein 4-like	chr20q11.22	216548_x_at	NR_002165
2.60	2.72	0.12	5.53E-01	8.29E-01	ZNF225	zinc finger protein 225	chr19q13.2	207125_at	NM_013362
4.06	4.17	0.11	5.53E-01	8.29E-01	SEZ6L	seizure related 6 homolog (mouse)-like	chr22q12.1	216047_x_at	NM_021115
2.21	2.31	0.11	5.53E-01	8.29E-01	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	chr10q22.3	214921_at	NM_001014797 /// NM_002247
2.88	2.98	0.09	5.53E-01	8.29E-01	LCP2	Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	chr5q33.1-qter	244556_at	NM_005565
1.96	2.03	0.07	5.53E-01	8.29E-01	TMEM87A	transmembrane protein 87A	chr15q15.1	223772_s_at	NM_001110503 /// NM_015497
3.04	3.14	0.10	5.53E-01	8.29E-01	EMX2OS	EMX2 opposite strand (non-protein coding)	chr10q26.1	232531_at	NR_002791
2.06	2.14	0.08	5.53E-01	8.29E-01	---	---	---	230211_at	---
4.55	4.63	0.08	5.53E-01	8.29E-01	---	---	---	229505_at	---
2.06	2.16	0.10	5.53E-01	8.29E-01	DCLK1	doublecortin-like kinase 1	chr13q13	215303_at	NM_004734
2.02	2.09	0.07	5.53E-01	8.29E-01	PAPOLB	poly(A) polymerase beta (testis specific)	chr7p22.1	208271_at	NM_020144

4.61	4.74	0.13	5.53E-01	8.29E-01	CPZ	carboxypeptidase Z	chr4p16.1	211062_s_at	NM_001014447 /// NM_001014448 /// NM_003652
2.32	2.43	0.11	5.53E-01	8.29E-01	CLUL1	clusterin-like 1 (retinal)	chr18p11.32	206556_at	NM_014410 /// NM_199167
4.24	4.33	0.09	5.53E-01	8.29E-01	CCDC97	coiled-coil domain containing 97	chr19q13.2	235495_at	NM_052848
1.94	2.03	0.08	5.53E-01	8.29E-01	---	---	---	237648_x_at	---
2.10	2.19	0.09	5.54E-01	8.29E-01	ART3	ADP-ribosyltransferase 3	chr4p15.1-p14|4p15.1-p14|4p15.1-p14	210147_at	NM_001130016 /// NM_001130017 /// NM_001179
3.99	4.07	0.08	5.54E-01	8.29E-01	---	---	---	1560639_at	---
2.35	2.45	0.09	5.54E-01	8.29E-01	RPP30	ribonuclease P/MRP 30kDa subunit	chr10q23.31	1556061_at	NM_001104546 /// NM_006413
5.98	6.52	0.55	5.54E-01	8.29E-01	---	---	---	227364_at	---
2.67	2.77	0.10	5.54E-01	8.29E-01	---	---	---	235596_at	---
2.68	2.75	0.07	5.54E-01	8.29E-01	HCN4	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	chr15q24-q25	206946_at	NM_005477
3.58	3.67	0.09	5.54E-01	8.29E-01	---	---	---	231963_at	---
2.33	2.43	0.10	5.54E-01	8.30E-01	LOC646241	hypothetical protein LOC646241	chr5p15.1	1559790_at	XM_933487
4.59	4.69	0.11	5.54E-01	8.30E-01	CHD7	chromodomain helicase DNA binding protein 7	chr8q12.2	222755_s_at	NM_017780
2.42	2.52	0.11	5.54E-01	8.30E-01	---	---	---	234383_x_at	---
3.00	3.09	0.08	5.54E-01	8.30E-01	CSHL1	chorionic somatomammotropin hormone-like 1	chr17q24.2	208294_x_at	NM_001318 /// NM_022579 /// NM_022580 /// NM_022581
6.72	6.87	0.15	5.54E-01	8.30E-01	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	chr10p15.3	212504_at	NM_014974
3.27	3.36	0.09	5.54E-01	8.30E-01	LOC375010	hypothetical LOC375010	chr1q12	1566147_a_at	XR_041271
2.95	3.06	0.11	5.54E-01	8.30E-01	FLJ44450	hypothetical gene supported by AK126414	chr2p21	237111_at	XM_001132353 /// XM_001133195 /// XM_001725012
2.80	2.90	0.09	5.54E-01	8.30E-01	---	---	---	222376_at	---
1.93	2.00	0.07	5.54E-01	8.30E-01	C18orf62	chromosome 18 open reading frame 62	chr18q22.3	1556288_at	NM_001037331
2.21	2.28	0.07	5.54E-01	8.30E-01	LOC283038	hypothetical protein LOC283038	chr10q26.2	1557591_at	---
7.35	7.66	0.31	5.55E-01	8.30E-01	NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like	chr1q21.2	214722_at	NM_203458
6.10	6.37	0.26	5.55E-01	8.30E-01	CNOT8	CCR4-NOT transcription complex, subunit 8	chr5q31-q33	202164_s_at	NM_004779
4.99	5.14	0.15	5.55E-01	8.30E-01	WDR22	WD repeat domain 22	chr14q23-q24.1	224697_at	NM_003861
2.46	2.57	0.11	5.55E-01	8.30E-01	---	---	---	1560826_at	---
3.92	4.03	0.11	5.55E-01	8.30E-01	---	---	---	235887_at	---
3.45	3.56	0.10	5.55E-01	8.30E-01	---	---	---	215353_at	---
2.54	2.63	0.09	5.55E-01	8.30E-01	SERPINA12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12	chr14q32.13	1552544_at	NM_173850
2.32	2.39	0.07	5.55E-01	8.30E-01	LOC100130155	Hypothetical protein LOC100130155	chr8q12.3	236693_at	XM_001720201 /// XM_001720202 /// XM_001720219
2.16	2.23	0.08	5.55E-01	8.30E-01	---	---	---	231181_at	---
2.63	2.74	0.11	5.55E-01	8.30E-01	FKBP8	FK506 binding protein 8, 38kDa	chr19p12	222007_s_at	NM_012181
2.13	2.22	0.08	5.55E-01	8.30E-01	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	chr4q13.3	1562644_at	NM_001004346
2.82	2.90	0.08	5.55E-01	8.30E-01	IRF4	interferon regulatory factor 4	chr6p25-p23	216986_s_at	NM_002460
3.17	3.32	0.15	5.55E-01	8.30E-01	SLC22A4	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	chr5q31.1	205896_at	NM_003059
2.94	3.08	0.14	5.55E-01	8.30E-01	---	---	---	1557852_at	---
2.95	3.05	0.11	5.55E-01	8.30E-01	LOC646778	hypothetical LOC646778	chr18q12.1	243452_at	XR_041105 /// XR_041106
2.34	2.42	0.09	5.55E-01	8.30E-01	---	---	---	237946_at	---
3.33	3.42	0.09	5.55E-01	8.30E-01	---	---	---	243207_at	---
2.61	2.69	0.08	5.55E-01	8.30E-01	CXorf23	chromosome X open reading frame 23	chrXp22.12	232087_at	NM_198279
5.76	5.95	0.19	5.55E-01	8.30E-01	SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	chr1p32-p31	209711_at	NM_015139
3.51	3.63	0.12	5.55E-01	8.30E-01	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	chr17p13	1555065_x_at	NM_004505
2.09	2.16	0.07	5.55E-01	8.30E-01	---	---	---	244291_x_at	---
4.12	4.20	0.08	5.55E-01	8.30E-01	C5orf24	Chromosome 5 open reading frame 24	chr5q31.1	229098_s_at	NM_152409
2.73	2.80	0.07	5.55E-01	8.30E-01	SPTBN1	Spectrin, beta, non-erythrocytic 1	chr2p21	228246_s_at	NM_003128 /// NM_178313
2.05	2.11	0.06	5.55E-01	8.30E-01	CRP	C-reactive protein, pentraxin-related	chr1q21-q23	37020_at	NM_000567
4.94	5.10	0.16	5.56E-01	8.30E-01	CD180	CD180 molecule	chr5q12	206206_at	NM_005582
3.98	4.11	0.13	5.56E-01	8.30E-01	FES	feline sarcoma oncogene	chr15q26.1	205418_at	NM_002005

9.73	9.86	0.13	5.56E-01	8.30E-01	VAT1	vesicle amine transport protein 1 homolog (T. californica)	chr17q21	208626_s_at	NM_006373
1.99	2.08	0.09	5.56E-01	8.30E-01	DLGAP1 /// LOC284214	discs, large (Drosophila) homolog-associated protein 1 /// hypothetical protein LOC284214	chr18p11.3 /// chr18p11.31	235527_at	NM_001003809 /// NM_004746
2.47	2.55	0.07	5.56E-01	8.30E-01	---	---	---	232292_at	---
3.98	4.13	0.15	5.56E-01	8.30E-01	HDAC9	histone deacetylase 9	chr7p21.1	205659_at	NM_014707 /// NM_058176 /// NM_058177 /// NM_178423 /// NM_178425
2.87	2.97	0.10	5.56E-01	8.30E-01	SLC39A3	solute carrier family 39 (zinc transporter), member 3	chr19p13.3	232115_at	NM_144564 /// NM_213568
3.82	3.92	0.10	5.56E-01	8.30E-01	---	---	---	229919_at	---
2.31	2.40	0.10	5.56E-01	8.30E-01	---	---	---	216808_at	---
2.41	2.51	0.10	5.56E-01	8.30E-01	ABP1	amiloride binding protein 1 (amine oxidase (copper-containing))	chr7q34-q36	203559_s_at	NM_001091
2.54	2.63	0.09	5.56E-01	8.30E-01	---	---	---	1562899_at	---
2.36	2.45	0.09	5.56E-01	8.30E-01	LOC100130648 /// SSX2 /// SSX2B	similar to Protein SSX2 (Synovial sarcoma, X breakpoint 2) (Cancer/testis antigen 5.2) (CT5.2) (SSX) (HOM-MEL-40) /// synovial sarcoma, X breakpoint 2 /// synovial sarcoma, X breakpoint 2B	chrXp11.22	207493_x_at	NM_003147 /// NM_175698 /// XM_001719568 /// XM_001720499
2.57	2.66	0.09	5.56E-01	8.30E-01	C2orf67	chromosome 2 open reading frame 67	chr2q34	1554791_a_at	NM_152519
11.41	11.48	0.07	5.56E-01	8.31E-01	GNAS	GNAS complex locus	chr20q13.3	214548_x_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259
2.57	2.64	0.07	5.56E-01	8.31E-01	---	---	---	222337_at	---
2.26	2.35	0.10	5.56E-01	8.31E-01	TRPM7	Transient receptor potential cation channel, subfamily M, member 7	chr15q21	1565887_at	NM_017672
5.95	6.14	0.19	5.56E-01	8.31E-01	C9orf97	chromosome 9 open reading frame 97	chr9q22.33	213161_at	NM_139246
4.61	4.74	0.12	5.56E-01	8.31E-01	NUDT16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	chr3q22.1	235002_at	NM_152395
3.19	3.31	0.12	5.56E-01	8.31E-01	TBC1D10A	TBC1 domain family, member 10A	chr22q12.1-qter	1570035_at	NM_031937
4.08	4.18	0.11	5.56E-01	8.31E-01	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5	chr19p13.2-p12	211123_at	NM_000453
2.25	2.34	0.09	5.56E-01	8.31E-01	---	---	---	1565723_at	---
2.80	2.88	0.08	5.56E-01	8.31E-01	FLRT1	fibronectin leucine rich transmembrane protein 1	chr11q12-q13	210414_at	NM_013280
5.63	5.86	0.23	5.56E-01	8.31E-01	CD47	CD47 molecule	chr3q13.1-q13.2	227259_at	NM_001025079 /// NM_001777 /// NM_198793
2.18	2.25	0.07	5.56E-01	8.31E-01	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	chr2q36-q37	216896_at	NM_000091 /// NM_031362 /// NM_031365 /// NM_031366
2.12	2.19	0.07	5.56E-01	8.31E-01	FAM66C	family with sequence similarity 66, member C	chr12p13.31	1570395_a_at	XR_040642 /// XR_040643
2.61	2.70	0.09	5.57E-01	8.31E-01	---	---	---	1558889_at	---
2.80	2.89	0.09	5.57E-01	8.31E-01	ITIH4	Inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	chr3p21-p14	241167_at	NM_002218
2.04	2.11	0.06	5.57E-01	8.31E-01	---	---	---	1563186_at	---
2.20	2.27	0.07	5.57E-01	8.31E-01	ZNF208	zinc finger protein 208	chr19p12	208542_x_at	NM_007153
2.02	2.08	0.06	5.57E-01	8.31E-01	---	---	---	234815_at	---
2.83	2.91	0.08	5.57E-01	8.31E-01	C12orf12	chromosome 12 open reading frame 12	chr12q21.33	236968_at	NM_152638
2.31	2.39	0.08	5.57E-01	8.31E-01	LRRIQ3	leucine-rich repeats and IQ motif containing 3	chr1p31.1	1553674_at	NM_001105659
3.75	3.85	0.10	5.57E-01	8.31E-01	UBXN10	UBX domain protein 10	chr1p36.12	232109_at	NM_152376
2.22	2.31	0.09	5.57E-01	8.31E-01	C1orf67 /// DNAH14 /// RP11-328N1.1	chromosome 1 open reading frame 67 /// dynein, axonemal, heavy chain 14 /// similar to CG7092-PA	chr1q42.12	242283_at	NM_144989 /// XM_001721899 /// XM_059166 /// XM_927520 /// XM_938194
2.45	2.54	0.09	5.57E-01	8.31E-01	---	---	---	240394_at	---
8.13	8.50	0.37	5.57E-01	8.31E-01	COL4A2	collagen, type IV, alpha 2	chr13q34	211964_at	NM_001846
2.15	2.24	0.09	5.57E-01	8.31E-01	---	---	---	1566902_at	---
5.02	5.19	0.18	5.57E-01	8.31E-01	BRD7	bromodomain containing 7	chr16q12	222737_s_at	NM_013263

9.06	9.18	0.13	5.57E-01	8.31E-01	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	chr11p15.1	201676_x_at	NM_002786 /// NM_148976
4.73	4.86	0.12	5.57E-01	8.31E-01	SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	chr16q22.1	209401_s_at	NM_005072
4.66	4.77	0.11	5.57E-01	8.31E-01	WNK2	WNK lysine deficient protein kinase 2	chr9q22.3	227217_at	NM_006648
6.18	6.44	0.26	5.57E-01	8.31E-01	EIF4E	eukaryotic translation initiation factor 4E	chr4q21-q25	201435_s_at	NM_001130678 /// NM_001130679 /// NM_001968
3.72	3.89	0.17	5.57E-01	8.31E-01	OR7E156P	olfactory receptor, family 7, subfamily E, member 156 pseudogene	chr13q21.31	222327_x_at	NR_002171
1.87	1.95	0.08	5.57E-01	8.31E-01	C1orf62	chromosome 1 open reading frame 62	chr1p13.3	1558834_s_at	NM_152763
3.42	3.56	0.15	5.57E-01	8.31E-01	C6orf52	chromosome 6 open reading frame 52	chr6p24.1	236504_x_at	XM_001718541 /// XM_371798 /// XM_938497
2.16	2.23	0.08	5.57E-01	8.31E-01	CDH26	cadherin-like 26	chr20q13.2-q13.33	232306_at	NM_021810 /// NM_177980
5.06	5.25	0.20	5.57E-01	8.31E-01	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	chr7q31.33	204354_at	NM_001042594 /// NM_015450 /// NR_003102 /// NR_003103 /// NR_003104
2.93	3.05	0.12	5.57E-01	8.31E-01	GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	chr22q11.2	223564_s_at	NM_053004
2.18	2.27	0.09	5.57E-01	8.31E-01	---	---	---	240789_at	---
2.31	2.38	0.07	5.57E-01	8.31E-01	NLN	neurolysin (metallopeptidase M3 family)	chr5q12.3	225942_at	NM_020726
3.53	3.65	0.12	5.57E-01	8.31E-01	LOC254128	hypothetical protein LOC254128	chr2q14.2	235132_at	---
2.84	2.93	0.09	5.58E-01	8.31E-01	NHLH2	nescient helix loop helix 2	chr1p12-p11	214497_s_at	NM_001111061 /// NM_005599
1.89	1.97	0.08	5.57E-01	8.31E-01	---	---	---	235326_at	---
1.87	1.94	0.08	5.57E-01	8.31E-01	TMEM196	transmembrane protein 196	chr7p15.3	236705_at	NM_152774
6.49	6.64	0.15	5.58E-01	8.31E-01	C18orf21	chromosome 18 open reading frame 21	chr18q12.2	223526_at	NM_031446
2.57	2.69	0.12	5.58E-01	8.31E-01	---	---	---	1563069_at	---
1.95	2.02	0.07	5.58E-01	8.31E-01	C14orf91	chromosome 14 open reading frame 91	chr14q22.1-q23.3	224213_at	---
2.99	3.23	0.23	5.58E-01	8.31E-01	ZNF138	zinc finger protein 138	chr7q11.21-q11.23	244743_x_at	NM_006524
2.63	2.72	0.09	5.58E-01	8.31E-01	SPATA13	spermatogenesis associated 13	chr13q12.12	1557470_at	NM_153023
1.95	2.03	0.08	5.58E-01	8.31E-01	---	---	---	233944_at	---
6.81	7.04	0.23	5.58E-01	8.31E-01	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	chr5q23.1	220454_s_at	NM_020796
4.13	4.26	0.14	5.58E-01	8.31E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	208325_s_at	NM_006738 /// NM_007200 /// NM_144767
3.32	3.43	0.11	5.58E-01	8.31E-01	OTUD7A	OTU domain containing 7A	chr15q13.3	1560399_a_at	NM_130901
2.08	2.18	0.10	5.58E-01	8.31E-01	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	1565080_at	NM_005417 /// NM_198291
2.73	2.84	0.11	5.58E-01	8.31E-01	---	---	---	240756_at	---
6.22	6.42	0.19	5.58E-01	8.31E-01	ARID4B	AT rich interactive domain 4B (RBP1-like)	chr1q42.1-q43	221230_s_at	NM_016374 /// NM_031371
4.11	4.26	0.15	5.58E-01	8.31E-01	GPIHBP1	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	chr8q24.3	238062_at	NM_178172
2.97	3.09	0.12	5.58E-01	8.31E-01	CDC2	cell division cycle 2, G1 to S and G2 to M	chr10q21.1	210559_s_at	NM_001130829 /// NM_001786 /// NM_033379
2.68	2.76	0.09	5.58E-01	8.31E-01	---	---	---	1569806_at	---
2.14	2.21	0.07	5.58E-01	8.31E-01	CD36	CD36 molecule (thrombospondin receptor)	chr7q11.2	242197_x_at	NM_000072 /// NM_001001547 /// NM_001001548 /// NM_001127443 /// NM_001127444
5.60	5.78	0.17	5.58E-01	8.31E-01	MOBKL1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)	chr4q13.3	225997_at	NM_173468
6.33	6.66	0.32	5.59E-01	8.32E-01	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	chr4q31	201872_s_at	NM_001040876 /// NM_002940
5.74	6.00	0.26	5.59E-01	8.32E-01	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	chr5q11.2	227447_at	NM_015360
6.15	6.35	0.20	5.59E-01	8.32E-01	MARCKS	myristoylated alanine-rich protein kinase C substrate	chr6q22.2	225897_at	NM_002356

3.62	3.75	0.13	5.59E-01	8.32E-01	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	chr11q13.5	208373_s_at	NM_004154 /// NM_176796 /// NM_176797 /// NM_176798																			
4.25	4.36	0.11	5.59E-01	8.32E-01	NOXO1	NADPH oxidase organizer 1	chr16p13.3	235329_at	NM_144603 /// NM_172167 /// NM_172168																			
2.65	2.76	0.11	5.58E-01	8.32E-01	MUC1	mucin 1, cell surface associated	chr1q21	211695_x_at	NM_001018016 /// NM_001018017 /// NM_001044390 /// NM_001044391 /// NM_001044392 /// NM_001044393 /// NM_002456																			
2.51	2.62	0.11	5.59E-01	8.32E-01	---	---	---	232883_at	---																			
2.32	2.43	0.10	5.59E-01	8.32E-01	---	---	---	211606_at	---																			
2.08	2.18	0.10	5.59E-01	8.32E-01	---	---	---	244330_at	---																			
3.21	3.30	0.09	5.59E-01	8.32E-01	RIN2	Ras and Rab interactor 2	chr20p11.22	233811_at	NM_018993																			
3.88	3.96	0.09	5.59E-01	8.32E-01	---	---	---	239908_at	---																			
2.26	2.34	0.08	5.59E-01	8.32E-01	TSGA10	testis specific, 10	chr2q11.2	220623_s_at	NM_025244 /// NM_182911																			
3.34	3.42	0.08	5.59E-01	8.32E-01	---	---	---	1556375_at	---																			
2.01	2.08	0.07	5.59E-01	8.32E-01	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	chr15q13-q15	218468_s_at	NM_013372																			
2.13	2.20	0.07	5.59E-01	8.32E-01	PRNP	prion protein	chr20p13	1556190_s_at	NM_000311 /// NM_001080121 /// NM_001080122 /// NM_001080123 /// NM_183079																			
2.53	2.60	0.07	5.59E-01	8.32E-01	KIAA1045	KIAA1045	chr9p13.3	37566_at	NM_015297																			
2.06	2.12	0.06	5.59E-01	8.32E-01	---	---	---	238305_at	---																			
3.77	4.03	0.26	5.59E-01	8.32E-01	PTPN12	protein tyrosine phosphatase, non-receptor type 12	chr7q11.23	216915_s_at	NM_001131008 /// NM_001131009 /// NM_002835																			
2.18	2.28	0.10	5.59E-01	8.32E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	234013_at	---																			
2.90	3.00	0.10	5.59E-01	8.32E-01	PFTK2	PFTAIRE protein kinase 2	chr2q33.2	1554826_at	NM_139158																			
8.45	8.60	0.15	5.59E-01	8.32E-01	HDDC2	HD domain containing 2	chr6q13-q24.3	203259_s_at	NM_016063																			
3.13	3.24	0.11	5.59E-01	8.32E-01	---	---	---	234251_at	---																			
2.05	2.14	0.08	5.59E-01	8.32E-01	---	---	---	1554281_at	---																			
4.84	5.08	0.25	5.59E-01	8.32E-01	SRPK2	SFRS protein kinase 2	chr7q22-q31.1	214931_s_at	NM_182691 /// NM_182692																			
5.45	5.56	0.11	5.59E-01	8.32E-01	LOC692247	hypothetical locus LOC692247	chr11p15.5	1561355_at	---																			
5.61	5.90	0.30	5.59E-01	8.32E-01	BCLAF1	BCL2-associated transcription factor 1	chr6q22-q23	214499_s_at	NM_001077440 /// NM_001077441 /// NM_014739																			
2.02	2.10	0.08	5.59E-01	8.32E-01	KRTAP3-2 /// LOC100128819	keratin associated protein 3-2 /// hypothetical protein LOC100128819	chr17q12-q21	233534_at	NM_031959 /// XM_001722596																			
7.41	7.57	0.16	5.60E-01	8.32E-01	CALCOCO2	calcium binding and coiled-coil domain 2	chr17q21.32	210817_s_at	NM_005831																			
5.68	5.87	0.20	5.60E-01	8.32E-01	---	---	---	238824_at	---																			
7.46	7.77	0.31	5.60E-01	8.32E-01	METAP2	methionyl aminopeptidase 2	chr12q22	209861_s_at	NM_006838																			
1.95	2.02	0.06	5.60E-01	8.32E-01	DIAPH3	diaphanous homolog 3 (Drosophila)	chr13q21.2	220997_s_at	NM_001042517 /// NM_030932																			
2.70	2.81	0.11	5.60E-01	8.32E-01	---	---	---	237231_at	---																			
5.02	5.10	0.08	5.60E-01	8.32E-01	---	---	---	224105_x_at	---																			
2.18	2.25	0.07	5.60E-01	8.32E-01	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	chr6q14	219532_at	NM_022726																			
2.06	2.12	0.06	5.60E-01	8.32E-01	C5orf22	chromosome 5 open reading frame 22	chr5p13.3	1565939_at	NM_018356																			
5.90	6.01	0.11	5.60E-01	8.32E-01	SLAIN2	SLAIN motif family, member 2	chr4p12	224845_s_at	NM_020846																			

2.24	2.33	0.08	5.60E-01	8.32E-01	ADRA1A	adrenergic, alpha-1A-, receptor	chr8p21-p11.2	211489_at	NM_000680 /// NM_033302 /// NM_033303 /// NM_033304
2.09	2.17	0.07	5.60E-01	8.32E-01	---	---	---	239280_at	---
2.20	2.26	0.07	5.60E-01	8.32E-01	---	---	---	1557434_at	---
5.14	5.54	0.41	5.60E-01	8.33E-01	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	chr1q44	225805_at	NM_004501 /// NM_031844
2.28	2.36	0.08	5.60E-01	8.33E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	209638_x_at	NM_002926 /// NM_198227 /// NM_198229
2.26	2.34	0.08	5.60E-01	8.33E-01	---	---	---	224350_at	---
4.30	4.54	0.24	5.60E-01	8.33E-01	FYB	FYN binding protein (FYB-120/130)	chr5p13.1	227266_s_at	NM_001465 /// NM_199335
2.41	2.51	0.09	5.60E-01	8.33E-01	LOC100132987	Hypothetical protein LOC100132987	chr10q22.3	1557807_a_at	XM_001716093 /// XM_001716355 /// XM_001716515
5.61	5.74	0.12	5.60E-01	8.33E-01	GBF1	golgi-specific brefeldin A resistance factor 1	chr10q24	201439_at	NM_004193
2.30	2.37	0.07	5.61E-01	8.33E-01	---	---	---	238380_s_at	---
4.27	4.40	0.13	5.61E-01	8.33E-01	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	chr6p22-p21	209293_x_at	NM_001546
7.16	7.37	0.21	5.61E-01	8.33E-01	ARL5A	ADP-ribosylation factor-like 5A	chr2q23.3	218150_at	NM_001037174 /// NM_012097 /// NM_177985
3.57	3.70	0.13	5.61E-01	8.33E-01	---	---	---	222096_x_at	---
4.64	4.76	0.12	5.61E-01	8.33E-01	ITFG2	integrin alpha FG-GAP repeat containing 2	chr12p13.33	220589_s_at	NM_018463
2.82	2.94	0.12	5.61E-01	8.33E-01	---	---	---	240779_at	---
2.50	2.61	0.11	5.61E-01	8.33E-01	---	---	---	231053_at	---
4.79	4.90	0.11	5.61E-01	8.33E-01	ZNF74	zinc finger protein 74	chr22q11.2|22q11.21	235997_at	NM_003426 /// NR_003253
5.82	5.92	0.11	5.61E-01	8.33E-01	---	---	---	215609_at	---
3.20	3.30	0.10	5.61E-01	8.33E-01	GPR68	G protein-coupled receptor 68	chr14q31	211249_at	NM_003485
4.91	5.01	0.10	5.61E-01	8.33E-01	SLC6A17	solute carrier family 6, member 17	chr1p13.3	233287_at	NM_001010898
3.61	3.70	0.10	5.61E-01	8.33E-01	KCTD17	potassium channel tetramerisation domain containing 17	chr22q12.3	1554566_at	NM_024681
2.19	2.28	0.09	5.61E-01	8.33E-01	---	---	---	1564760_at	---
2.24	2.32	0.08	5.61E-01	8.33E-01	---	---	---	238674_at	---
2.66	2.74	0.08	5.61E-01	8.33E-01	WT1	Wilms tumor 1	chr11p13	206067_s_at	NM_000378 /// NM_024424 /// NM_024425 /// NM_024426
2.21	2.29	0.08	5.61E-01	8.33E-01	CNOT4	CCR4-NOT transcription complex, subunit 4	chr7q22-qter	210203_at	NM_001008225 /// NM_013316
1.86	1.93	0.08	5.61E-01	8.33E-01	---	---	---	239253_at	---
2.52	2.59	0.07	5.61E-01	8.33E-01	HIST1H4A /// HIST1H4B /// HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	chr12p12.3 /// chr1q21 /// chr6p21.3 /// chr6p21.33 /// chr6p22-p21.3	208046_at	NM_001034077 /// NM_003495 /// NM_003538 /// NM_003539 /// NM_003540 /// NM_003541 /// NM_003542 /// NM_003543 /// NM_003544 /// NM_003545 /// NM_003546 /// NM_003548 /// NM_021968 /// NM_175054
1.89	1.96	0.06	5.61E-01	8.33E-01	---	---	---	243320_at	---

1.88	1.94	0.06	5.61E-01	8.33E-01	---	---	---	1566893_at	---
2.20	2.29	0.10	5.61E-01	8.33E-01	RP11-408E5.4	hCG1646718	chr13q12.11	234473_at	XR_040614 /// XR_040615 /// XR_040616
5.21	5.35	0.13	5.61E-01	8.33E-01	CAPRIN1	cell cycle associated protein 1	chr11p13	226990_at	NM_005898 /// NM_203364
2.94	3.13	0.20	5.61E-01	8.33E-01	LPHN3	latrophilin 3	chr4q13.1	242186_x_at	NM_015236
5.36	5.46	0.10	5.61E-01	8.33E-01	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	chr19q13.4	207104_x_at	NM_001081637 /// NM_001081638 /// NM_001081639 /// NM_006669
3.79	3.89	0.10	5.61E-01	8.33E-01	MEF2B	myocyte enhancer factor 2B	chr19p12	205124_at	NM_005919
6.18	6.53	0.35	5.61E-01	8.33E-01	---	---	---	1556589_at	---
4.28	4.37	0.09	5.62E-01	8.33E-01	LOC388796 /// SNORA71B	hypothetical LOC388796 /// small nucleolar RNA, H/ACA box 71B	chr20q11.23	1568249_at	NR_002910 /// NR_015366 /// XM_001720823 /// XM_001720894 /// XM_001721371
1.96	2.03	0.07	5.62E-01	8.33E-01	---	---	---	1560842_a_at	---
2.68	2.76	0.08	5.62E-01	8.33E-01	FRMD4B	FERM domain containing 4B	chr3p14.1	216134_at	NM_015123
3.07	3.18	0.11	5.62E-01	8.33E-01	SNX32	sorting nexin 32	chr11q13.1	231194_at	NM_152760
2.34	2.45	0.11	5.62E-01	8.33E-01	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	chr8p21.1	235588_at	NM_001017420
1.93	1.99	0.06	5.62E-01	8.33E-01	DST	dystonin	chr6p12.1	1553191_at	NM_001723 /// NM_015548 /// NM_020388 /// NM_183380
3.86	3.97	0.10	5.62E-01	8.33E-01	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	chr11q13	204936_at	NM_004579
3.56	3.65	0.10	5.62E-01	8.33E-01	LAS1L	LAS1-like (S. cerevisiae)	chrXq12-q13	235541_at	NM_031206
2.69	2.78	0.09	5.62E-01	8.33E-01	RP11-297H3.4	hypothetical protein LOC284688	chr1q24.2	1557682_a_at	XR_041574 /// XR_041575 /// XR_041576
1.81	1.89	0.07	5.62E-01	8.33E-01	C4orf33	chromosome 4 open reading frame 33	chr4q28.2	1552373_s_at	NM_001099783 /// NM_173487
1.91	1.96	0.06	5.62E-01	8.33E-01	MIB1	Mindbomb homolog 1 (Drosophila)	chr18q11.2	236573_at	NM_020774
3.09	3.19	0.10	5.62E-01	8.33E-01	LOC100131864	hypothetical protein LOC100131864	chr1p36.31	1564660_at	XM_001716604 /// XM_001718463 /// XM_001719743
2.07	2.16	0.09	5.62E-01	8.33E-01	PDE5A	Phosphodiesterase 5A, cGMP-specific	chr4q25-q27	1556787_s_at	NM_001083 /// NM_033430 /// NM_033437
2.17	2.26	0.09	5.62E-01	8.33E-01	TRPM3	transient receptor potential cation channel, subfamily M, member 3	chr9q21.11-q21.12	211422_at	NM_001007470 /// NM_001007471 /// NM_020952 /// NM_024971 /// NM_206944 /// NM_206945 /// NM_206946 /// NM_206947 /// NM_206948
2.18	2.27	0.09	5.62E-01	8.33E-01	---	---	---	229479_at	---
2.15	2.23	0.08	5.62E-01	8.33E-01	EHF	ets homologous factor	chr11p12	222932_at	NM_012153
1.99	2.08	0.08	5.62E-01	8.33E-01	RBL1	retinoblastoma-like 1 (p107)	chr20q11.2	205296_at	NM_002895 /// NM_183404
2.51	2.58	0.07	5.62E-01	8.33E-01	---	---	---	1563210_at	---
2.64	2.78	0.14	5.62E-01	8.34E-01	SOX17	SRY (sex determining region Y)-box 17	chr8q11.23	219993_at	NM_022454
4.37	4.64	0.27	5.62E-01	8.34E-01	DOCK5	Dedicator of cytokinesis 5	chr8p21.2	230207_s_at	NM_024940
3.24	3.34	0.10	5.62E-01	8.34E-01	KLF2	Kruppel-like factor 2 (lung)	chr19p13.13-p13.11	226646_at	NM_016270

2.07	2.17	0.10	5.62E-01	8.34E-01	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4	deleted in azoospermia 1 /// deleted in azoospermia 2 /// deleted in azoospermia 3 /// deleted in azoospermia 4	chrYq11.223	216922_x_at	NM_001005375 /// NM_001005785 /// NM_001005786 /// NM_004081 /// NM_020363 /// NM_020364 /// NM_020420 /// XM_001718583																					
6.87	7.16	0.30	5.62E-01	8.34E-01	RBMS3	RNA binding motif, single stranded interacting protein	chr3p24-p23	238447_at	NM_001003792 /// NM_001003793 /// NM_014483																					
4.24	4.62	0.39	5.62E-01	8.34E-01	MCOLN2	mucolipin 2	chr1p22	1555465_at	NM_153259																					
3.40	3.49	0.09	5.62E-01	8.34E-01	LOC729314	similar to POM121-like 2	chr22q11.21	1566037_at	XR_015506 /// XR_037423 /// XR_037995																					
2.62	2.70	0.08	5.62E-01	8.34E-01	CXorf48	chromosome X open reading frame 48	chrXq26.3	221121_at	NM_001031705 /// NM_017863																					
3.93	4.00	0.07	5.62E-01	8.34E-01	KYNU	kynureninase (L-kynurenine hydrolase)	chr2q22.2	204385_at	NM_001032998 /// NM_003937																					
2.23	2.31	0.08	5.62E-01	8.34E-01	NIN	ninein (GSK3B interacting protein)	chr14q22.1	223981_at	NM_016350 /// NM_020921 /// NM_182944 /// NM_182946																					
2.42	2.49	0.07	5.62E-01	8.34E-01	---	---	---	243300_at	---																					
2.97	3.09	0.12	5.63E-01	8.34E-01	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	chr14q22.1	207766_at	NM_004196																					
2.39	2.52	0.13	5.63E-01	8.34E-01	LOC100133432 /// LOC100133761 /// MUC6	similar to Mucin-6 precursor (Gastric mucin-6) /// similar to Mucin-6 precursor (Gastric mucin-6) /// mucin 6, oligomeric mucus/gel-forming	chr11p15.5-p15.4	1565666_s_at	NM_005961 /// XM_001714734 /// XM_001718792																					
3.07	3.18	0.11	5.63E-01	8.34E-01	---	---	---	232199_at	---																					
3.00	3.08	0.08	5.63E-01	8.34E-01	COL27A1	collagen, type XXVII, alpha 1	chr9q32	230603_at	NM_032888																					
2.46	2.53	0.07	5.63E-01	8.34E-01	---	---	---	236543_at	---																					
2.56	2.77	0.21	5.63E-01	8.34E-01	NPAS3	neuronal PAS domain protein 3	chr14q12-q13	229281_at	NM_022123 /// NM_173159																					
4.57	4.85	0.28	5.63E-01	8.34E-01	COG6	component of oligomeric golgi complex 6	chr13q13.3	225769_at	NM_020751																					
3.97	4.19	0.22	5.63E-01	8.34E-01	---	---	---	239266_at	---																					
2.79	2.92	0.13	5.63E-01	8.34E-01	---	---	---	242390_at	---																					
4.71	4.84	0.13	5.63E-01	8.34E-01	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	chr17q21	205095_s_at	NM_001130020 /// NM_001130021 /// NM_005177																					
2.64	2.72	0.08	5.63E-01	8.34E-01	ZBTB7C	zinc finger and BTB domain containing 7C	chr18q21.1	217675_at	NM_001039360																					
4.42	4.67	0.25	5.63E-01	8.34E-01	---	---	---	1563841_at	---																					
3.81	3.97	0.16	5.63E-01	8.34E-01	RNF19A	ring finger protein 19A	chr8q22	220483_s_at	NM_015435 /// NM_183419																					
2.67	2.75	0.08	5.63E-01	8.34E-01	---	---	---	1568847_at	---																					
6.14	6.37	0.23	5.63E-01	8.34E-01	UBR2	ubiquitin protein ligase E3 component n-recognin 2	chr6p21.1	212756_s_at	NM_015255																					
3.31	3.49	0.18	5.63E-01	8.34E-01	RABEP1	rabaptin, RAB GTPase binding effector protein 1	chr17p13.2	203223_at	NM_001083585 /// NM_004703																					
3.42	3.54	0.11	5.63E-01	8.34E-01	CACNG1	calcium channel, voltage-dependent, gamma subunit 1	chr17q24	206612_at	NM_000727																					
2.84	2.95	0.11	5.63E-01	8.34E-01	CST6	cystatin E/M	chr11q13	206595_at	NM_001323																					
2.24	2.35	0.11	5.63E-01	8.34E-01	---	---	---	240476_at	---																					
2.66	2.76	0.09	5.63E-01	8.34E-01	SOX2	SRY (sex determining region Y)-box 2	chr3q26.3-q27	214178_s_at	NM_003106																					
2.73	2.81	0.08	5.63E-01	8.34E-01	DYNLRB1	Dynein, light chain, roadblock-type 1	chr20q11.21	1565612_at	NM_014183																					
8.42	8.58	0.15	5.63E-01	8.34E-01	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	chr4q24	200669_s_at	NM_003340 /// NM_181886 /// NM_181887 /// NM_181888 /// NM_181889 /// NM_181890 /// NM_181891 /// NM_181892 /// NM_181893																					
2.33	2.43	0.09	5.63E-01	8.34E-01	NAG	neuroblastoma-amplified protein	chr2p24	240579_at	NM_015909																					
2.65	2.75	0.10	5.63E-01	8.34E-01	LOC730961	hypothetical protein LOC730961	---	239094_at	XM_001131308																					

2.28	2.36	0.08	5.63E-01	8.34E-01	SLC26A8	solute carrier family 26, member 8	chr6p21	237340_at	NM_052961 /// NM_138718
4.68	4.84	0.16	5.63E-01	8.34E-01	KIAA1618	KIAA1618	chr17q25.3	231956_at	NM_020954
5.34	5.52	0.18	5.64E-01	8.34E-01	C1orf165	chromosome 1 open reading frame 165	chr1p33	219670_at	NM_024603
2.28	2.34	0.06	5.64E-01	8.34E-01	POGK	pogo transposable element with KRAB domain	chr1q24.1	222564_at	NM_017542
2.15	2.23	0.07	5.64E-01	8.34E-01	PTPRC	protein tyrosine phosphatase, receptor type, C	chr1q31-q32	1569830_at	NM_002838 /// NM_080921 /// NM_080922 /// NM_080923
1.95	2.02	0.06	5.64E-01	8.34E-01	---	---	---	1559707_at	---
3.71	3.88	0.16	5.64E-01	8.34E-01	C21orf90	chromosome 21 open reading frame 90	chr21q22.3	1554953_a_at	XR_017894 /// XR_017992 /// XR_040133
2.78	2.88	0.10	5.64E-01	8.35E-01	---	---	---	216172_at	---
6.47	6.65	0.18	5.64E-01	8.35E-01	RABGEF1	RAB guanine nucleotide exchange factor (GEF) 1	chr7q11.21	218310_at	NM_014504
3.42	3.55	0.13	5.64E-01	8.35E-01	ACSS1	acyl-CoA synthetase short-chain family member 1	chr20p11.23-p11.21	234484_s_at	NM_032501
2.75	2.84	0.09	5.64E-01	8.35E-01	PLA2R1	phospholipase A2 receptor 1, 180kDa	chr2q23-q24	240039_at	NM_001007267 /// NM_007366
1.92	1.99	0.07	5.64E-01	8.35E-01	---	---	---	1570176_at	---
7.35	7.55	0.19	5.64E-01	8.35E-01	TJP1	tight junction protein 1 (zona occludens 1)	chr15q13	202011_at	NM_003257 /// NM_175610
2.85	2.98	0.12	5.64E-01	8.35E-01	IGSF6	immunoglobulin superfamily, member 6	chr16p12-p13	206420_at	NM_005849
2.24	2.32	0.08	5.64E-01	8.35E-01	---	---	---	229928_at	---
2.61	2.68	0.07	5.64E-01	8.35E-01	---	---	---	229243_at	---
3.18	3.25	0.07	5.64E-01	8.35E-01	---	---	---	242962_at	---
2.38	2.48	0.10	5.64E-01	8.35E-01	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	chr4q13.3	242370_at	NM_001004346
5.61	5.96	0.35	5.64E-01	8.35E-01	---	---	---	213156_at	---
1.90	1.97	0.07	5.64E-01	8.35E-01	---	---	---	1567380_at	---
4.56	4.99	0.44	5.64E-01	8.35E-01	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	chr1q25	212107_s_at	NM_001357
4.93	5.28	0.36	5.65E-01	8.35E-01	MGC24125	hypothetical protein MGC24125	chr4q35.1	1554733_at	XR_000543 /// XR_000648
4.42	4.62	0.19	5.65E-01	8.35E-01	---	---	---	235577_at	---
5.36	5.54	0.18	5.65E-01	8.35E-01	TXNDC10	thioredoxin domain containing 10	chr18q22	225302_at	NM_019022
6.34	6.49	0.15	5.65E-01	8.35E-01	---	---	---	242407_at	---
4.05	4.19	0.14	5.64E-01	8.35E-01	GFOD1	glucose-fructose oxidoreductase domain containing 1	chr6pter-p22.1	219821_s_at	NM_018988
5.42	5.53	0.11	5.64E-01	8.35E-01	WTIP	Wilms tumor 1 interacting protein	chr19q13.11	227411_at	NM_001080436
2.30	2.41	0.11	5.65E-01	8.35E-01	PROL1	proline rich, lacrimal 1	chr4q13.3	208004_at	NM_021225
2.74	2.83	0.09	5.65E-01	8.35E-01	C17orf46	chromosome 17 open reading frame 46	chr17q21.31	1553804_a_at	NM_152343
2.97	3.06	0.09	5.64E-01	8.35E-01	---	---	---	230354_at	---
2.66	2.74	0.09	5.64E-01	8.35E-01	C15orf45	chromosome 15 open reading frame 45	chr15q13.3	1561434_at	XR_041264 /// XR_041265 /// XR_041266
2.88	2.96	0.08	5.64E-01	8.35E-01	KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2	chr8q22	1554680_s_at	NM_020697
2.27	2.35	0.07	5.64E-01	8.35E-01	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	chr6p12	1553394_a_at	NM_003221
2.31	2.39	0.08	5.65E-01	8.35E-01	NEBL	nebulette	chr10p12	217585_at	NM_006393 /// NM_213569
2.16	2.24	0.08	5.65E-01	8.35E-01	OR2J3	olfactory receptor, family 2, subfamily J, member 3	chr6p22.1	217334_at	NM_001005216
3.01	3.41	0.40	5.65E-01	8.35E-01	TAC1	tachykinin, precursor 1	chr7q21-q22	206552_s_at	NM_003182 /// NM_013996 /// NM_013997 /// NM_013998
5.30	5.52	0.21	5.65E-01	8.35E-01	GNPDA2	glucosamine-6-phosphate deaminase 2	chr4p13	227022_at	NM_138335
2.94	3.07	0.13	5.65E-01	8.35E-01	MRO	maestro	chr18q21	231358_at	NM_001127174 /// NM_001127175 /// NM_001127176 /// NM_031939
3.03	3.13	0.11	5.65E-01	8.35E-01	LOC541473	FK506 binding protein 6, 36kDa pseudogene	chr7q11.23	1554318_at	NR_003602
2.32	2.42	0.10	5.65E-01	8.35E-01	---	---	---	1557875_at	---
2.08	2.15	0.07	5.65E-01	8.35E-01	---	---	---	237928_at	---
1.85	1.92	0.07	5.65E-01	8.35E-01	---	---	---	242958_x_at	---
4.74	4.85	0.11	5.65E-01	8.35E-01	---	---	---	237779_at	---
2.46	2.56	0.10	5.65E-01	8.35E-01	---	---	---	232622_at	---
6.64	6.75	0.11	5.65E-01	8.35E-01	---	---	---	231968_at	---
2.35	2.43	0.08	5.65E-01	8.35E-01	COX18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr4q13.3	230909_at	NM_173827
2.12	2.19	0.07	5.65E-01	8.35E-01	CRTAM	cytotoxic and regulatory T cell molecule	chr11q22-q23	206914_at	NM_019604

5.43	5.82	0.39	5.65E-01	8.35E-01	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	chr10q22.1	223721_s_at	NM_021800 /// NM_201262																				
3.58	3.72	0.14	5.65E-01	8.35E-01	MLPH	melanophilin	chr2q37.3	218211_s_at	NM_001042467 /// NM_024101																				
3.03	3.14	0.11	5.65E-01	8.35E-01	---	---	---	1554891_at	---																				
2.72	2.89	0.18	5.66E-01	8.35E-01	RC3H2	ring finger and CCCH-type zinc finger domains 2	chr9q34	238421_at	NM_001100588 /// NM_018835																				
3.03	3.14	0.11	5.66E-01	8.35E-01	DNM2	dynamin 2	chr19p13.2	216024_at	NM_001005360 /// NM_001005361 /// NM_001005362 /// NM_004945																				
2.59	2.67	0.08	5.66E-01	8.35E-01	---	---	---	240384_at	---																				
3.32	3.45	0.13	5.66E-01	8.35E-01	PNKD	paroxysmal nonkinesigenic dyskinesia	chr2q35	1555713_at	NM_001077399 /// NM_015488 /// NM_022572																				
3.79	3.91	0.12	5.66E-01	8.36E-01	MYH11	myosin, heavy chain 11, smooth muscle	chr16p13.11	201495_x_at	NM_001040113 /// NM_001040114 /// NM_002474 /// NM_022844																				
2.56	2.65	0.10	5.66E-01	8.36E-01	CYP4X1	cytochrome P450, family 4, subfamily X, polypeptide 1	chr1p33	227702_at	NM_178033																				
2.31	2.41	0.10	5.66E-01	8.36E-01	TAS2R39	taste receptor, type 2, member 39	chr7q34	1553553_at	NM_176881																				
4.04	4.13	0.09	5.66E-01	8.36E-01	IGSF3	immunoglobulin superfamily, member 3	chr1p13	1556163_a_at	NM_001007237 /// NM_001542																				
3.92	4.02	0.10	5.66E-01	8.36E-01	AKR1CL2	aldo-keto reductase family 1, member C-like 2	chr10p15.1	1559982_s_at	NM_001040177																				
2.42	2.49	0.06	5.66E-01	8.36E-01	---	---	---	1561817_at	---																				
7.22	7.38	0.16	5.66E-01	8.36E-01	RNF12	Ring finger protein 12	chrXq13-q21	225416_at	NM_016120 /// NM_183353																				
2.20	2.27	0.07	5.66E-01	8.36E-01	---	---	---	1560716_at	---																				
4.66	4.81	0.15	5.66E-01	8.36E-01	ASXL2	additional sex combs like 2 (Drosophila)	chr2p24.1	226251_at	NM_018263																				
2.50	2.61	0.11	5.66E-01	8.36E-01	CLDN18	claudin 18	chr3q22.3	214135_at	NM_001002026 /// NM_016369																				
6.74	6.87	0.13	5.66E-01	8.36E-01	RAB4B	RAB4B, member RAS oncogene family	chr19q13.2	219807_x_at	NM_016154																				
2.16	2.25	0.09	5.67E-01	8.36E-01	GPR82	G protein-coupled receptor 82	chrXp11.4	1553317_s_at	NM_080817																				
2.46	2.54	0.08	5.67E-01	8.36E-01	---	---	---	220898_at	---																				
7.09	7.47	0.38	5.67E-01	8.36E-01	CCT2	chaperonin containing TCP1, subunit 2 (beta)	chr12q15	201946_s_at	NM_006431																				
6.08	6.38	0.30	5.67E-01	8.36E-01	SLC39A6	solute carrier family 39 (zinc transporter), member 6	chr18q12.2	202089_s_at	NM_001099406 /// NM_012319																				
8.28	8.49	0.21	5.67E-01	8.36E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	201983_s_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284																				
7.80	8.00	0.20	5.67E-01	8.36E-01	CD59	CD59 molecule, complement regulatory protein	chr11p13	212463_at	NM_000611 /// NM_001127223 /// NM_001127225 /// NM_001127226 /// NM_001127227 /// NM_203329 /// NM_203330 /// NM_203331																				
3.11	3.28	0.17	5.67E-01	8.36E-01	PVRIG	poliovirus receptor related immunoglobulin domain containing	chr7q22.1	219812_at	NM_024070																				
3.95	4.08	0.14	5.67E-01	8.36E-01	GAB3	GRB2-associated binding protein 3	chrXq28	228410_at	NM_001081573 /// NM_080612																				
3.14	3.26	0.12	5.67E-01	8.36E-01	ATXN7L1	ataxin 7-like 1	chr7q22.2	227732_at	NM_020725 /// NM_152749																				

4.67	4.78	0.11	5.67E-01	8.36E-01	FGFR1	fibroblast growth factor receptor 1	chr8p11.2-p11.1	226705_at	NM_015850 /// NM_023105 /// NM_023106 /// NM_023107 /// NM_023108 /// NM_023110 /// NM_023111
2.23	2.33	0.09	5.67E-01	8.36E-01	---	---	---	236409_at	---
2.15	2.24	0.09	5.67E-01	8.36E-01	---	---	---	1563801_at	---
2.51	2.60	0.09	5.67E-01	8.36E-01	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	chr10q22.3	221583_s_at	NM_001014797 /// NM_002247
2.89	2.97	0.09	5.67E-01	8.36E-01	MAGEB4	melanoma antigen family B, 4	chrXp21.3	207581_s_at	NM_002367
2.08	2.14	0.07	5.67E-01	8.36E-01	---	---	---	1560909_x_at	---
2.05	2.13	0.08	5.67E-01	8.36E-01	---	---	---	216297_at	---
1.88	1.94	0.07	5.67E-01	8.36E-01	ANKRD32	ankyrin repeat domain 32	chr5q15	1558076_at	NM_032290
2.17	2.25	0.08	5.67E-01	8.36E-01	---	---	---	231394_at	---
7.82	8.07	0.25	5.67E-01	8.36E-01	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	chr17q23-q24	200604_s_at	NM_002734 /// NM_212471 /// NM_212472
2.66	2.77	0.11	5.67E-01	8.36E-01	ABHD1	abhydrolase domain containing 1	chr2p23.3	1560117_at	NM_032604
6.16	6.31	0.14	5.67E-01	8.36E-01	FKBP8	FK506 binding protein 8, 38kDa	chr19p12	40850_at	NM_012181
8.65	8.90	0.24	5.67E-01	8.37E-01	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	chr14q12-q13	1554241_at	NM_004086
5.43	5.86	0.44	5.68E-01	8.37E-01	---	---	---	241903_at	---
4.60	4.71	0.12	5.68E-01	8.37E-01	FAM155B	family with sequence similarity 155, member B	chrXq13.1	206299_at	NM_015686
1.92	1.99	0.07	5.68E-01	8.37E-01	---	---	---	216595_at	---
1.99	2.05	0.06	5.68E-01	8.37E-01	---	---	---	243678_at	---
4.78	5.07	0.29	5.68E-01	8.37E-01	RGPD5 /// RGPD6 /// RGPD8	RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 6 /// RANBP2-like and GRIP domain containing 8	chr2q13	210676_x_at	NM_001123363 /// NM_005054 /// NM_032260 /// XM_001133591 /// XM_001722279
4.74	5.00	0.27	5.68E-01	8.37E-01	---	---	---	232797_at	---
3.37	3.51	0.14	5.68E-01	8.37E-01	RAB3D	RAB3D, member RAS oncogene family	chr19p13.2	208466_at	NM_004283
2.71	2.79	0.09	5.68E-01	8.37E-01	PLG	plasminogen	chr6q26	209977_at	NM_000301
2.85	2.96	0.12	5.68E-01	8.37E-01	---	---	---	243398_at	---
4.18	4.27	0.09	5.68E-01	8.37E-01	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	chr5q33.1	202608_s_at	NM_001543
2.29	2.40	0.11	5.68E-01	8.37E-01	OR10H2	olfactory receptor, family 10, subfamily H, member 2	chr19p13.1	208543_at	NM_013939
3.11	3.18	0.07	5.68E-01	8.37E-01	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	chr9q34.3	205915_x_at	NM_000832 /// NM_007327 /// NM_021569
6.74	7.06	0.32	5.68E-01	8.37E-01	FUSIP1 /// LOC642558	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1	chr1p36.11	213594_x_at	NM_006625 /// NM_054016 /// XM_001713958 /// XM_001713979
2.48	2.59	0.11	5.68E-01	8.37E-01	PKD1L2	polycystic kidney disease 1-like 2	chr16q23.2	1554371_at	NM_001076780 /// NM_052892
4.45	4.55	0.10	5.68E-01	8.37E-01	---	---	---	242987_x_at	---
2.18	2.27	0.10	5.68E-01	8.37E-01	NKX2-2	NK2 homeobox 2	chr20pter-q11.23	206915_at	NM_002509
1.98	2.06	0.09	5.68E-01	8.37E-01	LDHAL6B	lactate dehydrogenase A-like 6B	chr15q22.2	210712_at	NM_033195
2.23	2.30	0.08	5.68E-01	8.37E-01	C15orf26	chromosome 15 open reading frame 26	chr15q25.1	1552950_at	NM_173528
2.09	2.16	0.07	5.68E-01	8.37E-01	---	---	---	240968_at	---
2.75	2.83	0.08	5.68E-01	8.37E-01	CXCR3	chemokine (C-X-C motif) receptor 3	chrXq13	207681_at	NM_001504
2.03	2.13	0.11	5.68E-01	8.37E-01	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	chr7q31.2-q31.3	1569450_at	NM_006136
4.93	5.06	0.13	5.68E-01	8.37E-01	VARS	valyl-tRNA synthetase	chr6p21.3	201796_s_at	NM_006295
11.13	11.21	0.08	5.68E-01	8.37E-01	BTF3	basic transcription factor 3	chr5q13.2	208517_x_at	NM_001037637 /// NM_001207
3.97	4.12	0.15	5.69E-01	8.37E-01	MIB2	Mindbomb homolog 2 (Drosophila)	chr1p36.33	241541_at	NM_080875
3.29	3.39	0.10	5.69E-01	8.37E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	217033_x_at	NM_001007156 /// NM_001012338 /// NM_002530
2.12	2.18	0.07	5.69E-01	8.37E-01	NUP54	nucleoporin 54kDa	chr4q21.1	215213_at	NM_017426
6.21	6.31	0.10	5.69E-01	8.37E-01	ZDHHC20	zinc finger, DHHC-type containing 20	chr13q12.11	225365_at	NM_153251
2.25	2.32	0.07	5.69E-01	8.37E-01	OR5AK4P	olfactory receptor, family 5, subfamily AK, member 4 pseudogene	chr11q12.1	1567023_at	---

4.47	4.56	0.09	5.69E-01	8.37E-01	---	---	---	240587_x_at	---
2.82	3.07	0.25	5.69E-01	8.37E-01	---	---	---	243366_s_at	---
4.98	5.23	0.25	5.69E-01	8.37E-01	EVI2A /// EVI2B	ecotropic viral integration site 2A /// ecotropic viral integration site 2B	chr17q11.2	204774_at	NM_001003927 /// NM_006495 /// NM_014210
1.77	1.86	0.09	5.69E-01	8.37E-01	CCDC67	coiled-coil domain containing 67	chr11q21	1558893_a_at	NM_181645
1.99	2.07	0.08	5.69E-01	8.37E-01	LOC121006	hypothetical protein LOC121006	chr12q13.13	1562317_at	XM_001714910 /// XM_001718353 /// XM_937469
2.07	2.13	0.07	5.69E-01	8.37E-01	---	---	---	1559621_at	---
3.62	3.72	0.10	5.69E-01	8.37E-01	---	---	---	227030_at	---
2.26	2.34	0.08	5.69E-01	8.37E-01	LOC388946	Hypothetical LOC388946	chr2p21	1556489_at	XM_001718876 /// XM_371491 /// XM_941345
2.75	2.82	0.07	5.69E-01	8.37E-01	PDE11A	phosphodiesterase 11A	chr2q31.2	221110_x_at	NM_001077196 /// NM_001077197 /// NM_001077358 /// NM_016953
4.48	4.56	0.08	5.69E-01	8.37E-01	---	---	---	237977_at	---
2.77	2.86	0.09	5.69E-01	8.37E-01	---	---	---	235573_at	---
2.72	2.80	0.08	5.69E-01	8.37E-01	TRAF4	TNF receptor-associated factor 4	chr17q11-q12	242473_at	NM_004295
7.25	7.46	0.22	5.69E-01	8.37E-01	SOD2	superoxide dismutase 2, mitochondrial	chr6q25.3	221477_s_at	NM_000636 /// NM_001024465 /// NM_001024466
2.14	2.22	0.08	5.69E-01	8.37E-01	FABP1	fatty acid binding protein 1, liver	chr2p11	205892_s_at	NM_001443
2.01	2.10	0.08	5.69E-01	8.37E-01	FAM83B	family with sequence similarity 83, member B	chr6p12.1	1563900_at	NM_001010872
2.66	2.75	0.09	5.69E-01	8.37E-01	---	---	---	237590_at	---
5.02	5.10	0.08	5.69E-01	8.37E-01	MPRIP	Myosin phosphatase Rho interacting protein	chr17p11.2	238329_at	NM_015134 /// NM_201274
4.01	4.29	0.28	5.69E-01	8.37E-01	FEM1B	fem-1 homolog b (C. elegans)	chr15q22	212373_at	NM_015322
4.11	4.24	0.14	5.69E-01	8.37E-01	C7orf44	chromosome 7 open reading frame 44	chr7p13	239490_at	NM_018224
2.36	2.43	0.07	5.69E-01	8.37E-01	LOC100129058	similar to hCG2038656	chr3p21.1	1564300_at	XM_001723374 /// XM_001725566 /// XM_001725887
2.69	2.81	0.12	5.69E-01	8.37E-01	RLBP1L1	retinaldehyde binding protein 1-like 1	chr8q12.2-q12.3	230217_at	NM_173519
3.72	3.84	0.12	5.69E-01	8.37E-01	---	---	---	234052_at	---
2.61	2.71	0.10	5.69E-01	8.37E-01	INSL4	insulin-like 4 (placenta)	chr9p24	206549_at	NM_002195
3.24	3.31	0.08	5.69E-01	8.37E-01	TESC	Tescalcin	chr12q24.22	240553_at	NM_017899
2.00	2.07	0.06	5.70E-01	8.37E-01	---	---	---	1569916_at	---
3.04	3.17	0.13	5.70E-01	8.38E-01	C6orf52	chromosome 6 open reading frame 52	chr6p24.1	239417_x_at	XM_001718541 /// XM_371798 /// XM_938497
2.09	2.16	0.08	5.70E-01	8.38E-01	LOC100128398	Hypothetical protein LOC100128398	chr19q13.43	1556725_a_at	XM_001725704 /// XM_001725733 /// XM_001726270
5.65	5.93	0.27	5.70E-01	8.38E-01	WAPAL	wings apart-like homolog (Drosophila)	chr10q23.2	212264_s_at	NM_015045
2.39	2.49	0.10	5.70E-01	8.38E-01	CA8	carbonic anhydrase VIII	chr8q11-q12	1555445_at	NM_004056
2.22	2.31	0.09	5.70E-01	8.38E-01	SPINT3	serine peptidase inhibitor, Kunitz type, 3	---	215503_at	NM_006652
5.07	5.16	0.09	5.70E-01	8.38E-01	---	---	---	243442_x_at	---
2.62	2.73	0.11	5.70E-01	8.38E-01	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	chr3q27	1558460_at	NM_001023587 /// NM_005688
4.30	4.40	0.10	5.70E-01	8.38E-01	PHKA2	phosphorylase kinase, alpha 2 (liver)	chrXp22.2-p22.1	1559705_s_at	NM_000292
6.09	6.43	0.34	5.70E-01	8.38E-01	REPS2	RALBP1 associated Eps domain containing 2	chrXp22.2	227425_at	NM_001080975 /// NM_004726
4.64	4.93	0.29	5.70E-01	8.38E-01	HSPA4	heat shock 70kDa protein 4	chr5q31.1-q31.2	211016_x_at	NM_002154

5.02	5.11	0.09	5.70E-01	8.38E-01	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	chr10q22	212669_at	NM_001222 /// NM_172169 /// NM_172170 /// NM_172171 /// NM_172173
2.14	2.23	0.09	5.70E-01	8.38E-01	GDEP	gene differentially expressed in prostate	chr4q21.1	231096_at	XR_000540 /// XR_000635
2.87	2.95	0.08	5.70E-01	8.38E-01	RNFT2	ring finger protein, transmembrane 2	chr12q24.22	1553209_at	NM_001109903 /// NM_032814
5.03	5.25	0.22	5.70E-01	8.38E-01	CTNS	cystinosis, nephropathic	chr17p13	36566_at	NM_001031681 /// NM_004937
6.75	6.93	0.18	5.70E-01	8.38E-01	FAM13A1	family with sequence similarity 13, member A1	chr4q22.1	202973_x_at	NM_001015045 /// NM_014883
2.30	2.37	0.07	5.70E-01	8.38E-01	---	---	---	241576_at	---
4.80	5.10	0.30	5.70E-01	8.38E-01	CD58	CD58 molecule	chr1p13	211744_s_at	NM_001779
6.19	6.44	0.25	5.70E-01	8.38E-01	C12orf31	chromosome 12 open reading frame 31	chr12q14.3	224446_at	NM_032338
2.52	2.64	0.13	5.70E-01	8.38E-01	SGOL2	shugoshin-like 2 (S. pombe)	chr2q33.1	235425_at	NM_152524
2.04	2.11	0.06	5.70E-01	8.38E-01	---	---	---	234510_at	---
4.44	4.58	0.14	5.70E-01	8.38E-01	ZNF79	zinc finger protein 79	chr9q34	214138_at	NM_007135
5.83	5.95	0.12	5.70E-01	8.38E-01	C1orf134	chromosome 1 open reading frame 134	chr1p36.13	244834_at	---
3.60	3.71	0.11	5.71E-01	8.38E-01	PLXNB2	Plexin B2	chr22q13.33	211472_at	NM_012401
2.10	2.19	0.09	5.71E-01	8.38E-01	ZBTB6	zinc finger and BTB domain containing 6	chr9q33.2	206098_at	NM_006626
1.98	2.05	0.06	5.70E-01	8.38E-01	---	---	---	1565608_at	---
2.66	2.78	0.12	5.71E-01	8.38E-01	FLJ34208	hypothetical gene supported by AK091527	chr3q29	1566760_at	XM_001713883 /// XM_001715353 /// XM_001719177
2.29	2.37	0.08	5.71E-01	8.38E-01	PTPRD	protein tyrosine phosphatase, receptor type, D	chr9p23-p24.3	213362_at	NM_001040712 /// NM_002839 /// NM_130391 /// NM_130392 /// NM_130393
2.05	2.13	0.07	5.71E-01	8.38E-01	---	---	---	238891_at	---
2.02	2.08	0.06	5.71E-01	8.38E-01	METT5D1	Methyltransferase 5 domain containing 1	chr11p14.1	1565898_at	NM_001113528 /// NM_152636
6.17	6.41	0.24	5.71E-01	8.38E-01	CYLD	cylindromatosis (turban tumor syndrome)	chr16q12.1	221903_s_at	NM_001042355 /// NM_001042412 /// NM_015247
3.35	3.43	0.08	5.71E-01	8.38E-01	---	---	---	237274_at	---
2.37	2.45	0.08	5.71E-01	8.38E-01	GGNBP2	gametogenetin binding protein 2	chr17q12	233937_at	NM_024835
2.59	2.68	0.10	5.71E-01	8.38E-01	CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	chr12p13.33	1552690_a_at	NM_172364
1.81	1.88	0.07	5.71E-01	8.38E-01	OLFM3	olfactomedin 3	chr1p22	1554526_at	NM_058170
2.45	2.52	0.07	5.71E-01	8.38E-01	---	---	---	238387_s_at	---
6.69	6.80	0.11	5.71E-01	8.38E-01	DBNL	drebrin-like	chr7p13	222429_at	NM_001014436 /// NM_001122956 /// NM_014063
2.15	2.22	0.06	5.71E-01	8.38E-01	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	chr1q25.2	242458_at	NM_018037 /// NM_152663
7.68	7.94	0.25	5.71E-01	8.38E-01	FNDC3B	fibronectin type III domain containing 3B	chr3q26.31	225032_at	NM_022763
3.35	3.51	0.16	5.71E-01	8.38E-01	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	chr9q31.1	216066_at	NM_005502
4.94	5.07	0.13	5.71E-01	8.38E-01	PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	chr2p23	201407_s_at	NM_002709 /// NM_206876
2.28	2.39	0.11	5.71E-01	8.38E-01	---	---	---	1563070_at	---
2.22	2.29	0.07	5.71E-01	8.38E-01	GSN	Gelsolin (amyloidosis, Finnish type)	chr9q33	227957_at	NM_000177 /// NM_001127662 /// NM_001127663 /// NM_001127664 /// NM_001127665 /// NM_001127666 /// NM_001127667 /// NM_198252
2.11	2.17	0.07	5.71E-01	8.38E-01	TMEM67	transmembrane protein 67	chr8q22.1	1552765_x_at	NM_153704

2.84	2.94	0.10	5.71E-01	8.38E-01	RP5-1000E10.4	suppressor of IKK epsilon	chr1p13.2	235294_at	NM_001102396 /// NM_025073
4.02	4.10	0.08	5.71E-01	8.38E-01	CEP250	centrosomal protein 250kDa	chr20q11.22-q12	210894_s_at	NM_001035518 /// NM_007186
2.25	2.32	0.07	5.71E-01	8.38E-01	---	---	---	232957_x_at	---
7.67	7.80	0.13	5.71E-01	8.38E-01	TOP1	topoisomerase (DNA) I	chr20q12-q13.1	208901_s_at	NM_003286
1.98	2.04	0.07	5.71E-01	8.39E-01	---	---	---	217479_at	---
2.00	2.08	0.07	5.71E-01	8.39E-01	LOC729296	Similar to hCG2017976	chr20q13.33	237806_s_at	XM_001129872 /// XM_001130699 /// XM_001717168
7.73	8.13	0.40	5.72E-01	8.39E-01	---	---	---	236699_at	---
3.15	3.28	0.13	5.72E-01	8.39E-01	C1orf61	chromosome 1 open reading frame 61	chr1q22	205103_at	NM_006365
1.98	2.08	0.09	5.72E-01	8.39E-01	---	---	---	241035_s_at	---
5.38	5.47	0.09	5.72E-01	8.39E-01	MRPS5	mitochondrial ribosomal protein S5	chr2p11.2-q11.2	224877_s_at	NM_031902
2.25	2.31	0.07	5.72E-01	8.39E-01	---	---	---	244437_at	---
2.63	2.79	0.16	5.72E-01	8.39E-01	---	---	---	1558959_at	---
2.87	3.00	0.13	5.72E-01	8.39E-01	MLN	motilin	chr6p21.3	207473_at	NM_001040109 /// NM_002418
3.69	3.79	0.10	5.72E-01	8.39E-01	ESPN	espin	chr1p36.31|1p36.31-p36.11	223549_s_at	NM_031475
6.70	7.09	0.39	5.72E-01	8.39E-01	PLEKHA5	pleckstrin homology domain containing, family A member 5	chr12p12	220952_s_at	NM_019012
5.03	5.17	0.14	5.72E-01	8.39E-01	SUSD2	sushi domain containing 2	chr22q11-q12	234310_s_at	NM_019601
2.89	3.03	0.14	5.72E-01	8.39E-01	---	---	---	1557804_at	---
3.54	3.65	0.11	5.72E-01	8.39E-01	---	---	---	1568639_a_at	---
4.78	4.93	0.16	5.72E-01	8.39E-01	THAP8	THAP domain containing 8	chr19q13.12	228500_at	NM_152658
2.69	2.79	0.10	5.72E-01	8.39E-01	CCK	cholecystokinin	chr3p22-p21.3	205827_at	NM_000729
2.21	2.30	0.09	5.72E-01	8.39E-01	SNTB2	Syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16q22-q23	213814_s_at	NM_006750
2.02	2.11	0.08	5.72E-01	8.39E-01	EPB41L1	erythrocyte membrane protein band 4.1-like 1	chr20q11.2-q12	230289_at	NM_012156 /// NM_177996
2.44	2.54	0.10	5.72E-01	8.39E-01	SYNPO2	synaptopodin 2	chr4q26	232119_at	NM_001128933 /// NM_001128934 /// NM_133477
1.92	2.00	0.08	5.72E-01	8.39E-01	---	---	---	1554887_at	---
2.10	2.16	0.06	5.72E-01	8.39E-01	IKZF1	Hypothetical protein LOC100132224	chr7p13-p11.1	1565816_at	NM_006060
3.17	3.28	0.11	5.72E-01	8.39E-01	---	---	---	232198_at	---
2.69	2.78	0.09	5.72E-01	8.39E-01	FAM69B	Family with sequence similarity 69, member B	chr9q34.3	226940_at	NM_152421
1.88	1.94	0.06	5.72E-01	8.39E-01	---	---	---	1557617_at	---
3.61	3.70	0.09	5.72E-01	8.39E-01	ASGR1	asialoglycoprotein receptor 1	chr17p13.2	206743_s_at	NM_001671
3.72	3.82	0.09	5.72E-01	8.39E-01	---	---	---	230922_x_at	---
3.22	3.30	0.08	5.72E-01	8.39E-01	---	---	---	1562861_at	---
2.07	2.14	0.07	5.72E-01	8.39E-01	---	---	---	1560453_at	---
2.63	2.70	0.07	5.73E-01	8.39E-01	NLRP12	NLR family, pyrin domain containing 12	chr19q13.41	1554952_s_at	NM_033297 /// NM_144687
6.34	6.55	0.21	5.73E-01	8.39E-01	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4	chr3q22.1	212740_at	NM_014602
2.16	2.24	0.08	5.73E-01	8.39E-01	---	---	---	1562399_at	---
2.55	2.63	0.08	5.73E-01	8.39E-01	THPO	thrombopoietin	chr3q27	211831_s_at	NM_000460
4.03	4.14	0.11	5.73E-01	8.39E-01	LILRA4	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	chr19q13.4	210313_at	NM_012276
2.55	2.63	0.08	5.73E-01	8.39E-01	---	---	---	233038_at	---
3.16	3.28	0.12	5.73E-01	8.39E-01	---	---	---	221852_at	---
4.32	4.42	0.10	5.73E-01	8.39E-01	ZNF554	zinc finger protein 554	chr19p13.3	232214_x_at	NM_001102651
2.15	2.22	0.07	5.73E-01	8.39E-01	---	---	---	241732_at	---
3.28	3.38	0.10	5.73E-01	8.39E-01	---	---	---	244366_at	---
1.75	1.81	0.06	5.73E-01	8.39E-01	COG6	component of oligomeric golgi complex 6	chr13q13.3	232786_at	NM_020751
4.10	4.27	0.17	5.73E-01	8.39E-01	TLR5	toll-like receptor 5	chr1q41-q42	210166_at	NM_003268
4.86	4.96	0.11	5.73E-01	8.39E-01	TRAF3IP1	TNF receptor-associated factor 3 interacting protein 1	chr2q37.3	238494_at	NM_015650
2.03	2.11	0.08	5.73E-01	8.39E-01	---	---	---	1567986_at	---
5.76	5.98	0.22	5.73E-01	8.39E-01	MTMR2	myotubularin related protein 2	chr11q22	203211_s_at	NM_016156 /// NM_201278 /// NM_201281 /// NR_023354 /// NR_023355 /// NR_023356
2.53	2.66	0.13	5.73E-01	8.39E-01	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	chr4q32.1	215992_s_at	NM_014247
2.66	2.75	0.09	5.73E-01	8.39E-01	---	---	---	244280_at	---
4.54	4.79	0.25	5.73E-01	8.39E-01	DLG1	discs, large homolog 1 (Drosophila)	chr3q29	202514_at	NM_001098424 /// NM_004087
2.95	3.05	0.10	5.73E-01	8.40E-01	---	---	---	236450_at	---
2.11	2.18	0.07	5.73E-01	8.40E-01	FMO9P	flavin containing monooxygenase 9 pseudogene	chr1q24.1	1553924_at	NR_002925

3.18	3.30	0.12	5.73E-01	8.40E-01	LOC150763	hypothetical protein LOC150763	chr2q11.2	235557_at	NM_207328
6.48	6.68	0.20	5.73E-01	8.40E-01	SYNJ2BP	synaptojanin 2 binding protein	chr14q24.2	227274_at	NM_018373
2.50	2.58	0.08	5.73E-01	8.40E-01	TAL2	T-cell acute lymphocytic leukemia 2	chr9q32	1553593_a_at	NM_005421
1.92	1.99	0.07	5.73E-01	8.40E-01	---	---	---	1561300_at	---
3.52	3.65	0.13	5.73E-01	8.40E-01	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	chr21q11	1555638_a_at	NM_022136
9.28	9.49	0.21	5.74E-01	8.40E-01	SERBP1	SERPINE1 mRNA binding protein 1	chr1p31	217724_at	NM_001018067 /// NM_001018068 /// NM_001018069 /// NM_015640
5.26	5.41	0.15	5.74E-01	8.40E-01	LOC283070	Hypothetical protein LOC283070	chr10p14	226959_at	---
2.41	2.49	0.09	5.74E-01	8.40E-01	---	---	---	241892_at	---
2.18	2.24	0.06	5.74E-01	8.40E-01	---	---	---	210914_at	---
1.90	1.97	0.07	5.74E-01	8.40E-01	---	---	---	215944_at	---
4.37	4.44	0.08	5.74E-01	8.40E-01	TRPV5	transient receptor potential cation channel, subfamily V, member 5	chr7q35	208267_at	NM_019841
3.53	3.68	0.15	5.74E-01	8.40E-01	LOC100129720	Hypothetical protein LOC100129720	chr3q25.1	235475_at	XM_001724737 /// XM_001724738 /// XM_001725428 /// XM_001725430 /// XM_001725771 /// XM_001725772
6.09	6.22	0.13	5.74E-01	8.40E-01	TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	chr1q23.2	214773_x_at	NM_001031800 /// NM_152902
1.96	2.04	0.08	5.74E-01	8.40E-01	---	---	---	216462_at	---
1.97	2.03	0.06	5.74E-01	8.40E-01	PANK2	Pantothenate kinase 2	chr20p13	228965_s_at	NM_024960 /// NM_153638 /// NM_153640
4.30	4.40	0.10	5.74E-01	8.40E-01	---	---	---	231280_at	---
2.59	2.71	0.12	5.74E-01	8.40E-01	CPT1A	carnitine palmitoyltransferase 1A (liver)	chr11q13.1-q13.2	203634_s_at	NM_001031847 /// NM_001876
2.27	2.34	0.07	5.74E-01	8.40E-01	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	chr2q24-q32	206633_at	NM_000079 /// NM_001039523
2.14	2.23	0.09	5.74E-01	8.40E-01	STOML3	stomatin (EPB72)-like 3	chr13q13.3	1553794_at	NM_145286
4.66	4.77	0.11	5.74E-01	8.40E-01	TSNARE1	t-SNARE domain containing 1	chr8q24.3	228862_at	NM_145003
3.01	3.11	0.10	5.74E-01	8.40E-01	SLC35E4	Solute carrier family 35, member E4	chr22q12.2	241078_at	NM_001001479
4.43	4.75	0.32	5.74E-01	8.40E-01	MBNL1	muscleblind-like (Drosophila)	chr3q25	201151_s_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297
6.94	7.05	0.11	5.74E-01	8.40E-01	ARHGEF19	Rho guanine nucleotide exchange factor (GEF) 19	chr1p36.13	226857_at	NM_153213
2.10	2.17	0.07	5.74E-01	8.40E-01	---	---	---	240969_at	---
1.78	1.84	0.07	5.74E-01	8.40E-01	OR5H1	olfactory receptor, family 5, subfamily H, member 1	chr3q11.2	1567246_at	NM_001005338
2.12	2.23	0.11	5.75E-01	8.40E-01	---	---	---	1560865_a_at	---
2.18	2.25	0.07	5.75E-01	8.40E-01	---	---	---	1566469_at	---
2.04	2.10	0.06	5.75E-01	8.40E-01	---	---	---	237124_at	---
4.70	4.90	0.20	5.75E-01	8.41E-01	SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin	chr20p13	219519_s_at	NM_023068
2.35	2.43	0.08	5.75E-01	8.41E-01	---	---	---	236422_at	---
1.86	1.94	0.07	5.75E-01	8.41E-01	ANKRD10	Ankyrin repeat domain 10	chr13q34	239116_at	NM_017664
2.22	2.30	0.08	5.75E-01	8.41E-01	C11orf37	chromosome 11 open reading frame 37	chr11q24.3	1562413_at	XR_040639 /// XR_040640 /// XR_040641
3.26	3.36	0.10	5.75E-01	8.41E-01	PTPN11	protein tyrosine phosphatase, non-receptor type 11	chr12q24	205867_at	NM_002834
2.24	2.31	0.07	5.75E-01	8.41E-01	MAPK4	Mitogen-activated protein kinase 4	chr18q12-q21	230732_s_at	NM_002747
2.49	2.61	0.12	5.75E-01	8.41E-01	ZNF19	zinc finger protein 19	chr16q22	234953_x_at	NM_006961
4.39	4.54	0.14	5.75E-01	8.41E-01	PDLIM7	PDZ and LIM domain 7 (enigma)	chr5q35.3	203370_s_at	NM_005451 /// NM_203352 /// NM_213636

2.15	2.24	0.10	5.75E-01	8.41E-01	LOC100130175	hypothetical protein LOC100130175	chr10q25.2	239864_at	XM_001722452 /// XM_001725810 /// XM_001726027
2.17	2.25	0.08	5.75E-01	8.41E-01	DSG2	desmoglein 2	chr18q12.1	1553105_s_at	NM_001943
2.52	2.65	0.13	5.75E-01	8.41E-01	ADAM23	ADAM metallopeptidase domain 23	chr2q33	244463_at	NM_003812
4.18	4.30	0.11	5.76E-01	8.41E-01	MFSD7	major facilitator superfamily domain containing 7	chr4p16.3	205144_at	NM_032219
5.53	5.71	0.19	5.76E-01	8.41E-01	NAT12	N-acetyltransferase 12	chr14q23.1	225679_at	NM_001011713
3.89	3.97	0.08	5.76E-01	8.41E-01	FAM91A1	family with sequence similarity 91, member A1	chr8q24.13	237045_at	NM_144963
5.39	5.53	0.14	5.76E-01	8.41E-01	AMICA1	adhesion molecule, interacts with CXADR antigen 1	chr11q23.3	228094_at	NM_001098526 /// NM_153206
2.52	2.64	0.13	5.76E-01	8.41E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	1559711_at	NM_014612
5.78	5.89	0.11	5.76E-01	8.41E-01	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	chr19q13.4	210225_x_at	NM_001081450 /// NM_006864
2.26	2.34	0.08	5.76E-01	8.41E-01	NMT2	N-myristoyltransferase 2	chr10p13	215069_at	NM_004808
1.97	2.04	0.08	5.76E-01	8.41E-01	---	---	---	1566896_at	---
5.25	5.39	0.14	5.76E-01	8.41E-01	MAPK1	mitogen-activated protein kinase 1	chr22q11.2|22q11.21	1552264_a_at	NM_002745 /// NM_138957
3.45	3.58	0.13	5.76E-01	8.41E-01	GPR44	G protein-coupled receptor 44	chr11q12-q13.3	216464_x_at	NM_004778
1.96	2.06	0.10	5.76E-01	8.41E-01	MPZL2	myelin protein zero-like 2	chr11q24	203779_s_at	NM_005797 /// NM_144765
4.14	4.30	0.16	5.76E-01	8.41E-01	BATF2	basic leucine zipper transcription factor, ATF-like 2	chr11q13.1	228439_at	NM_138456
4.18	4.48	0.30	5.76E-01	8.42E-01	TRBC1	T cell receptor beta constant 1	chr7q34	210915_x_at	---
2.64	2.75	0.10	5.76E-01	8.42E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	216133_at	---
2.31	2.40	0.09	5.76E-01	8.42E-01	---	---	---	1559067_a_at	---
2.09	2.18	0.08	5.76E-01	8.42E-01	PID1	phosphotyrosine interaction domain containing 1	chr2q36.3	237866_at	NM_001100818 /// NM_017933
3.30	3.41	0.10	5.76E-01	8.42E-01	PRDM8	PR domain containing 8	chr4q21	239111_at	NM_001099403 /// NM_020226
1.91	1.98	0.07	5.76E-01	8.42E-01	SIGLEC6	sialic acid binding Ig-like lectin 6	chr19q13.3	206519_x_at	NM_001245 /// NM_198845 /// NM_198846
2.50	2.59	0.09	5.76E-01	8.42E-01	DCC	Deleted in colorectal carcinoma	chr18q21.3	242653_at	NM_005215
2.60	2.74	0.14	5.76E-01	8.42E-01	---	---	---	1565567_at	---
2.98	3.16	0.18	5.76E-01	8.42E-01	KIAA0895	KIAA0895 protein	chr7p14.2	213424_at	NM_001100425 /// NM_015314
3.76	4.07	0.31	5.77E-01	8.42E-01	---	---	---	213429_at	---
3.44	3.56	0.12	5.77E-01	8.42E-01	IQCF1	IQ motif containing F1	chr3p21.1	1552997_a_at	NM_152397
2.34	2.42	0.08	5.77E-01	8.42E-01	---	---	---	241581_at	---
4.57	4.69	0.12	5.77E-01	8.42E-01	---	---	---	241680_at	---
2.40	2.48	0.07	5.77E-01	8.42E-01	ULK4	unc-51-like kinase 4 (C. elegans)	chr3p22.1	220958_at	NM_017886
3.92	4.09	0.16	5.77E-01	8.42E-01	IL2RB	interleukin 2 receptor, beta	chr22q13|22q13.1	205291_at	NM_000878
2.59	2.70	0.10	5.77E-01	8.42E-01	LOC283104	hypothetical protein LOC283104	chr11p15.4	1566831_at	XM_001724808 /// XM_932328 /// XM_944648
1.93	2.00	0.07	5.77E-01	8.42E-01	PHLDB2	pleckstrin homology-like domain, family B, member 2	chr3q13.2	1554778_at	NM_001134437 /// NM_001134438 /// NM_001134439 /// NM_145753
2.12	2.19	0.07	5.77E-01	8.42E-01	---	---	---	1562665_at	---
2.62	2.68	0.06	5.77E-01	8.42E-01	---	---	---	242747_at	---
3.57	3.72	0.15	5.77E-01	8.42E-01	PLLP	plasma membrane proteolipid (plasmolipin)	chr16q13	204519_s_at	NM_015993
2.44	2.50	0.06	5.77E-01	8.42E-01	FLI1	Friend leukemia virus integration 1	chr11q24.1-q24.3	237722_at	NM_002017
1.81	1.87	0.06	5.77E-01	8.42E-01	---	---	---	243164_s_at	---
6.11	6.30	0.18	5.77E-01	8.42E-01	DENND1A	DENN/MADD domain containing 1A	chr9q33.2	226849_at	NM_020946 /// NM_024820
3.85	3.97	0.12	5.77E-01	8.42E-01	AVIL	advillin	chr12q14.1	210507_s_at	NM_006576
10.37	10.48	0.11	5.77E-01	8.42E-01	SPTBN1	spectrin, beta, non-erythrocytic 1	chr2p21	212071_s_at	NM_003128 /// NM_178313
2.40	2.50	0.09	5.77E-01	8.42E-01	ZNF224	Zinc finger protein 224	chr19q13.2	232427_at	NM_013398
2.27	2.34	0.07	5.77E-01	8.42E-01	MTHFSD	methenyltetrahydrofolate synthetase domain containing	chr16q24.1	1554494_at	NM_022764
1.86	1.92	0.06	5.77E-01	8.42E-01	EAF2	ELL associated factor 2	chr3q13.33	1568673_s_at	NM_018456
5.43	5.67	0.23	5.78E-01	8.42E-01	SLC35A5	solute carrier family 35, member A5	chr3q13.2	218519_at	NM_017945

5.64	5.84	0.20	5.77E-01	8.42E-01	CAND1	cullin-associated and neddylation-dissociated 1	chr12q14	208838_at	NM_018448
4.59	4.76	0.17	5.78E-01	8.42E-01	SLC35B4	solute carrier family 35, member B4	chr7q33	225882_at	NM_032826
8.97	9.12	0.16	5.78E-01	8.42E-01	HIGD1A	HIG1 domain family, member 1A	chr3p22.1	217845_x_at	NM_001099668 /// NM_001099669 /// NM_014056
4.13	4.28	0.14	5.78E-01	8.42E-01	---	---	---	215828_at	---
5.18	5.32	0.14	5.78E-01	8.42E-01	SCAMP5	secretory carrier membrane protein 5	chr15q24.1-q24.2	212699_at	NM_138967
4.19	4.29	0.10	5.78E-01	8.42E-01	LOC399491	LOC399491 protein	chr16p13.1	214682_at	XR_041580
2.68	2.77	0.08	5.78E-01	8.42E-01	LOC554206	hypothetical LOC554206	chr16p12.1	1554185_at	XR_040102 /// XR_040103
2.16	2.24	0.08	5.77E-01	8.42E-01	---	---	---	232242_at	---
2.10	2.18	0.08	5.78E-01	8.42E-01	---	---	---	239032_at	---
5.67	5.74	0.07	5.77E-01	8.42E-01	ZDHHC8	zinc finger, DHHC-type containing 8	chr22q11.21	230731_x_at	NM_013373
2.26	2.33	0.07	5.77E-01	8.42E-01	---	---	---	1556879_at	---
7.76	7.99	0.23	5.78E-01	8.42E-01	SPTBN1	spectrin, beta, non-erythrocytic 1	chr2p21	200672_x_at	NM_003128 /// NM_178313
5.68	5.86	0.19	5.78E-01	8.42E-01	KPNA4	karyopherin alpha 4 (importin alpha 3)	chr3q25.33	225268_at	NM_002268
5.35	5.50	0.15	5.78E-01	8.42E-01	CPEB4	cytoplasmic polyadenylation element binding protein 4	chr5q21	242280_x_at	NM_030627
2.21	2.32	0.11	5.78E-01	8.42E-01	CCR6	chemokine (C-C motif) receptor 6	chr6q27	206983_at	NM_004367 /// NM_031409
2.25	2.35	0.10	5.78E-01	8.42E-01	GJC1	gap junction protein, gamma 1, 45kDa	chr17q21.31	243502_at	NM_001080383 /// NM_005497
3.26	3.35	0.09	5.78E-01	8.42E-01	NOBOX	NOBOX oogenesis homeobox	chr7q35	234519_at	NM_001080413
2.04	2.12	0.07	5.78E-01	8.42E-01	CCT8	chaperonin containing TCP1, subunit 8 (theta)	chr21q22.11	210436_at	NM_006585
1.93	1.99	0.07	5.78E-01	8.42E-01	---	---	---	224237_at	---
2.10	2.16	0.07	5.78E-01	8.42E-01	ARHGAP11A	Rho GTPase activating protein 11A	chr15q13.2	204492_at	NM_014783 /// NM_199357 /// XM_001714495
4.15	4.29	0.14	5.78E-01	8.42E-01	---	---	---	236143_at	---
6.62	6.82	0.20	5.78E-01	8.42E-01	ZFP106	zinc finger protein 106 homolog (mouse)	chr15q15.1	217781_s_at	NM_022473
2.26	2.36	0.10	5.78E-01	8.42E-01	ZRANB3	zinc finger, RAN-binding domain containing 3	chr2q21.3	244092_at	NM_032143
2.08	2.15	0.07	5.78E-01	8.42E-01	---	---	---	1558806_at	---
1.88	1.96	0.08	5.78E-01	8.42E-01	TTF2	transcription termination factor, RNA polymerase II	chr1p22	1555307_at	NM_003594
2.45	2.55	0.10	5.78E-01	8.42E-01	UBR5	Ubiquitin protein ligase E3 component n-recognin 5	chr8q22	1555888_at	NM_015902
1.93	2.00	0.07	5.78E-01	8.42E-01	DEPDC2	DEP domain containing 2	chr8q13.2	1569934_at	NM_024870 /// NM_025170
3.55	3.64	0.09	5.78E-01	8.42E-01	SPAG11A	sperm associated antigen 11A	chr8p23.1	210884_s_at	NM_001081552 /// XM_001713749
2.89	2.97	0.08	5.78E-01	8.42E-01	---	---	---	237079_at	---
5.48	5.63	0.15	5.78E-01	8.42E-01	PAPD1	PAP associated domain containing 1	chr10p11.23	233873_x_at	NM_018109
3.86	3.96	0.10	5.78E-01	8.42E-01	NID1	nidogen 1	chr1q43	1561082_at	NM_002508
3.12	3.21	0.09	5.78E-01	8.42E-01	IFNAR1	Interferon (alpha, beta and omega) receptor 1	chr21q22.1|21q22.11	236478_at	NM_000629
2.36	2.44	0.08	5.78E-01	8.42E-01	SLITRK6	SLIT and NTRK-like family, member 6	chr13q31.1	232481_s_at	NM_032229
2.41	2.49	0.08	5.78E-01	8.42E-01	---	---	---	234019_at	---
1.99	2.07	0.07	5.78E-01	8.42E-01	SNX31	sorting nexin 31	chr8q22.3	241987_x_at	NM_152628
2.73	2.79	0.07	5.78E-01	8.43E-01	---	---	---	244158_at	---
5.92	6.16	0.24	5.79E-01	8.43E-01	TYW3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	chr1p31.1	227141_at	NM_138467
3.90	4.04	0.14	5.79E-01	8.43E-01	PF4	platelet factor 4	chr4q12-q21	206390_x_at	NM_002619
5.86	6.12	0.26	5.79E-01	8.43E-01	SYTL5	synaptotagmin-like 5	chrXp21.1	242093_at	NM_138780
3.34	3.50	0.16	5.79E-01	8.43E-01	---	---	---	235295_at	---
4.16	4.31	0.15	5.79E-01	8.43E-01	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	chr5q33.1	226881_at	NM_152407
2.80	2.89	0.09	5.79E-01	8.43E-01	PRKCZ	Protein kinase C, zeta	chr1p36.33-p36.2	1569748_at	NM_001033581 /// NM_001033582 /// NM_002744
2.40	2.47	0.08	5.79E-01	8.43E-01	C8orf22	chromosome 8 open reading frame 22	chr8q11	235981_at	NM_001007176
2.03	2.10	0.07	5.79E-01	8.43E-01	---	---	---	1557647_a_at	---
1.86	1.92	0.06	5.79E-01	8.43E-01	TTC6	tetratricopeptide repeat domain 6	chr14q21.1	1556666_a_at	NM_001007795
3.99	4.06	0.07	5.79E-01	8.43E-01	WDR51A	WD repeat domain 51A	chr3p21.1	234749_s_at	NM_015426
3.30	3.37	0.07	5.79E-01	8.43E-01	---	---	---	240918_at	---
2.41	2.51	0.09	5.79E-01	8.43E-01	---	---	---	1561375_at	---
2.25	2.32	0.08	5.79E-01	8.43E-01	APOBEC1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	chr12p13.1	207158_at	NM_001644
2.13	2.19	0.06	5.79E-01	8.43E-01	---	---	---	244724_at	---
6.32	6.41	0.09	5.79E-01	8.43E-01	ZER1	zer-1 homolog (C. elegans)	chr9q34.11	202452_at	NM_006336
2.21	2.29	0.09	5.79E-01	8.43E-01	---	---	---	237770_at	---
2.19	2.27	0.08	5.79E-01	8.43E-01	---	---	---	1557339_at	---
3.58	3.80	0.22	5.79E-01	8.43E-01	---	---	---	239285_at	---

7.18	7.38	0.20	5.79E-01	8.43E-01	TMED8	transmembrane emp24 protein transport domain containing 8	chr14q24.3	225343_at	NM_213601
2.77	2.87	0.10	5.79E-01	8.43E-01	---	---	---	237854_at	---
1.83	1.90	0.07	5.79E-01	8.43E-01	---	---	---	244130_at	---
2.33	2.43	0.11	5.79E-01	8.43E-01	C22orf28	Chromosome 22 open reading frame 28	chr22q12	239980_at	NM_014306
2.58	2.67	0.09	5.79E-01	8.43E-01	LOC100130648 /// SSX2 /// SSX2B	similar to Protein SSX2 (Synovial sarcoma, X breakpoint 2) (Cancer/testis antigen 5.2) (CT5.2) (SSX) (HOM-MEL-40) /// synovial sarcoma, X breakpoint 2 /// synovial sarcoma, X breakpoint 2B	chrXp11.22	210497_x_at	NM_003147 /// NM_175698 /// XM_001719568 /// XM_001720499
3.01	3.14	0.13	5.80E-01	8.43E-01	PML	promyelocytic leukemia	chr15q22	239582_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250
2.63	2.70	0.07	5.80E-01	8.43E-01	SOX2	SRY (sex determining region Y)-box 2	chr3q26.3-q27	213722_at	NM_003106
1.88	1.94	0.06	5.80E-01	8.43E-01	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	chr14q31-q32.1	1554319_at	NM_004755 /// NM_182398
2.15	2.24	0.09	5.80E-01	8.43E-01	PCDH11X /// PCDH11Y	protocadherin 11 X-linked /// protocadherin 11 Y-linked	chrXq21.3 /// chrYp11.2	210292_s_at	NM_014522 /// NM_032967 /// NM_032968 /// NM_032969 /// NM_032971 /// NM_032972 /// NM_032973
1.96	2.05	0.09	5.80E-01	8.43E-01	LOC401387	hypothetical protein LOC401387	chr7q21.2	1569783_at	XM_934383 /// XM_934385 /// XM_936006 /// XM_936007 /// XM_945004 /// XM_945006
1.93	1.99	0.06	5.80E-01	8.43E-01	FANCB	Fanconi anemia, complementation group B	chrXp22.2	243597_at	NM_001018113 /// NM_152633
4.63	4.74	0.12	5.80E-01	8.43E-01	CDH24	cadherin-like 24	chr14q11.2	230157_at	NM_022478 /// NM_144985
3.19	3.33	0.14	5.80E-01	8.43E-01	POGK	pogo transposable element with KRAB domain	chr1q24.1	239392_s_at	NM_017542
3.88	4.10	0.22	5.80E-01	8.43E-01	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	chr4q24	227605_at	NM_004757
7.31	7.53	0.22	5.80E-01	8.43E-01	EIF3M	eukaryotic translation initiation factor 3, subunit M	chr11p13	202232_s_at	NM_006360
2.58	2.73	0.15	5.80E-01	8.43E-01	LOC285812	hypothetical protein LOC285812	chr6p23	230179_at	---
6.17	6.31	0.15	5.80E-01	8.43E-01	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	chr18p11.31-p11.21	202933_s_at	NM_005433
5.02	5.16	0.14	5.80E-01	8.43E-01	LYAR	Ly1 antibody reactive homolog (mouse)	chr4p16.2	223413_s_at	NM_017816
3.26	3.41	0.14	5.80E-01	8.43E-01	---	---	---	229206_at	---
2.91	3.04	0.13	5.80E-01	8.43E-01	CCDC87	coiled-coil domain containing 87	chr11q13.1	219887_at	NM_018219
3.52	3.62	0.10	5.80E-01	8.43E-01	hCG_1811732	hypothetical LOC151534	chr2p13.1	238422_at	XM_001726163 /// XM_001726563 /// XM_001726936
2.18	2.25	0.07	5.80E-01	8.43E-01	MNS1	meiosis-specific nuclear structural 1	chr15q21.3	219703_at	NM_018365
2.34	2.42	0.07	5.80E-01	8.43E-01	HMMR	hyaluronan-mediated motility receptor (RHAMM)	chr5q33.2-qter	207165_at	NM_012484 /// NM_012485
2.29	2.38	0.09	5.80E-01	8.43E-01	---	---	---	215626_at	---

3.20	3.31	0.11	5.80E-01	8.43E-01	ZNF167	zinc finger protein 167	chr3p22.3-p21.1	234292_s_at	NM_018651 /// NM_025169
4.82	4.96	0.15	5.80E-01	8.43E-01	LMBR1	limb region 1 homolog (mouse)	chr7q36	222506_at	NM_022458
2.90	2.98	0.08	5.80E-01	8.43E-01	---	---	---	1561756_at	---
2.22	2.32	0.10	5.80E-01	8.43E-01	ATL3	atlastin 3	chr11q13.1	223453_s_at	NM_015459
2.20	2.27	0.07	5.80E-01	8.43E-01	---	---	---	1566780_at	---
2.97	3.09	0.12	5.80E-01	8.43E-01	---	---	---	236528_at	---
5.59	5.70	0.12	5.80E-01	8.43E-01	MTMR2	myotubularin related protein 2	chr11q22	214649_s_at	NM_016156 /// NM_201278 /// NM_201281 /// NR_023354 /// NR_023355 /// NR_023356
2.67	2.72	0.06	5.80E-01	8.43E-01	CNTNAP5	contactin associated protein-like 5	chr2q14.3	1553418_a_at	NM_130773
3.05	3.24	0.19	5.80E-01	8.43E-01	THSD7A	thrombospondin, type I, domain containing 7A	chr7p21.3	230008_at	NM_015204
2.63	2.72	0.10	5.80E-01	8.43E-01	---	---	---	216794_at	---
4.10	4.37	0.27	5.80E-01	8.43E-01	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	chr2q32.3-q33	211139_s_at	NM_005966
3.19	3.30	0.10	5.80E-01	8.43E-01	---	---	---	234258_at	---
2.44	2.54	0.10	5.80E-01	8.43E-01	ZNF385C	zinc finger protein 385C	chr17q21.2	241383_at	NM_001013624
1.85	1.91	0.06	5.80E-01	8.43E-01	---	---	---	217306_at	---
2.46	2.56	0.10	5.81E-01	8.43E-01	---	---	---	1555488_at	---
4.07	4.15	0.08	5.80E-01	8.43E-01	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	chr13q11-q12	223379_s_at	NM_014572
2.96	3.17	0.20	5.81E-01	8.43E-01	---	---	---	1566442_at	---
2.13	2.22	0.09	5.81E-01	8.43E-01	---	---	---	240380_at	---
2.58	2.74	0.16	5.81E-01	8.43E-01	FBN2	fibrillin 2	chr5q23-q31	215717_s_at	NM_001999
8.17	8.30	0.13	5.81E-01	8.43E-01	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	chr2q33	211069_s_at	NM_001005781 /// NM_001005782 /// NM_003352
2.86	2.98	0.12	5.81E-01	8.43E-01	OPCML	opioid binding protein/cell adhesion molecule-like	chr11q25	206215_at	NM_001012393 /// NM_002545
3.17	3.28	0.11	5.81E-01	8.43E-01	NASP	Nuclear autoantigenic sperm protein (histone-binding)	chr1p34.1	237276_at	NM_002482 /// NM_152298 /// NM_172164
2.24	2.34	0.10	5.81E-01	8.43E-01	TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2	chr2q32.3	223557_s_at	NM_016192
2.81	2.88	0.07	5.81E-01	8.43E-01	---	---	---	244445_at	---
4.14	4.35	0.21	5.81E-01	8.43E-01	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	chr1p36.22	226075_at	NM_025106
2.59	2.70	0.11	5.81E-01	8.43E-01	ABHD6	abhydrolase domain containing 6	chr3p14.3	221678_at	NM_020676
2.15	2.24	0.09	5.81E-01	8.43E-01	LOC100131180	Hypothetical protein LOC100131180	chr9p13.3	241810_at	XM_001722021 /// XM_001723526 /// XM_001725594
2.85	2.96	0.11	5.81E-01	8.43E-01	---	---	---	242241_x_at	---
3.94	4.03	0.09	5.81E-01	8.44E-01	FUT6	Fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	chr19p13.3	1565659_at	NM_000150 /// NM_001040701
6.32	6.47	0.14	5.81E-01	8.44E-01	ARMC7	armadillo repeat containing 7	chr17q25.1	219096_at	NM_024585
6.71	6.78	0.07	5.81E-01	8.44E-01	C18orf45	chromosome 18 open reading frame 45	chr18q11.2	224493_x_at	NM_032933
2.18	2.27	0.09	5.81E-01	8.44E-01	C1orf98	chromosome 1 open reading frame 98	chr1q32.1	1562909_at	---
2.00	2.08	0.08	5.81E-01	8.44E-01	LOC285957	hypothetical protein LOC285957	chr7p13	243601_at	---
5.07	5.20	0.13	5.81E-01	8.44E-01	YARS	tyrosyl-tRNA synthetase	chr1p35.1	238760_at	NM_003680
2.24	2.32	0.09	5.81E-01	8.44E-01	---	---	---	1554220_a_at	---
1.99	2.06	0.08	5.81E-01	8.44E-01	---	---	---	243685_at	---
2.23	2.29	0.06	5.81E-01	8.44E-01	---	---	---	234831_at	---
7.25	7.55	0.31	5.81E-01	8.44E-01	CSNK1A1	casein kinase 1, alpha 1	chr5q32	206562_s_at	NM_001025105 /// NM_001892
2.50	2.57	0.07	5.82E-01	8.44E-01	---	---	---	1556110_at	---
1.80	1.86	0.06	5.81E-01	8.44E-01	LIPJ	lipase, family member J	chr10q23.31	1569873_at	NM_001010939
4.08	4.16	0.09	5.82E-01	8.44E-01	POU5F1P3	POU class 5 homeobox 1 pseudogene 3	chr12p13.31	210265_x_at	---
7.24	7.41	0.17	5.82E-01	8.44E-01	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	chr3p21.3	202788_at	NM_004635
6.04	6.19	0.15	5.82E-01	8.44E-01	LOC440434	hypothetical protein FLJ11822	chr17q12	214107_x_at	XM_001725426 /// XM_001725441
1.93	2.00	0.07	5.82E-01	8.44E-01	SLC35D3	solute carrier family 35, member D3	chr6q23.3	231341_at	NM_001008783
4.15	4.26	0.11	5.82E-01	8.44E-01	SNAI1	snail homolog 1 (Drosophila)	chr20q13.1-q13.2	219480_at	NM_005985
2.05	2.13	0.08	5.82E-01	8.44E-01	PTH	parathyroid hormone	chr11p15.3-p15.1	206977_at	NM_000315

2.45	2.53	0.08	5.82E-01	8.44E-01	HIST1H2AK	histone cluster 1, H2ak	chr6p22-p21.3	214644_at	NM_003510
6.48	6.66	0.18	5.82E-01	8.44E-01	ATMIN	ATM interactor	chr16q23.2	201854_s_at	NM_015251
2.21	2.28	0.08	5.82E-01	8.44E-01	C9orf122	chromosome 9 open reading frame 122	chr9p13.1	1557541_at	XR_041857
2.75	2.89	0.14	5.82E-01	8.44E-01	AHCTF1	AT hook containing transcription factor 1	chr1q44	1560224_at	NM_015446
3.86	3.96	0.11	5.82E-01	8.44E-01	ZNF182	zinc finger protein 182	chrXp22.11-p11.23	235810_at	NM_001007088 /// NM_006962
2.31	2.41	0.10	5.82E-01	8.44E-01	---	---	---	239978_at	---
3.81	3.91	0.10	5.82E-01	8.44E-01	ACRBP	acrosin binding protein	chr12p13.31	223717_s_at	NM_032489
2.59	2.68	0.09	5.82E-01	8.44E-01	SNX25	sorting nexin 25	chr4q35.1	232425_at	NM_031953
4.43	4.54	0.11	5.82E-01	8.44E-01	TNFSF13	Tumor necrosis factor (ligand) superfamily, member 12	chr17p13.1	229326_at	NM_003808 /// NM_172087 /// NM_172088
3.06	3.17	0.11	5.82E-01	8.44E-01	---	---	---	242181_at	---
2.20	2.29	0.09	5.82E-01	8.44E-01	UPK1B	uroplakin 1B	chr3q13.3-q21	210064_s_at	NM_006952
3.51	3.60	0.08	5.82E-01	8.44E-01	---	---	---	1563005_at	---
2.58	2.66	0.08	5.82E-01	8.44E-01	---	---	---	234867_at	---
2.53	2.61	0.08	5.82E-01	8.44E-01	---	---	---	1561909_at	---
2.33	2.41	0.07	5.82E-01	8.44E-01	C1orf101	chromosome 1 open reading frame 101	chr1q44	233578_at	NM_001130957 /// NM_173807
2.16	2.23	0.07	5.82E-01	8.44E-01	---	---	---	1564306_at	---
2.32	2.38	0.06	5.82E-01	8.44E-01	FLJ23834	hypothetical protein FLJ23834	chr7q22.2	235650_at	NM_152750
5.71	5.90	0.19	5.83E-01	8.44E-01	SMAD2	SMAD family member 2	chr18q21.1	203077_s_at	NM_001003652 /// NM_005901
1.87	1.94	0.06	5.83E-01	8.44E-01	---	---	---	1562737_at	---
5.99	6.17	0.18	5.83E-01	8.44E-01	---	---	---	230391_at	---
2.53	2.69	0.17	5.83E-01	8.44E-01	SCN3B	sodium channel, voltage-gated, type III, beta	chr11q23.3	204723_at	NM_001040151 /// NM_018400
2.42	2.50	0.08	5.83E-01	8.44E-01	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	chr2p12	241463_at	NM_004836
2.61	2.68	0.07	5.83E-01	8.44E-01	KRT24	keratin 24	chr17q11.2	220267_at	NM_019016
3.83	3.90	0.07	5.83E-01	8.44E-01	GATA1	GATA binding protein 1 (globin transcription factor 1)	chrXp11.23	210446_at	NM_002049
5.42	5.64	0.22	5.83E-01	8.45E-01	---	---	---	227838_at	---
3.12	3.23	0.12	5.83E-01	8.45E-01	SMOX	spermine oxidase	chr20p13	1555680_a_at	NM_175839 /// NM_175840 /// NM_175841 /// NM_175842
3.55	3.67	0.12	5.83E-01	8.45E-01	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	chr18q11.1	235854_x_at	NM_005406 /// XM_001713904 /// XM_001722015 /// XM_001723570
5.23	5.34	0.11	5.83E-01	8.45E-01	USP36	ubiquitin specific peptidase 36	chr17q25.3	224979_s_at	NM_025090
3.27	3.37	0.10	5.83E-01	8.45E-01	FLJ33065	hypothetical gene supported by AK057627; BC031275; BC045736	chr3p22.1	1557212_at	---
2.09	2.17	0.08	5.83E-01	8.45E-01	ZNF93	zinc finger protein 93	chr19p12	1569241_a_at	NM_031218
2.38	2.44	0.06	5.83E-01	8.45E-01	FAM26D	family with sequence similarity 26, member D	chr6q22.1	1553388_at	NM_153036
1.83	1.89	0.06	5.83E-01	8.45E-01	---	---	---	243530_at	---
4.24	4.34	0.09	5.83E-01	8.45E-01	ATCAY	ataxia, cerebellar, Cayman type	chr19p13.3	227365_at	NM_033064
8.54	8.91	0.37	5.83E-01	8.45E-01	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	chr2p16	201842_s_at	NM_001039348 /// NM_001039349 /// NM_004105
5.08	5.24	0.16	5.83E-01	8.45E-01	DNAH11	dynein, axonemal, heavy chain 11	chr7p21	1553159_at	NM_003777
2.41	2.52	0.11	5.83E-01	8.45E-01	SAMD4A	sterile alpha motif domain containing 4A	chr14q22.2	215496_at	NM_015589
2.90	3.00	0.10	5.83E-01	8.45E-01	LOC55908	hepatocellular carcinoma-associated gene TD26	chr19p13.2	220437_at	NM_018687
2.74	2.86	0.12	5.83E-01	8.45E-01	CGA	glycoprotein hormones, alpha polypeptide	chr6q12-q21	204637_at	NM_000735
2.87	2.97	0.10	5.83E-01	8.45E-01	LOC148189	Hypothetical protein LOC148189	chr19q12	242663_at	---
2.06	2.14	0.08	5.83E-01	8.45E-01	LOC148824	hypothetical protein LOC148824	chr1q44	232452_at	---
2.29	2.36	0.07	5.83E-01	8.45E-01	FAM62C	family with sequence similarity 62 (C2 domain containing), member C	chr3q22.3	1557793_at	NM_031913
9.52	9.71	0.19	5.83E-01	8.45E-01	EIF4B	eukaryotic translation initiation factor 4B	chr12q13.13	211937_at	NM_001417
1.92	1.98	0.06	5.83E-01	8.45E-01	---	---	---	232999_at	---
5.61	5.72	0.11	5.84E-01	8.45E-01	C2orf64	chromosome 2 open reading frame 64	chr2q11.2	225409_at	NM_001008215
3.33	3.44	0.11	5.84E-01	8.45E-01	TRERF1	transcriptional regulating factor 1	chr6p21.1-p12.1	238520_at	NM_033502
2.42	2.50	0.08	5.84E-01	8.45E-01	---	---	---	235563_at	---
2.79	2.86	0.07	5.84E-01	8.45E-01	---	---	---	229248_at	---
3.89	3.98	0.09	5.84E-01	8.45E-01	TSP50	testes-specific protease 50	chr3p14-p12	220126_at	NM_013270
3.18	3.34	0.16	5.84E-01	8.45E-01	---	---	---	220915_s_at	---
2.31	2.36	0.06	5.84E-01	8.45E-01	---	---	---	239330_at	---
4.27	4.39	0.12	5.84E-01	8.45E-01	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	chr12q23-q24.1	212362_at	NM_001681 /// NM_170665

1.90	1.96	0.06	5.84E-01	8.45E-01	HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	chr5p12	1556351_at	NM_021072
4.13	4.43	0.30	5.84E-01	8.45E-01	---	---	---	232978_at	---
4.72	4.88	0.16	5.84E-01	8.45E-01	---	---	---	242448_at	---
2.03	2.09	0.06	5.84E-01	8.45E-01	LMOD3	leiomodin 3 (fetal)	chr3p14.1	243346_at	NM_198271
6.22	6.35	0.13	5.84E-01	8.45E-01	---	---	---	244566_at	---
2.72	2.81	0.09	5.84E-01	8.45E-01	---	---	---	236330_at	---
3.34	3.41	0.07	5.84E-01	8.45E-01	C2orf19	chromosome 2 open reading frame 19	chr2q37.3	1554782_at	NM_001024676
5.02	5.37	0.35	5.85E-01	8.45E-01	EXOC6	exocyst complex component 6	chr10q23.33	233924_s_at	NM_001013848 /// NM_019053
6.44	6.68	0.24	5.85E-01	8.45E-01	C7orf28A /// C7orf28B	chromosome 7 open reading frame 28A /// chromosome 7 open reading frame 28B	chr7p22.1	208310_s_at	NM_015622 /// NM_198097 /// XM_001720226
6.65	6.86	0.21	5.85E-01	8.45E-01	---	---	---	226725_at	---
5.03	5.20	0.17	5.85E-01	8.45E-01	---	---	---	229189_s_at	---
2.88	3.04	0.16	5.85E-01	8.45E-01	PDPN	podoplanin	chr1p36.21	204879_at	NM_001006624 /// NM_001006625 /// NM_006474 /// NM_198389
5.82	5.97	0.15	5.85E-01	8.45E-01	TOX4	TOX high mobility group box family member 4	chr14q11.2	201685_s_at	NM_014828
4.73	4.84	0.12	5.85E-01	8.45E-01	FCHO1	FCH domain only 1	chr19p13.11	213669_at	NM_015122
3.82	3.94	0.12	5.85E-01	8.45E-01	LOC284889 /// MIF	hypothetical protein LOC284889 /// macrophage migration inhibitory factor (glycosylation-inhibiting factor)	chr22q11.23	1556316_s_at	NM_002415
2.41	2.50	0.09	5.85E-01	8.45E-01	ATG9B	ATG9 autophagy related 9 homolog B (S. cerevisiae)	chr7q36.1	1553390_at	NM_173681
2.50	2.59	0.09	5.85E-01	8.45E-01	TAF1A	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	chr1q42	206613_s_at	NM_005681 /// NM_139352
3.24	3.32	0.09	5.85E-01	8.45E-01	NUDT22	Nudix (nucleoside diphosphate linked moiety X)-type motif 22	chr11q13.1	1558848_at	NM_001128612 /// NM_001128613 /// NM_032344
2.06	2.11	0.06	5.85E-01	8.45E-01	C11orf57	chromosome 11 open reading frame 57	chr11q23.1	1560028_at	NM_001082969 /// NM_001082970 /// NM_018195
3.79	3.92	0.13	5.85E-01	8.45E-01	RCAN1	regulator of calcineurin 1	chr21q22.1-q22.2|21q22.12	215253_s_at	NM_004414 /// NM_203417 /// NM_203418
3.80	3.93	0.13	5.85E-01	8.45E-01	JPH4	junctophilin 4	chr14q11	226918_at	NM_032452
3.06	3.15	0.09	5.85E-01	8.45E-01	FTCD	formiminotransferase cyclodeaminase	chr21q22.3	233741_at	NM_006657 /// NM_206965
2.19	2.27	0.08	5.85E-01	8.45E-01	---	---	---	1564567_at	---
3.76	3.84	0.07	5.85E-01	8.45E-01	WNT3	wingless-type MMTV integration site family, member 3	chr17q21	231743_at	NM_030753
2.88	2.95	0.07	5.85E-01	8.45E-01	KRT7	Keratin 7	chr12q12-q13	214031_s_at	NM_005556
1.80	1.87	0.06	5.85E-01	8.45E-01	---	---	---	215514_at	---
2.19	2.25	0.06	5.85E-01	8.45E-01	---	---	---	1558489_at	---
8.90	9.07	0.17	5.85E-01	8.45E-01	CYBASC3	cytochrome b, ascorbate dependent 3	chr11q12.2	224735_at	NM_153611
2.93	3.05	0.12	5.85E-01	8.45E-01	FN3K	fructosamine 3 kinase	chr17q25.3	219744_at	NM_022158
3.10	3.21	0.11	5.85E-01	8.45E-01	TMEM184A	transmembrane protein 184A	chr7p22.3	1558281_a_at	NM_001097620
2.37	2.47	0.10	5.85E-01	8.45E-01	ZNF506	zinc finger protein 506	chr19p13.11	238493_at	NM_001099269
2.45	2.54	0.10	5.85E-01	8.45E-01	---	---	---	241582_at	---
3.06	3.19	0.13	5.85E-01	8.45E-01	MRPS26	Mitochondrial ribosomal protein S26	chr20p13	227118_s_at	NM_030811
2.96	3.07	0.11	5.85E-01	8.45E-01	---	---	---	1569270_at	---
2.44	2.52	0.08	5.85E-01	8.45E-01	---	---	---	242627_at	---
6.65	6.78	0.13	5.85E-01	8.46E-01	USP10	ubiquitin specific peptidase 10	chr16q24.1	209137_s_at	NM_005153
4.04	4.14	0.09	5.85E-01	8.46E-01	CAPS	calcyphosine	chr19p13.3	231728_at	NM_004058 /// NM_080590
2.98	3.06	0.08	5.85E-01	8.46E-01	---	---	---	1555237_at	---
6.71	7.01	0.30	5.85E-01	8.46E-01	LMOD1	leiomodin 1 (smooth muscle)	chr1q32	203766_s_at	NM_012134
5.65	5.79	0.14	5.86E-01	8.46E-01	ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	chrXp22.1	213876_x_at	NM_005089
4.05	4.19	0.14	5.85E-01	8.46E-01	CARHSP1	Calcium regulated heat stable protein 1, 24kDa	chr16p13.2	1566134_at	NM_001042476 /// NM_014316
2.60	2.74	0.14	5.85E-01	8.46E-01	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	chr2q36.3	1552508_at	NM_080671
2.41	2.51	0.09	5.86E-01	8.46E-01	---	---	---	1565732_at	---

3.41	3.50	0.09	5.86E-01	8.46E-01	COPE	coatomer protein complex, subunit epsilon	chr19p13.11	220469_at	NM_007263 /// NM_199442 /// NM_199444																				
2.16	2.24	0.08	5.86E-01	8.46E-01	CADM2	cell adhesion molecule 2	chr3p12.1	1555544_a_at	NM_153184																				
3.44	3.51	0.06	5.86E-01	8.46E-01	ZNF468	zinc finger protein 468	chr19q13.41	214751_at	NM_001008801 /// NM_199132																				
6.12	6.24	0.12	5.86E-01	8.46E-01	SLA	Src-like-adaptor	chr8q22.3-qter|8q24	203760_s_at	NM_001045556 /// NM_001045557 /// NM_006748																				
5.67	5.88	0.21	5.86E-01	8.46E-01	ARPP-19	cyclic AMP phosphoprotein, 19 kD	chr15q21.2	214553_s_at	NM_006628																				
3.03	3.12	0.09	5.86E-01	8.46E-01	PAX8	paired box 8	chr2q12-q14	221990_at	NM_003466 /// NM_013951 /// NM_013952 /// NM_013953 /// NM_013992																				
2.92	3.01	0.09	5.86E-01	8.46E-01	RPS15	Ribosomal protein S15	chr19p13.3	1563014_at	NM_001018																				
2.59	2.68	0.08	5.86E-01	8.46E-01	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	chr6p21.32	229604_at	NR_002174																				
2.78	2.85	0.08	5.86E-01	8.46E-01	CD40LG	CD40 ligand	chrXq26	207892_at	NM_000074																				
2.26	2.34	0.07	5.86E-01	8.46E-01	CENPI	centromere protein I	chrXq22.1	214804_at	NM_006733																				
2.28	2.38	0.09	5.86E-01	8.46E-01	PLA2G12B	phospholipase A2, group XIIB	chr10q22.1	231009_at	NM_032562																				
5.94	6.34	0.41	5.86E-01	8.46E-01	LOC283666	Hypothetical LOC283666	chr15q21.3	235567_at	---																				
5.95	6.30	0.35	5.86E-01	8.46E-01	---	---	---	236067_at	---																				
3.98	4.25	0.28	5.86E-01	8.46E-01	IGLV3-19	immunoglobulin lambda variable 3-19	chr22q11.2	216853_x_at	---																				
4.97	5.23	0.26	5.86E-01	8.46E-01	FBN1	fibrillin 1	chr15q21.1	202765_s_at	NM_000138																				
2.54	2.65	0.11	5.86E-01	8.46E-01	CCKAR	cholecystokinin A receptor	chr4p15.1-p15.2	211174_s_at	NM_000730																				
3.15	3.25	0.10	5.86E-01	8.46E-01	---	---	---	243453_at	---																				
3.57	3.67	0.10	5.86E-01	8.46E-01	FBXL18	F-box and leucine-rich repeat protein 18	chr7p22.2	216395_at	NM_024963																				
2.31	2.38	0.07	5.86E-01	8.46E-01	HEATR4	HEAT repeat containing 4	chr14q24.3	1560727_at	NM_203309																				
1.99	2.11	0.12	5.86E-01	8.46E-01	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	chr2q31.3	205884_at	NM_000885																				
2.08	2.16	0.09	5.86E-01	8.46E-01	---	---	---	243862_at	---																				
2.38	2.46	0.08	5.86E-01	8.46E-01	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	chr4q32.1	215987_at	NM_014247																				
2.77	2.84	0.08	5.86E-01	8.46E-01	---	---	---	239341_at	---																				
2.31	2.38	0.07	5.86E-01	8.46E-01	---	---	---	241766_at	---																				
1.99	2.06	0.07	5.86E-01	8.46E-01	UNC5D	Unc-5 homolog D (C. elegans)	chr8p12	231325_at	NM_080872																				
2.52	2.59	0.06	5.86E-01	8.46E-01	MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	chr22q11.21	231985_at	NM_001122731 /// NM_015241 /// XM_001721205 /// XM_001725408 /// XM_001726352																				
2.05	2.11	0.06	5.86E-01	8.46E-01	---	---	---	238392_at	---																				
2.29	2.38	0.08	5.86E-01	8.46E-01	KCNG3	potassium voltage-gated channel, subfamily G, member 3	chr2p21	1552898_a_at	NM_133329 /// NM_172344																				
6.97	7.10	0.13	5.86E-01	8.46E-01	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	chr4q12	205120_s_at	NM_000232																				
4.54	4.62	0.08	5.86E-01	8.46E-01	PRB1	proline-rich protein BstNI subfamily 1	chr12p13.2	210597_x_at	NM_005039 /// NM_199353 /// NM_199354																				
5.94	6.09	0.16	5.87E-01	8.46E-01	F11R	F11 receptor	chr1q21.2-q21.3	221664_s_at	NM_016946 /// NM_144503																				
4.66	4.82	0.15	5.87E-01	8.46E-01	TEAD4	TEA domain family member 4	chr12p13.3-p13.2	204281_at	NM_003213 /// NM_201441 /// NM_201443																				
2.36	2.46	0.10	5.87E-01	8.46E-01	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	chr3q27-q28	206449_s_at	NM_001031849 /// NM_001879 /// NM_139125																				
4.51	4.70	0.19	5.87E-01	8.46E-01	FKBP14	FK506 binding protein 14, 22 kDa	chr7p15.1	219390_at	NM_017946																				
6.13	6.29	0.16	5.87E-01	8.46E-01	CD4	CD4 molecule	chr12pter-p12	203547_at	NM_000616																				

2.64	2.76	0.11	5.87E-01	8.46E-01	ZNF837	Zinc finger protein 837	chr19q13.43	1556822_s_at	NM_001129730 /// NM_138466 /// XM_001725760 /// XM_001725797 /// XM_001726206 /// XM_001726207 /// XM_375665 /// XM_938741
2.10	2.19	0.09	5.87E-01	8.46E-01	ANO3	anoctamin 3	chr11p14.2	215241_at	NM_031418
2.92	3.01	0.09	5.87E-01	8.46E-01	WFDC10A	WAP four-disulfide core domain 10A	chr20q13.12	233913_at	NM_080753
3.44	3.55	0.11	5.87E-01	8.46E-01	PRSS33	protease, serine, 33	chr16p13.3	1552348_at	NM_152891
8.23	8.54	0.32	5.87E-01	8.46E-01	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	chr8q23.1	200641_s_at	NM_003406 /// NM_145690
4.54	4.75	0.21	5.87E-01	8.46E-01	CLCN3	chloride channel 3	chr4q33	201733_at	NM_001829 /// NM_173872
4.06	4.22	0.16	5.87E-01	8.46E-01	SYT9	synaptotagmin IX	chr11p15.4	1563658_a_at	NM_175733
5.37	5.47	0.09	5.87E-01	8.46E-01	WDR43	WD repeat domain 43	chr2p23.2	214662_at	NM_015131
2.56	2.64	0.08	5.87E-01	8.46E-01	---	---	---	216824_at	---
6.55	6.75	0.19	5.87E-01	8.46E-01	---	---	---	227531_at	---
2.13	2.21	0.08	5.87E-01	8.46E-01	CASD1	CAS1 domain containing 1	chr7q21.3	242000_at	NM_022900
3.75	3.82	0.08	5.87E-01	8.46E-01	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	chr20q11.23	1556701_at	NM_001042486 /// NM_014902 /// NM_183006
2.15	2.22	0.07	5.87E-01	8.46E-01	---	---	---	237537_at	---
3.49	3.59	0.10	5.87E-01	8.46E-01	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	chr9q13	205505_at	NM_001097633 /// NM_001097634 /// NM_001097635 /// NM_001097636 /// NM_001490
3.60	3.70	0.10	5.87E-01	8.46E-01	---	---	---	244349_at	---
2.18	2.28	0.10	5.87E-01	8.46E-01	LOC100133233 /// TRAF3IP3	hypothetical protein LOC100133233 /// TRAF3 interacting protein 3	chr1q32.2 /// chr1q32.3-q41	215275_at	NM_025228 /// XM_001718033 /// XM_001718553 /// XM_001720826
2.85	2.92	0.07	5.87E-01	8.46E-01	---	---	---	1560550_at	---
2.00	2.05	0.05	5.87E-01	8.47E-01	FLJ40176	hypothetical LOC121951	chr13q33.1	1566665_at	XM_926977 /// XM_937542
2.81	2.93	0.12	5.88E-01	8.47E-01	---	---	---	228493_at	---
1.99	2.07	0.09	5.88E-01	8.47E-01	STAP1	signal transducing adaptor family member 1	chr4q13.2	220059_at	NM_012108
1.92	2.00	0.08	5.88E-01	8.47E-01	HAPLN1	hyaluronan and proteoglycan link protein 1	chr5q14.3	205523_at	NM_001884
5.22	5.39	0.17	5.88E-01	8.47E-01	RPAP2	RNA polymerase II associated protein 2	chr1p22.1	222893_s_at	NM_024813
2.80	2.91	0.12	5.88E-01	8.47E-01	---	---	---	240482_at	---
2.51	2.63	0.11	5.88E-01	8.47E-01	SMOC2	SPARC related modular calcium binding 2	chr6q27	243946_at	NM_022138
2.74	2.84	0.10	5.88E-01	8.47E-01	LOC253264	hypothetical protein LOC253264	chr10q22.2	232684_at	---
3.66	3.74	0.08	5.88E-01	8.47E-01	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	chr1p36.2	230705_at	NM_003039
2.48	2.56	0.08	5.88E-01	8.47E-01	ZNF385D	zinc finger protein 385D	chr3p24.3	220117_at	NM_024697
2.50	2.59	0.09	5.88E-01	8.47E-01	RXRB	retinoid X receptor, beta	chr6p21.3	215098_at	NM_021976
2.23	2.29	0.06	5.88E-01	8.47E-01	TRA@ /// TRAC /// TRAJ17 /// TRAV20	T cell receptor alpha locus /// T cell receptor alpha constant /// T cell receptor alpha joining 17 /// T cell receptor alpha variable 20	chr14q11 /// chr14q11.2	215524_x_at	---
6.01	6.17	0.16	5.88E-01	8.47E-01	USP33	ubiquitin specific peptidase 33	chr1p31.1	214843_s_at	NM_015017 /// NM_201624 /// NM_201626
3.83	4.00	0.16	5.88E-01	8.47E-01	FAM126A	family with sequence similarity 126, member A	chr7p15.3	223625_at	NM_032581
3.19	3.27	0.08	5.88E-01	8.47E-01	---	---	---	1559362_at	---
2.84	2.94	0.10	5.88E-01	8.47E-01	C19orf30	chromosome 19 open reading frame 30	chr19p13.3	223913_s_at	XR_040340 /// XR_040341 /// XR_040342
5.01	5.14	0.13	5.88E-01	8.47E-01	SLC38A9	solute carrier family 38, member 9	chr5q11.2	235241_at	NM_173514
2.73	2.82	0.09	5.88E-01	8.47E-01	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	chr11q23.3	229010_at	NM_005188
4.38	4.58	0.20	5.88E-01	8.47E-01	FPGT	fucose-1-phosphate guanylyltransferase	chr1p31.1	205140_at	NM_003838

2.27	2.39	0.12	5.88E-01	8.47E-01	TNNI3K	TNNI3 interacting kinase	chr1p31.1	220415_at	NM_001112808 /// NM_015978
1.92	1.98	0.06	5.88E-01	8.47E-01	CSMD1	CUB and Sushi multiple domains 1	chr8p23.2	1562329_at	NM_033225
2.48	2.57	0.09	5.88E-01	8.47E-01	GATM	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	chr15q21.1	231590_at	NM_001482
2.62	2.71	0.10	5.88E-01	8.47E-01	C16orf78	chromosome 16 open reading frame 78	chr16q12.1	240209_at	NM_144602
1.96	2.05	0.08	5.89E-01	8.47E-01	SYTL3	synaptotagmin-like 3	chr6q25.3	236864_at	NM_001009991
4.72	4.79	0.08	5.89E-01	8.47E-01	FTCD	formiminotransferase cyclodeaminase	chr21q22.3	224299_x_at	NM_006657 /// NM_206965
3.28	3.38	0.10	5.89E-01	8.47E-01	KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	chr19p13.1	206231_at	NM_002248
1.98	2.06	0.08	5.89E-01	8.47E-01	POSTN	periostin, osteoblast specific factor	chr13q13.3	1555777_at	NM_006475
1.99	2.05	0.07	5.89E-01	8.47E-01	---	---	---	234428_at	---
1.99	2.06	0.07	5.89E-01	8.47E-01	---	---	---	1561676_at	---
2.00	2.06	0.06	5.89E-01	8.47E-01	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit	chr3p24-p21	224029_x_at	NM_014139
5.98	6.11	0.13	5.89E-01	8.47E-01	SKIP	skeletal muscle and kidney enriched inositol phosphatase	chr17p13.3	202782_s_at	NM_016532 /// NM_130766
2.34	2.43	0.09	5.89E-01	8.47E-01	---	---	---	240076_at	---
2.49	2.56	0.07	5.89E-01	8.47E-01	PRMT8	protein arginine methyltransferase 8	chr12p13.3	207772_s_at	NM_019854
2.09	2.16	0.07	5.89E-01	8.47E-01	ACAT1	acetyl-Coenzyme A acetyltransferase 1	chr11q22.3-q23.1	1554947_at	NM_000019
3.04	3.19	0.14	5.89E-01	8.47E-01	WNT5A	wingless-type MMTV integration site family, member 5A	chr3p21-p14	213425_at	NM_003392
4.21	4.32	0.11	5.89E-01	8.47E-01	C21orf45	chromosome 21 open reading frame 45	chr21q22.11	219004_s_at	NM_018944
2.52	2.62	0.10	5.89E-01	8.47E-01	---	---	---	221714_s_at	---
5.47	5.69	0.22	5.89E-01	8.47E-01	TRIP4	thyroid hormone receptor interactor 4	chr15q22.31	203732_at	NM_016213
2.12	2.20	0.08	5.89E-01	8.47E-01	C16orf65	chromosome 16 open reading frame 65	chr16p12.1	241572_at	NM_173806
2.12	2.18	0.06	5.89E-01	8.47E-01	---	---	---	217215_s_at	---
1.90	1.96	0.07	5.89E-01	8.48E-01	---	---	---	233821_at	---
4.10	4.27	0.17	5.89E-01	8.48E-01	SAR1A	SAR1 gene homolog A (S. cerevisiae)	chr10q22.1	210790_s_at	NM_020150
3.31	3.42	0.11	5.89E-01	8.48E-01	RIT1	Ras-like without CAAX 1	chr1q22	243463_s_at	NM_006912
2.93	3.03	0.10	5.89E-01	8.48E-01	LOC100129087 /// WIBG	hypothetical protein LOC100129087 /// within bgcn homolog (Drosophila)	chr12q13.2	1569428_at	NM_032345 /// XM_001715965 /// XM_001717673 /// XM_001718616
2.92	3.01	0.10	5.89E-01	8.48E-01	LRRC1	leucine rich repeat containing 1	chr6p12.1	207790_at	NM_018214
3.00	3.09	0.09	5.89E-01	8.48E-01	LYPD1	LY6/PLAUR domain containing 1	chr2q21.2	212909_at	NM_001077427 /// NM_144586
8.80	8.95	0.14	5.89E-01	8.48E-01	SERBP1	SERPINE1 mRNA binding protein 1	chr1p31	210466_s_at	NM_001018067 /// NM_001018068 /// NM_001018069 /// NM_015640
2.22	2.28	0.06	5.89E-01	8.48E-01	C3orf67	Chromosome 3 open reading frame 67	chr3p14.2	231539_at	NM_198463
2.23	2.28	0.06	5.89E-01	8.48E-01	---	---	---	1569816_at	---
1.97	2.03	0.06	5.89E-01	8.48E-01	---	---	---	236843_at	---
4.95	5.11	0.15	5.90E-01	8.48E-01	LOC100128155 /// VAV2	hypothetical protein LOC100128155 /// vav 2 guanine nucleotide exchange factor	chr9q34.1 /// chr9q34.2	205536_at	NM_001134398 /// NM_003371 /// XM_001719399 /// XM_001722275 /// XM_001722967
2.97	3.06	0.09	5.90E-01	8.48E-01	ZNF24	zinc finger protein 24	chr18q12	1554045_at	NM_006965
2.17	2.24	0.07	5.90E-01	8.48E-01	---	---	---	237385_at	---
8.38	8.55	0.17	5.90E-01	8.48E-01	NUDT4 /// NUDT4P1	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	chr12q21 /// chr1q21.1	212181_s_at	NM_019094 /// NM_199040 /// NR_002212
1.94	2.01	0.07	5.90E-01	8.48E-01	CAMK4	calcium/calmodulin-dependent protein kinase IV	chr5q21.3	241871_at	NM_001744
2.49	2.60	0.10	5.90E-01	8.48E-01	C8orf75	chromosome 8 open reading frame 75	chr8p12	232718_at	---
5.34	5.53	0.18	5.90E-01	8.48E-01	CLIP4	CAP-GLY domain containing linker protein family, member 4	chr2p23.2	226425_at	NM_024692
2.16	2.26	0.10	5.90E-01	8.48E-01	---	---	---	232805_at	---
3.24	3.37	0.12	5.90E-01	8.48E-01	LOC441242	Hypothetical LOC441242	chr7q11.21	243009_at	XR_041923 /// XR_041924
3.69	3.77	0.08	5.90E-01	8.48E-01	SLC25A18	solute carrier family 25 (mitochondrial carrier), member 18	chr22q11.2	1569793_at	NM_031481
4.88	5.13	0.25	5.90E-01	8.48E-01	CD52	CD52 molecule	chr1p36	204661_at	NM_001803
11.54	11.66	0.12	5.90E-01	8.48E-01	RPL24	ribosomal protein L24	chr3q12	200013_at	NM_000986

6.04	6.15	0.11	5.90E-01	8.48E-01	CD47	CD47 molecule	chr3q13.1-q13.2	213055_at	NM_001025079 /// NM_001777 /// NM_198793
5.42	5.55	0.13	5.90E-01	8.48E-01	C19orf45	chromosome 19 open reading frame 45	chr19p13.2	241862_x_at	NM_198534
2.11	2.21	0.11	5.90E-01	8.48E-01	---	---	---	228955_at	---
2.14	2.21	0.07	5.90E-01	8.48E-01	RNF145	Ring finger protein 145	chr5q33.3	239899_at	NM_144726
2.28	2.35	0.07	5.90E-01	8.48E-01	---	---	---	1560489_at	---
2.07	2.14	0.07	5.90E-01	8.48E-01	C12orf54	chromosome 12 open reading frame 54	chr12q13.11	240353_s_at	NM_152319
2.10	2.16	0.06	5.90E-01	8.48E-01	FLJ37396	hypothetical protein FLJ37396	chr6q21	1553446_at	XM_001722396 /// XM_001725471 /// XM_001726130
1.85	1.90	0.05	5.90E-01	8.48E-01	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	chr12q23.3	1556804_s_at	NM_018082
3.57	3.64	0.08	5.90E-01	8.48E-01	SIP1	survival of motor neuron protein interacting protein 1	chr14q13	210779_x_at	NM_001009182 /// NM_001009183 /// NM_003616
5.64	5.97	0.33	5.90E-01	8.48E-01	GTPBP4	GTP binding protein 4	chr10p15-p14	218238_at	NM_012341
4.99	5.12	0.13	5.90E-01	8.48E-01	MTMR9	myotubularin related protein 9	chr8p23-p22	233101_at	NM_015458
2.15	2.24	0.08	5.90E-01	8.48E-01	C6orf168	chromosome 6 open reading frame 168	chr6q16.2-q16.3	232067_at	NM_032511
1.97	2.05	0.08	5.90E-01	8.48E-01	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	chr19q13.2	206676_at	NM_001816
2.24	2.31	0.07	5.90E-01	8.48E-01	KIAA0317	KIAA0317	chr14q24.3	244137_at	NM_001039479
3.17	3.26	0.09	5.91E-01	8.48E-01	---	---	---	240057_at	---
1.96	2.04	0.08	5.91E-01	8.48E-01	RFX4	regulatory factor X, 4 (influences HLA class II expression)	chr12q24	1552809_at	NM_002920 /// NM_032491 /// NM_213594
6.07	6.26	0.19	5.91E-01	8.48E-01	ZNF493	zinc finger protein 493	chr19p12	1558486_at	NM_001076678 /// NM_175910
6.34	6.46	0.11	5.91E-01	8.48E-01	C1orf144	chromosome 1 open reading frame 144	chr1p36.13	212005_at	NM_001114600 /// NM_015609
4.04	4.18	0.15	5.91E-01	8.48E-01	---	---	---	225066_at	---
2.00	2.07	0.07	5.91E-01	8.48E-01	SOX5	SRY (sex determining region Y)-box 5	chr12p12.1	216561_x_at	NM_006940 /// NM_152989 /// NM_178010
7.43	7.60	0.17	5.91E-01	8.48E-01	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	chr1p34.3	218235_s_at	NM_016037
4.00	4.11	0.11	5.91E-01	8.48E-01	LOC728445	hypothetical protein LOC728445	chr8p11.21	1561579_at	XM_001127482
5.23	5.31	0.08	5.91E-01	8.48E-01	NOVA2	neuro-oncological ventral antigen 2	chr19q13.3	206477_s_at	NM_002516
5.22	5.45	0.23	5.91E-01	8.49E-01	PALLD	palladin, cytoskeletal associated protein	chr4q32.3	200906_s_at	NM_016081
5.21	5.29	0.08	5.91E-01	8.49E-01	LOC79999	hypothetical LOC79999	chr17p11.2	220849_at	XR_040955 /// XR_040956
3.26	3.33	0.08	5.91E-01	8.49E-01	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	chr2q37.3	1555548_at	NM_004544
4.38	4.47	0.09	5.91E-01	8.49E-01	TRIM8	Tripartite motif-containing 8	chr10q24.3	228015_s_at	NM_030912
2.17	2.25	0.07	5.91E-01	8.49E-01	---	---	---	215317_at	---
2.56	2.66	0.10	5.91E-01	8.49E-01	---	---	---	232743_at	---
2.02	2.08	0.07	5.91E-01	8.49E-01	ANAPC13	anaphase promoting complex subunit 13	chr3q22.1	215282_at	NM_015391
5.02	5.18	0.17	5.92E-01	8.49E-01	SMAD5	SMAD family member 5	chr5q31	225223_at	NM_001001419 /// NM_001001420 /// NM_005903
5.70	5.84	0.15	5.92E-01	8.49E-01	ARMC10	armadillo repeat containing 10	chr7q22.1	1554480_a_at	NM_031905
4.10	4.19	0.10	5.92E-01	8.49E-01	---	---	---	244032_at	---
5.14	5.21	0.07	5.92E-01	8.49E-01	LOC100129195	hypothetical protein LOC100129195	chr6p22.1	244730_x_at	XM_001715702 /// XM_001719301 /// XM_001722758
2.31	2.42	0.11	5.92E-01	8.49E-01	---	---	---	1560391_at	---
2.90	3.09	0.18	5.92E-01	8.49E-01	ZNF277	zinc finger protein 277	chr7q31.1	1555193_a_at	NM_021994
2.69	2.76	0.07	5.92E-01	8.49E-01	---	---	---	232189_at	---

2.91	3.02	0.11	5.92E-01	8.49E-01	MAPT	microtubule-associated protein tau	chr17q21.1	203929_s_at	NM_001123066 /// NM_001123067 /// NM_005910 /// NM_016834 /// NM_016835 /// NM_016841
3.15	3.25	0.10	5.92E-01	8.49E-01	---	---	---	241327_at	---
2.45	2.55	0.10	5.92E-01	8.49E-01	BCMO1	beta-carotene 15,15'-monooxygenase 1	chr16q21-q23	220087_at	NM_017429
5.27	5.36	0.09	5.92E-01	8.49E-01	GTPBP8	GTP-binding protein 8 (putative)	chr3q13.2	223486_at	NM_014170 /// NM_138485
3.13	3.22	0.09	5.92E-01	8.49E-01	VGLL1	vestigial like 1 (Drosophila)	chrXq26.3	205487_s_at	NM_016267
2.18	2.26	0.09	5.92E-01	8.49E-01	PTPN9	Protein tyrosine phosphatase, non-receptor type 9	chr15q24.2	230140_at	NM_002833
2.47	2.54	0.07	5.92E-01	8.49E-01	ARHGAP24	Rho GTPase activating protein 24	chr4q21.23-q21.3	221030_s_at	NM_001025616 /// NM_001042669 /// NM_031305
2.12	2.19	0.07	5.92E-01	8.49E-01	---	---	---	241539_at	---
5.11	5.22	0.11	5.92E-01	8.49E-01	DIDO1	death inducer-obliterator 1	chr20q13.33	218325_s_at	NM_022105 /// NM_033081 /// NM_080796 /// NM_080797
2.04	2.10	0.06	5.92E-01	8.49E-01	---	---	---	1560940_at	---
2.52	2.65	0.13	5.92E-01	8.49E-01	LOC439938	hypothetical gene supported by NM_178534	chr6p21.33	244424_at	---
2.10	2.17	0.07	5.92E-01	8.49E-01	---	---	---	234619_at	---
5.55	5.71	0.16	5.93E-01	8.49E-01	---	---	---	233068_at	---
3.17	3.31	0.13	5.93E-01	8.49E-01	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	chr3p14.3	243334_at	NM_000720 /// NM_001128839 /// NM_001128840
3.85	3.93	0.09	5.93E-01	8.49E-01	LOC389634	hypothetical LOC389634	chr12p13.31	1564426_x_at	XR_041469 /// XR_041470 /// XR_041471
2.80	2.86	0.06	5.93E-01	8.49E-01	EFNA5	Ephrin-A5	chr5q21	227955_s_at	NM_001962
9.60	9.82	0.22	5.93E-01	8.49E-01	SLC38A2	solute carrier family 38, member 2	chr12q	222982_x_at	NM_018976
4.00	4.19	0.19	5.93E-01	8.49E-01	RNF219	ring finger protein 219	chr13q31.1	219303_at	NM_024546
3.53	3.63	0.10	5.93E-01	8.49E-01	FCRLA	Fc receptor-like A	chr1q23.3	235372_at	NM_032738
1.92	1.99	0.06	5.93E-01	8.49E-01	---	---	---	242252_at	---
3.01	3.24	0.23	5.93E-01	8.49E-01	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	chr9q21.31	233575_s_at	NM_007005
2.52	2.61	0.09	5.93E-01	8.49E-01	---	---	---	241069_at	---
5.85	5.97	0.13	5.93E-01	8.49E-01	ST7	suppression of tumorigenicity 7	chr7q31.1-q31.3	207871_s_at	NM_018412 /// NM_021908
5.84	5.95	0.11	5.93E-01	8.49E-01	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	chr10p13	219678_x_at	NM_001033855 /// NM_001033857 /// NM_001033858 /// NM_022487
2.04	2.10	0.06	5.93E-01	8.49E-01	C6orf12	chromosome 6 open reading frame 12	chr6p21.33	234866_s_at	XR_041144 /// XR_041145
5.96	6.19	0.23	5.93E-01	8.50E-01	CTR9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr11p15.3	202060_at	NM_014633
3.42	3.60	0.17	5.93E-01	8.50E-01	---	---	---	235046_at	---
3.46	3.55	0.09	5.93E-01	8.50E-01	TF	transferrin	chr3q22.1	214063_s_at	NM_001063
3.58	3.69	0.11	5.93E-01	8.50E-01	---	---	---	1566576_at	---
2.32	2.40	0.08	5.93E-01	8.50E-01	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	chr10q21-q22	1570454_at	NM_004096
4.62	4.83	0.20	5.93E-01	8.50E-01	DOCK8	dedicator of cytokinesis 8	chr9p24.3	225502_at	NM_203447
3.88	4.01	0.13	5.93E-01	8.50E-01	QRSL1	Glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	chr6q21	241933_at	NM_018292
2.82	2.92	0.10	5.93E-01	8.50E-01	---	---	---	216286_at	---
2.32	2.41	0.09	5.93E-01	8.50E-01	---	---	---	240785_at	---
2.26	2.34	0.09	5.93E-01	8.50E-01	LOC440836	Similar to MGC52679 protein	chr22q13.33	243934_at	NM_001014440
2.71	2.80	0.08	5.93E-01	8.50E-01	PER4	period 4 pseudogene	chr7p21.3	1566844_at	NR_002790
3.76	3.84	0.08	5.93E-01	8.50E-01	RASA2	RAS p21 protein activator 2	chr3q22-q23	206636_at	NM_006506
2.67	2.75	0.08	5.93E-01	8.50E-01	---	---	---	1557540_at	---
2.15	2.22	0.08	5.93E-01	8.50E-01	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	chr15q11.2-q12	217280_x_at	NM_000810
2.29	2.36	0.08	5.93E-01	8.50E-01	---	---	---	240416_at	---
2.25	2.31	0.06	5.93E-01	8.50E-01	---	---	---	232962_x_at	---
7.28	7.59	0.31	5.94E-01	8.50E-01	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	chr11q12.2	218688_at	NM_015533

3.69	3.80	0.11	5.94E-01	8.50E-01	LOC100130262	hypothetical protein LOC100130262	chr1q44	227011_at	XM_001714091 /// XM_001724097 /// XM_001724354																				
2.20	2.30	0.10	5.94E-01	8.50E-01	LOC728052	similar to hCG2031213	chr6q12	1558796_a_at	XM_001126435 /// XM_001128968 /// XM_001717850																				
2.86	2.96	0.10	5.94E-01	8.50E-01	---	---	---	236510_at	---																				
2.54	2.63	0.09	5.94E-01	8.50E-01	---	---	---	210098_s_at	---																				
2.77	2.86	0.09	5.94E-01	8.50E-01	STIM2	stromal interaction molecule 2	chr4p15.2	225250_at	NM_020860																				
2.64	2.74	0.09	5.93E-01	8.50E-01	---	---	---	240183_at	---																				
3.08	3.17	0.09	5.94E-01	8.50E-01	---	---	---	244696_at	---																				
6.74	6.82	0.08	5.94E-01	8.50E-01	MAP4	microtubule-associated protein 4	chr3p21	33850_at	NM_001134364 /// NM_001134365 /// NM_002375 /// NM_030884 /// NM_030885																				
3.82	3.90	0.08	5.94E-01	8.50E-01	MEGF10	multiple EGF-like-domains 10	chr5q33	1555343_at	NM_032446																				
3.86	4.00	0.14	5.94E-01	8.50E-01	PDLIM7	PDZ and LIM domain 7 (enigma)	chr5q35.3	203369_x_at	NM_005451 /// NM_203352 /// NM_213636																				
6.88	7.05	0.17	5.94E-01	8.50E-01	IPO8	importin 8	chr12p11.21	225528_at	NM_006390																				
2.60	2.71	0.12	5.94E-01	8.50E-01	---	---	---	242599_at	---																				
4.48	4.57	0.09	5.94E-01	8.50E-01	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	chr10p13	1554572_a_at	NM_024670																				
2.81	2.89	0.07	5.94E-01	8.50E-01	---	---	---	1562771_at	---																				
2.40	2.48	0.07	5.94E-01	8.50E-01	CYP4F2 /// CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 2 /// cytochrome P450, family 4, subfamily F, polypeptide 3	chr19p13.2 /// chr19pter-p13.11	206514_s_at	NM_000896 /// NM_001082																				
6.53	6.69	0.15	5.94E-01	8.50E-01	DDAH2	dimethylarginine dimethylaminohydrolase 2	chr6p21.3	214909_s_at	NM_013974																				
6.83	6.96	0.14	5.94E-01	8.50E-01	CBX6	chromobox homolog 6	chr22q13.1	202047_s_at	NM_014292																				
7.01	7.13	0.12	5.94E-01	8.50E-01	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	chr5q33.1	202607_at	NM_001543																				
5.62	5.71	0.09	5.94E-01	8.50E-01	---	---	---	241344_at	---																				
2.34	2.42	0.08	5.94E-01	8.50E-01	OR51B5	olfactory receptor, family 51, subfamily B, member 5	chr11p15.4	1570516_s_at	NM_001005567																				
3.45	3.53	0.08	5.94E-01	8.50E-01	TRIM50	tripartite motif-containing 50	chr7q11.23	1556554_at	NM_178125																				
2.36	2.43	0.06	5.94E-01	8.50E-01	C20orf74	Chromosome 20 open reading frame 74	chr20p11.22	234934_at	NM_020343																				
3.50	3.59	0.08	5.94E-01	8.50E-01	NEUROD6	neurogenic differentiation 6	chr7p15.1	220045_at	NM_022728																				
2.06	2.13	0.07	5.94E-01	8.50E-01	NLRP3	NLR family, pyrin domain containing 3	chr1q44	216016_at	NM_001079821 /// NM_001127461 /// NM_001127462 /// NM_004895 /// NM_183395																				
2.36	2.45	0.09	5.94E-01	8.50E-01	YDD19	YDD19 protein	chr13q12	37079_at	---																				
4.93	5.21	0.27	5.94E-01	8.50E-01	TMEM119	transmembrane protein 119	chr12q24.11	227300_at	NM_181724																				
2.45	2.56	0.11	5.94E-01	8.50E-01	EDIL3	EGF-like repeats and discoidin I-like domains 3	chr5q14	1558643_s_at	NM_005711																				
1.99	2.06	0.07	5.94E-01	8.50E-01	PAP2D	phosphatidic acid phosphatase type 2	chr1p21.3	231397_at	NM_001010861 /// NM_001037317																				
4.70	4.83	0.13	5.94E-01	8.50E-01	CENTA1	centaurin, alpha 1	chr7p22.3	90265_at	NM_006869																				
4.42	4.61	0.19	5.95E-01	8.50E-01	---	---	---	235985_at	---																				
3.46	3.56	0.10	5.95E-01	8.50E-01	---	---	---	241149_at	---																				
2.19	2.25	0.07	5.95E-01	8.50E-01	ZC3H4	Zinc finger CCCH-type containing 4	chr19q13.32	240022_at	NM_015168																				
2.48	2.57	0.09	5.95E-01	8.50E-01	LOC494558	hypothetical locus LOC494558	chr9q21.11	236071_at	---																				
2.59	2.66	0.07	5.95E-01	8.50E-01	MGC3771	hypothetical LOC81854	chr16p13.3	208136_s_at	---																				
2.23	2.34	0.10	5.95E-01	8.50E-01	LOC728190	hypothetical LOC728190	chr10q23.2	229609_at	XR_040767																				
4.29	4.37	0.08	5.95E-01	8.50E-01	---	---	---	1558299_at	---																				
2.16	2.22	0.06	5.95E-01	8.50E-01	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	chr1p36	211786_at	NM_001561																				
4.74	4.90	0.16	5.95E-01	8.50E-01	EIF4E3	eukaryotic translation initiation factor 4E family member 3	chr3p14	225940_at	NM_001134649 /// NM_001134650 /// NM_001134651 /// NM_173359																				
5.52	5.63	0.11	5.95E-01	8.50E-01	CALCOCO2	calcium binding and coiled-coil domain 2	chr17q21.32	235076_at	NM_005831																				
2.32	2.40	0.08	5.95E-01	8.50E-01	---	---	---	243811_at	---																				
4.49	4.56	0.08	5.95E-01	8.50E-01	STAT5B	signal transducer and activator of transcription 5B	chr17q11.2	205026_at	NM_012448																				

5.30	5.43	0.12	5.95E-01	8.50E-01	LRRC8A	leucine rich repeat containing 8 family, member A	chr9q34.11	233487_s_at	NM_001127244 /// NM_001127245 /// NM_019594
2.13	2.21	0.08	5.95E-01	8.50E-01	RBM24	RNA binding motif protein 24	chr6p22.3	235004_at	NM_153020
2.54	2.62	0.08	5.95E-01	8.50E-01	---	---	---	237129_at	---
1.91	1.97	0.06	5.95E-01	8.50E-01	MAF	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	chr16q22-q23	1566323_at	NM_001031804 /// NM_005360
2.07	2.13	0.06	5.95E-01	8.50E-01	---	---	---	1561493_at	---
2.77	2.85	0.08	5.95E-01	8.50E-01	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	chr14q11.2	217248_s_at	NM_012244 /// NM_182728
2.16	2.24	0.08	5.95E-01	8.50E-01	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	chr11q12.1	210254_at	NM_001031666 /// NM_001031809 /// NM_006138
1.90	1.95	0.05	5.95E-01	8.50E-01	---	---	---	217694_at	---
2.58	2.65	0.07	5.95E-01	8.51E-01	SMC6	structural maintenance of chromosomes 6	chr2p24.2	236535_at	NM_024624
2.96	3.13	0.18	5.95E-01	8.51E-01	---	---	---	236335_at	---
3.03	3.10	0.07	5.95E-01	8.51E-01	---	---	---	1561702_at	---
1.96	2.01	0.06	5.95E-01	8.51E-01	---	---	---	237580_at	---
7.40	7.63	0.24	5.96E-01	8.51E-01	SNX5	sorting nexin 5	chr20p11	222417_s_at	NM_014426 /// NM_152227
8.26	8.39	0.13	5.96E-01	8.51E-01	NR2F2	nuclear receptor subfamily 2, group F, member 2	chr15q26	209121_x_at	NM_021005
2.08	2.16	0.08	5.96E-01	8.51E-01	---	---	---	240977_at	---
2.00	2.08	0.07	5.96E-01	8.51E-01	---	---	---	241855_s_at	---
2.51	2.58	0.06	5.96E-01	8.51E-01	LOC149684	hypothetical protein LOC149684	chr20q12	1563753_at	---
2.43	2.50	0.07	5.96E-01	8.51E-01	IL1F9	interleukin 1 family, member 9	chr2q12-q21	220322_at	NM_019618
2.49	2.55	0.06	5.96E-01	8.51E-01	FLJ30375	Hypothetical gene supported by AK054937	chr3q24	1557155_a_at	XM_001724993 /// XM_001725199 /// XM_001725628
1.99	2.06	0.07	5.96E-01	8.51E-01	CTNND2	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	chr5p15.2	209618_at	NM_001332
3.46	3.57	0.11	5.96E-01	8.51E-01	---	---	---	239117_at	---
5.47	5.58	0.11	5.96E-01	8.51E-01	VGF	VGF nerve growth factor inducible	chr7q22.1	205586_x_at	NM_003378
2.36	2.44	0.08	5.96E-01	8.51E-01	IL21R	interleukin 21 receptor	chr16p11	219971_at	NM_021798 /// NM_181078 /// NM_181079
3.00	3.08	0.08	5.96E-01	8.51E-01	MYOM3	myomesin family, member 3	chr1p36.11	230284_at	NM_152372
3.22	3.30	0.07	5.96E-01	8.51E-01	PHTF2	putative homeodomain transcription factor 2	chr7q11.23-q21	1554780_a_at	NM_001127357 /// NM_001127358 /// NM_001127359 /// NM_001127360 /// NM_020432
2.74	2.84	0.10	5.96E-01	8.51E-01	---	---	---	239652_at	---
3.09	3.17	0.07	5.96E-01	8.51E-01	PGAM5	phosphoglycerate mutase family member 5	chr12q24.33	1553837_at	NM_138575 /// XM_001713960
1.98	2.06	0.07	5.96E-01	8.51E-01	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	chr12q11-q12	207583_at	NM_005164
2.77	2.88	0.11	5.96E-01	8.51E-01	TRIM11	tripartite motif-containing 11	chr1q42.13	238797_at	NM_145214
4.19	4.27	0.08	5.96E-01	8.51E-01	TRIM29	tripartite motif-containing 29	chr11q22-q23	211002_s_at	NM_012101
4.03	4.15	0.12	5.96E-01	8.51E-01	LTBP4	latent transforming growth factor beta binding protein 4	chr19q13.1-q13.2	213176_s_at	NM_001042544 /// NM_001042545 /// NM_003573
2.32	2.41	0.09	5.96E-01	8.51E-01	CNDP1	carnosine dipeptidase 1 (metallopeptidase M20 family)	chr18q22.3	223699_at	NM_032649
2.59	2.68	0.09	5.96E-01	8.51E-01	CCDC88C	coiled-coil domain containing 88C	chr14q32.12	227228_s_at	NM_001080414
2.54	2.69	0.15	5.96E-01	8.51E-01	LRRC8B	leucine rich repeat containing 8 family, member B	chr1p22.2	212976_at	NM_001134476 /// NM_015350
1.95	2.02	0.07	5.97E-01	8.51E-01	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	chr2q24.3	209891_at	NM_020675
2.11	2.18	0.07	5.96E-01	8.51E-01	FILIP1L	filamin A interacting protein 1-like	chr3q12.1	1554965_at	NM_001042459 /// NM_014890 /// NM_182909
2.01	2.08	0.07	5.97E-01	8.51E-01	SLC26A3	Solute carrier family 26, member 3	chr7q31	215657_at	NM_000111

1.97	2.04	0.07	5.97E-01	8.51E-01	---	---	---	1560996_at	---
5.15	5.28	0.13	5.97E-01	8.51E-01	BCR	breakpoint cluster region	chr22q11|22q11.23	217223_s_at	NM_004327 /// NM_021574
7.94	8.12	0.18	5.97E-01	8.51E-01	ZFR	zinc finger RNA binding protein	chr5p13.3	201857_at	NM_016107
2.06	2.13	0.07	5.97E-01	8.51E-01	LOC641467	hypothetical LOC641467	---	237745_at	---
2.87	3.00	0.13	5.97E-01	8.51E-01	ANKRD13A	ankyrin repeat domain 13A	chr12q24.11	238851_at	NM_033121
5.68	5.79	0.11	5.97E-01	8.51E-01	LOC643837	hypothetical LOC643837	chr1p36.33	1557055_s_at	NR_015368 /// XM_927114
3.11	3.20	0.09	5.97E-01	8.51E-01	ZDHHC18	zinc finger, DHHC-type containing 18	chr1p36.11	1558327_at	NM_032283
3.55	3.70	0.15	5.97E-01	8.51E-01	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	chr18q21.3	1554616_at	NM_001031848 /// NM_002640 /// NM_198833
2.21	2.28	0.07	5.97E-01	8.51E-01	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	chr13q32	216513_at	NM_001129889 /// NM_001922
2.89	2.97	0.08	5.97E-01	8.51E-01	EFHC1	EF-hand domain (C-terminal) containing 1	chr6p12.3	231026_at	NM_018100
2.44	2.51	0.08	5.97E-01	8.51E-01	KCNG4	potassium voltage-gated channel, subfamily G, member 4	chr16q24.1	1552598_at	NM_133490 /// NM_172347
1.98	2.03	0.05	5.97E-01	8.51E-01	CLIP1	CAP-GLY domain containing linker protein 1	chr12q24.3	1568012_at	NM_002956 /// NM_198240
6.56	6.80	0.25	5.97E-01	8.51E-01	SMAD5	SMAD family member 5	chr5q31	225219_at	NM_001001419 /// NM_001001420 /// NM_005903
3.84	3.93	0.09	5.97E-01	8.51E-01	FGF21	fibroblast growth factor 21	chr19q13.1-qter	221433_at	NM_019113
1.98	2.06	0.07	5.97E-01	8.51E-01	MCM9	minichromosome maintenance complex component 9	chr6q22.31	1553759_at	NM_153255
2.07	2.14	0.07	5.97E-01	8.51E-01	C6orf65	chromosome 6 open reading frame 65	chr6p12.1	1568820_a_at	NM_152731
2.02	2.09	0.07	5.97E-01	8.51E-01	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	chr18q21.3	211906_s_at	NM_002974
4.11	4.21	0.10	5.97E-01	8.51E-01	PDIK1L	PDLIM1 interacting kinase 1 like	chr1p36.11	227255_at	NM_152835
2.47	2.55	0.08	5.97E-01	8.51E-01	MCF2L	MCF.2 cell line derived transforming sequence-like	chr13q34	1552743_at	NM_001112732 /// NM_024979
6.71	6.95	0.24	5.97E-01	8.51E-01	PLRG1	pleiotropic regulator 1 (PRL1 homolog, Arabidopsis)	chr4q31.2-q32.1	225194_at	NM_002669
5.05	5.23	0.18	5.97E-01	8.51E-01	RMND1	required for meiotic nuclear division 1 homolog (S. cerevisiae)	chr6q25.1	1555201_a_at	NM_017909
9.23	9.41	0.18	5.97E-01	8.51E-01	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	chr1q44	200594_x_at	NM_004501 /// NM_031844
4.53	4.71	0.18	5.97E-01	8.51E-01	AKT3	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	chr1q43-q44	242876_at	NM_005465 /// NM_181690
4.00	4.09	0.09	5.97E-01	8.51E-01	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	chr3p14.3	207998_s_at	NM_000720 /// NM_001128839 /// NM_001128840
2.00	2.07	0.07	5.97E-01	8.51E-01	---	---	---	243146_at	---
2.38	2.44	0.07	5.97E-01	8.51E-01	CP	ceruloplasmin (ferroxidase)	chr3q23-q25	227253_at	NM_000096
3.55	3.62	0.06	5.97E-01	8.51E-01	C21orf93	chromosome 21 open reading frame 93	chr21q22.3	1553832_at	XR_041771 /// XR_041772 /// XR_041773
4.65	4.72	0.06	5.97E-01	8.51E-01	---	---	---	224133_at	---
5.54	5.69	0.15	5.97E-01	8.51E-01	UBQLN1	ubiquilin 1	chr9q22|9q21.2-q21.3	222989_s_at	NM_013438 /// NM_053067
6.18	6.27	0.09	5.97E-01	8.51E-01	C9orf78	chromosome 9 open reading frame 78	chr9q34.11	218116_at	NM_016520
1.86	1.92	0.06	5.98E-01	8.51E-01	---	---	---	241796_x_at	---
4.34	4.47	0.12	5.98E-01	8.51E-01	TBX2	T-box 2	chr17q23	205993_s_at	NM_005994
6.91	7.06	0.15	5.98E-01	8.51E-01	ACLY	ATP citrate lyase	chr17q12-q21	210337_s_at	NM_001096 /// NM_198830
8.68	8.82	0.14	5.98E-01	8.51E-01	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	chr11p15.1	210759_s_at	NM_002786 /// NM_148976
3.31	3.44	0.12	5.98E-01	8.51E-01	GDF3	growth differentiation factor 3	chr12p13.1	220053_at	NM_020634
3.83	3.94	0.11	5.98E-01	8.51E-01	ESPNL	espin-like	chr2q37.3	1557002_x_at	NM_194312
2.14	2.23	0.09	5.98E-01	8.51E-01	---	---	---	233404_at	---
9.87	9.95	0.08	5.98E-01	8.51E-01	PTGES3	prostaglandin E synthase 3 (cytosolic)	chr12q13.3|12	200627_at	NM_006601
2.11	2.18	0.08	5.98E-01	8.51E-01	DTNB	dystrobrevin, beta	chr2p24	215565_at	NM_021907 /// NM_033147 /// NM_033148 /// NM_183360 /// NM_183361
2.20	2.28	0.07	5.98E-01	8.51E-01	---	---	---	236365_at	---
2.13	2.20	0.07	5.98E-01	8.51E-01	---	---	---	230650_at	---
2.11	2.17	0.07	5.98E-01	8.51E-01	PADI4	peptidyl arginine deiminase, type IV	chr1p36.13	211412_at	NM_012387
2.16	2.22	0.07	5.98E-01	8.51E-01	---	---	---	236576_at	---

1.77	1.82	0.05	5.98E-01	8.51E-01	C6orf12	chromosome 6 open reading frame 12	chr6p21.33	234457_at	XR_041144 /// XR_041145
3.65	3.75	0.11	5.98E-01	8.51E-01	NOTCH1	Notch homolog 1, translocation-associated (Drosophila)	chr9q34.3	223508_at	NM_017617
5.76	6.02	0.26	5.98E-01	8.51E-01	RBM34	RNA binding motif protein 34	chr1q42.3	212591_at	NM_015014
4.16	4.31	0.15	5.98E-01	8.51E-01	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	chr5q23-q31	239163_at	NM_003337
3.00	3.08	0.09	5.98E-01	8.52E-01	LOC255275	similar to myeloid-associated differentiation marker	chr17q25.3	242378_at	XR_041346 /// XR_041347 /// XR_041348
3.84	3.95	0.11	5.98E-01	8.52E-01	KCNK7	potassium channel, subfamily K, member 7	chr11q13	220412_x_at	NM_005714 /// NM_033347 /// NM_033348 /// NM_033455
6.44	6.64	0.20	5.98E-01	8.52E-01	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	chr5q33.1	201514_s_at	NM_005754 /// NM_198395
5.12	5.30	0.18	5.98E-01	8.52E-01	FBXO3	F-box protein 3	chr11p13	218432_at	NM_012175 /// NM_033406
2.57	2.67	0.09	5.98E-01	8.52E-01	---	---	---	233200_at	---
2.49	2.58	0.09	5.98E-01	8.52E-01	TCL6	T-cell leukemia/lymphoma 6	chr14q32.1	221054_s_at	NM_012468 /// NM_014418 /// NM_020550 /// NM_020552 /// NM_020553 /// NM_020554
2.64	2.73	0.08	5.98E-01	8.52E-01	LOC729355 /// TP53TG3	similar to TP53TG3 protein /// TP53TG3 protein	chr16p11.2 /// chr16p13	220167_s_at	NM_001099687 /// NM_016212
2.28	2.36	0.07	5.98E-01	8.52E-01	---	---	---	237517_at	---
2.14	2.21	0.06	5.98E-01	8.52E-01	---	---	---	241586_at	---
1.89	1.95	0.06	5.98E-01	8.52E-01	---	---	---	1564134_at	---
2.02	2.09	0.06	5.98E-01	8.52E-01	---	---	---	1562514_at	---
2.75	2.81	0.06	5.98E-01	8.52E-01	---	---	---	234206_at	---
2.26	2.37	0.11	5.99E-01	8.52E-01	---	---	---	241321_at	---
4.23	4.32	0.09	5.99E-01	8.52E-01	CADM3	cell adhesion molecule 3	chr1q21.2-q22	211677_x_at	NM_001127173 /// NM_021189
2.55	2.62	0.07	5.99E-01	8.52E-01	---	---	---	237774_at	---
3.16	3.24	0.08	5.99E-01	8.52E-01	---	---	---	1559675_at	---
3.15	3.21	0.07	5.99E-01	8.52E-01	---	---	---	237196_at	---
2.41	2.48	0.07	5.99E-01	8.52E-01	PSMD7	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	chr16q23-q24	244515_at	NM_002811
2.19	2.25	0.06	5.99E-01	8.52E-01	---	---	---	222178_s_at	---
8.41	8.55	0.14	5.99E-01	8.52E-01	ANTXR1	anthrax toxin receptor 1	chr2p13.1	224694_at	NM_018153 /// NM_032208 /// NM_053034
4.44	4.54	0.10	5.99E-01	8.52E-01	NANOS3	nanos homolog 3 (Drosophila)	chr19p13.12	240311_at	NM_001098622
1.94	2.00	0.06	5.99E-01	8.52E-01	KRTAP9-4 /// KRTAP9-9	keratin associated protein 9-4 /// keratin associated protein 9-9	chr17q12-q21	220972_s_at	NM_030975 /// NM_033191
2.40	2.48	0.08	5.99E-01	8.52E-01	AANAT	arylalkylamine N-acetyltransferase	chr17q25	207225_at	NM_001088
6.16	6.37	0.21	5.99E-01	8.52E-01	ORC4L	origin recognition complex, subunit 4-like (yeast)	chr2q22-q23	203351_s_at	NM_002552 /// NM_181741 /// NM_181742
4.89	5.02	0.13	5.99E-01	8.52E-01	HCRP1	hepatocellular carcinoma-related HCRP1	---	216176_at	XM_001722898 /// XM_001724271 /// XM_001725456
3.88	3.96	0.08	5.99E-01	8.52E-01	---	---	---	227710_s_at	---
2.16	2.22	0.06	5.99E-01	8.52E-01	NEUROG2	neurogenin 2	chr4q25	215632_at	NM_024019
1.96	2.03	0.06	5.99E-01	8.52E-01	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	chr2q36.1	1555733_s_at	NM_001039569
4.70	4.92	0.22	5.99E-01	8.52E-01	EEA1	early endosome antigen 1	chr12q22	225885_at	NM_003566
2.60	2.71	0.10	5.99E-01	8.52E-01	---	---	---	244787_at	---
2.60	2.69	0.09	5.99E-01	8.52E-01	---	---	---	1561228_at	---
3.08	3.20	0.11	5.99E-01	8.52E-01	---	---	---	240764_at	---
2.20	2.27	0.07	5.99E-01	8.52E-01	DICER1	dicer 1, ribonuclease type III	chr14q32.13	216280_s_at	NM_030621 /// NM_177438
5.75	6.02	0.27	6.00E-01	8.53E-01	---	---	---	226865_at	---
5.56	5.77	0.21	6.00E-01	8.53E-01	FAM13A1	family with sequence similarity 13, member A1	chr4q22.1	217047_s_at	NM_001015045 /// NM_014883
4.37	4.56	0.19	6.00E-01	8.53E-01	ANAPC10	anaphase promoting complex subunit 10	chr4q31	207845_s_at	NM_014885
4.66	4.75	0.09	6.00E-01	8.53E-01	---	---	---	1560560_at	---
5.25	5.35	0.10	6.00E-01	8.53E-01	DVL2	dishevelled, dsh homolog 2 (Drosophila)	chr17p13.2	218759_at	NM_004422
2.34	2.40	0.06	6.00E-01	8.53E-01	---	---	---	243824_at	---
3.18	3.25	0.08	6.00E-01	8.53E-01	SLC20A2	solute carrier family 20 (phosphate transporter), member 2	chr8p12-p11	202744_at	NM_006749

2.67	2.78	0.10	6.00E-01	8.53E-01	---	---	---	1560412_at	---
8.49	8.68	0.19	6.00E-01	8.53E-01	MCFD2	multiple coagulation factor deficiency 2	chr2p21	212245_at	NM_139279
4.62	4.73	0.11	6.00E-01	8.53E-01	ARHGAP23	Rho GTPase activating protein 23	chr17q12	231903_x_at	XM_001714948 /// XM_001716606 /// XM_290799
3.20	3.28	0.08	6.00E-01	8.53E-01	ZSCAN5A	zinc finger and SCAN domain containing 5A	chr19q13.43	219904_at	NM_024303
2.91	2.98	0.08	6.00E-01	8.53E-01	NEK11	NIMA (never in mitosis gene a)- related kinase 11	chr3q22.1	1554380_at	NM_024800 /// NM_145910
3.61	3.77	0.16	6.00E-01	8.53E-01	KIF2A	kinesin heavy chain member 2A	chr5q12-q13	203087_s_at	NM_001098511 /// NM_004520
2.42	2.50	0.09	6.00E-01	8.53E-01	---	---	---	241163_at	---
3.26	3.35	0.08	6.00E-01	8.53E-01	---	---	---	1557316_at	---
2.20	2.27	0.07	6.00E-01	8.53E-01	---	---	---	1555031_at	---
4.22	4.52	0.30	6.01E-01	8.53E-01	GFM2	G elongation factor, mitochondrial 2	chr5q13	231918_s_at	NM_032380 /// NM_170681 /// NM_170691
2.15	2.20	0.06	6.01E-01	8.53E-01	MTMR8	myotubularin related protein 8	chrXq11.1	220537_at	NM_017677
7.23	7.67	0.44	6.01E-01	8.53E-01	CD46	CD46 molecule, complement regulatory protein	chr1q32	211574_s_at	NM_002389 /// NM_153826 /// NM_172350 /// NM_172351 /// NM_172352 /// NM_172353 /// NM_172354 /// NM_172355 /// NM_172356 /// NM_172357 /// NM_172358 /// NM_172359 /// NM_172360 /// NM_172361
3.48	3.69	0.22	6.01E-01	8.53E-01	---	---	---	242457_at	---
4.45	4.54	0.09	6.01E-01	8.53E-01	PRMT8	protein arginine methyltransferase 8	chr12p13.3	230839_at	NM_019854
2.77	2.85	0.07	6.01E-01	8.53E-01	SBF1	SET binding factor 1	chr22q13.33	222084_s_at	NM_002972
5.71	5.86	0.14	6.01E-01	8.53E-01	C1orf50	chromosome 1 open reading frame 50	chr1p34.2	62212_at	NM_024097
2.11	2.17	0.06	6.01E-01	8.53E-01	---	---	---	233455_at	---
3.23	3.34	0.11	6.01E-01	8.53E-01	---	---	---	242989_at	---
2.05	2.11	0.07	6.01E-01	8.53E-01	MYO3B	myosin IIIB	chr2q31.1-q31.2	1560788_at	NM_001083615 /// NM_138995
7.40	7.53	0.14	6.01E-01	8.53E-01	GMFB	glia maturation factor, beta	chr14q22.2	202544_at	NM_004124
1.96	2.04	0.08	6.01E-01	8.53E-01	SSPN	Sarcospan (Kras oncogene-associated gene)	chr12p11.2	1561517_at	NM_005086
2.48	2.55	0.07	6.01E-01	8.53E-01	---	---	---	244722_at	---
6.31	6.56	0.25	6.01E-01	8.53E-01	PUM2	pumilio homolog 2 (Drosophila)	chr2p22-p21	201493_s_at	NM_015317
3.52	3.62	0.10	6.01E-01	8.53E-01	---	---	---	1558348_at	---
2.34	2.42	0.08	6.01E-01	8.53E-01	PSG6	pregnancy specific beta-1-glycoprotein 6	chr19q13.2	239910_at	NM_001031850 /// NM_002782
2.96	3.03	0.07	6.01E-01	8.53E-01	C17orf56	chromosome 17 open reading frame 56	chr17q25.3	238980_x_at	NM_144679
2.35	2.42	0.07	6.01E-01	8.53E-01	STK31	serine/threonine kinase 31	chr7p15.3	223883_s_at	NM_001122833 /// NM_031414 /// NM_032944
2.82	2.89	0.07	6.01E-01	8.53E-01	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	chr12q12	229751_s_at	NM_001098614 /// NM_001098615 /// NM_031292
2.12	2.19	0.06	6.01E-01	8.53E-01	RAD9B	RAD9 homolog B (S. cerevisiae)	chr12q24.11	1553285_s_at	NM_152442
2.18	2.24	0.06	6.01E-01	8.53E-01	---	---	---	229049_at	---
6.33	6.49	0.15	6.01E-01	8.53E-01	TP53TG1	TP53 target 1 (non-protein coding)	chr7q21.1	210886_x_at	NM_007233 /// NR_015381
4.34	4.43	0.10	6.01E-01	8.53E-01	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	chr6p21.3	230297_x_at	NM_001130066 /// NM_006772
2.28	2.34	0.07	6.02E-01	8.54E-01	DNAH7	dynein, axonemal, heavy chain 7	chr2q32.3	234727_at	NM_018897
1.98	2.04	0.06	6.02E-01	8.54E-01	SLC10A7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	chr4q31.22	224126_at	NM_001029998 /// NM_032128
1.91	1.99	0.08	6.02E-01	8.54E-01	RP4-662A9.2	hypothetical protein MGC34034	chr6q23.2	1552899_at	---
2.35	2.42	0.07	6.02E-01	8.54E-01	PI3	peptidase inhibitor 3, skin-derived (SKALP)	chr20q12-q13	41469_at	NM_002638
6.98	7.18	0.20	6.02E-01	8.54E-01	C6orf62	chromosome 6 open reading frame 62	chr6p22.2	208809_s_at	NM_030939
3.61	3.70	0.09	6.02E-01	8.54E-01	KIAA1609	KIAA1609	chr16q24.1	222261_at	NM_020947
4.36	4.45	0.09	6.02E-01	8.54E-01	PLD6	phospholipase D family, member 6	chr17p11.2	227037_at	NM_178836

2.32	2.40	0.08	6.02E-01	8.54E-01	---	---	---	243253_at	---
2.03	2.10	0.07	6.02E-01	8.54E-01	TRPM1	Transient receptor potential cation channel, subfamily M, member 1	chr15q13-q14	214410_at	NM_002420
2.73	2.80	0.07	6.02E-01	8.54E-01	FAM71F1	family with sequence similarity 71, member F1	chr7q32.1	236214_at	NM_032599
2.16	2.23	0.07	6.02E-01	8.54E-01	ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2	---	1552532_a_at	NM_001039362 /// NM_144583
3.10	3.17	0.07	6.02E-01	8.54E-01	LOC100128025	hypothetical protein LOC100128025	chr3q25.1	228629_s_at	XM_001717448 /// XM_001718324 /// XM_001718515
1.97	2.03	0.06	6.02E-01	8.54E-01	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	chr3p22	207603_at	NM_003615
3.19	3.35	0.16	6.02E-01	8.54E-01	CLASP2	cytoplasmic linker associated protein 2	chr3p22.3	1558759_s_at	NM_015097
3.29	3.37	0.08	6.02E-01	8.54E-01	---	---	---	242205_at	---
4.19	4.50	0.31	6.02E-01	8.54E-01	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	chr3q26.3	222678_s_at	NM_020640
5.69	5.86	0.17	6.02E-01	8.54E-01	MCM6	minichromosome maintenance complex component 6	chr2q21	201930_at	NM_005915
2.46	2.54	0.08	6.02E-01	8.54E-01	FLJ34521	hypothetical protein LOC646383	chr11q24.3	1562217_at	NM_001039787
2.67	2.73	0.06	6.02E-01	8.54E-01	IMPAD1	Inositol monophosphatase domain containing 1	chr8q12.1	227774_s_at	NM_017813
2.26	2.32	0.05	6.02E-01	8.54E-01	---	---	---	239089_at	---
3.42	3.56	0.13	6.03E-01	8.54E-01	---	---	---	1561640_at	---
6.90	6.99	0.10	6.03E-01	8.54E-01	CISD2	CDGSH iron sulfur domain 2	chr4q24	226689_at	NM_001008388
3.18	3.27	0.09	6.03E-01	8.54E-01	---	---	---	1557433_at	---
2.63	2.75	0.12	6.03E-01	8.54E-01	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	chr17p13	215114_at	NM_015670
2.12	2.19	0.07	6.03E-01	8.54E-01	---	---	---	1562688_at	---
2.64	2.74	0.10	6.03E-01	8.54E-01	CLIC6	chloride intracellular channel 6	chr21q22.12	227742_at	NM_053277
2.88	2.97	0.09	6.03E-01	8.54E-01	CSNK2A1	Casein kinase 2, alpha 1 polypeptide	chr20p13	229212_at	NM_001895 /// NM_177559 /// NM_177560
2.44	2.50	0.05	6.03E-01	8.54E-01	---	---	---	241195_at	---
3.17	3.42	0.25	6.03E-01	8.54E-01	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	chr1p22-p21	1554878_a_at	NM_001122674 /// NM_002858
6.43	6.65	0.22	6.03E-01	8.54E-01	---	---	---	230233_at	---
5.66	5.76	0.10	6.03E-01	8.54E-01	IGSF8	immunoglobulin superfamily, member 8	chr1q23.1	225025_at	NM_052868
3.49	3.57	0.08	6.03E-01	8.54E-01	---	---	---	233817_at	---
4.51	4.58	0.07	6.03E-01	8.54E-01	---	---	---	233103_at	---
2.24	2.37	0.13	6.03E-01	8.54E-01	---	---	---	1568365_at	---
2.46	2.56	0.10	6.03E-01	8.54E-01	GPR180	G protein-coupled receptor 180	chr13q32.1	232912_at	NM_180989
2.35	2.43	0.08	6.03E-01	8.54E-01	ZNF397 /// ZNF397OS	zinc finger protein 397 /// zinc finger protein 397 opposite strand	chr18q12.2	229133_s_at	NM_001112734 /// NM_032347 /// XM_001720071 /// XM_001722380 /// XM_001723235
2.19	2.28	0.09	6.03E-01	8.54E-01	---	---	---	233886_at	---
2.19	2.28	0.09	6.03E-01	8.54E-01	---	---	---	1561512_at	---
2.08	2.15	0.07	6.03E-01	8.54E-01	---	---	---	241566_at	---
2.51	2.61	0.10	6.03E-01	8.54E-01	---	---	---	238894_at	---
2.86	2.95	0.09	6.03E-01	8.54E-01	LOC100130264	similar to hCG2038397	chr20p11.23	1564444_at	XM_001717962 /// XM_001718300 /// XM_001718565
2.12	2.19	0.07	6.03E-01	8.54E-01	MBNL1	muscleblind-like (Drosophila)	chr3q25	215663_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297

2.39	2.46	0.07	6.03E-01	8.54E-01	OPRM1	opioid receptor, mu 1	chr6q24-q25	211359_s_at	NM_000914 /// NM_001008503 /// NM_001008504 /// NM_001008505
5.16	5.27	0.11	6.03E-01	8.54E-01	WDR68	WD repeat domain 68	chr17q23.3	221745_at	NM_005828
3.46	3.71	0.25	6.03E-01	8.55E-01	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	chr1q32.1	223661_at	NM_022731
4.62	4.85	0.24	6.04E-01	8.55E-01	ZNF131	zinc finger protein 131	chr5p12-p11	214741_at	NM_003432
3.34	3.53	0.19	6.04E-01	8.55E-01	GOLIM4	golgi integral membrane protein 4	chr3q26.2	204324_s_at	NM_014498
4.01	4.12	0.10	6.04E-01	8.55E-01	DRP2	dystrophin related protein 2	chrXq22	207648_at	NM_001939
3.35	3.45	0.09	6.04E-01	8.55E-01	KLK15	kallikrein-related peptidase 15	chr19q13.41	234966_at	NM_017509 /// NM_138563 /// NM_138564
2.39	2.47	0.08	6.04E-01	8.55E-01	FLJ37453	hypothetical protein LOC729614	chr1p36.21	227596_at	XR_042511 /// XR_042512 /// XR_042513
2.31	2.38	0.07	6.04E-01	8.55E-01	CTGLF2	Centaurin, gamma-like family, member 2	chr10q22.2	1565621_at	XM_001722569 /// XM_001722765
5.36	5.77	0.41	6.04E-01	8.55E-01	---	---	---	233276_at	---
3.55	3.68	0.13	6.04E-01	8.55E-01	STH	saitohin	chr17q21.1	1555752_at	NM_001007532
8.89	9.00	0.12	6.04E-01	8.55E-01	STOM	stomatin	chr9q34.1	201061_s_at	NM_004099 /// NM_198194
2.66	2.76	0.10	6.04E-01	8.55E-01	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	chrXq13.1	230597_at	NM_001048164 /// NM_032803
2.24	2.31	0.07	6.04E-01	8.55E-01	---	---	---	1564130_x_at	---
1.96	2.01	0.06	6.04E-01	8.55E-01	---	---	---	235336_at	---
5.92	6.06	0.13	6.04E-01	8.55E-01	WDR70	WD repeat domain 70	chr5p13.2	219193_at	NM_018034
2.31	2.41	0.10	6.04E-01	8.55E-01	---	---	---	236002_at	---
1.90	1.96	0.07	6.04E-01	8.55E-01	---	---	---	1557437_a_at	---
1.94	1.99	0.05	6.04E-01	8.55E-01	STX19	syntaxin 19	chr3q11	1555173_at	NM_001001850
7.92	8.05	0.13	6.04E-01	8.55E-01	TM9SF3	transmembrane 9 superfamily member 3	chr10q24.1	217758_s_at	NM_020123
6.55	6.82	0.27	6.04E-01	8.55E-01	FBN2	fibrillin 2	chr5q23-q31	203184_at	NM_001999
4.89	4.98	0.09	6.04E-01	8.55E-01	ODF3L2	outer dense fiber of sperm tails 3-like 2	chr19p13.3	237620_at	NM_182577
2.22	2.28	0.05	6.04E-01	8.55E-01	---	---	---	244436_at	---
5.61	5.71	0.10	6.04E-01	8.55E-01	CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	chr11q13	209850_s_at	NM_006779
3.76	3.85	0.09	6.04E-01	8.55E-01	---	---	---	1554972_at	---
4.83	4.92	0.09	6.04E-01	8.55E-01	---	---	---	233794_at	---
2.72	2.80	0.08	6.04E-01	8.55E-01	---	---	---	1562934_at	---
4.71	5.04	0.33	6.04E-01	8.55E-01	---	---	---	229704_at	---
2.45	2.52	0.07	6.04E-01	8.55E-01	MBTD1	mbt domain containing 1	chr17q21.33	207115_x_at	NM_017643
2.10	2.19	0.08	6.05E-01	8.55E-01	---	---	---	233635_at	---
2.17	2.23	0.06	6.05E-01	8.55E-01	---	---	---	237381_at	---
3.49	3.59	0.10	6.05E-01	8.55E-01	WDR33	WD repeat domain 33	chr2q14.3	223146_at	NM_001006622 /// NM_001006623 /// NM_018383
2.00	2.06	0.06	6.05E-01	8.55E-01	---	---	---	1560990_a_at	---
2.76	2.85	0.09	6.05E-01	8.55E-01	---	---	---	1561893_at	---
2.02	2.08	0.06	6.05E-01	8.55E-01	---	---	---	240020_at	---
2.89	2.99	0.10	6.05E-01	8.55E-01	LMO7	LIM domain 7	chr13q22.2	242722_at	NM_005358
2.10	2.18	0.08	6.05E-01	8.55E-01	F2RL2	coagulation factor II (thrombin) receptor-like 2	chr5q13	206795_at	NM_004101
2.48	2.56	0.08	6.05E-01	8.55E-01	FABP6	fatty acid binding protein 6, ileal	chr5q33.3-q34	1566123_at	NM_001040442 /// NM_001130958 /// NM_001445
7.27	7.50	0.23	6.05E-01	8.55E-01	MRFAP1L1	Morf4 family associated protein 1-like 1	chr4p16.1	212199_at	NM_152301 /// NM_203462
2.92	3.07	0.15	6.05E-01	8.55E-01	OSTM1	osteopetrosis associated transmembrane protein 1	chr6q21	235197_s_at	NM_014028
3.60	3.74	0.14	6.05E-01	8.55E-01	SLFN5	schlafen family member 5	chr17q12	243999_at	NM_144975
3.15	3.25	0.10	6.05E-01	8.55E-01	SNAPC5	small nuclear RNA activating complex, polypeptide 5, 19kDa	chr15q22.31	214592_s_at	NM_006049

3.52	3.62	0.10	6.05E-01	8.55E-01	TP63	tumor protein p63	chr3q28	211834_s_at	NM_001114978 /// NM_001114979 /// NM_001114980 /// NM_001114981 /// NM_001114982 /// NM_003722																				
5.66	5.75	0.09	6.05E-01	8.55E-01	LOC728344	similar to hCG1978918	chr6p25.2	216532_x_at	XR_015265 /// XR_018424 /// XR_037950																				
2.91	3.00	0.08	6.05E-01	8.55E-01	ERAP2	endoplasmic reticulum aminopeptidase 2	chr5q15	235104_at	NM_001130140 /// NM_022350																				
2.70	2.77	0.08	6.05E-01	8.55E-01	MYLK	myosin light chain kinase	chr3q21	1568770_at	NM_053025 /// NM_053026 /// NM_053027 /// NM_053028 /// NM_053031 /// NM_053032																				
2.23	2.30	0.07	6.05E-01	8.55E-01	---	---	---	233240_at	---																				
1.92	1.98	0.06	6.05E-01	8.55E-01	MARVELD2	MARVEL domain containing 2	chr5q13.2	235955_at	NM_001038603 /// NM_144724																				
2.42	2.52	0.10	6.05E-01	8.55E-01	ANKFY1	Ankyrin repeat and FYVE domain containing 1	chr17p13.3	1562495_at	NM_016376 /// NM_020740																				
2.20	2.28	0.08	6.05E-01	8.55E-01	---	---	---	1565823_at	---																				
3.04	3.14	0.10	6.05E-01	8.55E-01	SNIP	SNAP25-interacting protein	chr17q12	236838_at	NM_025248																				
4.44	4.76	0.32	6.06E-01	8.56E-01	NNT	nicotinamide nucleotide transhydrogenase	chr5p13.1-cen	202784_s_at	NM_012343 /// NM_182977																				
2.16	2.25	0.09	6.06E-01	8.56E-01	---	---	---	242464_at	---																				
2.12	2.17	0.05	6.06E-01	8.56E-01	C2orf58	chromosome 2 open reading frame 58	chr2p22.2	1553829_at	XR_040334 /// XR_040335 /// XR_040336																				
2.43	2.51	0.08	6.06E-01	8.56E-01	TTTY13	testis-specific transcript, Y-linked 13	chrYq11.223	224292_at	NR_001537																				
2.21	2.28	0.07	6.06E-01	8.56E-01	---	---	---	240361_at	---																				
2.17	2.24	0.07	6.06E-01	8.56E-01	---	---	---	1569525_s_at	---																				
2.60	2.66	0.07	6.06E-01	8.56E-01	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	chr19q13.12	207116_s_at	NM_014364																				
3.48	3.59	0.11	6.06E-01	8.56E-01	GAST	gastrin	chr17q21	208138_at	NM_000805																				
5.46	5.89	0.43	6.06E-01	8.56E-01	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	chrXp11.3-p11.23	201211_s_at	NM_001356																				
4.10	4.31	0.21	6.06E-01	8.56E-01	ADCY3	adenylate cyclase 3	chr2p23.3	209321_s_at	NM_004036																				
5.96	6.07	0.11	6.06E-01	8.56E-01	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	chr6q21	212897_at	NM_015076																				
2.57	2.64	0.07	6.06E-01	8.56E-01	LEKR1	leucine, glutamate and lysine rich 1	chr3q25.31-q25.32	1564653_s_at	NM_001004316 /// XM_001724269 /// XM_001725663 /// XM_001725985																				
2.35	2.42	0.07	6.06E-01	8.56E-01	---	---	---	241105_at	---																				
1.93	2.00	0.06	6.06E-01	8.56E-01	GPR115	G protein-coupled receptor 115	chr6p12.3	237690_at	NM_153838																				
2.33	2.40	0.06	6.06E-01	8.56E-01	---	---	---	1566608_at	---																				
4.57	4.70	0.13	6.06E-01	8.56E-01	---	---	---	217643_x_at	---																				
5.87	6.15	0.28	6.07E-01	8.56E-01	SNX10	sorting nexin 10	chr7p15.2	218404_at	NM_013322																				
3.21	3.30	0.10	6.07E-01	8.56E-01	UBE3B	ubiquitin protein ligase E3B	chr12q24.11	232301_at	NM_130466 /// NM_183415																				
1.98	2.06	0.08	6.07E-01	8.56E-01	CAPZA3	capping protein (actin filament) muscle Z-line, alpha 3	chr12p12.3	236888_at	NM_033328																				
4.98	5.04	0.06	6.07E-01	8.56E-01	LZIC	leucine zipper and CTNNBIP1 domain containing	chr1p36.22	226081_at	NM_032368																				
3.52	3.62	0.10	6.07E-01	8.56E-01	PIWIL2	piwi-like 2 (Drosophila)	chr8p21.3	217421_at	NM_018068																				
2.00	2.07	0.07	6.07E-01	8.56E-01	SPATA22	spermatogenesis associated 22	chr17p13.3	1558668_s_at	NM_032598																				
1.87	1.93	0.06	6.07E-01	8.56E-01	---	---	---	1563461_at	---																				
2.07	2.14	0.07	6.07E-01	8.56E-01	---	---	---	216189_at	---																				

4.87	5.07	0.20	6.07E-01	8.56E-01	ZNF226	zinc finger protein 226	chr19q13.2	233461_x_at	NM_001032372 /// NM_001032373 /// NM_001032374 /// NM_001032375 /// NM_015919
2.24	2.32	0.08	6.07E-01	8.56E-01	CCDC112	coiled-coil domain containing 112	chr5q22.3	235208_at	NM_001040440 /// NM_152549
4.51	4.60	0.09	6.07E-01	8.56E-01	SLC45A3	solute carrier family 45, member 3	chr1q32.1	228696_at	NM_033102
4.83	4.99	0.17	6.07E-01	8.56E-01	---	---	---	235680_at	---
2.46	2.53	0.06	6.07E-01	8.56E-01	---	---	---	216856_s_at	---
6.23	6.57	0.34	6.07E-01	8.56E-01	DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	chr17q23.1	222574_s_at	NM_024612
3.41	3.53	0.12	6.07E-01	8.56E-01	ALPI	alkaline phosphatase, intestinal	chr2q37.1	207140_at	NM_001631
3.37	3.47	0.10	6.07E-01	8.56E-01	PRDM15	PR domain containing 15	chr21q22.3	236061_at	NM_001040424 /// NM_022115
2.23	2.31	0.09	6.07E-01	8.56E-01	HIST1H3J	Histone cluster 1, H3j	chr6p22-p21.3	214646_at	NM_003535
2.23	2.31	0.08	6.07E-01	8.56E-01	---	---	---	244845_at	---
3.06	3.15	0.09	6.07E-01	8.56E-01	---	---	---	237970_at	---
2.11	2.17	0.07	6.07E-01	8.56E-01	---	---	---	242173_at	---
5.50	5.63	0.13	6.07E-01	8.56E-01	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	chr11q13.4	203756_at	NM_014786
8.92	9.17	0.26	6.08E-01	8.57E-01	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	chr1q42	200662_s_at	NM_014765
6.71	6.87	0.16	6.08E-01	8.57E-01	GOLGA7	golgi autoantigen, golgin subfamily a, 7	chr8p11.21	1554167_a_at	NM_001002296 /// NM_016099
2.18	2.25	0.06	6.08E-01	8.57E-01	---	---	---	1570491_at	---
2.49	2.56	0.07	6.08E-01	8.57E-01	---	---	---	243819_at	---
2.61	2.71	0.10	6.08E-01	8.57E-01	---	---	---	229952_at	---
4.87	4.97	0.10	6.08E-01	8.57E-01	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	chr19q13.3	1555620_a_at	NM_000960
2.46	2.56	0.10	6.08E-01	8.57E-01	---	---	---	227244_s_at	---
1.83	1.91	0.08	6.08E-01	8.57E-01	LOC283454	hypothetical protein LOC283454	chr12q24.23	1566734_at	---
7.26	7.40	0.15	6.08E-01	8.57E-01	SCP2	sterol carrier protein 2	chr1p32	211733_x_at	NM_001007098 /// NM_001007099 /// NM_001007100 /// NM_001007250 /// NM_002979
3.77	3.90	0.13	6.08E-01	8.57E-01	CNTFR	ciliary neurotrophic factor receptor	chr9p13	205723_at	NM_001842 /// NM_147164
2.18	2.25	0.07	6.08E-01	8.57E-01	ARMC8	Armadillo repeat containing 8	chr3q22.3	244528_at	NM_014154 /// NM_015396 /// NM_213654
2.61	2.72	0.11	6.08E-01	8.57E-01	---	---	---	1559354_a_at	---
2.44	2.51	0.07	6.08E-01	8.57E-01	---	---	---	1559678_s_at	---
2.82	2.91	0.08	6.08E-01	8.57E-01	DKFZP434B2016	similar to hypothetical protein LOC284701	chr16q24.3	231886_at	XM_932064 /// XM_932068 /// XM_932075
2.79	2.87	0.08	6.08E-01	8.57E-01	---	---	---	236683_at	---
4.27	4.42	0.15	6.08E-01	8.57E-01	ARHGAP20	Rho GTPase activating protein 20	chr11q22.3-q23.1	228368_at	NM_020809
2.26	2.33	0.07	6.08E-01	8.57E-01	---	---	---	230501_at	---
3.10	3.32	0.22	6.08E-01	8.57E-01	---	---	---	239945_at	---
5.81	5.96	0.15	6.08E-01	8.57E-01	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	chr2q36	203192_at	NM_005689
2.45	2.53	0.08	6.08E-01	8.57E-01	CCDC136	coiled-coil domain containing 136	chr7q33	232989_s_at	NM_022742
2.08	2.14	0.06	6.08E-01	8.57E-01	---	---	---	234616_at	---
2.53	2.60	0.06	6.09E-01	8.57E-01	---	---	---	231450_at	---
2.64	2.72	0.08	6.09E-01	8.57E-01	---	---	---	239653_at	---
5.21	5.46	0.25	6.09E-01	8.57E-01	---	---	---	239082_at	---
4.31	4.51	0.21	6.09E-01	8.57E-01	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	chr19q13.2	232078_at	NM_001042724 /// NM_002856
3.50	3.60	0.09	6.09E-01	8.57E-01	---	---	---	233256_at	---
2.10	2.19	0.09	6.09E-01	8.57E-01	RHBDL2	rhomboid, veinlet-like 2 (Drosophila)	chr1p34.3	1552502_s_at	NM_017821
4.21	4.29	0.08	6.09E-01	8.57E-01	GUSB	Glucuronidase, beta	chr7q21.11	230125_at	NM_000181
1.96	2.02	0.06	6.09E-01	8.57E-01	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	chr21q22.11	237551_at	NM_014825

1.83	1.89	0.06	6.09E-01	8.57E-01	HMGA2	high mobility group AT-hook 2	chr12q15	1568287_at	NM_003483 /// NM_003484
1.92	1.97	0.05	6.09E-01	8.57E-01	---	---	---	237992_at	---
3.37	3.47	0.10	6.09E-01	8.57E-01	AAK1	AP2 associated kinase 1	chr2p14	211186_s_at	NM_014911
2.04	2.12	0.08	6.09E-01	8.57E-01	---	---	---	1567181_x_at	---
2.10	2.18	0.07	6.09E-01	8.57E-01	SMR3B	submaxillary gland androgen regulated protein 3B	chr4q13.3	207441_at	NM_006685
2.69	2.80	0.11	6.09E-01	8.57E-01	---	---	---	235441_at	---
3.58	3.75	0.17	6.09E-01	8.57E-01	---	---	---	236583_at	---
2.34	2.41	0.08	6.09E-01	8.57E-01	CD80	CD80 molecule	chr3q13.3-q21	1554519_at	NM_005191
2.23	2.32	0.09	6.09E-01	8.57E-01	PRLR	prolactin receptor	chr5p14-p13	243755_at	NM_000949
2.16	2.22	0.06	6.09E-01	8.57E-01	---	---	---	239046_at	---
5.16	5.39	0.23	6.09E-01	8.58E-01	PKN2	protein kinase N2	chr1p22.2	212628_at	NM_006256
2.23	2.38	0.16	6.09E-01	8.58E-01	NOX5 /// SPESP1	NADPH oxidase, EF-hand calcium binding domain 5 /// sperm equatorial segment protein 1	chr15q23	229352_at	NM_024505 /// NM_145658
1.98	2.05	0.08	6.09E-01	8.58E-01	TRIM2	tripartite motif-containing 2	chr4q31.3	243945_at	NM_001130067 /// NM_015271
2.80	2.90	0.10	6.09E-01	8.58E-01	RGS11	regulator of G-protein signaling 11	chr16p13.3	206107_at	NM_003834 /// NM_183337
2.28	2.35	0.07	6.09E-01	8.58E-01	---	---	---	1558830_at	---
7.35	7.54	0.18	6.10E-01	8.58E-01	YIPF5	Yip1 domain family, member 5	chr5q32	224934_at	NM_001024947 /// NM_030799
5.32	5.49	0.17	6.10E-01	8.58E-01	---	---	---	233369_at	---
3.73	3.87	0.14	6.10E-01	8.58E-01	---	---	---	244592_at	---
3.41	3.50	0.09	6.10E-01	8.58E-01	GPSM1	G-protein signaling modulator 1 (AGS3-like, C. elegans)	chr9q34.3	1554259_at	NM_015597
3.72	3.81	0.08	6.10E-01	8.58E-01	SGSM1	small G protein signaling modulator 1	chr22q11.23	1562239_at	NM_001039948 /// NM_001098497 /// NM_001098498 /// NM_133454
2.53	2.60	0.07	6.10E-01	8.58E-01	GP6	glycoprotein VI (platelet)	chr19q13.4	220336_s_at	NM_001083899 /// NM_016363
3.76	3.86	0.09	6.10E-01	8.58E-01	CIP29	cytokine induced protein 29 kDa	chr12q13.2	229069_at	NM_033082
2.50	2.58	0.08	6.10E-01	8.58E-01	---	---	---	238107_at	---
2.49	2.58	0.09	6.10E-01	8.58E-01	SEC16B	SEC16 homolog B (S. cerevisiae)	chr1q25.2	1552880_at	NM_033127
1.84	1.91	0.07	6.10E-01	8.58E-01	CHML	choroideremia-like (Rab escort protein 2)	chr1q42-qter	1565951_s_at	NM_001821
2.08	2.14	0.06	6.10E-01	8.58E-01	C4orf39	chromosome 4 open reading frame 39	chr4q32.3	1553710_at	NM_153027
2.11	2.17	0.06	6.10E-01	8.58E-01	---	---	---	237933_at	---
2.23	2.29	0.06	6.10E-01	8.58E-01	AKAP12	A kinase (PRKA) anchor protein 12	chr6q24-q25	1555395_at	NM_005100 /// NM_144497
2.74	2.85	0.10	6.10E-01	8.58E-01	---	---	---	1560390_s_at	---
2.45	2.53	0.08	6.10E-01	8.58E-01	---	---	---	237979_at	---
2.17	2.24	0.07	6.10E-01	8.58E-01	---	---	---	1559134_a_at	---
2.31	2.39	0.07	6.10E-01	8.58E-01	EHF	ets homologous factor	chr11p12	232360_at	NM_012153
2.17	2.24	0.07	6.10E-01	8.58E-01	---	---	---	244568_at	---
2.16	2.22	0.06	6.10E-01	8.58E-01	---	---	---	216287_at	---
3.43	3.53	0.10	6.10E-01	8.58E-01	SAMD4A	sterile alpha motif domain containing 4A	chr14q22.2	215120_s_at	NM_015589
2.54	2.64	0.10	6.10E-01	8.58E-01	---	---	---	1556003_a_at	---
2.62	2.71	0.09	6.10E-01	8.58E-01	FLJ32575	hypothetical protein FLJ32575	chr22q11.21	1553658_at	XR_040381 /// XR_040382 /// XR_040383
3.25	3.34	0.09	6.10E-01	8.58E-01	DIO3OS	DIO3 opposite strand (non-protein coding)	chr14q32.31	1559326_at	NR_002770
2.89	2.96	0.08	6.10E-01	8.58E-01	RBM47	RNA binding motif protein 47	chr4p13-p12	229421_s_at	NM_001098634 /// NM_019027
1.89	1.95	0.06	6.10E-01	8.58E-01	LOC100131298	PRO1095	chr22q13.2	1570308_at	XM_001724044 /// XM_001725577 /// XM_001726814
4.00	4.10	0.10	6.10E-01	8.58E-01	MATN4	matrilin 4	chr20q13.1-q13.2	207123_s_at	NM_003833 /// NM_030590 /// NM_030592
3.99	4.21	0.22	6.10E-01	8.58E-01	ZNF322B	zinc finger protein 322B	chr9q22.33	219376_at	NM_199005
2.14	2.25	0.12	6.11E-01	8.58E-01	---	---	---	1562608_at	---
2.73	2.82	0.09	6.11E-01	8.58E-01	DNMT3L	DNA (cytosine-5-)-methyltransferase 3-like	chr21q22.3	220139_at	NM_013369 /// NM_175867
3.14	3.21	0.07	6.11E-01	8.58E-01	SNX20	sorting nexin 20	chr16q12.1	1563641_a_at	NM_182854
2.20	2.27	0.07	6.11E-01	8.58E-01	---	---	---	1562168_at	---

2.45	2.53	0.08	6.11E-01	8.58E-01	---	---	---	215896_at	---
2.45	2.54	0.08	6.11E-01	8.58E-01	DKK4	dickkopf homolog 4 (Xenopus laevis)	chr8p11.2-p11.1	206619_at	NM_014420
4.87	4.95	0.08	6.11E-01	8.58E-01	---	---	---	1557712_x_at	---
2.43	2.55	0.12	6.11E-01	8.59E-01	LRRC46	leucine rich repeat containing 46	chr17q21.32	230601_s_at	NM_033413
4.44	4.57	0.13	6.11E-01	8.59E-01	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	chr1q21.1	1558027_s_at	NM_005399
2.52	2.61	0.10	6.11E-01	8.59E-01	---	---	---	231444_at	---
3.08	3.17	0.09	6.11E-01	8.59E-01	TRAM2	translocation associated membrane protein 2	chr6p21.1-p12	1554383_a_at	NM_012288
2.69	2.76	0.07	6.11E-01	8.59E-01	C9orf117	chromosome 9 open reading frame 117	chr9q34.11	231172_at	NM_001012502
8.52	8.59	0.07	6.11E-01	8.59E-01	LMNA	lamin A/C	chr1q21.2-q21.3	212086_x_at	NM_005572 /// NM_170707 /// NM_170708
2.13	2.20	0.07	6.11E-01	8.59E-01	---	---	---	243886_at	---
2.89	2.97	0.07	6.11E-01	8.59E-01	---	---	---	242016_at	---
3.23	3.30	0.07	6.11E-01	8.59E-01	RCHY1	ring finger and CHY zinc finger domain containing 1	chr4q21.1	212743_at	NM_001008925 /// NM_001009922 /// NM_015436
2.47	2.55	0.08	6.11E-01	8.59E-01	LDB2	LIM domain binding 2	chr4p16	242360_at	NM_001130834 /// NM_001290
2.11	2.18	0.07	6.11E-01	8.59E-01	---	---	---	240059_at	---
4.35	4.46	0.11	6.11E-01	8.59E-01	---	---	---	235015_at	---
2.10	2.18	0.08	6.11E-01	8.59E-01	ZDHHC13	Zinc finger, DHHC-type containing 13	chr11p15.1	243250_at	NM_001001483 /// NM_019028
2.11	2.19	0.08	6.11E-01	8.59E-01	PKD1L2	polycystic kidney disease 1-like 2	chr16q23.2	244444_at	NM_001076780 /// NM_052892
2.26	2.34	0.08	6.11E-01	8.59E-01	PTPLAD2	Protein tyrosine phosphatase-like A domain containing 2	chr9p21.3	236939_at	NM_001010915
2.15	2.22	0.07	6.11E-01	8.59E-01	KIAA1211	KIAA1211 protein	chr4q12	1564828_at	NM_020722
2.39	2.44	0.06	6.11E-01	8.59E-01	LIPC	lipase, hepatic	chr15q21-q23	206606_at	NM_000236
2.22	2.27	0.06	6.11E-01	8.59E-01	LOC285000	hypothetical protein LOC285000	chr2q12.2	240428_at	---
6.81	6.93	0.12	6.12E-01	8.59E-01	RALBP1	ralA binding protein 1	chr18p11.3	202845_s_at	NM_006788
7.71	7.85	0.14	6.12E-01	8.59E-01	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	chr16q22-q23	209348_s_at	NM_001031804 /// NM_005360
7.07	7.16	0.09	6.12E-01	8.59E-01	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	chr20q13.33	216088_s_at	NM_002792
2.68	2.73	0.05	6.12E-01	8.59E-01	---	---	---	239429_at	---
4.19	4.34	0.15	6.12E-01	8.59E-01	FMO5	flavin containing monooxygenase 5	chr1q21.1	205776_at	NM_001461
2.19	2.27	0.08	6.12E-01	8.59E-01	---	---	---	1563379_at	---
2.40	2.47	0.07	6.12E-01	8.59E-01	LRP12	low density lipoprotein-related protein 12	chr8q22.2-q23.1	220254_at	NM_013437
2.34	2.40	0.07	6.12E-01	8.59E-01	ASPH	aspartate beta-hydroxylase	chr8q12.1	207284_s_at	NM_004318 /// NM_020164 /// NM_032466 /// NM_032467 /// NM_032468
2.24	2.36	0.12	6.12E-01	8.59E-01	---	---	---	243341_at	---
6.35	6.61	0.27	6.12E-01	8.59E-01	MED1	mediator complex subunit 1	chr17q12-q21.1	203497_at	NM_004774
2.27	2.35	0.08	6.12E-01	8.59E-01	---	---	---	239156_at	---
2.68	2.75	0.07	6.12E-01	8.59E-01	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	chr11q12.3	66053_at	NM_001079559
2.11	2.18	0.07	6.12E-01	8.59E-01	---	---	---	224238_at	---
2.10	2.16	0.06	6.12E-01	8.59E-01	RNF213	ring finger protein 213	chr17q25.3	1569078_at	NM_020914
3.03	3.13	0.10	6.12E-01	8.59E-01	FLII /// LLGL1	flightless I homolog (Drosophila) /// lethal giant larvae homolog 1 (Drosophila)	chr17p11.2	227302_s_at	NM_002018 /// NM_004140
2.65	2.72	0.07	6.12E-01	8.59E-01	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	chr7q22.1	239699_s_at	NR_003613
7.80	8.01	0.22	6.12E-01	8.59E-01	MEF2C	myocyte enhancer factor 2C	chr5q14	209200_at	NM_001131005 /// NM_002397
4.67	4.82	0.14	6.12E-01	8.59E-01	RHOBTB3	Rho-related BTB domain containing 3	chr5q15	240111_at	NM_014899
2.59	2.68	0.09	6.12E-01	8.59E-01	TMEM125	transmembrane protein 125	chr1p34.2	225822_at	NM_144626
1.97	2.04	0.08	6.12E-01	8.59E-01	OPA1	optic atrophy 1 (autosomal dominant)	chr3q28-q29|3q28-q29	241027_at	NM_015560 /// NM_130831 /// NM_130832 /// NM_130833 /// NM_130834 /// NM_130835 /// NM_130836 /// NM_130837
3.13	3.19	0.06	6.12E-01	8.59E-01	PGC	progastricsin (pepsinogen C)	chr6p21.3-p21.1	1555236_a_at	NM_002630
2.10	2.17	0.06	6.12E-01	8.59E-01	---	---	---	240681_at	---

6.32	6.52	0.20	6.12E-01	8.59E-01	PLSCR1	phospholipid scramblase 1	chr3q23	202446_s_at	NM_021105
4.14	4.24	0.10	6.13E-01	8.59E-01	FAM95B1 /// LOC100132340 /// LOC100133036 /// LOC644587 /// LOC90499 /// RP11-146D12.4	family with sequence similarity 95, member B1 /// similar to hCG1793603 /// hypothetical protein LOC100133036 /// similar to hCG1794531 /// hypothetical protein LOC90499 /// family with sequence similarity 95, member B1	chr2q11.1 /// chr9p11.2	239590_x_at	XM_001713909 /// XM_001714189 /// XM_001716755 /// XM_001716764 /// XM_001732879 /// XR_036896 /// XR_042126 /// XR_042127
2.30	2.40	0.09	6.13E-01	8.59E-01	---	---	---	241335_at	---
2.19	2.26	0.08	6.13E-01	8.59E-01	CAPSL	calcyphosine-like	chr5p13.2	236085_at	NM_001042625 /// NM_144647
4.05	4.11	0.07	6.13E-01	8.59E-01	---	---	---	1556327_a_at	---
2.37	2.44	0.07	6.13E-01	8.59E-01	---	---	---	243465_at	---
1.95	2.02	0.07	6.13E-01	8.59E-01	---	---	---	1568661_at	---
3.66	3.80	0.14	6.13E-01	8.59E-01	DOCK5	dedicator of cytokinesis 5	chr8p21.2	1570078_a_at	NM_024940
2.35	2.44	0.09	6.13E-01	8.59E-01	---	---	---	243965_at	---
2.40	2.48	0.08	6.13E-01	8.59E-01	---	---	---	240225_at	---
1.98	2.05	0.07	6.13E-01	8.59E-01	SFTA3	surfactant associated 3	chr14q13.3	228979_at	NM_001101341
4.35	4.45	0.10	6.13E-01	8.59E-01	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	chr1q31	226733_at	NM_001018053 /// NM_006212
1.87	1.93	0.07	6.13E-01	8.59E-01	---	---	---	1561450_at	---
3.24	3.56	0.32	6.13E-01	8.59E-01	PON1	paraoxonase 1	chr7q21.3	206345_s_at	NM_000446
4.47	4.68	0.21	6.13E-01	8.59E-01	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	chr3q29	202165_at	NM_006241
2.67	2.75	0.08	6.13E-01	8.59E-01	LOC283692	hypothetical protein LOC283692	chr15q25.1	1560030_at	---
2.09	2.16	0.07	6.13E-01	8.59E-01	WARS2	Tryptophanyl tRNA synthetase 2, mitochondrial	chr1p13.3-p13.1	1561297_at	NM_015836 /// NM_201263
1.95	2.00	0.05	6.13E-01	8.59E-01	C10orf93	chromosome 10 open reading frame 93	chr10q26.3	1555573_at	NM_173572
3.72	3.84	0.13	6.13E-01	8.59E-01	ZP1	zona pellucida glycoprotein 1 (sperm receptor)	chr11q12.2	237335_at	NM_207341
3.41	3.50	0.09	6.13E-01	8.59E-01	TLR9 /// TWF2	toll-like receptor 9 /// twinfilin, actin-binding protein, homolog 2 (Drosophila)	chr3p21.1 /// chr3p21.3	223903_at	NM_007284 /// NM_017442
9.32	9.40	0.09	6.13E-01	8.59E-01	BCAP31	B-cell receptor-associated protein 31	chrXq28	200837_at	NM_005745
2.23	2.31	0.08	6.13E-01	8.59E-01	NBPF5 /// NBPF6	neuroblastoma breakpoint family, member 5 /// neuroblastoma breakpoint family, member 6	chr1p13.3	1558862_at	XM_001714472 /// XM_926213
5.72	6.05	0.33	6.13E-01	8.59E-01	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	chr3q26	202687_s_at	NM_003810
2.80	2.90	0.11	6.13E-01	8.59E-01	MYBPC2	myosin binding protein C, fast type	chr19q13.33	206394_at	NM_004533
4.47	4.56	0.09	6.13E-01	8.59E-01	TRAK1	trafficking protein, kinesin binding 1	chr3p25.3-p24.1	226013_at	NM_001042646 /// NM_014965
2.25	2.33	0.08	6.13E-01	8.59E-01	---	---	---	243522_at	---
5.86	6.01	0.14	6.13E-01	8.59E-01	PCM1	pericentriolar material 1	chr8p22-p21.3	214118_x_at	NM_006197
2.48	2.57	0.09	6.13E-01	8.59E-01	---	---	---	1569004_at	---
3.24	3.34	0.11	6.13E-01	8.59E-01	NHLH1	nescient helix loop helix 1	chr1q22	214628_at	NM_005598
9.11	9.23	0.13	6.14E-01	8.59E-01	PKM2	pyruvate kinase, muscle	chr15q22	201251_at	NM_002654 /// NM_182470 /// NM_182471
2.21	2.30	0.09	6.13E-01	8.59E-01	F2RL3	coagulation factor II (thrombin) receptor-like 3	chr19p12	207221_at	NM_003950
3.63	3.71	0.08	6.14E-01	8.59E-01	ARL3	ADP-ribosylation factor-like 3	chr10q23.3	213433_at	NM_004311
4.37	4.45	0.08	6.14E-01	8.59E-01	CCDC74B	coiled-coil domain containing 74B	chr2q21.1	231657_s_at	NM_207310
2.98	3.06	0.07	6.14E-01	8.59E-01	LOC729994	hypothetical LOC729994	chr19q13.43	237899_at	XM_001131994 /// XM_001718478 /// XM_001719218
2.24	2.31	0.07	6.14E-01	8.59E-01	UBA6	ubiquitin-like modifier activating enzyme 6	chr4q13.2	220869_at	NM_018227
2.53	2.60	0.07	6.14E-01	8.59E-01	BCL2	B-cell CLL/lymphoma 2	chr18q21.33|18q21.3	203684_s_at	NM_000633 /// NM_000657
1.86	1.92	0.06	6.14E-01	8.59E-01	UBR3	Ubiquitin protein ligase E3 component n-recognin 3 (putative)	chr2q31.1	244121_at	NM_172070
2.14	2.20	0.06	6.14E-01	8.59E-01	SASS6	spindle assembly 6 homolog (C. elegans)	chr1p21.2	231895_at	NM_194292
2.42	2.48	0.06	6.14E-01	8.59E-01	TOX	thymocyte selection-associated high mobility group box	chr8q12.1	204530_s_at	NM_014729
2.72	2.77	0.05	6.13E-01	8.59E-01	SP1	Sp1 transcription factor	chr12q13.1	214732_at	NM_138473
2.19	2.27	0.08	6.14E-01	8.59E-01	---	---	---	238306_at	---
3.79	3.90	0.11	6.14E-01	8.59E-01	SRRM2	Serine/arginine repetitive matrix 2	chr16p13.3	216629_at	NM_016333
2.32	2.40	0.08	6.14E-01	8.59E-01	---	---	---	234442_at	---
3.96	4.04	0.08	6.14E-01	8.59E-01	BRD8	Bromodomain containing 8	chr5q31	242265_at	NM_006696 /// NM_139199 /// NM_183359
2.75	2.83	0.08	6.14E-01	8.60E-01	CNGB1	cyclic nucleotide gated channel beta 1	chr16q13	211099_s_at	NM_001297
2.72	2.81	0.09	6.14E-01	8.60E-01	FAM20A	family with sequence similarity 20, member A	chr17q24.2	226804_at	NM_017565

1.80	1.86	0.05	6.14E-01	8.60E-01	TMEM74	transmembrane protein 74	chr8q23.1	1552521_a_at	NM_153015
3.97	4.09	0.12	6.14E-01	8.60E-01	ZSCAN22	zinc finger and SCAN domain containing 22	chr19q13.43	228769_at	NM_181846
2.84	2.92	0.08	6.14E-01	8.60E-01	GPR77	G protein-coupled receptor 77	chr19q13.33	221149_at	NM_018485
2.14	2.20	0.06	6.14E-01	8.60E-01	---	---	---	1561713_at	---
3.99	4.06	0.08	6.14E-01	8.60E-01	RIT1	Ras-like without CAAX 1	chr1q22	239843_at	NM_006912
1.92	1.98	0.06	6.14E-01	8.60E-01	---	---	---	234448_at	---
6.79	6.91	0.11	6.14E-01	8.60E-01	MRPL48	mitochondrial ribosomal protein L48	chr11q13.4	218281_at	NM_016055
3.18	3.27	0.09	6.14E-01	8.60E-01	HPS1	Hermansky-Pudlak syndrome 1	chr10q23.1-q23.3	239382_at	NM_000195 /// NM_182639
4.11	4.20	0.09	6.14E-01	8.60E-01	EPB41L1	Erythrocyte membrane protein band 4.1-like 1	chr20q11.2-q12	222066_at	NM_012156 /// NM_177996
2.38	2.45	0.06	6.14E-01	8.60E-01	FRZB	Frizzled-related protein	chr2qter	244419_at	NM_001463
1.81	1.87	0.05	6.14E-01	8.60E-01	PRO2012	hypothetical protein PRO2012	chr1q42.13	1553546_at	---
2.71	2.84	0.13	6.15E-01	8.60E-01	LOC652755 /// NAIP	similar to Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein) /// NLR family, apoptosis inhibitory protein	chr5q13.1	204860_s_at	NM_004536 /// NM_022892 /// XM_001713981 /// XM_942384
2.88	2.97	0.09	6.15E-01	8.60E-01	---	---	---	235585_at	---
5.65	5.90	0.25	6.15E-01	8.60E-01	CD164	CD164 molecule, sialomucin	chr6q21	208653_s_at	NM_006016
4.92	5.15	0.23	6.15E-01	8.60E-01	MFN1	mitofusin 1	chr3q26.32	217043_s_at	NM_033540
2.76	2.84	0.08	6.15E-01	8.60E-01	VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	chr10q25.2	1552536_at	NM_145206
4.23	4.34	0.10	6.15E-01	8.60E-01	FLJ33706	hypothetical protein FLJ33706	chr20q11.21	1556722_a_at	XR_041128 /// XR_041129 /// XR_041130
2.57	2.64	0.07	6.15E-01	8.60E-01	SLC7A14	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	chr3q26.2	1556641_at	NM_020949 /// XM_001723366 /// XM_930209 /// XM_941578
2.19	2.25	0.06	6.15E-01	8.60E-01	---	---	---	1561319_at	---
2.52	2.60	0.07	6.15E-01	8.60E-01	PRTG	protogenin homolog (Gallus gallus)	chr15q21.3	1562590_at	NM_173814
7.14	7.33	0.19	6.15E-01	8.60E-01	SEC24B	SEC24 related gene family, member B (S. cerevisiae)	chr4q25	202798_at	NM_001042734 /// NM_006323
5.63	5.72	0.09	6.15E-01	8.60E-01	FBXO2	F-box protein 2	chr1p36.22	219305_x_at	NM_012168
5.54	5.63	0.09	6.15E-01	8.60E-01	CDH22	cadherin-like 22	chr20q13.1	215181_at	NM_021248
2.72	2.81	0.08	6.15E-01	8.60E-01	MINA	MYC induced nuclear antigen	chr3q11.2	229132_at	NM_001042533 /// NM_032778 /// NM_153182
2.45	2.54	0.08	6.15E-01	8.60E-01	SCN10A	sodium channel, voltage-gated, type X, alpha subunit	chr3p22-p21	208578_at	NM_006514
2.57	2.65	0.08	6.15E-01	8.60E-01	LOC100128511	hypothetical protein LOC100128511	chr10p12.31	239894_at	XM_001716027 /// XM_001716766 /// XM_001718701
2.39	2.46	0.06	6.15E-01	8.60E-01	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	chr7p11	203819_s_at	NM_006547
2.32	2.38	0.06	6.15E-01	8.60E-01	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	chr13q33-q34	207254_at	NM_005073
5.62	5.88	0.27	6.15E-01	8.60E-01	SENP6	SUMO1/sentrin specific peptidase 6	chr6q13-q14.3	202318_s_at	NM_001100409 /// NM_015571
5.76	5.99	0.23	6.15E-01	8.60E-01	FGF12	fibroblast growth factor 12	chr3q28	214589_at	NM_004113 /// NM_021032
7.03	7.22	0.19	6.15E-01	8.60E-01	---	---	---	224989_at	---
2.33	2.39	0.06	6.15E-01	8.60E-01	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	chr5q14.3	206653_at	NM_006467
2.28	2.37	0.08	6.16E-01	8.61E-01	---	---	---	243627_at	---
1.91	1.98	0.07	6.16E-01	8.61E-01	---	---	---	1567705_at	---
6.18	6.33	0.15	6.16E-01	8.61E-01	TEF	thyrotrophic embryonic factor	chr22q13|22q13.2	225840_at	NM_003216
5.42	5.53	0.12	6.16E-01	8.61E-01	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	chr1q24-q25	226893_at	NM_001100108 /// NM_005158 /// NM_007314
2.31	2.37	0.06	6.16E-01	8.61E-01	---	---	---	240938_at	---
2.66	2.78	0.11	6.16E-01	8.61E-01	CCL11	chemokine (C-C motif) ligand 11	chr17q21.1-q21.2	210133_at	NM_002986
3.12	3.23	0.11	6.16E-01	8.61E-01	C22orf23	chromosome 22 open reading frame 23	chr22q13.1	223706_at	NM_032561
2.56	2.62	0.06	6.16E-01	8.61E-01	---	---	---	221969_at	---
5.20	5.35	0.15	6.16E-01	8.61E-01	IPO7	Importin 7	chr11p15.4	200995_at	NM_006391
2.40	2.48	0.08	6.16E-01	8.61E-01	PTENP1	phosphatase and tensin homolog pseudogene 1	chr9p21	217494_s_at	NR_023917
6.29	6.54	0.25	6.16E-01	8.61E-01	TMOD1	tropomodulin 1	chr9q22.3	203661_s_at	NM_003275

2.49	2.57	0.08	6.16E-01	8.61E-01	---	---	---	234372_at	---
2.46	2.55	0.09	6.17E-01	8.61E-01	KRT2	keratin 2	chr12q11-q13	207908_at	NM_000423
3.28	3.36	0.08	6.17E-01	8.61E-01	C5orf46	chromosome 5 open reading frame 46	chr5q33.1	1554195_a_at	NM_206966
2.45	2.52	0.08	6.17E-01	8.61E-01	---	---	---	1561226_at	---
2.31	2.37	0.06	6.17E-01	8.61E-01	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)	chr4q35.1	1559661_at	NM_001080477
1.84	1.90	0.05	6.17E-01	8.61E-01	C10orf141	chromosome 10 open reading frame 141	chr10q26.2	244435_at	NM_001039762
1.95	2.01	0.06	6.17E-01	8.61E-01	FLJ43663	Hypothetical LOC378805	chr7q32.3	238874_at	XM_380146 /// XM_930545 /// XM_935361 /// XM_935362 /// XM_935363 /// XM_935364 /// XM_935365 /// XM_935366 /// XM_935367 /// XM_935688 /// XM_935957 /// XM_935958 /// XM_935959 /// XM_935960 /// XM_935961 /// XM_935962 /// XM_935963 /// XM_935964 /// XM_940526 /// XM_944629 /// XM_944633 /// XM_944638 /// XM_944640 /// XM_944641 /// XM_944643 /// XM_944645 /// XM_944647
2.22	2.29	0.07	6.17E-01	8.61E-01	CLSPN	claspin homolog (Xenopus laevis)	chr1p34.2	219621_at	NM_022111
6.90	7.04	0.14	6.17E-01	8.61E-01	---	---	---	235028_at	---
9.21	9.32	0.11	6.17E-01	8.61E-01	ATP6V0D1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	chr16q22	212041_at	NM_004691
4.03	4.13	0.10	6.17E-01	8.61E-01	FAM41AY	family with sequence similarity 41, member A, Y-linked	chrYq11.221	1561390_at	---
2.06	2.15	0.09	6.17E-01	8.61E-01	---	---	---	244539_at	---
2.38	2.46	0.08	6.17E-01	8.61E-01	LOC642864	spermatogenesis-related protein 7	chr1p13.3	231586_at	XR_041426 /// XR_041427 /// XR_041428
9.18	9.36	0.18	6.17E-01	8.61E-01	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	chr9q33-q34.1	211936_at	NM_005347
2.24	2.31	0.07	6.17E-01	8.61E-01	---	---	---	1559229_at	---
1.90	1.97	0.07	6.17E-01	8.61E-01	---	---	---	1559285_at	---
6.03	6.26	0.24	6.17E-01	8.61E-01	PNPT1	polyribonucleotide nucleotidyltransferase 1	chr2p15	225291_at	NM_033109
5.74	5.87	0.12	6.17E-01	8.61E-01	ZNF771	zinc finger protein 771	chr16p11.2	219781_s_at	NM_016643 /// XM_001721231 /// XM_001721234
2.99	3.19	0.20	6.17E-01	8.62E-01	MORF4L2	Mortality factor 4 like 2	chrXq22	243857_at	NM_012286
3.10	3.23	0.13	6.17E-01	8.62E-01	EIF4E3	eukaryotic translation initiation factor 4E family member 3	chr3p14	238461_at	NM_001134649 /// NM_001134650 /// NM_001134651 /// NM_173359
8.27	8.38	0.11	6.17E-01	8.62E-01	GRN	granulin	chr17q21.32	216041_x_at	NM_002087

4.57	4.67	0.10	6.17E-01	8.62E-01	KCNQ1DN	KCNQ1 downstream neighbor	chr11p15.4|11p15.5	220629_at	XR_039804 /// XR_039805 /// XR_039806																				
3.75	3.85	0.09	6.18E-01	8.62E-01	LAT2	linker for activation of T cells family, member 2	chr7q11.23	211768_at	NM_014146 /// NM_032463 /// NM_032464																				
7.33	7.69	0.35	6.18E-01	8.62E-01	INHA	inhibin, alpha	chr2q33-q36	210141_s_at	NM_002191																				
3.59	3.68	0.09	6.18E-01	8.62E-01	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	chr16p13.3	233360_at	NM_003345 /// NM_194259 /// NM_194260 /// NM_194261																				
2.46	2.54	0.08	6.18E-01	8.62E-01	TAS2R3	taste receptor, type 2, member 3	chr7q31.3-q32	221456_at	NM_016943																				
5.90	6.05	0.15	6.18E-01	8.62E-01	OSGEPL1	O-sialoglycoprotein endopeptidase-like 1	chr2q32.2	230032_at	NM_022353																				
2.53	2.60	0.07	6.18E-01	8.62E-01	---	---	---	240882_at	---																				
2.24	2.31	0.07	6.18E-01	8.62E-01	---	---	---	232943_at	---																				
3.80	3.97	0.17	6.18E-01	8.62E-01	AGRN	agrin	chr1p36.33	217419_x_at	NM_198576																				
4.25	4.36	0.12	6.18E-01	8.62E-01	---	---	---	241276_at	---																				
2.59	2.69	0.09	6.18E-01	8.62E-01	TMEM145	transmembrane protein 145	chr19q13.2	1553479_at	NM_173633																				
1.94	2.00	0.06	6.18E-01	8.62E-01	GAB1	GRB2-associated binding protein 1	chr4q31.21	1557030_at	NM_002039 /// NM_207123																				
2.53	2.60	0.07	6.18E-01	8.62E-01	PHCA	Phytoceramidase, alkaline	chr11q13.5	231321_s_at	NM_018367																				
5.91	6.05	0.14	6.18E-01	8.62E-01	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16q22-q23	226685_at	NM_006750																				
3.20	3.28	0.07	6.18E-01	8.62E-01	TMEM90A	transmembrane protein 90A	chr14q24.3	237053_at	NM_001105579																				
2.56	2.64	0.08	6.18E-01	8.62E-01	KAL1	Kallmann syndrome 1 sequence	chrXp22.32	229853_at	NM_000216																				
5.42	5.50	0.09	6.18E-01	8.62E-01	RAB11FIP1	RAB11 family interacting protein 1 (class I)	chr8p11.22	231830_x_at	NM_001002233 /// NM_001002814 /// NM_025151																				
2.57	2.63	0.06	6.18E-01	8.62E-01	C20orf200	chromosome 20 open reading frame 200	chr20q13.33	1553204_at	NM_152757																				
3.43	3.52	0.10	6.18E-01	8.62E-01	ZNF709	zinc finger protein 709	chr19p13.2	1570364_at	NM_152601																				
2.19	2.26	0.07	6.18E-01	8.62E-01	---	---	---	1569405_at	---																				
2.29	2.35	0.05	6.18E-01	8.62E-01	---	---	---	1566777_at	---																				
1.99	2.06	0.07	6.18E-01	8.62E-01	GNASAS	GNAS antisense	chr20q13.32	232881_at	NR_002785																				
1.94	2.00	0.06	6.18E-01	8.62E-01	EFCAB5	EF-hand calcium binding domain 5	chr17q11.2	1558301_a_at	NM_198529																				
1.87	1.92	0.05	6.18E-01	8.62E-01	---	---	---	1563052_at	---																				
4.40	4.56	0.15	6.19E-01	8.62E-01	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	chr10q	202405_at	NM_001033925 /// NM_003252																				
1.95	2.03	0.08	6.19E-01	8.62E-01	UNC13C	unc-13 homolog C (C. elegans)	chr15q21.3	1569969_a_at	NM_001080534																				
2.06	2.12	0.05	6.19E-01	8.62E-01	---	---	---	232268_at	---																				
2.25	2.30	0.05	6.19E-01	8.62E-01	MEP1A	meprin A, alpha (PABA peptide hydrolase)	chr6p12-p11	206000_at	NM_005588																				
6.70	6.90	0.20	6.19E-01	8.62E-01	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	chr2q21	225263_at	NM_004807																				
4.36	4.51	0.15	6.19E-01	8.62E-01	ITGA11	integrin, alpha 11	chr15q23	222899_at	NM_001004439																				
2.68	2.76	0.08	6.19E-01	8.62E-01	---	---	---	242124_at	---																				
1.89	1.95	0.05	6.19E-01	8.62E-01	---	---	---	216575_at	---																				
3.21	3.36	0.15	6.19E-01	8.62E-01	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	chr5q13.2	228050_at	NM_032175																				
5.66	5.79	0.14	6.19E-01	8.62E-01	LTC4S	leukotriene C4 synthase	chr5q35	206480_at	NM_145867																				
2.20	2.35	0.15	6.19E-01	8.62E-01	LOC100132881 /// LOC728715 /// OVOS /// OVOS2	hypothetical protein LOC100132881 /// similar to hCG38149 /// ovostatin /// ovostatin 2	chr12p11.21 /// chr12p13 /// chr12p13.31	228245_s_at	NM_001080502 /// XM_001128260 /// XM_001715897 /// XM_001716690 /// XM_001722912 /// XM_001723398 /// XM_001724047																				
1.79	1.86	0.07	6.19E-01	8.62E-01	---	---	---	1558793_at	---																				
2.08	2.15	0.07	6.19E-01	8.62E-01	LOC339874	hypothetical LOC339874	chr3q22.1	1562638_at	---																				
2.92	2.98	0.07	6.19E-01	8.62E-01	ADAM30	ADAM metallopeptidase domain 30	chr1p13-p11	221446_at	NM_021794																				
2.11	2.17	0.06	6.19E-01	8.62E-01	---	---	---	1569331_at	---																				
1.95	2.01	0.06	6.19E-01	8.62E-01	SYTL3	synaptotagmin-like 3	chr6q25.3	1561882_at	NM_001009991																				
2.79	2.90	0.11	6.19E-01	8.62E-01	---	---	---	1566836_at	---																				
3.24	3.34	0.10	6.19E-01	8.62E-01	EPO	erythropoietin	chr7q22	207257_at	NM_000799																				
6.19	6.32	0.13	6.19E-01	8.62E-01	XIAP	X-linked inhibitor of apoptosis	chrXq25	243026_x_at	NM_001167																				

4.44	4.56	0.12	6.19E-01	8.62E-01	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	chr8p21.2	236492_at	NM_002717
4.27	4.37	0.10	6.19E-01	8.62E-01	C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	chr7p14-p13	219439_at	NM_020156
2.14	2.23	0.08	6.19E-01	8.62E-01	CHRM1	cholinergic receptor, muscarinic 1	chr11q13	231783_at	NM_000738
2.47	2.53	0.06	6.19E-01	8.62E-01	CCDC46	coiled-coil domain containing 46	chr17q24.1-q24.2	1557886_at	NM_001037325 /// NM_145036
2.43	2.50	0.08	6.19E-01	8.62E-01	LOC550113	hypothetical LOC550113	chr4q13.2	1556992_at	---
3.63	3.72	0.10	6.20E-01	8.62E-01	---	---	---	244002_at	---
2.23	2.30	0.07	6.19E-01	8.62E-01	---	---	---	233094_at	---
2.64	2.71	0.07	6.20E-01	8.63E-01	---	---	---	214353_at	---
3.00	3.08	0.08	6.20E-01	8.63E-01	CNOT2	CCR4-NOT transcription complex, subunit 2	chr12q15	222181_at	NM_014515
3.96	4.11	0.15	6.20E-01	8.63E-01	---	---	---	1570588_at	---
4.39	4.66	0.27	6.20E-01	8.63E-01	---	---	---	240216_at	---
2.54	2.61	0.07	6.20E-01	8.63E-01	ADAM5P	ADAM metallopeptidase domain 5 pseudogene	chr8p11.23	216998_s_at	NR_001448
2.01	2.09	0.08	6.20E-01	8.63E-01	LOC285778	hypothetical protein LOC285778	chr6p25.1	1563662_at	---
5.64	5.72	0.08	6.20E-01	8.63E-01	TMIGD2	transmembrane and immunoglobulin domain containing 2	chr19p13.3	244716_x_at	NM_144615
3.09	3.25	0.16	6.20E-01	8.63E-01	KAL1	Kallmann syndrome 1 sequence	chrXp22.32	205206_at	NM_000216
2.51	2.59	0.08	6.20E-01	8.63E-01	---	---	---	217068_at	---
3.45	3.53	0.08	6.20E-01	8.63E-01	ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	chr11p15.1	210245_at	NM_000352
2.29	2.38	0.08	6.20E-01	8.63E-01	---	---	---	1556004_at	---
2.30	2.36	0.06	6.20E-01	8.63E-01	LOC441453	similar to olfactory receptor, family 7, subfamily A, member 17	chr11p15.1	217551_at	XR_041341 /// XR_041342 /// XR_041343
2.00	2.06	0.06	6.20E-01	8.63E-01	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit	chr3p24-p21	210853_at	NM_014139
2.07	2.12	0.05	6.20E-01	8.63E-01	DKFZp686A1627	putative PHD finger protein 2 pseudogene	chr13q11	1561961_at	NR_002801
2.17	2.25	0.08	6.20E-01	8.63E-01	---	---	---	242792_at	---
2.30	2.38	0.08	6.20E-01	8.63E-01	---	---	---	217345_at	---
4.13	4.32	0.19	6.21E-01	8.63E-01	NARG2	NMDA receptor regulated 2	chr15q22.2	218713_at	NM_001018089 /// NM_024611
4.70	4.89	0.19	6.21E-01	8.63E-01	---	---	---	227524_at	---
3.46	3.57	0.10	6.20E-01	8.63E-01	---	---	---	221382_at	---
5.45	5.55	0.10	6.20E-01	8.63E-01	CHD9	chromodomain helicase DNA binding protein 9	chr16q12.2	212615_at	NM_025134
5.41	5.51	0.10	6.21E-01	8.63E-01	ZCCHC14	zinc finger, CCHC domain containing 14	chr16q24.2	215427_s_at	NM_015144
2.06	2.14	0.08	6.21E-01	8.63E-01	---	---	---	1569786_at	---
3.18	3.26	0.08	6.21E-01	8.63E-01	LOC100130275	hypothetical protein LOC100130275	chr6p24.3	1557070_at	XM_001720213 /// XM_001724910 /// XM_001725291
3.11	3.23	0.12	6.21E-01	8.63E-01	---	---	---	239809_at	---
3.34	3.46	0.11	6.21E-01	8.63E-01	LOC220077	docking protein 1-like protein	chr11q13.4	216385_at	XR_017002 /// XR_019008 /// XR_041797
2.80	2.90	0.10	6.21E-01	8.63E-01	CAMK1G	calcium/calmodulin-dependent protein kinase IG	chr1q32-q41	217128_s_at	NM_020439
2.03	2.10	0.07	6.21E-01	8.63E-01	---	---	---	238213_at	---
3.06	3.13	0.07	6.21E-01	8.63E-01	MYC	Similar to ORF 114	chr8q24.21	244089_at	NM_002467
2.58	2.65	0.07	6.21E-01	8.63E-01	OR10J1	olfactory receptor, family 10, subfamily J, member 1	chr1q23.2	221346_at	NM_012351
1.91	1.97	0.06	6.21E-01	8.63E-01	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	chr10q22.2	1562236_at	NM_012330
3.34	3.43	0.10	6.21E-01	8.63E-01	KIAA1549	KIAA1549	chr7q34	238885_at	NM_020910
8.03	8.34	0.31	6.21E-01	8.63E-01	MRAP	melanocortin 2 receptor accessory protein	chr21q22.1	1554044_a_at	NM_178817 /// NM_206898
2.25	2.37	0.12	6.21E-01	8.63E-01	NCOA2	nuclear receptor coactivator 2	chr8q13.3	205732_s_at	NM_006540
4.35	4.44	0.09	6.21E-01	8.63E-01	SLC6A3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	chr5p15.3	206836_at	NM_001044
2.82	2.89	0.06	6.21E-01	8.63E-01	DPPA2	developmental pluripotency associated 2	chr3q13.13	240301_at	NM_138815
4.67	4.79	0.11	6.21E-01	8.63E-01	---	---	---	228866_at	---
2.50	2.61	0.11	6.21E-01	8.63E-01	FLRT3	fibronectin leucine rich transmembrane protein 3	chr20p11	222853_at	NM_013281 /// NM_198391
2.44	2.49	0.05	6.21E-01	8.63E-01	---	---	---	231428_at	---
5.49	6.50	1.01	6.21E-01	8.63E-01	LOC100133662 /// RPS4Y1	hypothetical protein LOC100133662 /// ribosomal protein S4, Y-linked 1	chrYp11.3	201909_at	NM_001008 /// XM_001713618
2.50	2.65	0.15	6.22E-01	8.63E-01	COG3	component of oligomeric golgi complex 3	chr13q14.12	1554339_a_at	NM_031431
7.76	7.95	0.19	6.22E-01	8.64E-01	CYBRD1	cytochrome b reductase 1	chr2q31.1	222453_at	NM_001127383 /// NM_024843
4.38	4.59	0.21	6.22E-01	8.64E-01	RPE	ribulose-5-phosphate-3-epimerase	chr2q32-q33.3	225039_at	NM_006916 /// NM_199229
5.54	5.65	0.11	6.22E-01	8.64E-01	AMZ1	archaelysin family metallopeptidase 1	chr7p22.2	1561179_s_at	NM_133463
5.32	5.43	0.10	6.22E-01	8.64E-01	LOC442240 /// ZNF259	similar to zinc finger protein 259 /// zinc finger protein 259	chr11q23.3 /// chr6q21	217185_s_at	NM_003904 /// XR_016496 /// XR_019092 /// XR_040401

3.23	3.30	0.08	6.22E-01	8.64E-01	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	chr10q24.1	216909_at	NM_015179
2.63	2.69	0.07	6.22E-01	8.64E-01	EXOSC3 /// SHB	exosome component 3 /// Src homology 2 domain containing adaptor protein B	chr9p11 /// chr9p13.2-p13.1	233495_at	NM_001002269 /// NM_003028 /// NM_016042
2.19	2.25	0.06	6.22E-01	8.64E-01	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2	chr8q13.2	208123_at	NM_004770
2.36	2.42	0.06	6.22E-01	8.64E-01	APOA2	apolipoprotein A-II	chr1q21-q23	219466_s_at	NM_001643
2.09	2.14	0.05	6.22E-01	8.64E-01	---	---	---	1567390_at	---
4.15	4.30	0.15	6.22E-01	8.64E-01	SLC35A3	Solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	chr1p21	226894_at	NM_012243
3.72	3.79	0.07	6.22E-01	8.64E-01	KIAA0485	hypothetical LOC57235	---	214294_at	---
2.33	2.39	0.06	6.22E-01	8.64E-01	PGBD1	piggyBac transposable element derived 1	chr6p22.1	235411_at	NM_032507
2.56	2.62	0.06	6.22E-01	8.64E-01	---	---	---	233074_at	---
5.86	5.97	0.11	6.22E-01	8.64E-01	FIT1	fat-inducing transcript 1	chr14q12	229567_at	NM_203402
3.19	3.28	0.09	6.22E-01	8.64E-01	FAAH2	fatty acid amide hydrolase 2	chrXp11.1	230792_at	NM_174912
2.74	2.83	0.09	6.22E-01	8.64E-01	CRTAC1	cartilage acidic protein 1	chr10q22	1555958_at	NM_018058
2.20	2.29	0.08	6.22E-01	8.64E-01	MYO7B	myosin VIIB	chr2q21.1	216660_at	NM_001080527
4.88	4.97	0.09	6.22E-01	8.64E-01	---	---	---	241415_at	---
3.06	3.17	0.12	6.22E-01	8.64E-01	C11orf21	chromosome 11 open reading frame 21	chr11p15.5	1568978_s_at	XR_042066 /// XR_042067 /// XR_042068
7.82	7.96	0.14	6.22E-01	8.64E-01	RAD23B	RAD23 homolog B (S. cerevisiae)	chr9q31.2	201222_s_at	NM_002874
2.75	2.82	0.08	6.22E-01	8.64E-01	BVES	blood vessel epicardial substance	chr6q21	228783_at	NM_007073 /// NM_147147
2.11	2.18	0.07	6.22E-01	8.64E-01	---	---	---	1560506_at	---
3.33	3.41	0.08	6.23E-01	8.64E-01	GPATCH4	G patch domain containing 4	chr1q22	220596_at	NM_015590 /// NM_182679
2.46	2.53	0.07	6.23E-01	8.64E-01	---	---	---	1554372_at	---
2.01	2.08	0.07	6.22E-01	8.64E-01	---	---	---	1563332_at	---
7.06	7.15	0.08	6.23E-01	8.64E-01	GGCT	gamma-glutamyl cyclotransferase	chr7p15-p14	215380_s_at	NM_024051
9.70	9.91	0.21	6.23E-01	8.64E-01	SORBS2	sorbin and SH3 domain containing 2	chr4q35.1	204288_s_at	NM_003603 /// NM_021069
2.48	2.59	0.11	6.23E-01	8.64E-01	MCTP1	multiple C2 domains, transmembrane 1	chr5q15	220122_at	NM_001002796 /// NM_024717
2.24	2.31	0.07	6.23E-01	8.64E-01	HAO1	hydroxyacid oxidase (glycolate oxidase) 1	chr20p12	220224_at	NM_017545
4.99	5.31	0.33	6.23E-01	8.64E-01	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	chr7p14.3	223585_x_at	NM_015483
5.55	5.71	0.16	6.23E-01	8.64E-01	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	chrXp21.2	227357_at	NM_152787
6.61	6.73	0.12	6.23E-01	8.64E-01	FBXO11	F-box protein 11	chr2p16.3	203255_at	NM_012167 /// NM_018693 /// NM_025133
2.76	2.85	0.10	6.23E-01	8.64E-01	41334	membrane-associated ring finger (C3HC4) 1	chr4q32.3	219574_at	NM_017923
2.02	2.09	0.07	6.23E-01	8.64E-01	PP8961	hypothetical protein LOC650662	chr14q32.12	1562396_at	NM_001080113
6.88	6.94	0.06	6.23E-01	8.64E-01	YIPF1	Yip1 domain family, member 1	chr1p33-p32.1	214733_s_at	NM_018982
2.07	2.13	0.06	6.23E-01	8.64E-01	D21S2091E	D21S2091E	---	1563385_at	---
2.97	3.07	0.10	6.23E-01	8.64E-01	---	---	---	239237_at	---
2.35	2.42	0.07	6.23E-01	8.64E-01	CST6	Cystatin E/M	chr11q13	231248_at	NM_001323
3.90	4.19	0.29	6.23E-01	8.64E-01	LOC145820	hypothetical protein LOC145820	chr15q26.2	1558881_at	XM_378546 /// XM_944060
1.98	2.04	0.06	6.23E-01	8.64E-01	LASS3	LAG1 homolog, ceramide synthase 3	chr15q26.3	1554252_a_at	NM_178842
7.16	7.37	0.20	6.23E-01	8.64E-01	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	chr9q32	224617_at	NM_005156
4.50	4.69	0.20	6.23E-01	8.64E-01	MFN1	mitofusin 1	chr3q26.32	211801_x_at	NM_033540
7.12	7.28	0.16	6.23E-01	8.64E-01	GHDC	GH3 domain containing	chr17q21.2	227159_at	NM_032484
5.55	5.70	0.15	6.23E-01	8.64E-01	ZNF252	zinc finger protein 252	chr8q24.3	228200_at	NR_023392 /// XM_001714325 /// XM_001714728 /// XM_001714801
5.32	5.47	0.15	6.23E-01	8.64E-01	LOC653786	otoancorin pseudogene	chr16p12.1	1557987_at	NR_003676 /// XR_017362
3.27	3.36	0.09	6.23E-01	8.64E-01	FLJ45224	FLJ45224 protein	chr9q34.3	1560488_at	NM_207510
2.00	2.07	0.07	6.23E-01	8.64E-01	FLJ22536 /// LOC729161	hypothetical locus LOC401237 /// similar to hCG1660466	chr6p22.3	241047_at	XM_001717403 /// XM_001718731 /// XM_001718838 /// XM_379398
2.80	2.86	0.06	6.23E-01	8.64E-01	---	---	---	208007_at	---
2.78	2.84	0.06	6.23E-01	8.64E-01	NOS1	nitric oxide synthase 1 (neuronal)	chr12q24.2-q24.31	1560974_s_at	NM_000620
1.96	2.02	0.06	6.23E-01	8.64E-01	---	---	---	231145_at	---

3.71	3.88	0.18	6.23E-01	8.64E-01	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	chr14q12-q13	217985_s_at	NM_013448 /// NM_182648
2.88	2.95	0.07	6.23E-01	8.64E-01	STYK1	serine/threonine/tyrosine kinase 1	chr12p13.2	221696_s_at	NM_018423
5.50	5.57	0.07	6.24E-01	8.64E-01	MEIS3	Meis homeobox 3	chr19q13.32	228327_x_at	NM_001009813 /// NM_020160
9.27	9.33	0.05	6.24E-01	8.64E-01	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	chr9q34.11-q34.12	200786_at	NM_002799
5.06	5.29	0.23	6.24E-01	8.64E-01	---	---	---	1558028_x_at	---
6.23	6.33	0.10	6.24E-01	8.64E-01	NLGN3	neuroligin 3	chrXq13.1	219726_at	NM_018977
2.32	2.40	0.08	6.24E-01	8.64E-01	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	chr13q14	211153_s_at	NM_003701 /// NM_033012
1.85	1.91	0.06	6.24E-01	8.64E-01	---	---	---	233703_x_at	---
1.93	1.99	0.06	6.24E-01	8.64E-01	C6orf12	chromosome 6 open reading frame 12	chr6p21.33	234097_s_at	XR_041144 /// XR_041145
5.13	5.29	0.17	6.24E-01	8.65E-01	NEK9	NIMA (never in mitosis gene a)- related kinase 9	chr14q24.3	214738_s_at	NM_033116
2.26	2.34	0.08	6.24E-01	8.65E-01	---	---	---	1560284_at	---
5.79	5.89	0.10	6.24E-01	8.65E-01	STK38	serine/threonine kinase 38	chr6p21	202951_at	NM_007271
2.15	2.22	0.07	6.24E-01	8.65E-01	SEZ6L	seizure related 6 homolog (mouse)-like	chr22q12.1	240709_at	NM_021115
3.71	3.92	0.21	6.24E-01	8.65E-01	---	---	---	239731_at	---
3.94	4.05	0.11	6.24E-01	8.65E-01	NUBPL	nucleotide binding protein-like	chr14q12	220176_at	NM_025152
2.41	2.49	0.09	6.24E-01	8.65E-01	---	---	---	1562169_at	---
2.49	2.58	0.09	6.24E-01	8.65E-01	PCDH10	protocadherin 10	chr4q28.3	228635_at	NM_020815 /// NM_032961
2.08	2.17	0.09	6.24E-01	8.65E-01	---	---	---	243170_at	---
2.54	2.63	0.09	6.24E-01	8.65E-01	IGFBPL1	insulin-like growth factor binding protein-like 1	chr9p13.1	227760_at	NM_001007563
3.94	4.02	0.07	6.24E-01	8.65E-01	ZNF44	zinc finger protein 44	chr19p13.2	223968_at	NM_016264 /// XM_001718561 /// XM_001719479 /// XM_001719639
2.21	2.28	0.07	6.24E-01	8.65E-01	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	chrXp11.23	210394_x_at	NM_001034832 /// NM_001040612 /// NM_005636 /// NM_175729 /// XM_001725018
3.11	3.18	0.07	6.24E-01	8.65E-01	KRT85	keratin 85	chr12q13	207670_at	NM_002283
1.84	1.91	0.07	6.24E-01	8.65E-01	MORC1	MORC family CW-type zinc finger 1	chr3q13	220850_at	NM_014429
2.12	2.19	0.07	6.24E-01	8.65E-01	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	chr19p13.3	231749_at	NM_012458
2.04	2.11	0.06	6.24E-01	8.65E-01	---	---	---	242340_at	---
2.48	2.55	0.06	6.24E-01	8.65E-01	---	---	---	237115_at	---
2.23	2.29	0.06	6.24E-01	8.65E-01	---	---	---	237669_at	---
2.37	2.43	0.06	6.24E-01	8.65E-01	---	---	---	239734_at	---
2.05	2.11	0.06	6.24E-01	8.65E-01	---	---	---	1557037_a_at	---
11.90	11.96	0.06	6.24E-01	8.65E-01	RPL38	ribosomal protein L38	chr17q23-q25	202029_x_at	NM_000999 /// NM_001035258
1.75	1.80	0.05	6.24E-01	8.65E-01	---	---	---	1563055_at	---
2.90	2.98	0.08	6.25E-01	8.65E-01	MMP23A /// MMP23B	matrix metallopeptidase 23A (pseudogene) /// matrix metallopeptidase 23B	chr1p36.3 /// chr1p36.33	207118_s_at	NM_006983 /// NR_002946
2.98	3.06	0.08	6.25E-01	8.65E-01	---	---	---	237184_at	---
2.45	2.52	0.07	6.25E-01	8.65E-01	---	---	---	243754_at	---
2.55	2.74	0.19	6.25E-01	8.65E-01	KCNT2	potassium channel, subfamily T, member 2	chr1q31.3	244455_at	NM_198503
7.70	7.84	0.14	6.25E-01	8.65E-01	KLHL9	kelch-like 9 (Drosophila)	chr9p22	213233_s_at	NM_018847
3.14	3.26	0.12	6.25E-01	8.65E-01	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	chr7p14-p13	235625_at	NM_014396 /// NM_080631
2.88	2.99	0.11	6.25E-01	8.65E-01	C15orf41	chromosome 15 open reading frame 41	chr15q14	232506_s_at	NM_001130010 /// NM_032499
4.77	4.87	0.10	6.25E-01	8.65E-01	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	chr19p13	210240_s_at	NM_001800 /// NM_079421
4.01	4.10	0.09	6.25E-01	8.65E-01	AUTS2	autism susceptibility candidate 2	chr7q11.22	243365_s_at	NM_001127231 /// NM_001127232 /// NM_015570
3.56	3.64	0.08	6.25E-01	8.65E-01	---	---	---	240632_at	---
2.49	2.57	0.08	6.25E-01	8.65E-01	ALPK3	alpha-kinase 3	chr15q25.2	228342_s_at	NM_020778

2.21	2.29	0.08	6.25E-01	8.65E-01	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	chr13q32	243928_s_at	NM_001105515 /// NM_005845
2.25	2.33	0.08	6.25E-01	8.65E-01	KIAA1524	KIAA1524	chr3q13.13	231855_at	NM_020890
2.62	2.69	0.07	6.25E-01	8.65E-01	LMO1	LIM domain only 1 (rhombotin 1)	chr11p15	206718_at	NM_002315
3.21	3.28	0.07	6.25E-01	8.65E-01	FAM26E	family with sequence similarity 26, member E	chr6q22.1	232217_at	NM_153711
2.01	2.07	0.06	6.25E-01	8.65E-01	---	---	---	1557215_at	---
2.16	2.22	0.06	6.25E-01	8.65E-01	---	---	---	1560614_at	---
2.11	2.17	0.06	6.25E-01	8.65E-01	DPY19L2P2	dpy-19-like 2 pseudogene 2 (C. elegans)	chr7q22.1	215143_at	NR_003561
1.97	2.03	0.05	6.25E-01	8.65E-01	---	---	---	1569539_at	---
4.72	4.90	0.18	6.25E-01	8.65E-01	METTL8	methyltransferase like 8	chr2q31.1	1554667_s_at	NM_024770
8.08	8.19	0.11	6.25E-01	8.65E-01	GLT8D1	glycosyltransferase 8 domain containing 1	chr3p21.1	218146_at	NM_001010983 /// NM_018446 /// NM_152932
3.22	3.32	0.10	6.25E-01	8.65E-01	RGMB	RGM domain family, member B	chr5q21.1	227340_s_at	NM_001012761 /// NM_173670
2.59	2.68	0.09	6.25E-01	8.65E-01	NEK4	NIMA (never in mitosis gene a)-related kinase 4	chr3p21.1	1554659_at	NM_003157
2.45	2.52	0.08	6.25E-01	8.65E-01	---	---	---	1569672_at	---
2.02	2.10	0.07	6.25E-01	8.65E-01	---	---	---	231340_at	---
2.30	2.37	0.07	6.25E-01	8.65E-01	GFRA1	GDNF family receptor alpha 1	chr10q26	205696_s_at	NM_005264 /// NM_145793
2.05	2.11	0.06	6.25E-01	8.65E-01	---	---	---	236773_at	---
2.08	2.14	0.05	6.25E-01	8.65E-01	ADAM18	ADAM metallopeptidase domain 18	chr8p11.22	1568970_at	NM_014237
2.88	2.93	0.05	6.25E-01	8.65E-01	---	---	---	1569915_at	---
7.13	7.38	0.25	6.25E-01	8.65E-01	LYZ	lysozyme (renal amyloidosis)	chr12q15	213975_s_at	NM_000239
5.57	5.73	0.16	6.26E-01	8.65E-01	DLAT	dihydrolipoamide S-acetyltransferase	chr11q23.1	211150_s_at	NM_001931
8.53	8.67	0.14	6.26E-01	8.65E-01	PMPCB	peptidase (mitochondrial processing) beta	chr7q22.1	201682_at	NM_004279
3.54	3.66	0.12	6.25E-01	8.65E-01	RAB30	RAB30, member RAS oncogene family	chr11q12-q14	206530_at	NM_014488
4.82	4.92	0.11	6.26E-01	8.65E-01	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	chr11q12.3	35179_at	NM_012200
3.75	3.85	0.10	6.26E-01	8.65E-01	C12orf47	chromosome 12 open reading frame 47	chr12q24.12	212868_x_at	NR_015404 /// XR_017874 /// XR_017973
2.02	2.09	0.07	6.26E-01	8.65E-01	---	---	---	243997_x_at	---
6.75	6.82	0.07	6.26E-01	8.65E-01	VWA5A	von Willebrand factor A domain containing 5A	chr11q23	205011_at	NM_001130142 /// NM_014622 /// NM_198315
2.54	2.59	0.06	6.26E-01	8.65E-01	TKTL1	transketolase-like 1	chrXq28	216370_s_at	NM_012253
4.28	4.36	0.09	6.26E-01	8.65E-01	HSPA14	heat shock 70kDa protein 14	chr10p13	226887_at	NM_016299
4.29	4.38	0.09	6.26E-01	8.65E-01	AMOTL1	angiomotin like 1	chr11q14.3	228840_at	NM_130847
2.18	2.25	0.07	6.26E-01	8.65E-01	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	chr17q21.32	211579_at	NM_000212
2.66	2.72	0.07	6.26E-01	8.65E-01	MUC4	mucin 4, cell surface associated	chr3q29	217109_at	NM_004532 /// NM_018406 /// NM_138297
2.16	2.23	0.06	6.26E-01	8.65E-01	HTRA4	HtrA serine peptidase 4	chr8p11.23	1553706_at	NM_153692
5.06	5.14	0.08	6.26E-01	8.65E-01	TUBGCP2	tubulin, gamma complex associated protein 2	chr10q26.3	202476_s_at	NM_006659
2.87	2.93	0.07	6.26E-01	8.65E-01	---	---	---	231652_at	---
2.75	2.83	0.08	6.26E-01	8.65E-01	---	---	---	1561341_at	---
3.99	4.11	0.13	6.26E-01	8.65E-01	SYNJ1	synaptojanin 1	chr21q22.2	212990_at	NM_003895 /// NM_203446
3.19	3.29	0.09	6.26E-01	8.65E-01	MYEOV2	myeloma overexpressed 2	chr2q37.3	1553515_at	NM_138336
2.95	3.02	0.07	6.26E-01	8.65E-01	---	---	---	207917_at	---
5.18	5.35	0.17	6.26E-01	8.65E-01	STAT1	signal transducer and activator of transcription 1, 91kDa	chr2q32.2	AFFX-HUMISGF3A/M97935_MA_at	NM_007315 /// NM_139266
2.45	2.52	0.08	6.26E-01	8.65E-01	---	---	---	1563340_at	---
2.15	2.22	0.07	6.26E-01	8.65E-01	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	chr13q12-q14	206566_at	NM_003045
3.05	3.18	0.13	6.26E-01	8.65E-01	CEP350	centrosomal protein 350kDa	chr1p36.13-q41	213957_s_at	NM_014810
2.32	2.39	0.07	6.26E-01	8.65E-01	LOC283624	Hypothetical protein LOC283624	chr14q11.2	240902_at	---
3.29	3.37	0.08	6.26E-01	8.65E-01	---	---	---	234070_at	---
2.08	2.15	0.07	6.27E-01	8.65E-01	ZNF396	zinc finger protein 396	chr18q12	1552825_at	NM_145756
2.79	2.86	0.07	6.27E-01	8.65E-01	FGF19	fibroblast growth factor 19	chr11q13.1	223761_at	NM_005117
6.38	6.48	0.10	6.27E-01	8.65E-01	KIAA0319L	KIAA0319-like	chr1p34.2	217929_s_at	NM_024874 /// NM_182686
5.62	5.77	0.15	6.27E-01	8.65E-01	C6orf130	chromosome 6 open reading frame 130	chr6p21.1	213322_at	NM_145063
3.32	3.45	0.14	6.27E-01	8.65E-01	UTX	ubiquitously transcribed tetratricopeptide repeat, X chromosome	chrXp11.2	203990_s_at	NM_021140
5.65	5.78	0.13	6.27E-01	8.65E-01	UNC5B	unc-5 homolog B (C. elegans)	chr10q22.1	226899_at	NM_170744
2.54	2.63	0.09	6.27E-01	8.65E-01	OR10C1	olfactory receptor, family 10, subfamily C, member 1	chr6p22.1	221339_at	NM_013941
1.94	1.99	0.06	6.27E-01	8.65E-01	---	---	---	1555344_at	---
2.80	2.89	0.10	6.27E-01	8.65E-01	C6orf35 /// LOC730074	chromosome 6 open reading frame 35 /// hypothetical LOC730074	chr6q25.3	230457_at	NM_018452 /// XM_001133047 /// XM_001713717

4.33	4.43	0.09	6.27E-01	8.65E-01	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)	chr11q22.3	237040_at	NM_152434
3.10	3.19	0.08	6.27E-01	8.65E-01	RIMS3	regulating synaptic membrane exocytosis 3	chr1pter-p22.2	210991_s_at	NM_014747
7.32	7.40	0.08	6.27E-01	8.65E-01	---	---	---	233702_x_at	---
2.28	2.35	0.08	6.27E-01	8.65E-01	---	---	---	235229_at	---
2.82	2.89	0.07	6.27E-01	8.65E-01	LOC100132971	hypothetical protein LOC100132971	chr10q26.13	240283_at	XM_001713948
2.84	2.91	0.07	6.27E-01	8.65E-01	S1PR5	sphingosine-1-phosphate receptor 5	chr19p13.2	233743_x_at	NM_030760
1.92	1.98	0.06	6.27E-01	8.65E-01	LOC145663	hypothetical protein LOC145663	chr15q15.1	1566860_at	---
4.69	4.83	0.14	6.27E-01	8.65E-01	CEP170	centrosomal protein 170kDa	chr1q44	207719_x_at	NM_001042404 /// NM_001042405 /// NM_014812
3.74	3.81	0.07	6.27E-01	8.65E-01	MAPK12	mitogen-activated protein kinase 12	chr22q13.33	1556341_s_at	NM_002969
2.87	2.93	0.06	6.27E-01	8.65E-01	---	---	---	234183_at	---
2.00	2.06	0.06	6.27E-01	8.65E-01	---	---	---	216136_at	---
3.05	3.15	0.10	6.27E-01	8.66E-01	LOC728377	similar to rho guanine nucleotide exchange factor 5	chr7q35	228596_at	XR_041051 /// XR_041052
2.62	2.69	0.07	6.27E-01	8.66E-01	---	---	---	243721_at	---
3.42	3.56	0.14	6.27E-01	8.66E-01	GLCE	glucuronic acid epimerase	chr15q23	213552_at	NM_015554
2.63	2.71	0.08	6.27E-01	8.66E-01	---	---	---	216292_at	---
7.25	7.43	0.17	6.27E-01	8.66E-01	BXDC5	brix domain containing 5	chr1p22.3	218462_at	NM_025065
7.92	8.07	0.15	6.28E-01	8.66E-01	FKBP1A	FK506 binding protein 1A, 12kDa	chr20p13	214119_s_at	NM_000801 /// NM_054014
2.70	2.81	0.11	6.28E-01	8.66E-01	---	---	---	1558474_at	---
2.11	2.17	0.07	6.27E-01	8.66E-01	FARSB	phenylalanyl-tRNA synthetase, beta subunit	chr2q36.1	223036_at	NM_005687
2.19	2.26	0.07	6.27E-01	8.66E-01	---	---	---	233546_at	---
3.17	3.24	0.07	6.27E-01	8.66E-01	LOC100134355 /// PRIM2	similar to Primase, DNA, polypeptide 2 (58kDa) /// primase, DNA, polypeptide 2 (58kDa)	chr6p12-p11.1	215709_at	NM_000947 /// XR_037800
2.07	2.12	0.06	6.28E-01	8.66E-01	---	---	---	1562306_at	---
2.06	2.11	0.05	6.28E-01	8.66E-01	---	---	---	237780_at	---
2.53	2.59	0.05	6.28E-01	8.66E-01	LOC100128239	hypothetical LOC100128239	chr11q25	238872_at	XM_001720464 /// XM_001726645 /// XM_001726660
5.24	5.51	0.27	6.28E-01	8.66E-01	MBNL2	muscleblind-like 2 (Drosophila)	chr13q32.1	205017_s_at	NM_144778 /// NM_207304
8.19	8.32	0.12	6.28E-01	8.66E-01	QDPR	quinoid dihydropteridine reductase	chr4p15.31	209123_at	NM_000320
2.08	2.16	0.08	6.28E-01	8.66E-01	TNIP3	TNFAIP3 interacting protein 3	chr4q27	220655_at	NM_001128843 /// NM_024873
3.43	3.50	0.07	6.28E-01	8.66E-01	CAPN12	calpain 12	chr19q13.2	228705_at	NM_144691
4.79	4.87	0.08	6.28E-01	8.66E-01	LOC255654	hypothetical protein LOC255654	chr1q44	1563074_at	---
2.07	2.13	0.06	6.28E-01	8.66E-01	LOC100133308	Ras suppressor protein 1 pseudogene	chr10q11.21	1561482_at	XM_001717581
1.84	1.90	0.06	6.28E-01	8.66E-01	---	---	---	1568919_at	---
4.25	4.37	0.12	6.28E-01	8.66E-01	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	chr3p21.3	201905_s_at	NM_001008392 /// NM_005808
2.68	2.79	0.11	6.28E-01	8.66E-01	SLC25A13	Solute carrier family 25, member 13 (citrin)	chr7q21.3	229081_at	NM_014251
3.22	3.30	0.08	6.28E-01	8.66E-01	KRT9	keratin 9	chr17q21.1-q21.2	208188_at	NM_000226
2.49	2.56	0.07	6.28E-01	8.66E-01	OR51M1	olfactory receptor, family 51, subfamily M, member 1	chr11p15.4	234777_at	NM_001004756
4.22	4.36	0.15	6.28E-01	8.66E-01	TUBGCP4	tubulin, gamma complex associated protein 4	chr15q15	211337_s_at	NM_014444
7.44	7.68	0.24	6.28E-01	8.66E-01	SELM	selenoprotein M	chr22q12.2	226051_at	NM_080430
8.76	8.88	0.12	6.28E-01	8.66E-01	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	chr5q31.3-q32	212667_at	NM_003118
2.98	3.09	0.11	6.28E-01	8.66E-01	SUGT1P	suppressor of G2 allele of SKP1 pseudogene (S. cerevisiae)	chr9p13.3	1555614_at	NR_003667 /// XR_000597
3.08	3.18	0.10	6.28E-01	8.66E-01	ASXL3	additional sex combs like 3 (Drosophila)	chr18q11	232838_at	NM_030632
3.37	3.46	0.09	6.28E-01	8.66E-01	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	chr1q43-q44	219393_s_at	NM_005465 /// NM_181690
2.14	2.21	0.08	6.28E-01	8.66E-01	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	chr7p15.3	1563882_a_at	NM_012294
4.21	4.28	0.08	6.28E-01	8.66E-01	ASGR2	asialoglycoprotein receptor 2	chr17p	206130_s_at	NM_001181 /// NM_080912 /// NM_080913 /// NM_080914
1.99	2.04	0.06	6.28E-01	8.66E-01	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	chr22q11.2|22q11.21	1569560_at	NM_003325
7.61	7.74	0.13	6.29E-01	8.66E-01	PPAP2A	phosphatidic acid phosphatase type 2A	chr5q11	210946_at	NM_003711 /// NM_176895
12.86	12.98	0.11	6.29E-01	8.66E-01	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	chr6q14.1	204892_x_at	NM_001402
2.19	2.27	0.08	6.29E-01	8.66E-01	---	---	---	244883_at	---
2.12	2.19	0.07	6.29E-01	8.66E-01	---	---	---	234260_at	---
4.86	5.15	0.28	6.29E-01	8.66E-01	GSTM3	glutathione S-transferase M3 (brain)	chr1p13.3	235867_at	NM_000849
2.83	2.92	0.08	6.29E-01	8.66E-01	---	---	---	1555129_at	---

2.66	2.73	0.07	6.29E-01	8.66E-01	---	---	---	241281_at	---
2.23	2.29	0.06	6.29E-01	8.66E-01	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	chr7q21.1	210755_at	NM_000601 /// NM_001010931 /// NM_001010932 /// NM_001010933 /// NM_001010934
2.59	2.68	0.10	6.29E-01	8.66E-01	SUB1	SUB1 homolog (S. cerevisiae)	chr5p13.3	237784_at	NM_006713
4.00	4.08	0.09	6.29E-01	8.66E-01	---	---	---	237004_at	---
3.67	3.76	0.10	6.29E-01	8.66E-01	---	---	---	229316_at	---
1.98	2.03	0.06	6.29E-01	8.66E-01	---	---	---	1561593_at	---
4.28	4.48	0.19	6.29E-01	8.66E-01	HPS3	Hermansky-Pudlak syndrome 3	chr3q24	238539_at	NM_032383
6.94	7.12	0.18	6.29E-01	8.66E-01	---	---	---	226191_at	---
2.76	2.85	0.08	6.29E-01	8.66E-01	---	---	---	236985_at	---
3.05	3.12	0.07	6.29E-01	8.66E-01	---	---	---	240281_at	---
4.49	4.62	0.13	6.29E-01	8.66E-01	MTA3	metastasis associated 1 family, member 3	chr2p21	226852_at	NM_020744
2.47	2.53	0.06	6.29E-01	8.66E-01	KIAA0802	KIAA0802	chr18p11.22	213358_at	NM_015210
4.43	4.61	0.19	6.29E-01	8.66E-01	SGMS1	sphingomyelin synthase 1	chr10q11.2	212989_at	NM_147156
2.47	2.53	0.05	6.29E-01	8.66E-01	---	---	---	1566689_at	---
2.48	2.57	0.09	6.29E-01	8.66E-01	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	chr10p13	221546_at	NM_003675
5.42	5.54	0.12	6.29E-01	8.66E-01	STBD1	starch binding domain 1	chr4q24-q25	203986_at	NM_003943
8.17	8.33	0.16	6.30E-01	8.66E-01	HBP1	HMG-box transcription factor 1	chr7q22-q31	209102_s_at	NM_012257
6.48	6.64	0.15	6.30E-01	8.66E-01	---	---	---	229647_at	---
7.48	7.59	0.11	6.30E-01	8.66E-01	RBKS	ribokinase	chr2p23.3	219222_at	NM_022128
3.00	3.10	0.10	6.30E-01	8.66E-01	EML4	Echinoderm microtubule associated protein like 4	chr2p22-p21	1556732_at	NM_019063
2.22	2.32	0.10	6.30E-01	8.66E-01	INTS4	integrator complex subunit 4	chr11q14.1	1553670_at	NM_033547
3.99	4.08	0.09	6.30E-01	8.66E-01	HFE	hemochromatosis	chr6p21.3	211331_x_at	NM_000410 /// NM_139003 /// NM_139004 /// NM_139006 /// NM_139007 /// NM_139008 /// NM_139009 /// NM_139010 /// NM_139011
3.53	3.62	0.09	6.30E-01	8.66E-01	CENPM	centromere protein M	chr22q13.2	218741_at	NM_001002876 /// NM_001110215 /// NM_024053
2.61	2.69	0.08	6.30E-01	8.66E-01	---	---	---	1565644_at	---
1.91	1.97	0.06	6.30E-01	8.66E-01	---	---	---	1561351_at	---
7.86	8.06	0.20	6.30E-01	8.66E-01	C19orf2	chromosome 19 open reading frame 2	chr19q12	214173_x_at	NM_003796 /// NM_134447
7.36	7.49	0.13	6.30E-01	8.66E-01	SEC24A	SEC24 related gene family, member A (S. cerevisiae)	chr5q31.1	212900_at	NM_021982
3.89	4.06	0.17	6.30E-01	8.67E-01	RPESP	RPE-spondin	chr8q21.11	235210_s_at	NM_153225
4.12	4.29	0.17	6.30E-01	8.67E-01	USP48	ubiquitin specific peptidase 48	chr1p36.12	229812_at	NM_001032730 /// NM_032236
4.85	4.97	0.12	6.30E-01	8.67E-01	LETM1	leucine zipper-EF-hand containing transmembrane protein 1	chr4p16.3	218939_at	NM_012318
6.13	6.23	0.10	6.30E-01	8.67E-01	UQCC	ubiquinol-cytochrome c reductase complex chaperone	chr20q11.22	222470_s_at	NM_018244 /// NM_199487
2.44	2.52	0.08	6.30E-01	8.67E-01	GNAS	GNAS complex locus	chr20q13.3	217057_s_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259
1.91	1.97	0.06	6.30E-01	8.67E-01	---	---	---	1562095_at	---
1.99	2.04	0.05	6.30E-01	8.67E-01	RIG	regulated in glioma	chr11p15.1	221126_at	XM_932493 /// XM_944753
5.16	5.34	0.18	6.30E-01	8.67E-01	MAP3K8	Mitogen-activated protein kinase kinase kinase 8	chr10p11.23	235421_at	NM_005204
9.90	9.98	0.08	6.30E-01	8.67E-01	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	chr2p25.1	213699_s_at	NM_006826
2.65	2.72	0.07	6.30E-01	8.67E-01	SSX3	synovial sarcoma, X breakpoint 3	chrXp11.23	211731_x_at	NM_021014 /// NM_175711

2.32	2.37	0.05	6.30E-01	8.67E-01	IL1F8	interleukin 1 family, member 8 (eta)	chr2q12-q14.1	224230_at	NM_014438 /// NM_173178
9.54	9.67	0.13	6.30E-01	8.67E-01	DDB1	damage-specific DNA binding protein 1, 127kDa	chr11q12-q13	208619_at	NM_001923
2.97	3.05	0.08	6.30E-01	8.67E-01	TTC30A	tetratricopeptide repeat domain 30A	chr2q31.2	213679_at	NM_152275
3.64	3.71	0.07	6.30E-01	8.67E-01	ARS2	arsenate resistance protein 2	chr7q21	222046_at	NM_001128852 /// NM_001128853 /// NM_001128854 /// NM_015908 /// NM_182800
2.04	2.10	0.06	6.30E-01	8.67E-01	C6orf146 /// LOC100128499	chromosome 6 open reading frame 146 /// hypothetical protein LOC100128499	chr6p25.2	1560838_at	NM_173563 /// XM_001714481 /// XM_001718202 /// XM_001718333
6.24	6.35	0.11	6.30E-01	8.67E-01	SLC25A44	solute carrier family 25, member 44	chr1q22	212683_at	NM_014655
1.95	2.00	0.05	6.30E-01	8.67E-01	CALCRL	calcitonin receptor-like	chr2q32.1	234996_at	NM_005795
3.00	3.08	0.08	6.31E-01	8.67E-01	SH2D1A	SH2 domain protein 1A	chrXq25-q26	211210_x_at	NM_001114937 /// NM_002351
2.12	2.18	0.07	6.31E-01	8.67E-01	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	chr7q31.2	217026_at	NM_000492
3.53	3.64	0.11	6.31E-01	8.67E-01	VMO1	vitelline membrane outer layer 1 homolog (chicken)	chr17p13.2	241894_at	NM_182566
2.17	2.24	0.06	6.31E-01	8.67E-01	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	chr15q22.2	232386_at	NM_001018088 /// NM_017684 /// NM_018080 /// NM_020821
3.69	3.77	0.08	6.31E-01	8.67E-01	MFGE8	milk fat globule-EGF factor 8 protein	chr15q25	1567540_at	NM_001114614 /// NM_005928
4.43	4.51	0.08	6.31E-01	8.67E-01	HIC2	hypermethylated in cancer 2	chr22q11.21	216911_s_at	NM_015094
3.84	3.94	0.10	6.31E-01	8.67E-01	LHX6	LIM homeobox 6	chr9q33.2	224556_s_at	NM_014368 /// NM_199160
3.48	3.57	0.09	6.31E-01	8.67E-01	---	---	---	1554752_a_at	---
3.54	3.62	0.08	6.31E-01	8.67E-01	CHN2	chimerin (chimaerin) 2	chr7p15.3	207486_x_at	NM_001039936 /// NM_004067
2.21	2.28	0.08	6.31E-01	8.67E-01	---	---	---	234690_at	---
5.33	5.63	0.31	6.31E-01	8.67E-01	PHACTR2	phosphatase and actin regulator 2	chr6q24.2	204047_s_at	NM_001100164 /// NM_001100165 /// NM_001100166 /// NM_014721
2.52	2.61	0.09	6.31E-01	8.67E-01	STMN4	stathmin-like 4	chr8p21.2	221236_s_at	NM_030795
2.17	2.24	0.07	6.31E-01	8.67E-01	SATB2	SATB homeobox 2	chr2q33	215591_at	NM_015265
6.26	6.45	0.19	6.31E-01	8.67E-01	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	chr14q32.1	202376_at	NM_001085
10.06	10.17	0.11	6.31E-01	8.67E-01	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	chr22q13.2-q13.31	200792_at	NM_001469
5.62	5.81	0.19	6.31E-01	8.67E-01	C11orf54	chromosome 11 open reading frame 54	chr11q21	229851_s_at	NM_014039
2.60	2.69	0.09	6.31E-01	8.67E-01	MAS1	MAS1 oncogene	chr6q25.3-q26	208210_at	NM_002377
5.08	5.24	0.16	6.31E-01	8.67E-01	CSNK1A1	casein kinase 1, alpha 1	chr5q32	208866_at	NM_001025105 /// NM_001892
2.74	2.84	0.09	6.31E-01	8.67E-01	KIAA1659	KIAA1659 protein	---	215750_at	XM_001723799 /// XM_001725435 /// XM_001726785
8.14	8.20	0.06	6.31E-01	8.67E-01	---	---	---	220856_x_at	---
4.44	4.71	0.28	6.32E-01	8.68E-01	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	chr10q23.3	222562_s_at	NM_025235
5.65	5.79	0.13	6.32E-01	8.68E-01	BIRC6	baculoviral IAP repeat-containing 6	chr2p22-p21	233093_s_at	NM_016252
2.46	2.54	0.08	6.32E-01	8.68E-01	---	---	---	1557026_at	---
4.84	4.92	0.08	6.32E-01	8.68E-01	ZNF445	zinc finger protein 445	chr3p21.32	233992_x_at	NM_181489
2.59	2.66	0.07	6.32E-01	8.68E-01	CHD6	chromodomain helicase DNA binding protein 6	chr20q12	1555463_a_at	NM_032221
4.10	4.17	0.06	6.32E-01	8.68E-01	LOC100129656	hypothetical protein LOC100129656	chr1q44	221639_x_at	XM_001717015 /// XM_001717020
3.75	3.90	0.16	6.32E-01	8.68E-01	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	chr2q23.3	209649_at	NM_005843

2.92	3.01	0.09	6.32E-01	8.68E-01	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	chr1q32.2	201510_at	NM_001114309 /// NM_004433
3.70	3.78	0.08	6.32E-01	8.68E-01	C16orf71	chromosome 16 open reading frame 71	chr16p13.3	222089_s_at	NM_139170
2.59	2.66	0.07	6.32E-01	8.68E-01	---	---	---	239578_at	---
1.88	1.94	0.06	6.32E-01	8.68E-01	ZNF277	zinc finger protein 277	chr7q31.1	1555192_at	NM_021994
2.13	2.18	0.05	6.32E-01	8.68E-01	MGC11082	hypothetical LOC84777	chr18p11.31	1560019_at	---
3.20	3.27	0.07	6.32E-01	8.68E-01	IFT52	intraflagellar transport 52 homolog (Chlamydomonas)	---	233532_x_at	NM_016004
4.40	4.48	0.07	6.32E-01	8.68E-01	FBF1	Fas (TNFRSF6) binding factor 1	chr17q25.1	1554468_s_at	NM_001080542
2.02	2.07	0.06	6.32E-01	8.68E-01	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	chr21q21.3	1558636_s_at	NM_007038
2.80	2.87	0.07	6.32E-01	8.68E-01	RP2	retinitis pigmentosa 2 (X-linked recessive)	chrXp11.4-p11.21	205191_at	NM_006915
5.31	5.40	0.09	6.32E-01	8.68E-01	ADCK2	aarF domain containing kinase 2	chr7q32-q34	221894_at	NM_052853
2.00	2.05	0.06	6.32E-01	8.68E-01	LOC338579	hypothetical protein LOC338579	chr10q11.21	1570474_s_at	XM_936973
1.94	1.99	0.05	6.32E-01	8.68E-01	---	---	---	1562520_at	---
3.34	3.44	0.10	6.32E-01	8.68E-01	---	---	---	1562487_at	---
2.23	2.30	0.07	6.32E-01	8.68E-01	TAAR2	trace amine associated receptor 2	chr6q24	221394_at	NM_001033080 /// NM_014626
2.47	2.53	0.06	6.32E-01	8.68E-01	---	---	---	1561035_at	---
3.22	3.29	0.07	6.32E-01	8.68E-01	---	---	---	238223_at	---
4.89	5.08	0.19	6.33E-01	8.68E-01	CCDC74A /// CCDC74B	coiled-coil domain containing 74A /// coiled-coil domain containing 74B	chr2q21.1	227966_s_at	NM_138770 /// NM_207310
2.23	2.28	0.05	6.33E-01	8.68E-01	SLC39A8	solute carrier family 39 (zinc transporter), member 8	chr4q22-q24	216504_s_at	NM_022154
8.60	8.71	0.11	6.33E-01	8.68E-01	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	chr1p13.2	208374_s_at	NM_006135
3.25	3.37	0.12	6.33E-01	8.68E-01	TTTY5	testis-specific transcript, Y-linked 5	chrYq11.223	224040_at	NR_001541
2.07	2.14	0.06	6.33E-01	8.68E-01	---	---	---	224047_at	---
2.97	3.03	0.06	6.33E-01	8.68E-01	ZSCAN12L1	zinc finger and SCAN domain containing 12-like 1	chr6p21.33	239157_at	NR_024063
2.57	2.63	0.06	6.33E-01	8.68E-01	PCSK6	proprotein convertase subtilisin/kexin type 6	chr15q26.3	1553531_at	NM_002570 /// NM_138319 /// NM_138320 /// NM_138321 /// NM_138322 /// NM_138323 /// NM_138324 /// NM_138325
2.42	2.52	0.09	6.33E-01	8.68E-01	---	---	---	1556932_at	---
2.17	2.23	0.05	6.33E-01	8.68E-01	---	---	---	1566114_at	---
2.58	2.65	0.07	6.33E-01	8.68E-01	WWC2	WW and C2 domain containing 2	chr4q35.1	237656_at	NM_024949
6.81	6.89	0.07	6.33E-01	8.68E-01	FKBP15	FK506 binding protein 15, 133kDa	chr9q32	212663_at	NM_015258
3.41	3.48	0.07	6.33E-01	8.69E-01	---	---	---	234879_at	---
9.23	9.38	0.14	6.33E-01	8.69E-01	DSTN	destrin (actin depolymerizing factor)	chr20p12.1	201021_s_at	NM_001011546 /// NM_006870
5.70	5.80	0.10	6.33E-01	8.69E-01	TMEM110	Transmembrane protein 110	chr3p21.1	227078_at	NM_198563
3.16	3.25	0.09	6.33E-01	8.69E-01	LILRA1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	chr19q13.4	207872_s_at	NM_006863
2.13	2.19	0.06	6.33E-01	8.69E-01	---	---	---	1556917_a_at	---
2.13	2.18	0.06	6.33E-01	8.69E-01	NHLH2	nescient helix loop helix 2	chr1p12-p11	215228_at	NM_001111061 /// NM_005599
5.92	6.27	0.35	6.33E-01	8.69E-01	NAMPT	nicotinamide phosphoribosyltransferase	chr7q22.2	217739_s_at	NM_005746
2.92	3.01	0.09	6.33E-01	8.69E-01	LMLN	leishmanolysin-like (metallopeptidase M8 family)	chr3q29	238037_at	NM_033029
2.16	2.23	0.07	6.33E-01	8.69E-01	LOC553137	Hypothetical LOC553137	chr6q21	237889_s_at	NR_015365 /// XR_001059 /// XR_001268
4.02	4.20	0.18	6.33E-01	8.69E-01	---	---	---	237330_at	---
2.28	2.34	0.07	6.33E-01	8.69E-01	---	---	---	216477_at	---
1.88	1.94	0.05	6.33E-01	8.69E-01	ENAM	Enamelin	chr4q13.3	240586_at	NM_031889
3.08	3.27	0.19	6.34E-01	8.69E-01	CETP	cholesteryl ester transfer protein, plasma	chr16q21	206210_s_at	NM_000078
3.27	3.34	0.08	6.34E-01	8.69E-01	RGR	retinal G protein coupled receptor	chr10q23	207070_at	NM_001012720 /// NM_001012722 /// NM_002921
2.04	2.10	0.06	6.34E-01	8.69E-01	---	---	---	1558852_at	---
4.85	5.06	0.21	6.34E-01	8.69E-01	LRRC8C	leucine rich repeat containing 8 family, member C	chr1p22.2	228314_at	NM_032270
3.12	3.22	0.10	6.34E-01	8.69E-01	GUK1	Guanylate kinase 1	chr1q32-q41	213621_s_at	NM_000858
2.37	2.43	0.06	6.34E-01	8.69E-01	---	---	---	213968_at	---
5.68	5.83	0.15	6.34E-01	8.69E-01	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	chr14q24.3-q31	203128_at	NM_004863
2.00	2.08	0.08	6.34E-01	8.69E-01	---	---	---	242067_at	---
3.83	3.91	0.08	6.34E-01	8.69E-01	---	---	---	239932_at	---
3.17	3.23	0.06	6.34E-01	8.69E-01	---	---	---	240672_at	---
6.25	6.47	0.22	6.34E-01	8.69E-01	ATXN7	ataxin 7	chr3p21.1-p12	209964_s_at	NM_000333 /// NM_001128149

3.22	3.28	0.05	6.34E-01	8.69E-01	FGF23	fibroblast growth factor 23	chr12p13.3	221166_at	NM_020638
5.59	5.89	0.30	6.34E-01	8.69E-01	---	---	---	217617_at	---
2.15	2.20	0.06	6.34E-01	8.69E-01	---	---	---	1562152_at	---
2.00	2.06	0.05	6.34E-01	8.69E-01	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	chr22q13.1-q13.2	210873_x_at	NM_145699
2.90	2.97	0.07	6.34E-01	8.69E-01	---	---	---	1558604_a_at	---
2.87	2.93	0.07	6.34E-01	8.69E-01	---	---	---	241301_at	---
2.03	2.10	0.08	6.34E-01	8.69E-01	---	---	---	236544_at	---
4.22	4.33	0.11	6.34E-01	8.69E-01	ZBTB39	zinc finger and BTB domain containing 39	chr12q13.3	205256_at	NM_014830
5.13	5.23	0.11	6.34E-01	8.69E-01	DDA1	DET1 and DDB1 associated 1	chr19p13.11	227472_at	NM_024050
3.54	3.62	0.08	6.35E-01	8.69E-01	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	chr7q22.1	1558179_at	NM_001003713 /// NM_001003714 /// NM_001039178 /// NM_004889
6.01	6.27	0.26	6.35E-01	8.69E-01	DCTN4	dynactin 4 (p62)	chr5q31-q32	218013_x_at	NM_016221
2.89	3.02	0.13	6.35E-01	8.69E-01	IL2RA	interleukin 2 receptor, alpha	chr10p15-p14	211269_s_at	NM_000417
4.28	4.40	0.12	6.35E-01	8.69E-01	ZNF187	zinc finger protein 187	chr6p21.31	213218_at	NM_001023560 /// NM_001111039 /// NM_152736
2.17	2.26	0.08	6.35E-01	8.69E-01	CD24	CD24 molecule	chr6q21	208650_s_at	NM_013230 /// XM_001725629
2.07	2.14	0.07	6.35E-01	8.69E-01	---	---	---	1570022_at	---
4.34	4.41	0.07	6.35E-01	8.69E-01	---	---	---	1569294_at	---
2.46	2.54	0.08	6.35E-01	8.69E-01	NEFL	neurofilament, light polypeptide 68kDa	chr8p21	221801_x_at	NM_006158
2.28	2.34	0.06	6.35E-01	8.69E-01	---	---	---	230299_s_at	---
1.91	1.98	0.06	6.35E-01	8.69E-01	EVI1	ecotropic viral integration site 1	chr3q24-q28	243277_x_at	NM_001105077 /// NM_001105078 /// NM_005241
2.19	2.25	0.06	6.35E-01	8.69E-01	---	---	---	234614_at	---
7.73	7.88	0.15	6.35E-01	8.69E-01	PLS3	plastin 3 (T isoform)	chrXq23	201215_at	NM_005032
5.59	5.71	0.12	6.35E-01	8.70E-01	LOC729970	hypothetical LOC729970	chr1p21.3	230433_at	XM_001129522 /// XM_001134179 /// XM_001720397
4.42	4.48	0.06	6.35E-01	8.70E-01	DLL3	Delta-like 3 (Drosophila)	chr19q13	229755_x_at	NM_016941 /// NM_203486
2.54	2.60	0.07	6.35E-01	8.70E-01	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	chr12q24.2	207359_at	NM_006549 /// NM_153499 /// NM_153500 /// NM_172214 /// NM_172215 /// NM_172216 /// NM_172226
7.76	7.91	0.15	6.35E-01	8.70E-01	PDCD6IP	programmed cell death 6 interacting protein	chr3p22.3	217746_s_at	NM_013374
2.14	2.21	0.06	6.35E-01	8.70E-01	SH3TC2	SH3 domain and tetratricopeptide repeats 2	chr5q32	219710_at	NM_024577
2.33	2.42	0.09	6.35E-01	8.70E-01	STK38	Serine/threonine kinase 38	chr6p21	216727_at	NM_007271
3.59	3.66	0.07	6.35E-01	8.70E-01	LOC339988	hypothetical protein LOC339988	chr4p16.1	1562697_at	---
8.06	8.19	0.13	6.35E-01	8.70E-01	PDIA6	protein disulfide isomerase family A, member 6	chr2p25.1	207668_x_at	NM_005742
2.58	2.68	0.09	6.35E-01	8.70E-01	ANKLE2	Ankyrin repeat and LEM domain containing 2	chr12q24.33	213962_s_at	NM_015114
1.99	2.04	0.05	6.35E-01	8.70E-01	---	---	---	238748_at	---
2.23	2.31	0.08	6.36E-01	8.70E-01	LOC285441	hypothetical protein LOC285441	chr4q35.2	1557233_at	---
2.31	2.38	0.07	6.36E-01	8.70E-01	---	---	---	231607_at	---
2.05	2.10	0.06	6.36E-01	8.70E-01	---	---	---	237168_at	---
4.48	4.74	0.26	6.36E-01	8.70E-01	PTPRC	protein tyrosine phosphatase, receptor type, C	chr1q31-q32	207238_s_at	NM_002838 /// NM_080921 /// NM_080922 /// NM_080923
7.08	7.19	0.11	6.36E-01	8.70E-01	MEGF8	multiple EGF-like-domains 8	chr19q12	227327_at	NM_001410
2.26	2.37	0.11	6.36E-01	8.70E-01	LOC100130428	Similar to IGYY565	chr11q24.2	236059_at	XM_001717173 /// XM_001726476 /// XM_001726507
2.60	2.70	0.10	6.36E-01	8.70E-01	KIF20A	kinesin family member 20A	chr5q31	218755_at	NM_005733
2.54	2.64	0.10	6.36E-01	8.70E-01	---	---	---	238338_at	---
2.67	2.76	0.09	6.36E-01	8.70E-01	---	---	---	1559375_s_at	---

2.52	2.59	0.08	6.36E-01	8.70E-01	---	---	---	215378_at	---
2.58	2.65	0.06	6.36E-01	8.70E-01	LOC642924	hypothetical protein LOC642924	chr8q22.1	238244_at	XM_931168
2.63	2.69	0.06	6.36E-01	8.70E-01	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	chr11q23.1	216615_s_at	NM_000869 /// NM_213621
2.58	2.66	0.08	6.36E-01	8.70E-01	C6orf151	chromosome 6 open reading frame 151	chr6p24.3	1553274_a_at	NM_152551
2.40	2.46	0.06	6.36E-01	8.70E-01	CCDC23	Coiled-coil domain containing 23	chr1p34.2	244013_at	NM_199342
2.46	2.62	0.16	6.36E-01	8.70E-01	FNDC3B	fibronectin type III domain containing 3B	chr3q26.31	222693_at	NM_022763
4.01	4.14	0.13	6.36E-01	8.70E-01	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	chr14q24.3	1554930_a_at	NM_004480 /// NM_178154 /// NM_178155 /// NM_178156 /// NM_178157
3.49	3.59	0.10	6.36E-01	8.70E-01	HIGD1A	HIG1 domain family, member 1A	chr3p22.1	242317_at	NM_001099668 /// NM_001099669 /// NM_014056
2.32	2.39	0.08	6.36E-01	8.70E-01	---	---	---	240534_at	---
5.65	5.84	0.20	6.37E-01	8.70E-01	ZNF644	zinc finger protein 644	chr1p22.2	222580_at	NM_016620 /// NM_032186 /// NM_201269
3.25	3.39	0.14	6.37E-01	8.70E-01	RAB30	RAB30, member RAS oncogene family	chr11q12-q14	227842_at	NM_014488
3.69	3.79	0.10	6.37E-01	8.70E-01	ZNF777	zinc finger protein 777	chr7q36.1	226983_at	NM_015694
2.84	2.93	0.09	6.37E-01	8.70E-01	---	---	---	240803_at	---
4.27	4.35	0.08	6.37E-01	8.70E-01	NT5DC3	5'-nucleotidase domain containing 3	chr12q22-q23.1	218786_at	NM_001031701 /// NM_016575
2.00	2.09	0.08	6.37E-01	8.70E-01	---	---	---	229951_x_at	---
2.38	2.46	0.08	6.37E-01	8.70E-01	---	---	---	240755_at	---
3.40	3.47	0.07	6.37E-01	8.70E-01	CNKSR1	connector enhancer of kinase suppressor of Ras 1	chr1p36.11	204740_at	NM_006314 /// NR_023345
2.38	2.46	0.07	6.37E-01	8.70E-01	RAB40C	RAB40C, member RAS oncogene family	chr16p13.3	227269_s_at	NM_021168
2.13	2.20	0.07	6.37E-01	8.70E-01	EIF5A2	eukaryotic translation initiation factor 5A2	chr3q26.2	235289_at	NM_020390
2.64	2.70	0.06	6.37E-01	8.70E-01	GPM6A	glycoprotein M6A	chr4q34	236024_at	NM_005277 /// NM_201591 /// NM_201592
2.28	2.34	0.06	6.37E-01	8.70E-01	OBSL1	obscurin-like 1	chr2q35	214928_at	NM_015311
3.04	3.09	0.05	6.37E-01	8.70E-01	---	---	---	230975_at	---
2.59	2.67	0.07	6.37E-01	8.70E-01	ANKRD50	ankyrin repeat domain 50	chr4q28.1	236189_at	NM_020337
2.77	2.83	0.06	6.37E-01	8.70E-01	---	---	---	1563068_at	---
5.62	5.71	0.08	6.37E-01	8.70E-01	KIAA0999	KIAA0999 protein	chr11q23.3	204155_s_at	NM_025164
2.01	2.06	0.05	6.37E-01	8.70E-01	---	---	---	1561363_a_at	---
4.43	4.50	0.07	6.37E-01	8.70E-01	IGSF3	immunoglobulin superfamily, member 3	chr1p13	1556162_at	NM_001007237 /// NM_001542
2.65	2.71	0.06	6.37E-01	8.70E-01	PDLIM2	PDZ and LIM domain 2 (mystique)	chr8p21.2	232302_at	NM_021630 /// NM_176871 /// NM_198042
8.10	8.30	0.19	6.37E-01	8.70E-01	C14orf147	chromosome 14 open reading frame 147	chr14q13.1	213508_at	NM_138288
7.37	7.51	0.14	6.37E-01	8.70E-01	SH3GLB1	SH3-domain GRB2-like endophilin B1	chr1p22	209091_s_at	NM_016009
8.60	8.69	0.09	6.37E-01	8.70E-01	ETFB	electron-transfer-flavoprotein, beta polypeptide	chr19q13.3	202942_at	NM_001014763 /// NM_001985
3.60	3.77	0.16	6.37E-01	8.71E-01	SLC25A13	solute carrier family 25, member 13 (citrin)	chr7q21.3	229061_s_at	NM_014251
4.77	4.99	0.22	6.37E-01	8.71E-01	OLFML2B	olfactomedin-like 2B	chr1q23.3	213125_at	NM_015441
1.83	1.88	0.05	6.37E-01	8.71E-01	PSMG4	proteasome (prosome, macropain) assembly chaperone 4	chr6p25.2	242623_x_at	NM_001128591 /// NM_001128592 /// XR_017743 /// XR_017905 /// XR_041314
7.67	7.90	0.23	6.38E-01	8.71E-01	LOC100133166 /// NBR1	similar to neighbor of BRCA1 gene 1 /// neighbor of BRCA1 gene 1	chr17q21.31	201384_s_at	NM_005899 /// NM_031858 /// NM_031862 /// XM_001719040
5.05	5.23	0.17	6.38E-01	8.71E-01	GRB10	growth factor receptor-bound protein 10	chr7p12-p11.2	210999_s_at	NM_001001549 /// NM_001001550 /// NM_001001555 /// NM_005311
4.04	4.19	0.15	6.38E-01	8.71E-01	CCDC34	coiled-coil domain containing 34	chr11p14.1	226287_at	NM_030771 /// NM_080654
2.02	2.10	0.09	6.38E-01	8.71E-01	---	---	---	231464_at	---
4.19	4.27	0.09	6.38E-01	8.71E-01	C1orf172	chromosome 1 open reading frame 172	chr1p36.11	236058_at	NM_152365

2.92	2.98	0.06	6.38E-01	8.71E-01	ATF7	activating transcription factor 7	chr12q13	206684_s_at	NM_001130059 /// NM_001130060 /// NM_006856																				
3.01	3.10	0.09	6.38E-01	8.71E-01	C4orf10	chromosome 4 open reading frame 10	chr4p16.3	214123_s_at	NR_015453																				
2.18	2.26	0.07	6.38E-01	8.71E-01	KCNV2	potassium channel, subfamily V, member 2	chr9p24.2	217522_at	NM_133497																				
2.18	2.27	0.09	6.38E-01	8.71E-01	---	---	---	1561670_at	---																				
2.17	2.22	0.05	6.38E-01	8.71E-01	---	---	---	217394_at	---																				
2.34	2.41	0.07	6.38E-01	8.71E-01	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	chr11p15	217607_x_at	NM_001042559 /// NM_001418																				
5.38	5.49	0.11	6.38E-01	8.71E-01	FBXO8	F-box protein 8	chr4q34.1	223240_at	NM_012180																				
3.82	3.88	0.06	6.38E-01	8.71E-01	LOC728777	hypothetical LOC728777	chr10p14	241196_at	XM_001128452 /// XM_001128728 /// XM_001723773																				
7.18	7.47	0.29	6.38E-01	8.71E-01	FBLN1 /// LOC100133843	fibulin 1 /// similar to Fibulin 1	chr22q13.31	201787_at	NM_001996 /// NM_006485 /// NM_006486 /// NM_006487 /// XM_001718348																				
3.45	3.70	0.25	6.38E-01	8.71E-01	PCDH9	protocadherin 9	chr13q14.3-q21.1	219737_s_at	NM_020403 /// NM_203487																				
5.19	5.31	0.12	6.38E-01	8.71E-01	FMNL1	formin-like 1	chr17q21	204789_at	NM_005892																				
2.63	2.70	0.07	6.38E-01	8.71E-01	---	---	---	237348_at	---																				
1.78	1.84	0.06	6.38E-01	8.71E-01	RAB3IP	RAB3A interacting protein (rabin3)	chr12q14.3	1565799_at	NM_001024647 /// NM_022456 /// NM_175623 /// NM_175624 /// NM_175625																				
2.30	2.35	0.05	6.38E-01	8.71E-01	---	---	---	1558885_at	---																				
5.27	5.35	0.09	6.38E-01	8.71E-01	RBBP6	retinoblastoma binding protein 6	chr16p12.2	212781_at	NM_006910 /// NM_018703 /// NM_032626																				
4.08	4.15	0.07	6.38E-01	8.71E-01	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	chr5q33-q34	214492_at	NM_000337 /// NM_001128209 /// NM_172244																				
3.43	3.54	0.11	6.39E-01	8.71E-01	MAGIX	MAGI family member, X-linked	chrXp11.23	1563318_s_at	NM_001099680 /// NM_001099681 /// NM_001099682 /// NM_024859																				
3.12	3.19	0.07	6.39E-01	8.71E-01	---	---	---	233890_at	---																				
2.57	2.66	0.09	6.39E-01	8.71E-01	STON1 /// STON1-GTF2A1L	stonin 1 /// STON1-GTF2A1L	chr2p16.3	231795_at	NM_006873 /// NM_172311																				
2.90	2.98	0.08	6.39E-01	8.71E-01	LOC100129104	similar to hydroxyproline-rich glycoprotein VSP-3	chr8q24.22	244074_at	XM_001713915 /// XM_001718186 /// XM_001718293																				
7.02	7.15	0.13	6.39E-01	8.71E-01	FKBP1A	FK506 binding protein 1A, 12kDa	chr20p13	210186_s_at	NM_000801 /// NM_054014																				
2.32	2.38	0.06	6.39E-01	8.71E-01	CADPS	Ca++-dependent secretion activator	chr3p14.2	239884_at	NM_003716 /// NM_183393 /// NM_183394																				
4.94	5.17	0.23	6.39E-01	8.71E-01	IVNS1ABP	influenza virus NS1A binding protein	chr1q25.1-q31.1	201362_at	NM_006469																				
4.29	4.48	0.19	6.39E-01	8.71E-01	TMEM136	transmembrane protein 136	chr11q23.3	238497_at	NM_174926																				
4.14	4.27	0.12	6.39E-01	8.71E-01	SLC7A6OS	solute carrier family 7, member 6 opposite strand	chr16q22.1	229153_at	NM_032178																				
2.12	2.20	0.08	6.39E-01	8.71E-01	LOC440416	hypothetical gene supported by BC072410	chr17p11.2	229669_at	---																				
2.38	2.45	0.07	6.39E-01	8.71E-01	GPR82	G protein-coupled receptor 82	chrXp11.4	1553316_at	NM_080817																				
2.14	2.21	0.07	6.39E-01	8.71E-01	---	---	---	237538_at	---																				
3.16	3.22	0.06	6.39E-01	8.71E-01	---	---	---	243702_at	---																				
2.55	2.61	0.06	6.39E-01	8.71E-01	SNORA65	small nucleolar RNA, H/ACA box 65	chr9q34	1558081_at	NR_002449																				

2.09	2.14	0.05	6.39E-01	8.71E-01	---	---	---	1561854_at	---
2.03	2.08	0.05	6.39E-01	8.71E-01	GPR137C	G protein-coupled receptor 137C	chr14q22.1	242592_at	NM_001099652
1.98	2.02	0.05	6.39E-01	8.71E-01	---	---	---	244303_at	---
2.04	2.08	0.05	6.39E-01	8.71E-01	LOC647107	hypothetical protein LOC647107	chr3q26.1	1561492_at	XM_934376
4.28	4.36	0.08	6.39E-01	8.71E-01	C15orf17	chromosome 15 open reading frame 17	chr15q24.1	224805_s_at	NM_020447
4.90	5.10	0.20	6.39E-01	8.72E-01	---	---	---	229828_at	---
2.54	2.61	0.08	6.39E-01	8.72E-01	---	---	---	243461_at	---
2.26	2.32	0.07	6.39E-01	8.72E-01	---	---	---	230535_s_at	---
2.07	2.13	0.06	6.40E-01	8.72E-01	---	---	---	241146_at	---
4.68	4.83	0.14	6.40E-01	8.72E-01	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	chr2q33-q35	202019_s_at	NM_006055
3.03	3.16	0.13	6.40E-01	8.72E-01	SOBP	sine oculis binding protein homolog (Drosophila)	chr6q21	1563906_at	NM_018013
2.27	2.34	0.08	6.40E-01	8.72E-01	LRP2	low density lipoprotein-related protein 2	chr2q24-q31	205710_at	NM_004525
2.16	2.22	0.06	6.40E-01	8.72E-01	SLC5A12	solute carrier family 5 (sodium/glucose cotransporter), member 12	chr11p14.2	1561951_at	NM_178498
2.80	2.91	0.11	6.40E-01	8.72E-01	---	---	---	1558630_at	---
2.03	2.09	0.06	6.40E-01	8.72E-01	ZNF485	zinc finger protein 485	chr10q11.21	1552427_at	NM_145312
4.33	4.46	0.12	6.40E-01	8.72E-01	TMEM191B	transmembrane protein 191B	chr22q11.21	223628_at	XM_001128423 /// XM_001722071 /// XM_001725853
2.78	2.89	0.11	6.40E-01	8.72E-01	---	---	---	215330_at	---
4.07	4.15	0.09	6.40E-01	8.72E-01	C10orf35	chromosome 10 open reading frame 35	chr10q21.3	226313_at	NM_145306
2.15	2.20	0.05	6.40E-01	8.72E-01	INVS	inversin	chr9q31	211055_s_at	NM_014425 /// NM_183245
2.19	2.25	0.06	6.40E-01	8.72E-01	---	---	---	244733_at	---
6.37	6.50	0.14	6.40E-01	8.72E-01	---	---	---	227277_at	---
2.28	2.35	0.07	6.40E-01	8.72E-01	---	---	---	215928_at	---
2.11	2.17	0.06	6.40E-01	8.72E-01	---	---	---	241551_at	---
2.96	3.07	0.12	6.40E-01	8.72E-01	LOC729143 /// MPRIP	similar to Myosin phosphatase Rho-interacting protein (Rho-interacting protein 3) (M-RIP) (RIP3) (p116Rip) /// myosin phosphatase Rho interacting protein	chr17p11.2 /// chr3p21.32	214694_at	NM_015134 /// NM_201274 /// XR_015907 /// XR_015979 /// XR_037739
4.75	4.94	0.19	6.41E-01	8.72E-01	NRBF2	nuclear receptor binding factor 2	chr10q21.2	223650_s_at	NM_030759
5.14	5.24	0.10	6.41E-01	8.72E-01	IRF5	interferon regulatory factor 5	chr7q32	205469_s_at	NM_001098627 /// NM_001098628 /// NM_001098629 /// NM_001098630 /// NM_001098631 /// NM_002200 /// NM_032643
2.89	2.97	0.08	6.41E-01	8.72E-01	NSFL1C	NSFL1 (p97) cofactor (p47)	chr20p13	232519_at	NM_016143 /// NM_018839 /// NM_182483
2.10	2.15	0.05	6.41E-01	8.72E-01	TAS2R8	taste receptor, type 2, member 8	chr12p13	221398_at	NM_023918
2.20	2.31	0.10	6.41E-01	8.72E-01	FAM153B	family with sequence similarity 153, member B	chr5q35.2	1563845_at	NM_001079529
4.21	4.38	0.17	6.41E-01	8.72E-01	LRRC25	leucine rich repeat containing 25	chr19p13.11	1559502_s_at	NM_145256
3.20	3.30	0.10	6.41E-01	8.72E-01	---	---	---	237570_x_at	---
2.17	2.24	0.07	6.41E-01	8.72E-01	DCC	deleted in colorectal carcinoma	chr18q21.3	206939_at	NM_005215
6.83	7.13	0.31	6.41E-01	8.72E-01	RGS5	regulator of G-protein signaling 5	chr1q23.1	218353_at	NM_003617
2.56	2.64	0.08	6.41E-01	8.72E-01	KIR3DL2 /// LOC727787	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 /// similar to killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I NK cell receptor) (Natural killer-associated transcript 4) (NKAT-4) (p70 natural killer cell receptor clone CL-5) (CD158k antigen)	chr19q13.4	216907_x_at	NM_006737 /// XM_001718625
6.20	6.41	0.21	6.41E-01	8.72E-01	KIAA0232	KIAA0232	chr4p16.1	212441_at	NM_001100590 /// NM_014743
4.27	4.35	0.08	6.41E-01	8.72E-01	TMEM19	transmembrane protein 19	chr12q21.1	230676_s_at	NM_018279
2.39	2.46	0.07	6.41E-01	8.72E-01	DGCR10	DiGeorge syndrome critical region gene 10	chr22q11	1557451_at	---

1.85	1.89	0.05	6.41E-01	8.72E-01	LOC100134745 /// PP12708	hypothetical protein LOC100134745 /// hypothetical LOC100130609	chr7q34	1570115_at	XM_001723609 /// XM_001724282 /// XM_001726626 /// XM_001726720																				
3.22	3.32	0.10	6.41E-01	8.72E-01	MCHR2	melanin-concentrating hormone receptor 2	chr6q16	224408_at	NM_001040179 /// NM_032503																				
4.81	4.96	0.15	6.41E-01	8.72E-01	---	---	---	228811_at	---																				
3.36	3.49	0.13	6.41E-01	8.72E-01	ITGA6	integrin, alpha 6	chr2q31.1	201656_at	NM_000210 /// NM_001079818																				
2.25	2.31	0.05	6.41E-01	8.72E-01	---	---	---	1560776_at	---																				
2.23	2.28	0.05	6.41E-01	8.72E-01	SUZ12	Suppressor of zeste 12 homolog (Drosophila)	chr17q11.2	1566190_at	NM_015355																				
6.79	6.95	0.16	6.41E-01	8.73E-01	TPR	translocated promoter region (to activated MET oncogene)	chr1q25	201731_s_at	NM_003292																				
4.86	4.94	0.09	6.41E-01	8.73E-01	---	---	---	228271_at	---																				
4.03	4.16	0.13	6.41E-01	8.73E-01	LOC100133609 /// MARCH3	similar to membrane-associated ring finger (C3HC4) 3 /// membrane-associated ring finger (C3HC4) 3	chr5q23.2	213256_at	NM_178450 /// XM_001720815																				
4.38	4.53	0.15	6.42E-01	8.73E-01	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	chr20q11.22-q11.23	209744_x_at	NM_031483																				
3.89	3.96	0.07	6.42E-01	8.73E-01	GINS2	GINS complex subunit 2 (Psf2 homolog)	chr16q24.1	221521_s_at	NM_016095																				
4.03	4.09	0.06	6.42E-01	8.73E-01	AQP6	aquaporin 6, kidney specific	chr12q13	216219_at	NM_001652																				
2.31	2.36	0.05	6.42E-01	8.73E-01	KLHL10	kelch-like 10 (Drosophila)	chr17q21.2	1552424_at	NM_152467																				
2.04	2.09	0.05	6.42E-01	8.73E-01	FBXO3	F-box protein 3	chr11p13	232851_at	NM_012175 /// NM_033406																				
3.89	4.07	0.18	6.42E-01	8.73E-01	CCDC88A	coiled-coil domain containing 88A	chr2p16.1	225045_at	NM_018084																				
2.51	2.63	0.11	6.42E-01	8.73E-01	FRYL	FRY-like	chr4p12	1563687_a_at	NM_015030																				
6.74	6.85	0.11	6.42E-01	8.73E-01	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	chr9p22.3	206542_s_at	NM_003070 /// NM_139045																				
2.80	2.89	0.09	6.42E-01	8.73E-01	---	---	---	1559645_at	---																				
4.26	4.35	0.09	6.42E-01	8.73E-01	CCDC21	coiled-coil domain containing 21	chr1p36.11	227818_at	NM_022778																				
4.07	4.16	0.09	6.42E-01	8.73E-01	---	---	---	235917_at	---																				
9.72	9.80	0.08	6.42E-01	8.73E-01	CS	citrate synthase	chr12q13.2-q13.3	208660_at	NM_004077 /// NM_198324																				
8.24	8.36	0.12	6.42E-01	8.73E-01	FBLN5	fibulin 5	chr14q32.1	203088_at	NM_006329																				
3.61	3.70	0.09	6.42E-01	8.73E-01	PROZ	protein Z, vitamin K-dependent plasma glycoprotein	chr13q34	208034_s_at	NM_003891																				
5.15	5.42	0.27	6.42E-01	8.73E-01	SLMAP	sarcolemma associated protein	chr3p21.2-p14.3	224149_x_at	NM_007159																				
3.12	3.18	0.06	6.42E-01	8.73E-01	---	---	---	241857_at	---																				
2.65	2.71	0.06	6.42E-01	8.73E-01	---	---	---	1559565_x_at	---																				
5.23	5.38	0.15	6.42E-01	8.73E-01	C5orf22	chromosome 5 open reading frame 22	chr5p13.3	203738_at	NM_018356																				
1.86	1.92	0.06	6.42E-01	8.73E-01	---	---	---	1556877_at	---																				
2.65	2.72	0.06	6.42E-01	8.73E-01	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	chr6p21	222179_at	NM_001253																				
1.84	1.90	0.06	6.42E-01	8.73E-01	FCRL1	Fc receptor-like 1	chr1q21-q22	243968_x_at	NM_052938																				
1.99	2.04	0.05	6.42E-01	8.73E-01	CDC20B	cell division cycle 20 homolog B (S. cerevisiae)	chr5q11.2	1555346_at	NM_152623																				
2.99	3.06	0.07	6.42E-01	8.73E-01	GLP1R	glucagon-like peptide 1 receptor	chr6p21	211232_x_at	NM_002062																				
4.47	4.70	0.23	6.43E-01	8.73E-01	---	---	---	213904_at	---																				
8.02	8.12	0.10	6.43E-01	8.73E-01	FNTA	farnesyltransferase, CAAX box, alpha	chr8p11	200090_at	NM_001018676 /// NM_001018677 /// NM_002027																				
2.16	2.24	0.08	6.43E-01	8.73E-01	PAR5	Prader-Willi/Angelman syndrome-5	chr15q11-q13	214834_at	NR_001292 /// NR_001294 /// NR_022008																				
2.38	2.44	0.06	6.43E-01	8.73E-01	---	---	---	1560131_at	---																				
4.72	4.81	0.09	6.43E-01	8.73E-01	ELL	elongation factor RNA polymerase II	chr19p13.1	204095_s_at	NM_006532																				
2.03	2.09	0.06	6.43E-01	8.73E-01	LOC100128286	PRO2300	chr15q23	224114_at	XM_001724752 /// XM_001725394 /// XM_001726717																				
2.32	2.39	0.07	6.43E-01	8.73E-01	---	---	---	1560794_at	---																				
2.21	2.28	0.07	6.43E-01	8.73E-01	TAT	Tyrosine aminotransferase	chr16q22.1	214413_at	NM_000353																				
2.12	2.19	0.06	6.43E-01	8.73E-01	---	---	---	1558473_at	---																				
5.54	5.62	0.08	6.43E-01	8.73E-01	SCYL2	SCY1-like 2 (S. cerevisiae)	chr12q23.1	224961_at	NM_017988																				
2.59	2.68	0.08	6.43E-01	8.73E-01	C10orf103	chromosome 10 open reading frame 103	chr10q22.2	1557827_at	---																				
3.10	3.18	0.08	6.43E-01	8.73E-01	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	chr7q11.23	211313_s_at	NM_032408																				
2.70	2.77	0.07	6.43E-01	8.73E-01	---	---	---	236542_at	---																				
2.59	2.65	0.07	6.43E-01	8.73E-01	CCDC68	coiled-coil domain containing 68	chr18q21	220180_at	NM_025214																				

2.33	2.39	0.06	6.43E-01	8.73E-01	PSIP1	PC4 and SFRS1 interacting protein 1	chr9p22.3	1554933_at	NM_001128217 /// NM_021144 /// NM_033222
2.37	2.43	0.06	6.43E-01	8.73E-01	---	---	---	236823_at	---
2.28	2.34	0.05	6.43E-01	8.73E-01	AP4E1	adaptor-related protein complex 4, epsilon 1 subunit	chr15q21.2	220228_at	NM_007347
2.13	2.18	0.05	6.43E-01	8.73E-01	---	---	---	1563303_at	---
4.83	4.97	0.14	6.43E-01	8.73E-01	C17orf42	chromosome 17 open reading frame 42	---	219146_at	NM_024683
6.65	6.79	0.14	6.43E-01	8.73E-01	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	chr9q21.11	226110_at	NM_001099666
2.05	2.13	0.08	6.43E-01	8.73E-01	---	---	---	1558922_at	---
2.17	2.24	0.08	6.43E-01	8.73E-01	AAK1	AP2 associated kinase 1	chr2p14	214956_at	NM_014911
3.45	3.64	0.19	6.43E-01	8.73E-01	---	---	---	228045_at	---
5.21	5.32	0.11	6.43E-01	8.73E-01	---	---	---	219731_at	---
2.92	3.03	0.11	6.43E-01	8.73E-01	---	---	---	1561454_at	---
4.12	4.22	0.10	6.43E-01	8.73E-01	LOC126147	hypothetical protein BC018697	chr19q13.33	1553890_s_at	NM_145807
2.17	2.22	0.05	6.43E-01	8.73E-01	KNG1	kininogen 1	chr3q27	217512_at	NM_000893 /// NM_001102416
2.24	2.29	0.05	6.43E-01	8.73E-01	---	---	---	235895_at	---
4.26	4.38	0.12	6.43E-01	8.73E-01	ALOX5	arachidonate 5-lipoxygenase	chr10q11.2	214366_s_at	NM_000698
4.02	4.13	0.10	6.44E-01	8.73E-01	RNF144B	ring finger 144B	chr6p22.3	239704_at	NM_182757
2.36	2.43	0.06	6.44E-01	8.73E-01	AMPH	amphiphysin	chr7p14-p13	205257_s_at	NM_001635 /// NM_139316
2.22	2.28	0.06	6.44E-01	8.73E-01	---	---	---	220670_at	---
2.01	2.06	0.05	6.44E-01	8.73E-01	PURG	purine-rich element binding protein G	chr8p11	220860_at	NM_001015508 /// NM_013357
5.60	5.76	0.17	6.44E-01	8.73E-01	SEC23A	Sec23 homolog A (S. cerevisiae)	chr14q21.1	204344_s_at	NM_006364
2.64	2.72	0.08	6.44E-01	8.73E-01	ZEB1	zinc finger E-box binding homeobox 1	chr10p11.2	239952_at	NM_001128128 /// NM_030751
8.54	8.62	0.08	6.44E-01	8.73E-01	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	chr8q21.11	202824_s_at	NM_005648
6.77	6.87	0.09	6.44E-01	8.73E-01	TMEM161A	transmembrane protein 161A	chr19p13.11	218745_x_at	NM_017814
2.76	2.85	0.09	6.44E-01	8.73E-01	FLJ45513	hypothetical LOC729220	chr17q21.33	239400_at	XM_001133597 /// XM_001133619 /// XM_001723161
3.05	3.14	0.09	6.44E-01	8.74E-01	NCKIPSD	NCK interacting protein with SH3 domain	chr3p21	216116_at	NM_016453 /// NM_184231
3.39	3.50	0.11	6.44E-01	8.74E-01	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	chr11p11.2	217487_x_at	NM_001014986 /// NM_004476
2.34	2.41	0.07	6.44E-01	8.74E-01	LOC285378	hypothetical protein LOC285378	chr3p25.1	236363_at	---
6.56	6.79	0.22	6.44E-01	8.74E-01	RUFY3	RUN and FYVE domain containing 3	chr4q13.3	213939_s_at	NM_001037442 /// NM_001130709 /// NM_014961
5.32	5.46	0.15	6.44E-01	8.74E-01	---	---	---	235938_at	---
2.97	3.08	0.10	6.44E-01	8.74E-01	CC2D1A	coiled-coil and C2 domain containing 1A	chr19p13.12	207083_s_at	NM_017721
2.14	2.21	0.07	6.44E-01	8.74E-01	CD28	CD28 molecule	chr2q33	206545_at	NM_006139
1.93	1.99	0.06	6.44E-01	8.74E-01	---	---	---	241764_at	---
2.47	2.52	0.05	6.44E-01	8.74E-01	FLJ42875	hypothetical LOC440556	chr1p36.32	242269_at	XM_928346 /// XM_932794 /// XM_942662 /// XM_946195
2.18	2.23	0.05	6.44E-01	8.74E-01	TRPM3	transient receptor potential cation channel, subfamily M, member 3	chr9q21.11-q21.12	1554722_at	NM_001007470 /// NM_001007471 /// NM_020952 /// NM_024971 /// NM_206944 /// NM_206945 /// NM_206946 /// NM_206947 /// NM_206948
4.79	4.98	0.18	6.44E-01	8.74E-01	ETV1	ets variant gene 1	chr7p21.3	206501_x_at	NM_004956
3.31	3.44	0.12	6.44E-01	8.74E-01	C1orf201	chromosome 1 open reading frame 201	chr1p36.11	233693_at	NM_178122

2.34	2.42	0.08	6.44E-01	8.74E-01	---	---	---	1560087_a_at	---
3.85	3.92	0.07	6.44E-01	8.74E-01	SOBP	sine oculis binding protein homolog (Drosophila)	chr6q21	244279_at	NM_018013
2.20	2.27	0.07	6.44E-01	8.74E-01	---	---	---	233507_at	---
2.78	2.85	0.06	6.44E-01	8.74E-01	---	---	---	1565821_at	---
2.72	2.78	0.06	6.44E-01	8.74E-01	---	---	---	236568_at	---
2.43	2.54	0.10	6.45E-01	8.74E-01	SHANK2	SH3 and multiple ankyrin repeat domains 2	chr11q13.3	213308_at	NM_012309 /// NM_133266
3.86	3.95	0.09	6.45E-01	8.74E-01	MCHR1	melanin-concentrating hormone receptor 1	chr22q13.2	223855_s_at	NM_005297
2.40	2.49	0.08	6.44E-01	8.74E-01	---	---	---	242227_at	---
2.28	2.34	0.06	6.44E-01	8.74E-01	MGC16025	hypothetical protein MGC16025	chr2q37.3	1553747_at	XM_001719489 /// XM_001722002 /// XM_001724457
5.21	5.27	0.06	6.45E-01	8.74E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	228849_at	NM_001007156 /// NM_001012338 /// NM_002530
2.41	2.46	0.05	6.45E-01	8.74E-01	ACSBG1	acyl-CoA synthetase bubblegum family member 1	chr15q23-q24	206466_at	NM_015162
3.84	3.95	0.11	6.45E-01	8.74E-01	LOC730496	hypothetical protein LOC730496	---	238639_x_at	XM_001126091
2.35	2.43	0.08	6.45E-01	8.74E-01	LETM2	leucine zipper-EF-hand containing transmembrane protein 2	chr8p12	1552546_a_at	NM_144652
2.44	2.51	0.07	6.45E-01	8.74E-01	KIAA1429	KIAA1429	chr8q22.1	238818_at	NM_015496 /// NM_183009
2.47	2.55	0.09	6.45E-01	8.74E-01	KLRD1	killer cell lectin-like receptor subfamily D, member 1	chr12p13	210606_x_at	NM_001114396 /// NM_002262 /// NM_007334
2.76	2.86	0.10	6.45E-01	8.74E-01	---	---	---	228032_s_at	---
3.54	3.61	0.07	6.45E-01	8.74E-01	SLC38A7	solute carrier family 38, member 7	chr16q21	222215_at	NM_018231
2.13	2.19	0.05	6.45E-01	8.74E-01	---	---	---	241083_at	---
2.72	2.81	0.09	6.45E-01	8.74E-01	---	---	---	242339_at	---
1.88	1.94	0.06	6.45E-01	8.74E-01	UGT2A3	UDP glucuronosyltransferase 2 family, polypeptide A3	chr4q13.2	219948_x_at	NM_024743 /// NR_024010
2.04	2.09	0.06	6.45E-01	8.74E-01	---	---	---	234218_at	---
6.49	6.58	0.09	6.45E-01	8.74E-01	ALAD	aminolevulinate, delta-, dehydratase	chr9q33.1	218489_s_at	NM_000031 /// NM_001003945
3.83	3.93	0.10	6.45E-01	8.74E-01	---	---	---	239641_at	---
2.40	2.45	0.06	6.45E-01	8.74E-01	HES2	hairy and enhancer of split 2 (Drosophila)	chr1p36.31-p36.11	214521_at	NM_019089
3.68	3.87	0.19	6.46E-01	8.74E-01	JAK2	Janus kinase 2 (a protein tyrosine kinase)	chr9p24	205842_s_at	NM_004972
2.25	2.31	0.06	6.46E-01	8.74E-01	TBX20	T-box 20	chr7p15-p14	1564945_at	NM_001077653 /// NM_020417
2.75	2.83	0.08	6.46E-01	8.74E-01	CCT8L2	chaperonin containing TCP1, subunit 8 (theta)-like 2	chr22q11.1	220508_at	NM_014406
2.20	2.29	0.09	6.46E-01	8.74E-01	TAS2R45	taste receptor, type 2, member 45	---	234108_at	NM_176886
3.54	3.67	0.13	6.46E-01	8.74E-01	SSFA2	Sperm specific antigen 2	chr2q31.3	229744_at	NM_001130445 /// NM_006751
2.70	2.76	0.06	6.46E-01	8.74E-01	MKRN3	makorin ring finger protein 3	chr15q11-q13	206585_at	NM_005664
4.65	4.81	0.16	6.46E-01	8.74E-01	HDGFRP3	hepatoma-derived growth factor, related protein 3	chr15q25.2	228266_s_at	NM_016073
2.17	2.22	0.05	6.46E-01	8.74E-01	---	---	---	1553275_s_at	---
5.17	5.25	0.08	6.46E-01	8.74E-01	ATG16L1	ATG16 autophagy related 16-like 1 (S. cerevisiae)	chr2q37.1	232612_s_at	NM_017974 /// NM_030803
2.87	2.94	0.06	6.46E-01	8.74E-01	RDH11	Retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	chr14q24.1	232359_at	NM_016026
7.86	7.99	0.12	6.46E-01	8.74E-01	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	chr4q21-q25	208847_s_at	NM_000671
3.09	3.16	0.07	6.46E-01	8.74E-01	---	---	---	234836_at	---
5.07	5.23	0.15	6.46E-01	8.75E-01	HIPK1	homeodomain interacting protein kinase 1	chr1p13.2	1552516_a_at	NM_152696 /// NM_181358 /// NM_198268 /// NM_198269
2.26	2.33	0.07	6.46E-01	8.75E-01	SIRPB1	signal-regulatory protein beta 1	chr20p13	1554624_a_at	NM_001083910 /// NM_006065
6.08	6.27	0.19	6.46E-01	8.75E-01	NR1D2	nuclear receptor subfamily 1, group D, member 2	chr3p24.2	225768_at	NM_005126
8.01	8.15	0.15	6.46E-01	8.75E-01	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	chr2p15-p13	212811_x_at	NM_003038
2.43	2.49	0.06	6.46E-01	8.75E-01	AGBL1	ATP/GTP binding protein-like 1	chr15q25.3	1553447_at	NM_152336
2.85	2.99	0.14	6.46E-01	8.75E-01	BBX	bobby sox homolog (Drosophila)	chr3q13.1	1557239_at	NM_020235
6.93	7.03	0.11	6.46E-01	8.75E-01	XIAP	X-linked inhibitor of apoptosis	chrXq25	235222_x_at	NM_001167
2.12	2.20	0.08	6.46E-01	8.75E-01	---	---	---	1560482_at	---
4.83	4.94	0.11	6.46E-01	8.75E-01	ALKBH4	alkB, alkylation repair homolog 4 (E. coli)	chr7q22.1	222228_s_at	NM_017621
3.07	3.15	0.09	6.46E-01	8.75E-01	PLCB2	phospholipase C, beta 2	chr15q15	210388_at	NM_004573

2.73	2.80	0.07	6.47E-01	8.75E-01	PLAC1	placenta-specific 1	chrXq26	219702_at	NM_021796
5.32	5.45	0.13	6.47E-01	8.75E-01	PALB2	partner and localizer of BRCA2	chr16p12.1	219530_at	NM_024675
3.69	3.75	0.06	6.47E-01	8.75E-01	MYLC2PL	myosin light chain 2, precursor lymphocyte-specific	chr7q22.1	221659_s_at	NM_138403
4.24	4.30	0.06	6.47E-01	8.75E-01	C20orf181	chromosome 20 open reading frame 181	---	1567036_at	---
2.98	3.19	0.21	6.47E-01	8.75E-01	RCAN3	RCAN family member 3	chr1p35.3-p33	226272_at	NM_013441
6.60	6.79	0.18	6.47E-01	8.75E-01	ERCC5	excision repair cross-complementing rodent repair deficiency, complementation group 5	chr13q33	202414_at	NM_000123
3.24	3.33	0.09	6.47E-01	8.75E-01	TFR2	transferrin receptor 2	chr7q22	210215_at	NM_003227
2.03	2.10	0.07	6.47E-01	8.75E-01	NCOA6	nuclear receptor coactivator 6	chr20q11	1568874_at	NM_014071
2.13	2.19	0.05	6.47E-01	8.75E-01	---	---	---	231127_at	---
1.87	1.92	0.05	6.47E-01	8.75E-01	---	---	---	233415_at	---
2.97	3.04	0.07	6.47E-01	8.75E-01	PHTF1	putative homeodomain transcription factor 1	chr1p13	235844_at	NM_006608
5.42	5.58	0.16	6.47E-01	8.75E-01	EVI2B	ecotropic viral integration site 2B	chr17q11.2	211742_s_at	NM_006495
7.65	7.78	0.13	6.47E-01	8.75E-01	PARP4	poly (ADP-ribose) polymerase family, member 4	chr13q11	202239_at	NM_006437
2.78	2.89	0.11	6.47E-01	8.75E-01	---	---	---	1559965_at	---
2.25	2.34	0.09	6.47E-01	8.75E-01	SLC8A3	solute carrier family 8 (sodium/calcium exchanger), member 3	chr14q24.1	1562403_a_at	NM_001130417 /// NM_033262 /// NM_058240 /// NM_182932 /// NM_182936 /// NM_183002
2.59	2.67	0.08	6.47E-01	8.75E-01	---	---	---	1556543_at	---
2.80	2.88	0.07	6.47E-01	8.75E-01	---	---	---	1561061_at	---
2.03	2.10	0.07	6.47E-01	8.75E-01	LOC285084	hypothetical protein LOC285084	chr2q31.1	1557570_a_at	---
2.56	2.63	0.07	6.47E-01	8.75E-01	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	chr13q32.2	1562426_a_at	NM_001001715 /// NM_005766
2.63	2.69	0.06	6.47E-01	8.75E-01	---	---	---	240445_at	---
2.73	2.79	0.06	6.47E-01	8.75E-01	---	---	---	233129_at	---
4.67	4.79	0.12	6.47E-01	8.75E-01	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	chr21q22.3	236988_x_at	NM_000211 /// NM_001127491
7.22	7.37	0.15	6.47E-01	8.75E-01	CCDC28A	coiled-coil domain containing 28A	chr6q23.1-q24.1	209479_at	NM_015439
2.72	2.82	0.10	6.47E-01	8.75E-01	GPR113	G protein-coupled receptor 113	chr2p23.3	1553016_at	NM_153835
3.51	3.60	0.09	6.47E-01	8.75E-01	MNT	MAX binding protein	chr17p13.3	236749_at	NM_020310
4.35	4.44	0.09	6.47E-01	8.75E-01	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	chr20q13.33	231200_at	NM_144703
3.10	3.19	0.09	6.47E-01	8.75E-01	MGC87042	similar to Six transmembrane epithelial antigen of prostate	chr7p15.3	217553_at	XM_001721690 /// XM_001723244 /// XM_001723293 /// XM_001724556
2.51	2.60	0.09	6.47E-01	8.75E-01	BRWD3	bromodomain and WD repeat domain containing 3	chrXq21.1	1553252_a_at	NM_153252
2.07	2.16	0.08	6.47E-01	8.75E-01	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	chr7q32	244171_at	NM_013255
3.21	3.29	0.08	6.47E-01	8.75E-01	---	---	---	243425_at	---
2.88	2.95	0.08	6.47E-01	8.75E-01	PHC3 /// SPACA3	polyhomeotic homolog 3 (Drosophila) /// sperm acrosome associated 3	chr17q11.2 /// chr3q26.2	243621_at	NM_024947 /// NM_173847
2.20	2.26	0.06	6.47E-01	8.75E-01	---	---	---	1570263_at	---
2.37	2.44	0.06	6.47E-01	8.75E-01	---	---	---	234786_at	---
2.02	2.07	0.05	6.47E-01	8.75E-01	---	---	---	1555929_s_at	---
3.72	3.90	0.18	6.48E-01	8.75E-01	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	chr11q23.2	202884_s_at	NM_002716 /// NM_181699
3.45	3.55	0.10	6.48E-01	8.75E-01	CENTB2	centaurin, beta 2	chr3q29	1552472_a_at	NM_012287
2.32	2.41	0.09	6.48E-01	8.75E-01	GRHL3	grainyhead-like 3 (Drosophila)	chr1p36.11	232116_at	NM_021180 /// NM_198173 /// NM_198174
5.71	5.80	0.09	6.48E-01	8.75E-01	LYRM2	LYR motif containing 2	chr6q14.2-q16.1	227797_x_at	NM_020466
2.95	3.03	0.08	6.48E-01	8.75E-01	C20orf26	chromosome 20 open reading frame 26	chr20p11.23	233389_at	NM_015585
3.09	3.17	0.08	6.48E-01	8.75E-01	LOC415056	Hypothetical gene LOC415056	chr9p13	237604_at	---
1.97	2.04	0.07	6.48E-01	8.75E-01	---	---	---	230927_at	---
3.06	3.12	0.06	6.48E-01	8.75E-01	LOC643837	hypothetical LOC643837	chr1p36.33	231942_at	NR_015368 /// XM_927114
2.08	2.13	0.05	6.48E-01	8.75E-01	---	---	---	241250_at	---
3.34	3.43	0.10	6.48E-01	8.75E-01	SYN1	synapsin I	chrXp11.23	221914_at	NM_006950 /// NM_133499
2.43	2.51	0.08	6.48E-01	8.75E-01	EPHA5	EPH receptor A5	chr4q13.1	216837_at	NM_004439 /// NM_182472
7.16	7.23	0.07	6.48E-01	8.75E-01	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	chr1p32	211792_s_at	NM_001262 /// NM_078626
7.52	7.67	0.15	6.48E-01	8.75E-01	RAB14	RAB14, member RAS oncogene family	chr9q32-q34.11	200927_s_at	NM_016322
4.12	4.18	0.06	6.48E-01	8.75E-01	---	---	---	233583_at	---
5.86	5.98	0.11	6.48E-01	8.75E-01	---	---	---	239363_at	---
2.18	2.26	0.08	6.48E-01	8.75E-01	TTLL9	tubulin tyrosine ligase-like family, member 9	chr20q11.21	234336_s_at	NM_001008409

2.56	2.63	0.07	6.48E-01	8.75E-01	AP4B1	adaptor-related protein complex 4, beta 1 subunit	chr1p13.2	231962_at	NM_006594
2.04	2.11	0.07	6.48E-01	8.75E-01	---	---	---	1560034_a_at	---
1.98	2.03	0.05	6.48E-01	8.75E-01	ZNF611	zinc finger protein 611	chr19q13.41	1559059_s_at	NM_030972
2.00	2.05	0.05	6.48E-01	8.75E-01	---	---	---	1556147_at	---
7.43	7.59	0.16	6.48E-01	8.75E-01	BCAS2	breast carcinoma amplified sequence 2	chr1p21-p13.3	203053_at	NM_005872
7.01	7.13	0.12	6.48E-01	8.75E-01	ABHD6 /// LOC643635	abhydrolase domain containing 6 /// similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11	chr1p36.33 /// chr3p14.3	221552_at	NM_020676 /// XM_926939
5.04	5.15	0.11	6.48E-01	8.75E-01	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	chr10pter-q25.3	202523_s_at	NM_001134434 /// NM_014767
2.48	2.57	0.09	6.48E-01	8.75E-01	---	---	---	231606_at	---
5.48	5.57	0.09	6.48E-01	8.75E-01	BOP1	block of proliferation 1	chr8q24.3	216397_s_at	NM_015201
4.14	4.21	0.08	6.48E-01	8.75E-01	---	---	---	232374_s_at	---
4.23	4.30	0.06	6.48E-01	8.75E-01	FGF17	fibroblast growth factor 17	chr8p21	221376_at	NM_003867
6.00	6.14	0.14	6.49E-01	8.75E-01	PHLDA3	pleckstrin homology-like domain, family A, member 3	chr1q31	218634_at	NM_012396
2.28	2.38	0.10	6.49E-01	8.75E-01	PRNT	prion protein (testis specific)	chr20p13	233975_at	NM_177549
2.56	2.65	0.08	6.49E-01	8.75E-01	---	---	---	1556090_at	---
2.35	2.43	0.08	6.49E-01	8.75E-01	TMF1	TATA element modulatory factor 1	chr3p21-p12	242243_at	NM_007114
2.43	2.50	0.08	6.49E-01	8.75E-01	PDCD2	Programmed cell death 2	chr6q27	243773_at	NM_002598 /// NM_144781
2.94	3.04	0.10	6.49E-01	8.76E-01	TRBV24-1	T cell receptor beta variable 24-1	chr7q34	234886_at	---
11.12	11.20	0.08	6.49E-01	8.76E-01	RPS27A /// UBB /// UBC	ribosomal protein S27a /// ubiquitin B /// ubiquitin C	chr12q24.3 /// chr17p12-p11.2 /// chr2p16	200017_at	NM_002954 /// NM_018955 /// NM_021009
2.61	2.70	0.09	6.49E-01	8.76E-01	B4GALNT2	beta-1,4-N-acetyl-galactosaminyl transferase 2	chr17q21.32	1552903_at	NM_153446
2.93	3.00	0.07	6.49E-01	8.76E-01	KSR1	kinase suppressor of ras 1	chr17q11.1	213767_at	NM_014238
2.90	3.00	0.10	6.49E-01	8.76E-01	ODZ3	Odz, odd Oz/ten-m homolog 3 (Drosophila)	chr4q35.1	227050_at	NM_001080477
3.72	3.79	0.07	6.49E-01	8.76E-01	GBP4	guanylate binding protein 4	chr1p22.2	235574_at	NM_052941
5.16	5.26	0.10	6.49E-01	8.76E-01	---	---	---	243459_x_at	---
3.54	3.62	0.09	6.49E-01	8.76E-01	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta	chr1p|1p36.3	208457_at	NM_000815
2.10	2.16	0.06	6.49E-01	8.76E-01	---	---	---	234340_at	---
4.38	4.49	0.12	6.49E-01	8.76E-01	LRRC4	leucine rich repeat containing 4	chr7q31.3	223552_at	NM_022143
3.79	3.87	0.08	6.49E-01	8.76E-01	---	---	---	230816_at	---
2.26	2.32	0.07	6.49E-01	8.76E-01	LOC339568	hypothetical protein LOC339568	chr20q12	1562829_at	---
3.84	3.94	0.09	6.49E-01	8.76E-01	KCNIP2	Kv channel interacting protein 2	chr10q24	223727_at	NM_014591 /// NM_173191 /// NM_173192 /// NM_173193 /// NM_173194 /// NM_173195 /// NM_173197
2.31	2.39	0.08	6.49E-01	8.76E-01	GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	chr11p15.3	233188_at	NM_198516
4.38	4.44	0.06	6.49E-01	8.76E-01	LHX5	LIM homeobox 5	chr12q24	208333_at	NM_022363
2.15	2.21	0.06	6.49E-01	8.76E-01	EHF	ets homologous factor	chr11p12	219850_s_at	NM_012153
3.99	4.11	0.12	6.49E-01	8.76E-01	FLJ37464	hypothetical protein FLJ37464	chr16q22.1	228903_at	NM_173815
2.60	2.67	0.07	6.49E-01	8.76E-01	---	---	---	235319_at	---
6.74	6.96	0.22	6.50E-01	8.76E-01	ARID5B	AT rich interactive domain 5B (MRF1-like)	chr10q21.2	212614_at	NM_032199
4.88	5.01	0.13	6.50E-01	8.76E-01	C12orf29	chromosome 12 open reading frame 29	chr12q21.32	213701_at	NM_001009894
11.74	11.86	0.12	6.50E-01	8.76E-01	RPL17	ribosomal protein L17	chr18q21	200038_s_at	NM_000985 /// NM_001035006
2.94	3.04	0.10	6.50E-01	8.76E-01	FLJ35946	hypothetical protein FLJ35946	chr5q21.1	1558899_s_at	XM_001724664 /// XM_931448 /// XM_944650
3.11	3.19	0.08	6.49E-01	8.76E-01	TBCEL	tubulin folding cofactor E-like	chr11q23.3	231997_at	NM_001130047 /// NM_152715
2.89	2.97	0.08	6.50E-01	8.76E-01	HOXB9	homeobox B9	chr17q21.3	216417_x_at	NM_024017
2.64	2.71	0.07	6.50E-01	8.76E-01	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	chr3q27.2	223963_s_at	NM_001007225 /// NM_006548
6.42	6.48	0.07	6.50E-01	8.76E-01	GFER	growth factor, augmenter of liver regeneration	chr16p13.3-p13.12	204660_at	NM_005262
2.36	2.43	0.07	6.50E-01	8.76E-01	DUSP27	dual specificity phosphatase 27 (putative)	chr1q22-q24	232252_at	NM_001080426
2.17	2.23	0.06	6.50E-01	8.76E-01	LOC100134410 /// POU6F2	similar to POU domain, class 6, transcription factor 2 (Retina-derived POU domain factor 1) (RPF-1) /// POU class 6 homeobox 2	chr7p14-p13	207450_s_at	NM_007252 /// XM_001716900
3.35	3.41	0.06	6.49E-01	8.76E-01	HAPLN1	hyaluronan and proteoglycan link protein 1	chr5q14.3	205524_s_at	NM_001884
2.75	2.87	0.12	6.50E-01	8.76E-01	ITGBL1	Integrin, beta-like 1 (with EGF-like repeat domains)	chr13q33	231993_at	NM_004791

4.66	4.76	0.10	6.50E-01	8.76E-01	GPR162 /// LEPREL2	G protein-coupled receptor 162 /// leprecan-like 2	chr12p13 /// chr12q13	204854_at	NM_014262 /// NM_014449 /// NM_019858
3.49	3.58	0.09	6.50E-01	8.76E-01	TRIM14	tripartite motif-containing 14	chr9q22.33	203147_s_at	NM_014788 /// NM_033219 /// NM_033220 /// NM_033221
4.76	4.84	0.09	6.50E-01	8.76E-01	MED16	mediator complex subunit 16	chr19p13.3	221544_s_at	NM_005481
3.28	3.35	0.07	6.50E-01	8.76E-01	---	---	---	240654_at	---
4.20	4.27	0.07	6.50E-01	8.76E-01	ECE2	endothelin converting enzyme 2	chr3q27.1|.	1555306_a_at	NM_001037324 /// NM_001100120 /// NM_001100121 /// NM_014693 /// NM_032331
2.35	2.41	0.06	6.50E-01	8.76E-01	ANKH	Ankylosis, progressive homolog (mouse)	chr5p15.1	1560369_at	NM_054027
2.81	2.87	0.06	6.50E-01	8.76E-01	---	---	---	238608_at	---
2.62	2.67	0.05	6.50E-01	8.76E-01	---	---	---	207985_at	---
4.34	4.72	0.37	6.50E-01	8.76E-01	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	chr6p25.2	211090_s_at	NM_003913
5.10	5.47	0.37	6.50E-01	8.76E-01	AQP1	aquaporin 1 (Colton blood group)	chr7p14	207542_s_at	NM_198098
5.88	6.08	0.20	6.50E-01	8.76E-01	SLC25A36	solute carrier family 25, member 36	chr3q23	201918_at	NM_001104647 /// NM_018155
3.62	3.82	0.20	6.50E-01	8.76E-01	FLJ20160	FLJ20160 protein	chr2q32.2	219858_s_at	NM_017694
4.70	4.87	0.17	6.50E-01	8.76E-01	AGA	aspartylglucosaminidase	chr4q32-q33	204333_s_at	NM_000027
6.30	6.45	0.15	6.50E-01	8.76E-01	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	chr19p13.3	226010_at	NM_024103
3.23	3.35	0.12	6.50E-01	8.76E-01	---	---	---	230486_at	---
3.92	4.02	0.10	6.50E-01	8.76E-01	STS	steroid sulfatase (microsomal), isozyme S	chrXp22.32	203769_s_at	NM_000351
2.51	2.59	0.08	6.50E-01	8.76E-01	CHD9	Chromodomain helicase DNA binding protein 9	chr16q12.2	242157_at	NM_025134
2.25	2.33	0.08	6.50E-01	8.76E-01	---	---	---	242924_at	---
3.29	3.37	0.07	6.50E-01	8.76E-01	UHRF1BP1	UHRF1 binding protein 1	chr6p21	233245_at	NM_017754
2.58	2.65	0.07	6.50E-01	8.76E-01	GGA2	Golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	214233_at	NM_015044
2.24	2.32	0.07	6.50E-01	8.76E-01	---	---	---	242766_at	---
5.16	5.23	0.07	6.50E-01	8.76E-01	---	---	---	237239_at	---
2.04	2.11	0.07	6.50E-01	8.76E-01	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	chrXp22.11	206751_s_at	NM_004845
2.23	2.29	0.06	6.50E-01	8.76E-01	LOC285194	hypothetical LOC285194	chr3q13.31	1558602_a_at	XR_040367 /// XR_040368 /// XR_040369
3.02	3.07	0.05	6.50E-01	8.76E-01	---	---	---	1570318_at	---
2.64	2.73	0.10	6.50E-01	8.76E-01	GLUD1	glutamate dehydrogenase 1	chr10q23.3	244802_at	NM_005271
2.21	2.29	0.07	6.50E-01	8.76E-01	IFNE1	interferon epsilon 1	chr9p21.3	1553574_at	NM_176891
2.12	2.20	0.08	6.50E-01	8.76E-01	---	---	---	1561422_at	---
2.59	2.66	0.06	6.50E-01	8.76E-01	MS4A14	membrane-spanning 4-domains, subfamily A, member 14	chr11q12.2	229510_at	NM_001079692 /// NM_032597
2.38	2.44	0.06	6.50E-01	8.76E-01	---	---	---	243023_at	---
3.12	3.18	0.06	6.51E-01	8.76E-01	RGL4	ral guanine nucleotide dissociation stimulator-like 4	chr22q11.23	235816_s_at	NM_153615
4.02	4.13	0.11	6.51E-01	8.76E-01	MKL1	megakaryoblastic leukemia (translocation) 1	chr22q13	215292_s_at	NM_020831
2.82	2.91	0.08	6.51E-01	8.76E-01	IL17F	interleukin 17F	chr6p12	234408_at	NM_052872
2.42	2.56	0.14	6.51E-01	8.76E-01	NR5A2	nuclear receptor subfamily 5, group A, member 2	chr1q32.1	210174_at	NM_003822 /// NM_205860
2.62	2.72	0.10	6.51E-01	8.76E-01	OSR1	odd-skipped related 1 (Drosophila)	chr2p24.1	228399_at	NM_145260
2.70	2.77	0.07	6.51E-01	8.76E-01	GGA2	Golgi associated, gamma adaptin ear containing, ARF binding protein 2	chr16p12	214189_s_at	NM_015044
2.16	2.22	0.06	6.51E-01	8.76E-01	---	---	---	220666_at	---
2.09	2.14	0.05	6.51E-01	8.76E-01	LOC100134306 /// MYT1L	hypothetical protein LOC100134306 /// myelin transcription factor 1-like	chr2p25.3	210016_at	NM_015025 /// XM_001715519
2.06	2.13	0.07	6.51E-01	8.76E-01	RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	chr14q11.2	217093_at	NM_002933 /// NM_198232 /// NM_198234 /// NM_198235
2.00	2.06	0.06	6.51E-01	8.76E-01	TPTE	transmembrane phosphatase with tensin homology	chr21p11	220205_at	NM_199259 /// NM_199260 /// NM_199261
3.30	3.42	0.12	6.51E-01	8.76E-01	SNN	stannin	chr16p13	218033_s_at	NM_003498
4.63	4.85	0.22	6.52E-01	8.76E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	232865_at	NM_014423
5.26	5.43	0.18	6.52E-01	8.76E-01	MED23	mediator complex subunit 23	chr6q22.33-q24.1	223947_s_at	NM_004830 /// NM_015979
8.25	8.42	0.17	6.52E-01	8.76E-01	COPB2	coatomer protein complex, subunit beta 2 (beta prime)	chr3q23	201098_at	NM_004766 /// NR_023350
6.07	6.22	0.15	6.52E-01	8.76E-01	FBXO30	F-box protein 30	chr6q24	226541_at	NM_032145
4.14	4.29	0.15	6.52E-01	8.76E-01	---	---	---	213383_at	---

6.29	6.40	0.10	6.51E-01	8.76E-01	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	chr22q12.3-q13.1|22q13.1	216061_x_at	NM_002608 /// NM_033016
9.16	9.27	0.10	6.51E-01	8.76E-01	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	chr11p15.1	211746_x_at	NM_002786 /// NM_148976
4.27	4.37	0.10	6.51E-01	8.76E-01	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	chr10q26.13	219024_at	NM_001001974 /// NM_021622
5.60	5.69	0.09	6.51E-01	8.76E-01	ZNF445	zinc finger protein 445	chr3p21.32	229766_at	NM_181489
3.08	3.17	0.09	6.52E-01	8.76E-01	NKX6-3	NK6 homeobox 3	chr8p11.21	1552884_at	NM_152568
3.97	4.05	0.08	6.52E-01	8.76E-01	VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	chr10q25.2	235923_at	NM_145206
5.09	5.17	0.08	6.51E-01	8.76E-01	C4orf23	chromosome 4 open reading frame 23	chr4p16.1	1554192_s_at	NM_152544
4.17	4.26	0.08	6.51E-01	8.76E-01	PSEN1	presenilin 1	chr14q24.3	238816_at	NM_000021 /// NM_007318
2.39	2.47	0.08	6.52E-01	8.76E-01	MGC33407	hypothetical protein MGC33407	chr19p13.2	243208_x_at	NM_178525
3.07	3.15	0.08	6.51E-01	8.76E-01	---	---	---	239826_at	---
3.39	3.46	0.08	6.51E-01	8.76E-01	SHROOM3	Shroom family member 3	chr4q21.1	243653_at	NM_020859
5.55	5.62	0.07	6.52E-01	8.76E-01	IGFBP5	insulin-like growth factor binding protein 5	chr2q33-q36	203426_s_at	NM_000599
2.96	3.03	0.07	6.52E-01	8.76E-01	LOC342918	similar to mCG134545	chr19q13.33	230814_at	XM_001718942 /// XM_292779 /// XM_936809
2.70	2.77	0.07	6.51E-01	8.76E-01	KLK2	kallikrein-related peptidase 2	chr19q13.41	1555545_at	NM_001002231 /// NM_005551
4.16	4.22	0.07	6.51E-01	8.76E-01	CXYorf10	chromosome X and Y open reading frame 10	chrXp22.33; Yp11.3	232463_at	---
9.08	9.14	0.06	6.52E-01	8.76E-01	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	chr12q22	223244_s_at	NM_018838
2.23	2.28	0.06	6.52E-01	8.76E-01	---	---	---	231510_at	---
2.64	2.70	0.06	6.52E-01	8.76E-01	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	1565082_x_at	NM_005417 /// NM_198291
2.74	2.80	0.06	6.51E-01	8.76E-01	---	---	---	240397_x_at	---
2.66	2.72	0.06	6.52E-01	8.76E-01	---	---	---	242526_at	---
1.85	1.90	0.05	6.52E-01	8.76E-01	---	---	---	237007_at	---
2.28	2.34	0.05	6.51E-01	8.76E-01	LOC401074	hypothetical LOC401074	chr3p12.3	1559827_at	XM_001714392
2.12	2.17	0.05	6.52E-01	8.76E-01	PANK2	Pantothenate kinase 2	chr20p13	228966_at	NM_024960 /// NM_153638 /// NM_153640
4.42	4.47	0.05	6.51E-01	8.76E-01	WIPI2	WD repeat domain, phosphoinositide interacting 2	chr7p22.1	214699_x_at	NM_001033518 /// NM_001033519 /// NM_001033520 /// NM_015610 /// NM_016003
1.82	1.87	0.05	6.51E-01	8.76E-01	---	---	---	1562611_at	---
1.92	1.97	0.05	6.52E-01	8.76E-01	C2orf13	chromosome 2 open reading frame 13	chr2p14	241379_at	NM_173545
1.90	1.95	0.05	6.51E-01	8.76E-01	SCN2A	sodium channel, voltage-gated, type II, alpha subunit	chr2q23-q24	229057_at	NM_001040142 /// NM_001040143 /// NM_021007
1.99	2.04	0.05	6.52E-01	8.76E-01	CAPN13	calpain 13	chr2p22-p21	234709_at	NM_144575
5.80	5.93	0.13	6.52E-01	8.76E-01	BLMH	bleomycin hydrolase	chr17q11.2	202179_at	NM_000386
3.09	3.15	0.07	6.52E-01	8.76E-01	CCDC37	coiled-coil domain containing 37	chr3q21.2	243758_at	NM_182628
5.28	5.38	0.09	6.52E-01	8.76E-01	C1orf25	chromosome 1 open reading frame 25	chr1q25.2	220992_s_at	NM_030934
4.84	5.01	0.17	6.52E-01	8.76E-01	ZNF45	zinc finger protein 45	chr19q13.2	222028_at	NM_003425
3.31	3.43	0.12	6.52E-01	8.76E-01	AFAP1L1	actin filament associated protein 1-like 1	chr5q33.1	226955_at	NM_152406
3.99	4.07	0.08	6.52E-01	8.76E-01	---	---	---	235929_s_at	---
2.39	2.47	0.07	6.52E-01	8.76E-01	C16orf3	chromosome 16 open reading frame 3	chr16q24.3	207615_s_at	NM_001214
3.27	3.34	0.07	6.52E-01	8.76E-01	---	---	---	240593_x_at	---
1.86	1.91	0.05	6.52E-01	8.76E-01	---	---	---	1561216_at	---
6.55	6.72	0.17	6.52E-01	8.77E-01	RAB27A	RAB27A, member RAS oncogene family	chr15q15-q21.1	209515_s_at	NM_004580 /// NM_183234 /// NM_183235 /// NM_183236
2.76	2.83	0.07	6.52E-01	8.77E-01	FERMT1	fermitin family homolog 1 (Drosophila)	chr20p12.3	232479_at	NM_017671
2.31	2.36	0.06	6.52E-01	8.77E-01	TCERG1	Transcription elongation regulator 1	chr5q31	238838_at	NM_001040006 /// NM_006706
6.13	6.24	0.11	6.52E-01	8.77E-01	NT5DC1	5'-nucleotidase domain containing 1	chr6q22.1	223177_at	NM_152729
5.95	6.14	0.19	6.52E-01	8.77E-01	TMEM47	transmembrane protein 47	chrXp11.4	209655_s_at	NM_031442

2.24	2.30	0.06	6.52E-01	8.77E-01	KRTAP4-9	keratin associated protein 4-9	chr17q12-q21	234685_x_at	XM_001715848 /// XM_001716829
4.31	4.38	0.07	6.53E-01	8.77E-01	TBRG1	transforming growth factor beta regulator 1	chr11q24.2	230320_at	NM_032811 /// NR_016021
4.71	4.87	0.16	6.53E-01	8.77E-01	UBA6	ubiquitin-like modifier activating enzyme 6	chr4q13.2	222602_at	NM_018227
3.93	4.03	0.10	6.53E-01	8.77E-01	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	chr6q24	216079_at	NM_001018041 /// NM_005670
4.95	5.15	0.19	6.53E-01	8.77E-01	PPM1K	protein phosphatase 1K (PP2C domain containing)	chr4q22.1	235061_at	NM_152542
2.24	2.31	0.07	6.53E-01	8.77E-01	---	---	---	233105_at	---
2.36	2.44	0.09	6.53E-01	8.77E-01	GABARAPL3	GABA(A) receptors associated protein like 3 (pseudogene)	chr15q26.1	211457_at	---
1.96	2.02	0.06	6.53E-01	8.77E-01	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	chr17q23.3	1559953_at	NM_007372 /// NM_203499
4.79	4.86	0.08	6.53E-01	8.77E-01	JMJD2B	jumonji domain containing 2B	chr19p13.3	216023_at	NM_015015
5.04	5.28	0.24	6.53E-01	8.77E-01	ATF1	activating transcription factor 1	chr12q13	1565269_s_at	NM_005171
4.09	4.28	0.19	6.53E-01	8.77E-01	RARB	retinoic acid receptor, beta	chr3p24	208530_s_at	NM_000965 /// NM_016152
3.98	4.12	0.14	6.53E-01	8.77E-01	---	---	---	237456_at	---
3.38	3.49	0.11	6.53E-01	8.77E-01	GDF15	Growth differentiation factor 15	chr19p13.11	229868_s_at	NM_004864
3.97	4.07	0.10	6.53E-01	8.77E-01	C19orf44	chromosome 19 open reading frame 44	chr19p13.11	232730_at	NM_032207
1.88	1.95	0.07	6.53E-01	8.77E-01	---	---	---	1557735_at	---
2.95	3.02	0.07	6.53E-01	8.77E-01	---	---	---	238676_at	---
1.91	1.96	0.06	6.53E-01	8.77E-01	---	---	---	240356_s_at	---
1.99	2.05	0.06	6.53E-01	8.77E-01	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	chr2q32	214378_at	NM_001032281 /// NM_006287
2.75	2.82	0.06	6.53E-01	8.77E-01	GPR45	G protein-coupled receptor 45	chr2q11.1-q12	211175_at	NM_007227
6.24	6.40	0.16	6.53E-01	8.77E-01	SPG11	spastic paraplegia 11 (autosomal recessive)	chr15q14	203513_at	NM_025137
2.38	2.47	0.08	6.54E-01	8.77E-01	SSX2	synovial sarcoma, X breakpoint 2	chrXp11.22	215885_at	NM_003147 /// NM_175698
2.44	2.51	0.06	6.53E-01	8.77E-01	OCR1	ovarian cancer-related protein 1	chr1q32.1	224270_at	XM_001723410 /// XM_001725251 /// XM_001726794
1.85	1.91	0.06	6.54E-01	8.77E-01	RDH10	retinol dehydrogenase 10 (all-trans)	chr8q21.11	1552379_at	NM_172037
2.37	2.42	0.06	6.54E-01	8.77E-01	SMG6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr17p13.3	220347_at	NM_017575
2.04	2.09	0.06	6.54E-01	8.77E-01	LOC286184	hypothetical protein LOC286184	chr8q12.3	1560337_at	---
2.27	2.33	0.06	6.54E-01	8.77E-01	GRIK2	glutamate receptor, ionotropic, kainate 2	chr6q16.3-q21	1560265_at	NM_021956 /// NM_175768
2.57	2.66	0.08	6.54E-01	8.77E-01	---	---	---	240964_at	---
3.47	3.66	0.19	6.54E-01	8.77E-01	CXorf36	chromosome X open reading frame 36	chrXp11.3	222911_s_at	NM_024689 /// NM_176819
4.87	5.02	0.14	6.54E-01	8.77E-01	ERMAP	erythroblast membrane-associated protein (Scianna blood group)	chr1p34.2	219905_at	NM_001017922 /// NM_018538
3.28	3.37	0.10	6.54E-01	8.77E-01	LOC730139	hypothetical protein LOC730139	chr3q27.3	1561571_at	XM_001134281
2.78	2.88	0.09	6.54E-01	8.77E-01	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	chr19p13.2	211447_s_at	NM_001111307 /// NM_001111308 /// NM_001111309 /// NM_006202
3.18	3.27	0.09	6.54E-01	8.77E-01	PGLYRP4	peptidoglycan recognition protein 4	chr1q21	220944_at	NM_020393
2.25	2.32	0.06	6.54E-01	8.77E-01	LOC730168	hypothetical LOC730168	chr3q26.32	243994_at	XM_001132555 /// XM_001132775 /// XM_001716621
2.18	2.24	0.06	6.54E-01	8.77E-01	C21orf135	chromosome 21 open reading frame 135	chr21q22.3	1568849_at	---
6.16	6.43	0.27	6.54E-01	8.77E-01	41519	septin 2	chr2q37	1554747_a_at	NM_001008491 /// NM_001008492 /// NM_004404 /// NM_006155
2.33	2.41	0.08	6.54E-01	8.77E-01	---	---	---	1562065_at	---
2.10	2.15	0.05	6.54E-01	8.77E-01	---	---	---	1562297_at	---
2.50	2.56	0.06	6.54E-01	8.78E-01	---	---	---	1563271_at	---
2.33	2.41	0.08	6.54E-01	8.78E-01	---	---	---	1568735_at	---
3.63	3.69	0.07	6.54E-01	8.78E-01	---	---	---	233111_at	---
1.86	1.91	0.06	6.54E-01	8.78E-01	---	---	---	1552975_x_at	---

2.08	2.13	0.05	6.54E-01	8.78E-01	H2BFM /// H2BFXP	H2B histone family, member M /// H2B histone family, member X, pseudogene	chrXq22.2	230664_at	NR_003238 /// XM_001714135 /// XM_001723437 /// XM_936705
4.23	4.33	0.10	6.55E-01	8.78E-01	C7orf64	chromosome 7 open reading frame 64	chr7q21.2	232661_s_at	NM_032120
2.86	2.96	0.10	6.55E-01	8.78E-01	EIF3C	eukaryotic translation initiation factor 3, subunit C	chr16p11.2	236700_at	NM_001037808 /// NM_003752
2.49	2.57	0.07	6.55E-01	8.78E-01	C20orf82	chromosome 20 open reading frame 82	chr20p12.1	232888_at	NM_080826
2.97	3.04	0.07	6.55E-01	8.78E-01	USP49	ubiquitin specific peptidase 49	chr6p21	243392_at	NM_018561
2.40	2.46	0.07	6.54E-01	8.78E-01	---	---	---	232562_at	---
2.20	2.26	0.06	6.55E-01	8.78E-01	LOC647500	phosphodiesterase 4D interacting protein-like	chr1q21.1	230837_at	XR_041430 /// XR_041431 /// XR_041432
2.28	2.33	0.05	6.55E-01	8.78E-01	---	---	---	1564378_a_at	---
3.17	3.21	0.05	6.54E-01	8.78E-01	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	chr5p15.33	238177_at	NM_001003841 /// XM_001716583 /// XM_001720416 /// XM_001722996
4.95	5.10	0.15	6.55E-01	8.78E-01	ACVRL1	activin A receptor type II-like 1	chr12q11-q14	226950_at	NM_000020 /// NM_001077401
5.38	5.52	0.14	6.55E-01	8.78E-01	STX7	syntaxin 7	chr6q23.1	212631_at	NM_003569
8.63	8.73	0.10	6.55E-01	8.78E-01	ANXA7	annexin A7	chr10q21.1-q21.2	209860_s_at	NM_001156 /// NM_004034
3.33	3.41	0.08	6.55E-01	8.78E-01	MYOZ3	myozenin 3	chr5q33.1	1553070_a_at	NM_001122853 /// NM_133371
3.75	3.82	0.07	6.55E-01	8.78E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHD /// IGHG1 /// IGHG3 /// IGHG4 /// IGHM /// IGHV4-31 /// LOC100126583 /// LOC100134331 /// LOC642131 /// LOC652128	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant gamma 4 (G4m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical LOC100126583 /// similar to hCG1812074 /// similar to hCG1812074 /// similar to Ig heavy chain V-II region ARH-77 precursor	chr14q32.33 /// chr15q11.2	211835_at	XM_001716198 /// XM_001716834 /// XM_001717736 /// XM_001724554 /// XM_941465
2.60	2.65	0.06	6.55E-01	8.78E-01	---	---	---	243662_at	---
3.08	3.14	0.05	6.55E-01	8.78E-01	FZD8	frizzled homolog 8 (Drosophila)	chr10p11.21	216587_s_at	NM_031866
1.94	1.99	0.05	6.55E-01	8.78E-01	TEX9	Testis expressed 9	chr15q21.3	1566605_at	NM_198524
5.64	6.01	0.36	6.55E-01	8.78E-01	---	---	---	227061_at	---
5.94	6.16	0.21	6.55E-01	8.78E-01	---	---	---	228746_s_at	---
7.90	8.03	0.13	6.55E-01	8.78E-01	DLC1	deleted in liver cancer 1	chr8p22	210762_s_at	NM_006094 /// NM_024767 /// NM_182643
3.22	3.34	0.12	6.55E-01	8.78E-01	KIAA0368	KIAA0368	chr9q31.3	212427_at	NM_001080398
4.39	4.48	0.08	6.55E-01	8.78E-01	C1orf61	chromosome 1 open reading frame 61	chr1q22	1559402_a_at	NM_006365
2.60	2.66	0.07	6.55E-01	8.78E-01	CTAG2	cancer/testis antigen 2	chrXq28	215733_x_at	NM_020994 /// NM_172377 /// XM_001714637
2.03	2.09	0.06	6.55E-01	8.78E-01	FLJ25770	hypothetical protein FLJ25770	chr4q21.1	1554846_at	NM_001042784
2.31	2.36	0.06	6.55E-01	8.78E-01	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)	chr3q21	1563794_s_at	NM_018262 /// NM_052985 /// NM_052989 /// NM_052990
2.15	2.20	0.05	6.55E-01	8.78E-01	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	chr2q36-q37	216368_s_at	NM_000091 /// NM_031362 /// NM_031365 /// NM_031366
6.91	7.02	0.11	6.55E-01	8.78E-01	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	chr1q41-q42	217788_s_at	NM_004481
2.56	2.65	0.10	6.55E-01	8.78E-01	PASK	PAS domain containing serine/threonine kinase	chr2q37.3	216945_x_at	NM_015148

2.39	2.44	0.06	6.55E-01	8.78E-01	TBC1D30	TBC1 domain family, member 30	chr12q14.3	213913_s_at	XM_001716833 /// XM_037557 /// XM_939476
2.90	2.99	0.08	6.56E-01	8.78E-01	---	---	---	237165_at	---
3.51	3.59	0.08	6.55E-01	8.78E-01	---	---	---	239158_at	---
2.17	2.24	0.07	6.56E-01	8.78E-01	---	---	---	244459_at	---
2.07	2.13	0.06	6.55E-01	8.78E-01	---	---	---	1569772_x_at	---
2.48	2.54	0.06	6.55E-01	8.78E-01	---	---	---	1556649_at	---
6.25	6.38	0.13	6.56E-01	8.78E-01	ETF1	eukaryotic translation termination factor 1	chr5q31.1	201573_s_at	NM_004730
2.10	2.16	0.05	6.56E-01	8.78E-01	---	---	---	1562353_x_at	---
2.11	2.16	0.05	6.56E-01	8.78E-01	---	---	---	1562009_a_at	---
3.37	3.46	0.09	6.56E-01	8.78E-01	ASMTL /// DUX1 /// DUX3 /// DUX4 /// DUX5 /// HPX-2 /// LOC100133977 /// LOC440014 /// LOC651709 /// LOC652119 /// LOC652291 /// LOC653548	acetylserotonin O-methyltransferase-like /// double homeobox, 1 /// double homeobox, 3 /// double homeobox, 4 /// double homeobox, 5 /// similar to double homeobox, 4 /// similar to double homeobox, 4 /// similar to Double homeobox protein 4 (Double homeobox protein 10) (Double homeobox protein 4/10) /// similar to double homeobox, 4 /// similar to double homeobox 4c /// similar to double homeobox, 4 /// double homeobox, 4-like	chr10q26.3 /// chr4q35 /// chr4q35.2 /// chrXp22.3; Yp11.3	208201_at	NM_004192 /// NM_012146 /// NM_012148 /// NM_012149 /// NM_033178 /// XM_001713702 /// XM_001719278 /// XM_001720798 /// XM_001722088 /// XM_001724713 /// XM_001732813 /// XM_001732890 /// XM_495855 /// XM_928023 /// XM_941455 /// XR_019487
6.06	6.14	0.07	6.56E-01	8.78E-01	TCP1	t-complex 1	chr6q25.3-q26	222010_at	NM_001008897 /// NM_030752
2.09	2.16	0.06	6.56E-01	8.78E-01	---	---	---	240850_at	---
3.69	3.79	0.10	6.56E-01	8.78E-01	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	chr7q36	203030_s_at	NM_002847 /// NM_130842 /// NM_130843
2.61	2.68	0.07	6.56E-01	8.78E-01	---	---	---	233452_at	---
2.90	2.95	0.06	6.56E-01	8.78E-01	SOCS7	suppressor of cytokine signaling 7	chr17q12	214015_at	NM_014598
4.45	4.59	0.15	6.56E-01	8.78E-01	XRCC6BP1	XRCC6 binding protein 1	chr12q14.1	227678_at	NM_033276
4.58	4.67	0.10	6.56E-01	8.78E-01	SLC12A4	Solute carrier family 12 (potassium/chloride transporters), member 4	chr16q22.1	228644_s_at	NM_005072
4.99	5.09	0.09	6.56E-01	8.78E-01	HDAC10	histone deacetylase 10	chr22q13.31	232870_at	NM_032019
4.32	4.41	0.08	6.56E-01	8.78E-01	---	---	---	211691_x_at	---
2.22	2.28	0.06	6.56E-01	8.78E-01	C17orf74	chromosome 17 open reading frame 74	chr17p13.1	240082_s_at	NM_175734
2.10	2.15	0.05	6.56E-01	8.78E-01	HDAC9	histone deacetylase 9	chr7p21.1	1552758_at	NM_014707 /// NM_058176 /// NM_058177 /// NM_178423 /// NM_178425
2.88	2.93	0.05	6.56E-01	8.78E-01	TLN2	talin 2	chr15q15-q21	232625_at	NM_015059
3.38	3.48	0.10	6.56E-01	8.78E-01	GOLGA6	golgi autoantigen, golgin subfamily a, 6	chr15q24.1	232813_s_at	NM_001038640
2.83	2.95	0.11	6.56E-01	8.78E-01	---	---	---	239516_at	---
2.73	2.80	0.07	6.56E-01	8.78E-01	BAT2D1	BAT2 domain containing 1	chr1q23.3	211947_s_at	NM_015172
2.78	2.85	0.07	6.56E-01	8.78E-01	---	---	---	239518_at	---
3.45	3.52	0.07	6.56E-01	8.78E-01	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	chr10q22.1	208252_s_at	NM_004273
1.94	1.99	0.05	6.56E-01	8.78E-01	IRAK2	interleukin-1 receptor-associated kinase 2	chr3p25.3	1553739_at	NM_001570
4.89	4.99	0.10	6.56E-01	8.78E-01	ZMYND8	zinc finger, MYND-type containing 8	chr20q13.12	230533_at	NM_012408 /// NM_183047 /// NM_183048
1.89	1.95	0.05	6.56E-01	8.78E-01	---	---	---	222342_at	---
5.36	5.43	0.07	6.57E-01	8.78E-01	DLEU1	deleted in lymphocytic leukemia 1 (non-protein coding)	chr13q14.3	205677_s_at	NR_002605 /// XR_041406 /// XR_041407 /// XR_041408
5.21	5.36	0.14	6.57E-01	8.78E-01	---	---	---	228611_s_at	---
2.16	2.21	0.05	6.57E-01	8.78E-01	---	---	---	238103_at	---
2.49	2.56	0.06	6.57E-01	8.78E-01	BRUNOL5	bruno-like 5, RNA binding protein (Drosophila)	chr19p13	230497_at	NM_021938
6.22	6.38	0.15	6.57E-01	8.79E-01	MAP3K1	mitogen-activated protein kinase kinase kinase 1	chr5q11.2	225927_at	NM_005921

3.44	3.49	0.05	6.57E-01	8.79E-01	C9orf130	chromosome 9 open reading frame 130	chr9q22.32	239799_at	NR_023389 /// NR_023390 /// XM_001722853 /// XM_001724349 /// XM_001732875
4.61	4.89	0.28	6.57E-01	8.79E-01	PRPS2	Phosphoribosyl pyrophosphate synthetase 2	chrXp22.3-p22.2	230352_at	NM_001039091 /// NM_002765
5.94	6.15	0.21	6.57E-01	8.79E-01	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	chr3q13.12	218100_s_at	NM_018010
2.05	2.13	0.08	6.57E-01	8.79E-01	CYP4Z2P	cytochrome P450, family 4, subfamily Z, polypeptide 2 pseudogene	chr1p33	1553434_at	NR_002788 /// XR_042146
2.85	2.93	0.08	6.57E-01	8.79E-01	OSCAR	osteoclast associated, immunoglobulin-like receptor	chr19q13.42	1554503_a_at	NM_130771 /// NM_133168 /// NM_133169 /// NM_206818
2.24	2.30	0.06	6.57E-01	8.79E-01	---	---	---	1562671_s_at	---
2.25	2.30	0.06	6.57E-01	8.79E-01	---	---	---	237072_at	---
2.22	2.29	0.06	6.57E-01	8.79E-01	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	chr17q22	1555606_a_at	NM_182569
5.14	5.28	0.14	6.57E-01	8.79E-01	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	chr16q24.3	205458_at	NM_002386
2.08	2.16	0.07	6.57E-01	8.79E-01	ZNF311	zinc finger protein 311	chr6p22.1	236550_s_at	NM_001010877
2.26	2.32	0.06	6.57E-01	8.79E-01	---	---	---	231302_at	---
5.38	5.57	0.19	6.57E-01	8.79E-01	CYP4V2	cytochrome P450, family 4, subfamily V, polypeptide 2	chr4q35.2	228391_at	NM_207352
6.71	6.82	0.11	6.57E-01	8.79E-01	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	213070_at	NM_002645
2.30	2.35	0.05	6.57E-01	8.79E-01	KIF19	kinesin family member 19	chr17q25.1	1553314_a_at	NM_153209
2.17	2.24	0.07	6.57E-01	8.79E-01	---	---	---	234193_at	---
4.92	5.06	0.14	6.57E-01	8.79E-01	PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	chr20q13.33	208879_x_at	NM_012469
2.39	2.52	0.13	6.58E-01	8.79E-01	---	---	---	233302_at	---
2.51	2.61	0.10	6.58E-01	8.79E-01	---	---	---	239646_at	---
2.01	2.07	0.06	6.58E-01	8.79E-01	---	---	---	1563173_at	---
3.44	3.50	0.05	6.58E-01	8.79E-01	CRLF1	cytokine receptor-like factor 1	chr19p12	1564568_at	NM_004750
2.28	2.33	0.05	6.58E-01	8.79E-01	WDR33	WD repeat domain 33	chr2q14.3	243832_at	NM_001006622 /// NM_001006623 /// NM_018383
2.03	2.09	0.06	6.58E-01	8.79E-01	---	---	---	1569835_at	---
2.76	2.82	0.06	6.58E-01	8.79E-01	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	chr7q22	223995_at	NM_020246
4.15	4.22	0.07	6.58E-01	8.79E-01	HPS6	Hermansky-Pudlak syndrome 6	chr10q24.32	230371_at	NM_024747
4.28	4.38	0.11	6.58E-01	8.79E-01	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	chr19p13.3	213298_at	NM_005597 /// NM_205843
1.99	2.06	0.07	6.58E-01	8.79E-01	---	---	---	1560570_a_at	---
2.03	2.09	0.06	6.58E-01	8.79E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	210833_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719
2.06	2.11	0.06	6.58E-01	8.79E-01	ZNF236	zinc finger protein 236	chr18q22-q23	219171_s_at	NM_007345
4.79	4.90	0.11	6.58E-01	8.79E-01	LOC283267	hypothetical LOC283267	chr11p13	226793_at	---
2.18	2.25	0.06	6.58E-01	8.79E-01	---	---	---	234930_at	---
3.59	3.72	0.13	6.58E-01	8.79E-01	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	chr12q15	202470_s_at	NM_007007
4.63	4.74	0.11	6.58E-01	8.79E-01	CNOT1	CCR4-NOT transcription complex, subunit 1	chr16q21	1554052_at	NM_016284 /// NM_206999
2.56	2.61	0.06	6.58E-01	8.79E-01	HES1	hairy and enhancer of split 1, (Drosophila)	chr3q28-q29	203393_at	NM_005524
2.07	2.13	0.06	6.58E-01	8.79E-01	---	---	---	239387_at	---
3.16	3.25	0.09	6.58E-01	8.79E-01	TTC39A	tetratricopeptide repeat domain 39A	chr1p32.3	217101_at	NM_001080494
8.21	8.39	0.17	6.58E-01	8.79E-01	CREBL2	cAMP responsive element binding protein-like 2	chr12p13	201990_s_at	NM_001310
4.75	4.85	0.10	6.58E-01	8.79E-01	---	---	---	236209_at	---
6.68	6.77	0.09	6.58E-01	8.79E-01	SNAPC5	small nuclear RNA activating complex, polypeptide 5, 19kDa	chr15q22.31	213203_at	NM_006049
2.16	2.25	0.09	6.59E-01	8.79E-01	CADPS	Ca++-dependent secretion activator	chr3p14.2	234220_at	NM_003716 /// NM_183393 /// NM_183394
7.26	7.34	0.08	6.59E-01	8.79E-01	MARK4	MAP/microtubule affinity-regulating kinase 4	chr19q13.3	221560_at	NM_031417

4.54	4.62	0.08	6.59E-01	8.79E-01	SYK	spleen tyrosine kinase	chr9q22	207540_s_at	NM_003177
2.38	2.45	0.07	6.59E-01	8.79E-01	---	---	---	243115_at	---
1.99	2.05	0.06	6.58E-01	8.79E-01	TMEM67	transmembrane protein 67	chr8q22.1	238229_at	NM_153704
2.05	2.11	0.06	6.59E-01	8.79E-01	DCLK1	doublecortin-like kinase 1	chr13q13	230962_at	NM_004734
8.91	8.96	0.05	6.59E-01	8.79E-01	SDHALP1	succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1	chr3q29	222021_x_at	NR_003264 /// XR_042174
6.27	6.44	0.16	6.59E-01	8.79E-01	---	---	---	227623_at	---
2.85	2.91	0.06	6.59E-01	8.79E-01	C18orf10	chromosome 18 open reading frame 10	chr18q12.2	244233_at	NM_015476
1.91	1.96	0.06	6.59E-01	8.79E-01	---	---	---	240726_at	---
5.04	5.13	0.09	6.59E-01	8.80E-01	CADM4	cell adhesion molecule 4	chr19q13.31	222293_at	NM_145296
2.06	2.17	0.11	6.59E-01	8.80E-01	METT5D1	methyltransferase 5 domain containing 1	chr11p14.1	242247_at	NM_001113528 /// NM_152636
5.28	5.37	0.10	6.59E-01	8.80E-01	PLCB2	phospholipase C, beta 2	chr15q15	204046_at	NM_004573
6.71	6.84	0.13	6.59E-01	8.80E-01	GTF2E1	general transcription factor IIE, polypeptide 1, alpha 56kDa	chr3q21-q24	205930_at	NM_005513
2.21	2.27	0.06	6.59E-01	8.80E-01	---	---	---	1561268_at	---
2.16	2.22	0.06	6.59E-01	8.80E-01	---	---	---	1568732_at	---
2.05	2.13	0.07	6.59E-01	8.80E-01	PLAC1L	placenta-specific 1-like	chr11q12.1	1557085_at	NM_173801
6.54	6.71	0.17	6.59E-01	8.80E-01	UBE2Q2	ubiquitin-conjugating enzyme E2Q family member 2	chr15q24.2	224747_at	NM_173469
2.48	2.55	0.07	6.59E-01	8.80E-01	---	---	---	244594_x_at	---
6.78	6.86	0.08	6.59E-01	8.80E-01	NIT2	nitrilase family, member 2	chr3q12.2	218557_at	NM_020202
4.27	4.34	0.06	6.59E-01	8.80E-01	---	---	---	229021_at	---
2.31	2.36	0.05	6.59E-01	8.80E-01	LOC550631	hypothetical LOC550631	chr22q12.2	232920_at	NM_001017437
2.64	2.74	0.09	6.59E-01	8.80E-01	KLK4	kallikrein-related peptidase 4	chr19q13.41	1555737_a_at	NM_004917
1.95	2.02	0.07	6.59E-01	8.80E-01	C6orf10	chromosome 6 open reading frame 10	chr6p21.3	207523_at	NM_006781
4.98	5.15	0.17	6.60E-01	8.80E-01	ZZZ3	zinc finger, ZZ-type containing 3	chr1p31.1	212893_at	NM_015534
2.44	2.50	0.06	6.60E-01	8.80E-01	PNPLA2	Patatin-like phospholipase domain containing 2	chr11p15.5	213862_at	NM_020376
5.35	5.44	0.09	6.60E-01	8.80E-01	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	chr20q11.23	202572_s_at	NM_001042486 /// NM_014902 /// NM_183006
4.81	4.95	0.14	6.60E-01	8.80E-01	---	---	---	236370_at	---
5.10	5.21	0.11	6.60E-01	8.80E-01	---	---	---	229810_at	---
2.77	2.86	0.08	6.60E-01	8.80E-01	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	chr5q11.2	212649_at	NM_019030
2.06	2.13	0.06	6.60E-01	8.80E-01	C11orf64	chromosome 11 open reading frame 64	chr11q12.2	1563145_at	XR_039987 /// XR_039988 /// XR_039989
2.17	2.22	0.05	6.60E-01	8.80E-01	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	chr8p11.2	224077_at	NM_017778 /// NM_023034
1.97	2.03	0.05	6.60E-01	8.80E-01	PAH	phenylalanine hydroxylase	chr12q22-q24.2	244742_at	NM_000277
2.20	2.26	0.06	6.60E-01	8.80E-01	TAS2R9	taste receptor, type 2, member 9	chr12p13	221461_at	NM_023917
2.08	2.14	0.06	6.60E-01	8.80E-01	---	---	---	216636_at	---
2.92	3.02	0.09	6.60E-01	8.80E-01	---	---	---	1557835_at	---
5.23	5.41	0.18	6.60E-01	8.80E-01	PCGF5	polycomb group ring finger 5	chr10q23.32	229194_at	NM_032373
9.64	9.74	0.10	6.60E-01	8.80E-01	RAB1A	RAB1A, member RAS oncogene family	chr2p14	208724_s_at	NM_004161
3.26	3.34	0.08	6.60E-01	8.80E-01	---	---	---	229735_s_at	---
2.71	2.78	0.07	6.60E-01	8.80E-01	PARVB	parvin, beta	chr22q13.2-q13.33	216254_at	NM_001003828 /// NM_013327
1.86	1.91	0.05	6.60E-01	8.80E-01	---	---	---	1568871_at	---
3.78	3.95	0.17	6.60E-01	8.81E-01	---	---	---	235429_at	---
4.31	4.42	0.11	6.61E-01	8.81E-01	GP1BB /// SEPT5	glycoprotein Ib (platelet), beta polypeptide /// septin 5	chr22q11.21 /// chr22q11.21-q11.23|22q11.21	209767_s_at	NM_000407 /// NM_002688
2.37	2.46	0.08	6.61E-01	8.81E-01	MAGEA8	melanoma antigen family A, 8	chrXq28	210274_at	NM_005364
2.41	2.48	0.07	6.60E-01	8.81E-01	SYNE2	spectrin repeat containing, nuclear envelope 2	chr14q23.2	242774_at	NM_015180 /// NM_182910 /// NM_182913 /// NM_182914
5.13	5.36	0.22	6.61E-01	8.81E-01	NFYB	nuclear transcription factor Y, beta	chr12q22-q23	218127_at	NM_006166
3.81	3.92	0.11	6.61E-01	8.81E-01	CHD9	Chromodomain helicase DNA binding protein 9	chr16q12.2	239654_at	NM_025134
3.28	3.37	0.09	6.61E-01	8.81E-01	CHRNA4	cholinergic receptor, nicotinic, alpha 4	chr20q13.2-q13.3	206736_x_at	NM_000744
6.71	6.93	0.22	6.61E-01	8.81E-01	EIF5	eukaryotic translation initiation factor 5	chr14q32.32	208708_x_at	NM_001969 /// NM_183004
7.73	7.82	0.09	6.61E-01	8.81E-01	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	chr11q23.3	208745_at	NM_006476
2.62	2.69	0.07	6.61E-01	8.81E-01	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	chr5q14.2	207774_at	NM_001131028 /// NM_031482
5.72	5.85	0.12	6.61E-01	8.81E-01	UBE2E2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	chr3p24.2	225651_at	NM_152653
2.20	2.27	0.07	6.61E-01	8.81E-01	---	---	---	242890_at	---
2.11	2.16	0.05	6.61E-01	8.81E-01	STXBP3	syntaxin binding protein 3	chr1p13.3	1560486_at	NM_007269
3.01	3.17	0.16	6.61E-01	8.81E-01	---	---	---	234082_at	---
4.93	5.06	0.14	6.61E-01	8.81E-01	SLC43A3	solute carrier family 43, member 3	chr11q11	213113_s_at	NM_014096 /// NM_017611 /// NM_199329

1.99	2.05	0.06	6.61E-01	8.81E-01	PCDH15	protocadherin 15	chr10q21.1	1560330_at	NM_033056
2.98	3.05	0.07	6.61E-01	8.81E-01	---	---	---	1561591_at	---
4.46	4.66	0.20	6.62E-01	8.81E-01	LIFR	leukemia inhibitory factor receptor alpha	chr5p13-p12	227771_at	NM_001127671 /// NM_002310
3.31	3.50	0.18	6.62E-01	8.81E-01	MIER3	mesoderm induction early response 1, family member 3	chr5q11.2	1554450_s_at	NM_152622
7.09	7.27	0.18	6.62E-01	8.81E-01	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	chr20q13.13	218098_at	NM_006420
4.21	4.37	0.16	6.62E-01	8.81E-01	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	chr3q22.1	211137_s_at	NM_001001485 /// NM_001001486 /// NM_001001487 /// NM_014382
3.86	4.03	0.16	6.62E-01	8.81E-01	TRA@ /// TRAC	T cell receptor alpha locus /// T cell receptor alpha constant	chr14q11 /// chr14q11.2	209671_x_at	---
2.93	3.03	0.11	6.61E-01	8.81E-01	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	chr18q21	210017_at	NM_006785 /// NM_173844
4.60	4.70	0.10	6.62E-01	8.81E-01	ATL3	atlastin 3	chr11q13.1	223452_s_at	NM_015459
3.76	3.85	0.08	6.61E-01	8.81E-01	LTA	lymphotoxin alpha (TNF superfamily, member 1)	chr6p21.3	206975_at	NM_000595
3.12	3.20	0.08	6.62E-01	8.81E-01	LOC651900	hypothetical protein LOC651900	---	1563119_at	XM_941161
4.13	4.20	0.07	6.62E-01	8.81E-01	C1orf201	chromosome 1 open reading frame 201	chr1p36.11	227694_at	NM_178122
3.98	4.05	0.07	6.62E-01	8.81E-01	MSL3L1	male-specific lethal 3-like 1 (Drosophila)	chrXp22.3	214009_at	NM_006800 /// NM_078628 /// NM_078629 /// NM_078630
3.02	3.08	0.07	6.61E-01	8.81E-01	---	---	---	1566424_at	---
2.97	3.03	0.07	6.62E-01	8.81E-01	CXorf42	chromosome X open reading frame 42	chrXq24	236493_at	XR_017748 /// XR_017897 /// XR_041218
2.75	2.82	0.06	6.62E-01	8.81E-01	HPDL	4-hydroxyphenylpyruvate dioxygenase-like	chr1p34.1	229332_at	NM_032756
3.12	3.18	0.06	6.62E-01	8.81E-01	RTKN	Rhotekin	chr2p13.1	239226_at	NM_001015055 /// NM_001015056 /// NM_033046
2.83	2.89	0.06	6.62E-01	8.81E-01	ACTG2	actin, gamma 2, smooth muscle, enteric	chr2p13.1	241148_at	NM_001615
2.58	2.64	0.06	6.61E-01	8.81E-01	FAM83H	family with sequence similarity 83, member H	chr8q24.3	241406_at	NM_198488
2.30	2.36	0.06	6.62E-01	8.81E-01	MGC33556	hypothetical LOC339541	chr1p34.1	242520_s_at	XR_039961 /// XR_039962 /// XR_039963
6.95	7.16	0.21	6.62E-01	8.81E-01	CXorf26	chromosome X open reading frame 26	chrXq13.3	223294_at	NM_016500
5.43	5.53	0.10	6.62E-01	8.81E-01	ZNF688	zinc finger protein 688	chr16p11.2	213527_s_at	NM_001024683 /// NM_145271
4.33	4.42	0.09	6.62E-01	8.81E-01	ZKSCAN3	zinc finger with KRAB and SCAN domains 3	chr6p22.1	211773_s_at	NM_024493
2.75	2.83	0.08	6.62E-01	8.81E-01	MYH13	myosin, heavy chain 13, skeletal muscle	chr17p13	208208_at	NM_003802
4.22	4.30	0.08	6.62E-01	8.81E-01	ZNF696	zinc finger protein 696	chr8q24.3	220967_s_at	NM_030895
2.64	2.71	0.07	6.62E-01	8.81E-01	OR7A10	olfactory receptor, family 7, subfamily A, member 10	chr19p13.12	217316_at	NM_001005190
2.92	2.98	0.07	6.62E-01	8.81E-01	C7orf52	chromosome 7 open reading frame 52	chr7q22.1	240784_at	NM_198571
2.20	2.27	0.07	6.62E-01	8.81E-01	GATAD1	GATA zinc finger domain containing 1	chr7q21-q22	242634_at	NM_021167
2.49	2.55	0.07	6.62E-01	8.81E-01	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	chr6p24	204653_at	NM_001032280 /// NM_001042425 /// NM_003220
2.38	2.43	0.05	6.62E-01	8.81E-01	OR7E24	olfactory receptor, family 7, subfamily E, member 24	chr19p13.2	215463_at	NM_001079935
2.13	2.18	0.05	6.62E-01	8.81E-01	---	---	---	241730_at	---
3.03	3.11	0.08	6.62E-01	8.81E-01	PKD1L2	polycystic kidney disease 1-like 2	chr16q23.2	1559261_a_at	NM_001076780 /// NM_052892
6.20	6.41	0.20	6.62E-01	8.81E-01	ZNF638	zinc finger protein 638	chr2p13.2-p13.1	211257_x_at	NM_001014972 /// NM_014497
4.01	4.08	0.07	6.62E-01	8.81E-01	C20orf141	chromosome 20 open reading frame 141	chr20p13	1554042_s_at	NM_080739
2.23	2.29	0.06	6.62E-01	8.81E-01	---	---	---	1561370_at	---
3.21	3.26	0.05	6.62E-01	8.81E-01	LOC284080	hypothetical protein LOC284080	chr17q21.33	1557608_a_at	---
2.87	2.95	0.07	6.62E-01	8.81E-01	---	---	---	215327_at	---
2.05	2.13	0.08	6.62E-01	8.81E-01	---	---	---	1566285_at	---
10.50	10.62	0.13	6.63E-01	8.81E-01	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	chr3q28	200912_s_at	NM_001967
6.08	6.18	0.10	6.63E-01	8.81E-01	STK4	serine/threonine kinase 4	chr20q11.2-q13.2	236259_at	NM_006282

7.45	7.54	0.09	6.62E-01	8.81E-01	APIP	APAF1 interacting protein	chr11p13	218698_at	NM_015957
2.75	2.81	0.06	6.63E-01	8.81E-01	---	---	---	242731_x_at	---
4.80	4.99	0.19	6.63E-01	8.81E-01	CDC42EP5	CDC42 effector protein (Rho GTPase binding) 5	chr19q13.42	227850_x_at	NM_145057
5.64	5.79	0.15	6.63E-01	8.81E-01	COMMD10	COMM domain containing 10	chr5q23.1	222637_at	NM_016144
2.50	2.57	0.07	6.63E-01	8.81E-01	---	---	---	242954_at	---
3.07	3.14	0.07	6.63E-01	8.81E-01	AGBL4	ATP/GTP binding protein-like 4	chr1p33	1553412_at	NM_032785
6.45	6.62	0.17	6.63E-01	8.81E-01	SLMAP	sarcolemma associated protein	chr3p21.2-p14.3	225243_s_at	NM_007159
2.15	2.23	0.08	6.63E-01	8.81E-01	---	---	---	240244_at	---
2.18	2.25	0.07	6.63E-01	8.81E-01	ENO3	enolase 3 (beta, muscle)	chr17pter-p11	237691_x_at	NM_001976 /// NM_053013
6.64	6.71	0.07	6.63E-01	8.81E-01	KCNIP3	Kv channel interacting protein 3, calsenilin	chr2q21.1	234647_at	NM_001034914 /// NM_013434
2.64	2.68	0.05	6.63E-01	8.81E-01	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	chr6p22.3-p22.1	244844_at	NM_020662
2.23	2.33	0.10	6.63E-01	8.81E-01	LIN28B	lin-28 homolog B (C. elegans)	chr6q21	229349_at	NM_001004317
2.42	2.50	0.08	6.63E-01	8.81E-01	LOC286299	hypothetical protein LOC286299	chr9p22.2	1565998_at	---
2.38	2.44	0.07	6.63E-01	8.81E-01	KLKBL4	plasma kallikrein-like protein 4	chr16q21	231287_s_at	NM_001080492
1.90	1.95	0.05	6.63E-01	8.81E-01	---	---	---	240447_at	---
4.48	4.56	0.08	6.63E-01	8.81E-01	SP3	Sp3 transcription factor	chr2q31	238035_at	NM_001017371 /// NM_003111
3.35	3.52	0.17	6.63E-01	8.82E-01	IGSF10	immunoglobulin superfamily, member 10	chr3q25.1	1556579_s_at	NM_178822
2.51	2.59	0.08	6.63E-01	8.82E-01	OR1G1	olfactory receptor, family 1, subfamily G, member 1	chr17p13.3	221375_at	NM_003555
2.93	2.99	0.06	6.63E-01	8.82E-01	---	---	---	216046_at	---
2.40	2.45	0.05	6.63E-01	8.82E-01	---	---	---	1565713_at	---
2.33	2.39	0.06	6.63E-01	8.82E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	1554528_at	NM_033364
2.04	2.10	0.05	6.63E-01	8.82E-01	CCDC110	coiled-coil domain containing 110	chr4q35.1	230900_at	NM_152775
5.04	5.28	0.24	6.64E-01	8.82E-01	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	chr22q13.1	213998_s_at	NM_001098504 /// NM_001098505 /// NM_006386 /// NM_030881
3.44	3.51	0.07	6.64E-01	8.82E-01	PPP1R11	Protein phosphatase 1, regulatory (inhibitor) subunit 11	chr6p21.3	1566301_at	NM_021959
2.34	2.39	0.05	6.64E-01	8.82E-01	---	---	---	234392_at	---
7.97	8.10	0.12	6.64E-01	8.82E-01	YTHDF2	YTH domain family, member 2	chr1p35	222430_s_at	NM_016258
5.63	5.74	0.11	6.64E-01	8.82E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	1555948_s_at	NM_014612
2.58	2.64	0.06	6.64E-01	8.82E-01	SLC25A18	solute carrier family 25 (mitochondrial carrier), member 18	chr22q11.2	223605_at	NM_031481
1.95	2.00	0.04	6.64E-01	8.82E-01	---	---	---	1563351_at	---
6.30	6.52	0.22	6.64E-01	8.82E-01	SSB	Sjogren syndrome antigen B (autoantigen La)	chr2q31.1	201138_s_at	NM_003142
4.00	4.09	0.09	6.64E-01	8.82E-01	FAM116B	family with sequence similarity 116, member B	chr22q13.33	228678_at	NM_001001794
2.44	2.52	0.08	6.64E-01	8.82E-01	---	---	---	233293_at	---
5.11	5.19	0.08	6.64E-01	8.82E-01	GNB3	guanine nucleotide binding protein (G protein), beta polypeptide 3	chr12p13	206047_at	NM_002075
3.60	3.66	0.06	6.64E-01	8.82E-01	FAM53A	Family with sequence similarity 53, member A	chr4p16.3	236206_at	NM_001013622
3.25	3.37	0.12	6.64E-01	8.82E-01	FOXD1	forkhead box D1	chr5q12-q13	206307_s_at	NM_004472
2.74	2.85	0.11	6.64E-01	8.82E-01	---	---	---	1562416_at	---
4.82	4.93	0.10	6.64E-01	8.82E-01	ZNF503	zinc finger protein 503	chr10q22.2	228684_at	NM_032772
3.26	3.33	0.07	6.64E-01	8.82E-01	RBMS2	RNA binding motif, single stranded interacting protein 2	chr12q13.3	205228_at	NM_002898
2.31	2.37	0.07	6.64E-01	8.82E-01	CSH1 /// CSH2 /// FCHO2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// FCH domain only 2 /// growth hormone 1	chr17q24.2 /// chr5q13.2	202493_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645 /// NM_138782
2.08	2.13	0.05	6.64E-01	8.82E-01	OLIG1	oligodendrocyte transcription factor 1	chr21q22.11	228170_at	NM_138983
2.77	2.82	0.05	6.64E-01	8.82E-01	tcag7.1228	hypothetical protein FLJ25778	chr7q34	238349_at	NM_173569
2.42	2.49	0.06	6.64E-01	8.82E-01	---	---	---	234959_at	---
7.45	7.60	0.15	6.65E-01	8.82E-01	CDC16	cell division cycle 16 homolog (S. cerevisiae)	chr13q34	209659_s_at	NM_001078645 /// NM_003903

2.05	2.12	0.07	6.64E-01	8.82E-01	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	chr1q31	219918_s_at	NM_018136
5.57	5.64	0.07	6.65E-01	8.82E-01	---	---	---	242398_x_at	---
2.03	2.09	0.06	6.65E-01	8.82E-01	THOC5	THO complex 5	chr22q12.2	209419_at	NM_001002877 /// NM_001002878 /// NM_001002879 /// NM_003678
2.10	2.16	0.06	6.65E-01	8.82E-01	---	---	---	238873_at	---
5.78	5.89	0.11	6.65E-01	8.83E-01	FLJ11151	hypothetical protein FLJ11151	chr16p13.12	222686_s_at	NM_001099455 /// NM_018340
3.82	3.87	0.05	6.65E-01	8.83E-01	MYLIP	Myosin regulatory light chain interacting protein	chr6p23-p22.3	227707_at	NM_013262
5.01	5.09	0.08	6.65E-01	8.83E-01	CCDC109A	coiled-coil domain containing 109A	chr10q22.1	225320_at	NM_138357
1.94	1.98	0.05	6.65E-01	8.83E-01	CCDC67	coiled-coil domain containing 67	chr11q21	1554071_at	NM_181645
5.97	6.10	0.12	6.65E-01	8.83E-01	DLAT	dihydrolipoamide S-acetyltransferase	chr11q23.1	213149_at	NM_001931
2.10	2.17	0.07	6.65E-01	8.83E-01	---	---	---	1570269_at	---
2.86	2.93	0.07	6.65E-01	8.83E-01	KCNK9	Potassium channel, subfamily K, member 9	chr8q24.3	238870_at	NM_016601
5.86	6.00	0.15	6.65E-01	8.83E-01	AKTIP	AKT interacting protein	chr16q12.2	218373_at	NM_001012398 /// NM_022476
2.49	2.58	0.09	6.65E-01	8.83E-01	---	---	---	216062_at	---
5.58	5.69	0.11	6.66E-01	8.83E-01	LYL1	lymphoblastic leukemia derived sequence 1	chr19p13.2	210044_s_at	NM_005583
2.46	2.55	0.09	6.66E-01	8.83E-01	RHOQ	ras homolog gene family, member Q	chr2p21	212122_at	NM_012249
2.69	2.77	0.08	6.66E-01	8.83E-01	---	---	---	215614_at	---
2.32	2.38	0.06	6.66E-01	8.83E-01	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	chr4q27	203362_s_at	NM_002358
2.05	2.10	0.05	6.66E-01	8.83E-01	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	chr1p31	238441_at	NM_006252
2.04	2.09	0.04	6.65E-01	8.83E-01	---	---	---	244831_at	---
4.53	4.60	0.07	6.66E-01	8.83E-01	ZNF438	zinc finger protein 438	chr10p11.23	229743_at	NM_182755
2.60	2.66	0.06	6.66E-01	8.83E-01	---	---	---	216827_at	---
8.76	8.91	0.15	6.66E-01	8.83E-01	HIGD1A	HIG1 domain family, member 1A	chr3p22.1	221896_s_at	NM_001099668 /// NM_001099669 /// NM_014056
5.25	5.40	0.14	6.66E-01	8.83E-01	---	---	---	222824_at	---
2.07	2.12	0.05	6.66E-01	8.83E-01	---	---	---	1563087_at	---
9.82	9.94	0.12	6.66E-01	8.83E-01	RPL36AL	ribosomal protein L36a-like	chr14q21	207585_s_at	NM_001001
2.84	2.92	0.08	6.66E-01	8.83E-01	LOC100130360	hypothetical protein LOC100130360	chr6p22.3	244570_at	XM_001717221 /// XM_001718619 /// XM_001718724
2.29	2.36	0.06	6.66E-01	8.83E-01	---	---	---	235859_at	---
7.61	7.73	0.12	6.66E-01	8.83E-01	CYYR1	cysteine/tyrosine-rich 1	chr21q21.2	228665_at	NM_052954
4.82	4.88	0.05	6.66E-01	8.83E-01	---	---	---	222339_x_at	---
1.85	1.90	0.05	6.66E-01	8.83E-01	---	---	---	234833_at	---
4.29	4.44	0.15	6.66E-01	8.83E-01	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	chr4q22	209735_at	NM_004827
4.59	4.95	0.36	6.66E-01	8.83E-01	---	---	---	240038_at	---
3.43	3.56	0.14	6.66E-01	8.83E-01	LHX6	LIM homeobox 6	chr9q33.2	219884_at	NM_014368 /// NM_199160
6.17	6.27	0.10	6.67E-01	8.83E-01	MPZL1	myelin protein zero-like 1	chr1q24.2	210594_x_at	NM_003953 /// NM_024569
3.79	3.87	0.08	6.67E-01	8.83E-01	HAO2	hydroxyacid oxidase 2 (long chain)	chr1p13.3-p13.1	220801_s_at	NM_001005783 /// NM_016527
3.86	3.98	0.12	6.67E-01	8.83E-01	WEE1	WEE1 homolog (S. pombe)	chr11p15.3-p15.1	215711_s_at	NM_003390
3.03	3.09	0.06	6.67E-01	8.83E-01	LOC286442	hypothetical protein LOC286442	chrXp11.4	1564460_at	---
4.77	4.82	0.05	6.67E-01	8.83E-01	OSBPL10	oxysterol binding protein-like 10	chr3p22.3	222818_at	NM_017784
2.02	2.07	0.05	6.67E-01	8.83E-01	ALS2CR11	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	chr2q33.1	1556757_a_at	NM_152525
4.97	5.07	0.10	6.67E-01	8.83E-01	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	chr10q21-q24	207927_at	NM_000872 /// NM_019859 /// NM_019860
3.53	3.60	0.07	6.67E-01	8.83E-01	---	---	---	234159_at	---
2.07	2.11	0.04	6.67E-01	8.83E-01	---	---	---	1561260_at	---
6.65	6.73	0.08	6.67E-01	8.83E-01	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	chr3p21.3	211800_s_at	NM_003363 /// NM_199443
6.67	6.76	0.09	6.67E-01	8.83E-01	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	chr11q24	208404_x_at	NM_000890
2.78	2.86	0.07	6.67E-01	8.83E-01	ELAC1	elaC homolog 1 (E. coli)	chr18q21	219325_s_at	NM_018696

1.96	2.03	0.07	6.67E-01	8.83E-01	LOC727945	similar to hCG1651100	chr6q12	233996_x_at	XM_001715536 /// XM_001724639 /// XM_001724715
2.16	2.20	0.04	6.67E-01	8.83E-01	---	---	---	1562588_at	---
3.83	3.94	0.12	6.67E-01	8.83E-01	---	---	---	238172_at	---
2.19	2.25	0.06	6.67E-01	8.83E-01	UGT1A6 /// UGT1A8 /// UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A8 /// UDP glucuronosyltransferase 1 family, polypeptide A9	chr2q37	221305_s_at	NM_001072 /// NM_019076 /// NM_021027 /// NM_205862
3.17	3.22	0.05	6.67E-01	8.83E-01	LOC654056 /// SIRPB1	similar to Signal-regulatory protein beta-1 precursor (SIRP-beta-1) /// signal-regulatory protein beta 1	chr20p13	217240_at	NM_001083910 /// NM_006065 /// XM_001720569 /// XM_938485
3.30	3.36	0.06	6.67E-01	8.83E-01	ANKRD26	ankyrin repeat domain 26	chr10pter-q22.1	205706_s_at	NM_014915
8.17	8.34	0.17	6.67E-01	8.83E-01	BZW1	basic leucine zipper and W2 domains 1	chr2q33	200777_s_at	NM_014670
4.70	4.79	0.09	6.67E-01	8.83E-01	PRB1 /// PRB2 /// PRB4 /// PRH1 /// PRH2	proline-rich protein BstNI subfamily 1 /// proline-rich protein BstNI subfamily 2 /// proline-rich protein BstNI subfamily 4 /// proline-rich protein HaeIII subfamily 1 /// proline-rich protein HaeIII subfamily 2	chr12p13.2	207752_x_at	NM_001110213 /// NM_002723 /// NM_005039 /// NM_005042 /// NM_006248 /// NM_006250 /// NM_199353 /// NM_199354
4.86	4.95	0.08	6.67E-01	8.83E-01	ATN1	atrophin 1	chr12p13.31	1555754_s_at	NM_001007026 /// NM_001940
2.35	2.43	0.08	6.67E-01	8.83E-01	---	---	---	1565860_at	---
3.53	3.61	0.08	6.67E-01	8.83E-01	EPC1	enhancer of polycomb homolog 1 (Drosophila)	chr10p11	223875_s_at	NM_025209
1.96	2.01	0.05	6.67E-01	8.83E-01	ZNF709	zinc finger protein 709	chr19p13.2	1553247_a_at	NM_152601
2.61	2.69	0.07	6.67E-01	8.83E-01	OTOA	otoancorin	chr16p12.2|16p12.2	1553432_s_at	NM_144672 /// NM_170664
2.15	2.21	0.06	6.67E-01	8.84E-01	COL22A1 /// LOC100134109	collagen, type XXII, alpha 1 /// similar to collagen, type XXII, alpha 1	chr8q24.23	243301_at	NM_152888 /// XM_001714227
2.66	2.76	0.10	6.68E-01	8.84E-01	C5orf24	chromosome 5 open reading frame 24	chr5q31.1	224875_at	NM_152409
2.98	3.06	0.08	6.68E-01	8.84E-01	METT10D	methyltransferase 10 domain containing	chr17p13.3	238931_at	NM_024086
2.16	2.21	0.05	6.68E-01	8.84E-01	---	---	---	232556_at	---
2.63	2.70	0.07	6.68E-01	8.84E-01	ZNF550	zinc finger protein 550	chr19q13.43	215124_at	NM_001039654
7.92	8.06	0.14	6.68E-01	8.84E-01	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	chr7q31.2-q31.3	201238_s_at	NM_006136
2.66	2.74	0.07	6.68E-01	8.84E-01	HTR7P	5-hydroxytryptamine (serotonin) receptor 7 pseudogene	chr12p13.1	216099_at	NR_002774
6.60	6.76	0.16	6.68E-01	8.84E-01	CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	chr6p22.3	212551_at	NM_006366
8.93	9.03	0.10	6.68E-01	8.84E-01	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	chr19q13.2-q13.3	208074_s_at	NM_004069 /// NM_021575
3.59	3.67	0.09	6.68E-01	8.84E-01	CMTM5	CKLF-like MARVEL transmembrane domain containing 5	chr14q11.2	230942_at	NM_001037288 /// NM_138460
2.27	2.33	0.06	6.68E-01	8.84E-01	ADAM7	ADAM metallopeptidase domain 7	chr8p21.2	239079_at	NM_003817
2.11	2.16	0.05	6.68E-01	8.84E-01	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	chr3q25.2	233903_s_at	NM_015595
5.61	5.76	0.15	6.68E-01	8.84E-01	TOM1L1	target of myb1 (chicken)-like 1	chr17q23.2	204485_s_at	NM_005486 /// XM_001723684 /// XM_001725529 /// XM_001726674
3.31	3.42	0.12	6.68E-01	8.84E-01	CD109	CD109 molecule	chr6q13	226545_at	NM_133493
5.28	5.37	0.09	6.68E-01	8.84E-01	CREB1	cAMP responsive element binding protein 1	chr2q34	225572_at	NM_004379 /// NM_134442
3.60	3.68	0.09	6.68E-01	8.84E-01	---	---	---	1554103_at	---
2.66	2.72	0.06	6.68E-01	8.84E-01	---	---	---	1557286_at	---
2.01	2.06	0.05	6.68E-01	8.84E-01	---	---	---	243713_at	---
2.60	2.72	0.12	6.68E-01	8.84E-01	MAP7D2	MAP7 domain containing 2	chrXp22.12	228262_at	NM_152780

2.03	2.08	0.05	6.68E-01	8.84E-01	NT5DC4	5'-nucleotidase domain containing 4	chr2q13	1560204_at	XM_001715677 /// XM_001716359 /// XM_001716541
1.76	1.81	0.04	6.68E-01	8.84E-01	PKD1L1	polycystic kidney disease 1 like 1	chr7p12.3	1563465_at	NM_138295
2.56	2.66	0.10	6.69E-01	8.84E-01	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	chr9p22-p13	220867_s_at	NM_020344
2.45	2.53	0.09	6.69E-01	8.84E-01	MIER3	mesoderm induction early response 1, family member 3	chr5q11.2	1553336_a_at	NM_152622
2.06	2.13	0.07	6.68E-01	8.84E-01	PMCHL2	pro-melanin-concentrating hormone-like 2	chr5q13	224423_x_at	NR_003922
2.01	2.07	0.06	6.69E-01	8.84E-01	---	---	---	233023_at	---
1.92	1.98	0.05	6.68E-01	8.84E-01	---	---	---	240812_at	---
3.38	3.50	0.12	6.69E-01	8.84E-01	C1orf27	chromosome 1 open reading frame 27	chr1q25	222720_x_at	NM_017847
1.98	2.03	0.05	6.69E-01	8.84E-01	GMCL1 /// GMCL1L	germ cell-less homolog 1 (Drosophila) /// germ cell-less homolog 1 (Drosophila)-like	chr2p13.3 /// chr5q35.3	234488_s_at	NM_178439 /// NR_003281
9.93	10.02	0.09	6.69E-01	8.84E-01	ZNF275	zinc finger protein 275	chrXq28	225383_at	NM_001080485
6.55	6.68	0.13	6.69E-01	8.84E-01	ZNF791	zinc finger protein 791	chr19p13.2-p13.13	1553703_at	NM_153358
2.57	2.64	0.07	6.69E-01	8.84E-01	LOC283868	hypothetical protein LOC283868	chr16p13.3	1564683_at	---
2.02	2.08	0.06	6.69E-01	8.84E-01	ZNF583	zinc finger protein 583	chr19q13.43	1563725_at	NM_152478
5.02	5.14	0.13	6.69E-01	8.84E-01	UBN1	ubinuclein 1	chr16p13.3	209088_s_at	NM_001079514 /// NM_016936
5.29	5.49	0.20	6.69E-01	8.84E-01	SEC24A	SEC24 related gene family, member A (S. cerevisiae)	chr5q31.1	212902_at	NM_021982
2.15	2.21	0.06	6.69E-01	8.84E-01	---	---	---	239902_at	---
7.37	7.51	0.14	6.69E-01	8.84E-01	FKBP3	FK506 binding protein 3, 25kDa	chr14q21.3	218003_s_at	NM_002013
2.96	3.04	0.09	6.69E-01	8.84E-01	NEUROD4	neurogenic differentiation 4	chr12q13.2	221318_at	NM_021191
2.36	2.43	0.07	6.69E-01	8.84E-01	OR51B5	olfactory receptor, family 51, subfamily B, member 5	chr11p15.4	234775_at	NM_001005567
2.58	2.62	0.05	6.69E-01	8.84E-01	AFF3	AF4/FMR2 family, member 3	chr2q11.2-q12	205735_s_at	NM_001025108 /// NM_002285
4.47	4.56	0.09	6.69E-01	8.84E-01	---	---	---	242365_at	---
5.44	5.57	0.13	6.69E-01	8.84E-01	UQCRB	ubiquinol-cytochrome c reductase binding protein	chr8q22	209065_at	NM_006294
5.40	5.48	0.09	6.69E-01	8.84E-01	RANGRF	RAN guanine nucleotide release factor	chr17p13	223554_s_at	NM_016492
7.02	7.10	0.08	6.69E-01	8.84E-01	YY1	YY1 transcription factor	chr14q	224711_at	NM_003403
2.04	2.11	0.07	6.69E-01	8.84E-01	LOC283745	hypothetical protein LOC283745	chr15q14	1557627_at	---
3.59	3.65	0.06	6.69E-01	8.84E-01	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	chr15q23	1567079_at	NM_017882
3.42	3.60	0.18	6.70E-01	8.84E-01	---	---	---	226498_at	---
2.79	2.85	0.06	6.70E-01	8.84E-01	C4orf44	chromosome 4 open reading frame 44	chr4p16.2	237434_x_at	NM_001012982 /// NM_001042690
2.55	2.64	0.09	6.70E-01	8.84E-01	---	---	---	1564291_at	---
3.06	3.12	0.06	6.70E-01	8.84E-01	PLA2G4D	phospholipase A2, group IVD (cytosolic)	chr15q15.1	1554914_at	NM_178034
3.10	3.15	0.06	6.70E-01	8.84E-01	---	---	---	244788_at	---
5.27	5.38	0.11	6.70E-01	8.84E-01	CFLAR	CASP8 and FADD-like apoptosis regulator	chr2q33-q34	239629_at	NM_001127183 /// NM_001127184 /// NM_003879
5.34	5.45	0.11	6.70E-01	8.84E-01	LTK	leukocyte receptor tyrosine kinase	chr15q15.1-q21.1	207106_s_at	NM_002344 /// NM_206961
5.71	5.80	0.09	6.70E-01	8.84E-01	---	---	---	1566887_x_at	---
2.20	2.26	0.06	6.70E-01	8.84E-01	ZNF92	zinc finger protein 92	chr7q11.21	1564962_at	NM_007139 /// NM_152626
2.25	2.31	0.06	6.70E-01	8.85E-01	---	---	---	241019_at	---
7.07	7.19	0.12	6.70E-01	8.85E-01	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	chr6q24-q25	210156_s_at	NM_005389
3.65	3.72	0.07	6.70E-01	8.85E-01	ZNF506	zinc finger protein 506	chr19p13.11	221626_at	NM_001099269
4.62	4.82	0.20	6.70E-01	8.85E-01	MEIS1	Meis homeobox 1	chr2p14-p13	242172_at	NM_002398
3.08	3.26	0.18	6.70E-01	8.85E-01	TLR1	toll-like receptor 1	chr4p14	210176_at	NM_003263
7.42	7.60	0.17	6.70E-01	8.85E-01	GBAS	glioblastoma amplified sequence	chr7p12	201816_s_at	NM_001483
6.60	6.76	0.17	6.70E-01	8.85E-01	MTDH	metadherin	chr8q22.1	212250_at	NM_178812
2.83	2.94	0.11	6.70E-01	8.85E-01	PRKCQ	protein kinase C, theta	chr10p15	210038_at	NM_006257
3.03	3.13	0.10	6.70E-01	8.85E-01	PDLIM4	PDZ and LIM domain 4	chr5q31.1	211564_s_at	NM_001131027 /// NM_003687
4.57	4.67	0.10	6.70E-01	8.85E-01	CENPF	centromere protein F, 350/400ka (mitosin)	chr1q32-q41	207828_s_at	NM_016343
5.93	6.01	0.08	6.70E-01	8.85E-01	SERGEF	secretion regulating guanine nucleotide exchange factor	chr11p14.3	232983_s_at	NM_012139
2.89	2.95	0.06	6.70E-01	8.85E-01	C8orf68	chromosome 8 open reading frame 68	chr8p23.3	1554978_at	XM_001719813 /// XM_001721201 /// XM_927505
8.16	8.35	0.19	6.70E-01	8.85E-01	S100A4	S100 calcium binding protein A4	chr1q21	203186_s_at	NM_002961 /// NM_019554
2.51	2.59	0.08	6.70E-01	8.85E-01	---	---	---	1566569_at	---

2.48	2.55	0.07	6.70E-01	8.85E-01	DMRTC1 /// LOC728656	DMRT-like family C1 /// doublesex-mab-3-like	chrXq13.1	1553998_at	NM_001080851 /// NM_033053
2.05	2.11	0.07	6.70E-01	8.85E-01	---	---	---	239509_at	---
2.11	2.16	0.05	6.70E-01	8.85E-01	---	---	---	234101_at	---
2.28	2.33	0.05	6.70E-01	8.85E-01	---	---	---	237119_at	---
1.94	2.01	0.07	6.70E-01	8.85E-01	---	---	---	1570332_at	---
5.70	5.78	0.07	6.71E-01	8.85E-01	RRP1	ribosomal RNA processing 1 homolog (S. cerevisiae)	chr21q22.3	222733_x_at	NM_003683
6.59	6.70	0.11	6.71E-01	8.85E-01	TXNDC9	thioredoxin domain containing 9	chr2q11.2	211758_x_at	NM_005783
3.10	3.18	0.09	6.71E-01	8.85E-01	THOC2	THO complex 2	chrXq25-q26.3	226628_at	NM_001081550 /// NM_020449
8.72	8.80	0.08	6.71E-01	8.85E-01	---	---	---	229465_s_at	---
2.49	2.55	0.07	6.71E-01	8.85E-01	ZSCAN1	zinc finger and SCAN domain containing 1	chr19q13.43	1562651_at	NM_182572
2.36	2.42	0.06	6.71E-01	8.85E-01	TAF7L	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa	chrXq22.1	220325_at	NM_024885
2.68	2.73	0.06	6.71E-01	8.85E-01	NLRP14	NLR family, pyrin domain containing 14	chr11p15.4	1553523_at	NM_176822
7.48	7.56	0.08	6.71E-01	8.85E-01	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	chr20p12	201204_s_at	NM_001042576 /// NM_004587
2.90	2.97	0.07	6.71E-01	8.85E-01	FAM71F2	family with sequence similarity 71, member F2	chr7q32.1	237320_at	NM_001012454 /// NM_001128926
4.24	4.30	0.06	6.71E-01	8.85E-01	BCORL1	BCL6 co-repressor-like 1	chrXq25-q26.1	233572_s_at	NM_021946
2.15	2.20	0.05	6.71E-01	8.85E-01	---	---	---	241656_at	---
2.38	2.45	0.07	6.71E-01	8.85E-01	ACSM2A /// ACSM2B	acyl-CoA synthetase medium-chain family member 2A /// acyl-CoA synthetase medium-chain family member 2B	chr16p12.3	241915_at	NM_001010845 /// NM_001105069 /// NM_182617 /// XM_001724180 /// XM_001724186 /// XM_001724187
2.06	2.12	0.06	6.71E-01	8.85E-01	ZNF643	zinc finger protein 643	chr1p34.2	207219_at	NM_023070
3.62	3.70	0.08	6.71E-01	8.85E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	1561937_x_at	---
3.81	3.88	0.08	6.71E-01	8.85E-01	CST4	cystatin S	chr20p11.21	206994_at	NM_001899
2.29	2.36	0.06	6.71E-01	8.85E-01	---	---	---	230778_at	---
2.53	2.57	0.04	6.71E-01	8.85E-01	---	---	---	239994_at	---
5.78	5.93	0.15	6.71E-01	8.85E-01	KIAA0020	KIAA0020	chr9p24.2	203712_at	NM_014878
2.03	2.09	0.07	6.71E-01	8.85E-01	CDK6	cyclin-dependent kinase 6	chr7q21-q22	235287_at	NM_001259
2.51	2.58	0.07	6.72E-01	8.85E-01	GRAMD2	GRAM domain containing 2	chr15q23	229616_s_at	NM_001012642
3.18	3.22	0.05	6.72E-01	8.85E-01	HECA	Headcase homolog (Drosophila)	chr6q23-q24	230582_at	NM_016217
4.43	4.70	0.27	6.72E-01	8.85E-01	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	chr11q13.1	231735_s_at	NR_002819
4.01	4.09	0.08	6.72E-01	8.85E-01	FAM149B1	family with sequence similarity 149, member B1	chr10q22.2	213896_x_at	NM_173348 /// XM_001721910 /// XM_001722273 /// XM_001723052
2.42	2.48	0.06	6.72E-01	8.85E-01	LOC728904	hypothetical LOC728904	chr5q14.1	244138_at	XM_001127594 /// XM_001128764 /// XM_001714622
5.75	5.85	0.10	6.72E-01	8.85E-01	C21orf2	chromosome 21 open reading frame 2	chr21q22.3	203995_at	NM_004928
9.54	9.64	0.10	6.72E-01	8.85E-01	RPN2	ribophorin II	chr20q12-q13.1	213399_x_at	NM_002951
4.35	4.41	0.06	6.72E-01	8.85E-01	ZNF496	zinc finger protein 496	chr1q44	225333_at	NM_032752
4.44	4.49	0.05	6.72E-01	8.85E-01	RTCD1	RNA terminal phosphate cyclase domain 1	chr1p21.2	238087_at	NM_001130841 /// NM_003729
2.59	2.66	0.08	6.72E-01	8.85E-01	---	---	---	217030_at	---
2.43	2.50	0.07	6.72E-01	8.85E-01	---	---	---	242333_at	---
2.46	2.52	0.06	6.72E-01	8.85E-01	MET	met proto-oncogene (hepatocyte growth factor receptor)	chr7q31	213807_x_at	NM_000245 /// NM_001127500
3.07	3.13	0.06	6.72E-01	8.85E-01	DHRS7C	dehydrogenase/reductase (SDR family) member 7C	chr17p13.1	230915_at	NM_001105571
2.00	2.06	0.06	6.72E-01	8.85E-01	---	---	---	1556944_at	---
2.23	2.29	0.06	6.72E-01	8.85E-01	---	---	---	1569841_x_at	---
2.03	2.07	0.04	6.72E-01	8.85E-01	TPMT	Thiopurine S-methyltransferase	chr6p22.3	238272_at	NM_000367
2.47	2.54	0.07	6.72E-01	8.85E-01	---	---	---	238471_at	---

2.89	2.95	0.06	6.72E-01	8.85E-01	RCCD1	RCC1 domain containing 1	chr15q26.1	231290_at	NM_001017919 /// NM_033544																					
2.60	2.66	0.05	6.72E-01	8.85E-01	SNORD8	small nucleolar RNA, C/D box 8	chr14q11.2	1566340_at	NR_002916																					
2.64	2.70	0.06	6.72E-01	8.85E-01	---	---	---	243404_at	---																					
2.75	2.82	0.07	6.72E-01	8.85E-01	ZFHX3	zinc finger homeobox 3	chr16q22.3-q23.1	233752_s_at	NM_006885																					
6.66	6.71	0.06	6.72E-01	8.85E-01	ATAD3B	ATPase family, AAA domain containing 3B	chr1p36.33	223617_x_at	NM_031921																					
4.67	4.75	0.08	6.73E-01	8.86E-01	SNX29	sorting nexin 29	chr16p13.13-p13.12	225608_at	NM_001080530																					
2.76	2.84	0.08	6.73E-01	8.86E-01	RGR	retinal G protein coupled receptor	chr10q23	1559714_at	NM_001012720 /// NM_001012722 /// NM_002921																					
5.51	5.68	0.17	6.73E-01	8.86E-01	IPO5	importin 5	chr13q32.2	211953_s_at	NM_002271																					
2.48	2.55	0.07	6.73E-01	8.86E-01	---	---	---	230843_at	---																					
7.19	7.47	0.28	6.73E-01	8.86E-01	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	chr4p15.3	201386_s_at	NM_001358																					
5.96	6.05	0.09	6.73E-01	8.86E-01	DKC1	dyskeratosis congenita 1, dyskerin	chrXq28	216212_s_at	NM_001363																					
6.79	6.98	0.19	6.73E-01	8.86E-01	---	---	---	224769_at	---																					
3.98	4.11	0.13	6.73E-01	8.86E-01	ERC1	ELKS/RAB6-interacting/CAST family member 1	chr12p13.3	1552663_a_at	NM_015064 /// NM_178037 /// NM_178038 /// NM_178039 /// NM_178040																					
4.24	4.32	0.08	6.73E-01	8.86E-01	---	---	---	216751_at	---																					
2.47	2.53	0.06	6.73E-01	8.86E-01	PCOLCE2	procollagen C-endopeptidase enhancer 2	chr3q21-q24	219295_s_at	NM_013363																					
4.86	5.07	0.21	6.73E-01	8.86E-01	CLASP2	cytoplasmic linker associated protein 2	chr3p22.3	212306_at	NM_015097																					
3.25	3.38	0.13	6.73E-01	8.86E-01	---	---	---	236766_at	---																					
3.35	3.42	0.07	6.73E-01	8.86E-01	SLC1A4	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	chr2p15-p13	244377_at	NM_003038																					
1.97	2.04	0.07	6.73E-01	8.86E-01	---	---	---	237634_at	---																					
2.92	3.00	0.08	6.73E-01	8.86E-01	KLF14	Kruppel-like factor 14	chr7q32.2	1552814_a_at	NM_138693																					
3.62	3.82	0.21	6.73E-01	8.86E-01	GZMK	granzyme K (granzyme 3; tryptase II)	chr5q11-q12	206666_at	NM_002104																					
2.77	2.84	0.07	6.73E-01	8.86E-01	NLRP1	NLR family, pyrin domain containing 1	chr17p13.2	1562256_at	NM_001033053 /// NM_014922 /// NM_033004 /// NM_033006 /// NM_033007																					
3.72	3.79	0.07	6.73E-01	8.86E-01	---	---	---	232474_at	---																					
2.46	2.53	0.06	6.73E-01	8.86E-01	CLCN4	Chloride channel 4	chrXp22.3	231066_s_at	NM_001830																					
7.01	7.16	0.15	6.73E-01	8.86E-01	RAG1AP1	recombination activating gene 1 activating protein 1	chr1q22	219125_s_at	NM_001122837 /// NM_001122839 /// NM_018845																					
2.36	2.45	0.08	6.73E-01	8.86E-01	---	---	---	1562719_at	---																					
1.89	1.94	0.05	6.73E-01	8.86E-01	---	---	---	1561486_at	---																					
3.82	3.92	0.10	6.74E-01	8.86E-01	---	---	---	244732_at	---																					
4.50	4.59	0.09	6.74E-01	8.86E-01	STMN1	stathmin 1/oncoprotein 18	chr1p36.1-p35	200783_s_at	NM_005563 /// NM_203399 /// NM_203401																					
2.18	2.25	0.07	6.74E-01	8.86E-01	---	---	---	1566748_at	---																					
2.38	2.43	0.05	6.74E-01	8.86E-01	B3GALT1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	chr2q24.3	222969_at	NM_020981																					
1.94	1.98	0.04	6.74E-01	8.86E-01	---	---	---	237302_at	---																					
2.04	2.09	0.05	6.74E-01	8.86E-01	---	---	---	243378_at	---																					
2.16	2.20	0.04	6.74E-01	8.86E-01	---	---	---	1569954_at	---																					
3.38	3.52	0.15	6.74E-01	8.86E-01	---	---	---	241789_at	---																					
3.54	3.61	0.07	6.74E-01	8.86E-01	TRIM31	tripartite motif-containing 31	chr6p21.3	210159_s_at	NM_007028																					
5.28	5.54	0.26	6.74E-01	8.86E-01	THBS1	thrombospondin 1	chr15q15	201109_s_at	NM_003246																					
8.14	8.32	0.18	6.74E-01	8.86E-01	EID1	EP300 interacting inhibitor of differentiation 1	chr15q21.1-q21.2	208670_s_at	NM_014335																					
5.30	5.47	0.16	6.74E-01	8.86E-01	ENAH	enabled homolog (Drosophila)	chr1q42.12	217820_s_at	NM_001008493 /// NM_018212																					
3.70	3.77	0.07	6.74E-01	8.86E-01	FLCN	folliculin	chr17p11.2	215645_at	NM_144606 /// NM_144997																					
2.32	2.37	0.05	6.74E-01	8.86E-01	---	---	---	241462_at	---																					
6.20	6.39	0.19	6.74E-01	8.86E-01	MTRF1L	mitochondrial translational release factor 1-like	chr6q25-q26	225215_s_at	NM_001114184 /// NM_019041																					

3.97	4.09	0.12	6.74E-01	8.86E-01	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	chr7q21.1	209960_at	NM_000601 /// NM_001010931 /// NM_001010932 /// NM_001010933 /// NM_001010934
4.04	4.13	0.08	6.74E-01	8.86E-01	PTCHD2	patched domain containing 2	chr1p36.22	230019_s_at	NM_020780
7.71	7.79	0.07	6.74E-01	8.86E-01	USF2	upstream transcription factor 2, c-fos interacting	chr19q13	215737_x_at	NM_003367 /// NM_207291
2.87	2.94	0.07	6.74E-01	8.86E-01	C21orf58	chromosome 21 open reading frame 58	chr21q22.3	1555197_a_at	NM_058180
2.43	2.49	0.07	6.74E-01	8.86E-01	REG1B	regenerating islet-derived 1 beta	chr2p12	205886_at	NM_006507
1.96	2.01	0.06	6.74E-01	8.86E-01	---	---	---	243878_at	---
3.03	3.09	0.06	6.74E-01	8.86E-01	PAPPA2	pappalysin 2	chr1q23-q25	211918_x_at	NM_020318 /// NM_021936
2.11	2.16	0.05	6.74E-01	8.86E-01	ZNF250	zinc finger protein 250	chr8q24.3	241738_at	NM_001109689 /// NM_021061
2.40	2.45	0.05	6.74E-01	8.86E-01	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	chr11q14.3	1558964_at	NM_001008781
2.26	2.32	0.05	6.75E-01	8.86E-01	---	---	---	242834_at	---
3.87	4.00	0.13	6.75E-01	8.86E-01	CABLES2	Cdk5 and Abl enzyme substrate 2	chr20q13.33	226004_at	NM_031215
3.68	3.91	0.23	6.75E-01	8.86E-01	TDGF1 /// TDGF3	teratocarcinoma-derived growth factor 1 /// teratocarcinoma-derived growth factor 3, pseudogene	chr3p21.31 /// chrXq22.3	206286_s_at	NM_003212 /// NR_002718
4.84	4.99	0.15	6.75E-01	8.86E-01	C5orf41	chromosome 5 open reading frame 41	chr5q35.2	238476_at	NM_153607
1.90	1.95	0.05	6.75E-01	8.86E-01	---	---	---	1561364_at	---
3.86	3.95	0.09	6.75E-01	8.86E-01	AKT2	v-akt murine thymoma viral oncogene homolog 2	chr19q13.1-q13.2	236664_at	NM_001626
2.33	2.40	0.07	6.75E-01	8.86E-01	LOC283480	hypothetical protein LOC283480	chr13q33.1	237392_at	XR_041482 /// XR_041483 /// XR_041484
2.61	2.67	0.05	6.75E-01	8.86E-01	LOC100129884	Hypothetical protein LOC100129884	chr13q22.1	234757_at	XM_001718836 /// XM_001722013 /// XM_001723940
1.79	1.84	0.04	6.75E-01	8.86E-01	---	---	---	234597_at	---
3.50	3.59	0.09	6.75E-01	8.86E-01	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	chr18q12.1	236746_at	NM_020474
5.84	5.91	0.07	6.75E-01	8.86E-01	MED28	mediator complex subunit 28	chr4p16	222635_s_at	NM_025205
10.14	10.20	0.06	6.75E-01	8.86E-01	GSTO1	glutathione S-transferase omega 1	chr10q25.1	201470_at	NM_004832
2.24	2.29	0.06	6.75E-01	8.86E-01	---	---	---	235975_at	---
9.18	9.26	0.07	6.75E-01	8.86E-01	DYNLRB1	dynein, light chain, roadblock-type 1	chr20q11.21	217917_s_at	NM_014183
3.95	4.09	0.15	6.75E-01	8.86E-01	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	chr2p11.2	221016_s_at	NM_031283
2.85	2.91	0.06	6.75E-01	8.86E-01	GATA4	GATA binding protein 4	chr8p23.1-p22	1570276_a_at	NM_002052
2.22	2.28	0.05	6.75E-01	8.86E-01	---	---	---	1561345_at	---
1.88	1.93	0.04	6.75E-01	8.86E-01	---	---	---	240093_x_at	---
3.96	4.03	0.06	6.75E-01	8.87E-01	MYO1G	myosin IG	chr7p13-p11.2	244654_at	NM_033054
2.49	2.55	0.06	6.75E-01	8.87E-01	LOC400965	hypothetical gene supported by AK098018	chr2p11.2	1563860_at	XR_017841 /// XR_017946
2.09	2.14	0.05	6.75E-01	8.87E-01	---	---	---	1566804_at	---
2.43	2.48	0.05	6.75E-01	8.87E-01	GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	chr9q31.1	233171_at	NM_133445
6.63	6.75	0.12	6.75E-01	8.87E-01	FLOT2	flotillin 2	chr17q11-q12	201350_at	NM_004475
2.67	2.78	0.12	6.75E-01	8.87E-01	XCL1 /// XCL2	chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	chr1q23 /// chr1q23-q25	214567_s_at	NM_002995 /// NM_003175
5.63	5.72	0.10	6.76E-01	8.87E-01	COMTD1	catechol-O-methyltransferase domain containing 1	chr10q22.2	226870_at	NM_144589
6.74	6.81	0.07	6.76E-01	8.87E-01	FAM120AOS	family with sequence similarity 120A opposite strand	chr9q22.31	225395_s_at	NM_198841
6.78	6.95	0.17	6.76E-01	8.87E-01	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	chr1q25.3	1555797_a_at	NM_005717
3.51	3.66	0.15	6.76E-01	8.87E-01	TMF1	TATA element modulatory factor 1	chr3p21-p12	235566_at	NM_007114
3.46	3.60	0.13	6.76E-01	8.87E-01	---	---	---	1560271_at	---
2.55	2.65	0.10	6.76E-01	8.87E-01	---	---	---	1565928_at	---
5.07	5.15	0.08	6.76E-01	8.87E-01	CTRB2	chymotrypsinogen B2	chr16q23.1	214411_x_at	NM_001025200
2.29	2.35	0.06	6.76E-01	8.87E-01	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	chrXq26.2	1552767_a_at	NM_001077188 /// NM_147175
1.83	1.89	0.06	6.76E-01	8.87E-01	LRRTM4	leucine rich repeat transmembrane neuronal 4	chr2p12	220345_at	NM_001134745 /// NM_024993
1.89	1.94	0.05	6.76E-01	8.87E-01	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	chr1q43	240509_s_at	NM_022469
3.08	3.16	0.09	6.76E-01	8.87E-01	---	---	---	243350_at	---
2.65	2.73	0.08	6.76E-01	8.87E-01	SKP2	S-phase kinase-associated protein 2 (p45)	chr5p13	203626_s_at	NM_005983 /// NM_032637

2.27	2.34	0.07	6.76E-01	8.87E-01	FCRL5	Fc receptor-like 5	chr1q21	224404_s_at	NM_031281
2.26	2.33	0.07	6.76E-01	8.87E-01	---	---	---	228534_s_at	---
7.14	7.30	0.16	6.76E-01	8.87E-01	RANBP6	RAN binding protein 6	chr9p24.1	213019_at	NM_012416 /// NR_024094 /// NR_024095
3.72	3.78	0.06	6.76E-01	8.87E-01	FXYD3	FXYD domain containing ion transport regulator 3	chr19q13.11-q13.12	202489_s_at	NM_005971 /// NM_021910
2.17	2.23	0.06	6.76E-01	8.87E-01	NAP1L4	nucleosome assembly protein 1-like 4	chr11p15.5	244001_at	NM_005969
2.38	2.43	0.05	6.76E-01	8.87E-01	---	---	---	241588_at	---
4.71	4.92	0.21	6.76E-01	8.87E-01	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	chr10q24	202731_at	NM_014456 /// NM_145341
5.18	5.28	0.10	6.76E-01	8.87E-01	SLC22A14	solute carrier family 22, member 14	chr3p21.3	207408_at	NM_004803
4.05	4.14	0.09	6.76E-01	8.87E-01	GEMIN7	gem (nuclear organelle) associated protein 7	chr19q13.32	219085_s_at	NM_001007269 /// NM_001007270 /// NM_024707
11.65	11.72	0.07	6.76E-01	8.87E-01	RPL14	ribosomal protein L14	chr3p22-p21.2	213588_x_at	NM_001034996 /// NM_003973
2.05	2.12	0.07	6.76E-01	8.87E-01	---	---	---	242795_at	---
2.89	2.96	0.07	6.76E-01	8.87E-01	C9orf144 /// LOC259308 /// RP11-251H13.2	chromosome 9 open reading frame 144 /// hypothetical LOC259308 /// similar to hCG2039876	chr9p12 /// chr9p13.2 /// chr9p13.3	243269_s_at	NM_001126494 /// XM_001721471 /// XM_001723970 /// XM_001725790 /// XR_040555 /// XR_040556 /// XR_040557 /// XR_041842 /// XR_041843
2.26	2.32	0.06	6.76E-01	8.87E-01	---	---	---	238552_at	---
2.26	2.31	0.05	6.76E-01	8.87E-01	---	---	---	240704_at	---
2.11	2.17	0.06	6.77E-01	8.87E-01	LOC100131508	PRO2122	chr6q14.1	224351_at	XM_001719407 /// XM_001720073 /// XM_001725343
4.25	4.49	0.24	6.77E-01	8.87E-01	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	chr14q11.2	233827_s_at	NM_007192
2.51	2.58	0.07	6.77E-01	8.87E-01	FXYD4	FXYD domain containing ion transport regulator 4	chr10q11.21	231058_at	NM_173160
4.89	5.10	0.20	6.77E-01	8.87E-01	---	---	---	239545_at	---
3.28	3.39	0.12	6.77E-01	8.87E-01	---	---	---	221648_s_at	---
3.70	3.81	0.11	6.77E-01	8.87E-01	LOC440028	hypothetical gene supported by BC040853	chr11p15.4	1566830_at	---
1.88	1.93	0.05	6.77E-01	8.87E-01	ZNF620	zinc finger protein 620	chr3p22.1	1558743_at	NM_175888 /// NR_024114
2.42	2.46	0.05	6.77E-01	8.87E-01	ACCN2	amiloride-sensitive cation channel 2, neuronal	chr12q12	37953_s_at	NM_001095 /// NM_020039
5.61	5.77	0.16	6.77E-01	8.87E-01	CLASP2	cytoplasmic linker associated protein 2	chr3p22.3	212309_at	NM_015097
1.98	2.04	0.06	6.77E-01	8.87E-01	GJA3	gap junction protein, alpha 3, 46kDa	chr13q11-q12	239572_at	NM_021954
3.27	3.36	0.09	6.77E-01	8.87E-01	---	---	---	1557676_at	---
8.11	8.17	0.07	6.77E-01	8.87E-01	ACTN4	actinin, alpha 4	chr19q13	200601_at	NM_004924
2.10	2.16	0.06	6.77E-01	8.87E-01	C14orf25	chromosome 14 open reading frame 25	chr14q21.1	1562299_at	XM_001129346 /// XM_001131984
5.32	5.49	0.17	6.77E-01	8.87E-01	PTPN2	protein tyrosine phosphatase, non-receptor type 2	chr18p11.3-p11.2	213137_s_at	NM_002828 /// NM_080422 /// NM_080423
2.25	2.33	0.07	6.77E-01	8.87E-01	C11orf41	chromosome 11 open reading frame 41	chr11p13	244584_at	NM_012194
6.04	6.11	0.07	6.77E-01	8.87E-01	DDO	D-aspartate oxidase	chr6q21	222134_at	NM_003649 /// NM_004032
2.70	2.77	0.06	6.77E-01	8.87E-01	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	chr7q21-q22.1	205939_at	NM_000765
2.02	2.08	0.06	6.77E-01	8.87E-01	---	---	---	234230_at	---
2.71	2.77	0.06	6.77E-01	8.87E-01	---	---	---	244232_at	---
2.43	2.49	0.06	6.77E-01	8.87E-01	LGALS3	lectin, galactoside-binding, soluble, 3	chr14q21-q22	1557197_a_at	NM_002306 /// NR_003225
4.02	4.09	0.07	6.78E-01	8.87E-01	NMT1	N-myristoyltransferase 1	chr17q21.31	201159_s_at	NM_021079
2.80	2.86	0.06	6.78E-01	8.87E-01	PAFAH1B2	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kDa	chr11q23	1569431_at	NM_002572

2.42	2.49	0.07	6.78E-01	8.87E-01	PHTF2	putative homeodomain transcription factor 2	chr7q11.23-q21	215286_s_at	NM_001127357 /// NM_001127358 /// NM_001127359 /// NM_001127360 /// NM_020432																				
2.12	2.18	0.06	6.78E-01	8.87E-01	ZNF273	zinc finger protein 273	chr7q11.21	215239_x_at	NM_021148 /// NR_003099																				
2.52	2.57	0.05	6.78E-01	8.87E-01	SPINLW1 /// WFDC6	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin) /// WAP four-disulfide core domain 6	chr20q12-q13.2 /// chr20q13.12	1552396_at	NM_020398 /// NM_080827 /// NM_181502																				
2.29	2.37	0.07	6.78E-01	8.87E-01	PRLR	prolactin receptor	chr5p14-p13	211917_s_at	NM_000949																				
4.14	4.20	0.06	6.78E-01	8.87E-01	TMED8	transmembrane emp24 protein transport domain containing 8	chr14q24.3	232913_at	NM_213601																				
2.73	2.78	0.05	6.78E-01	8.87E-01	TTC12	Tetratricopeptide repeat domain 12	chr11q23.1	215598_at	NM_017868																				
4.90	4.97	0.07	6.78E-01	8.88E-01	CIZ1	CDKN1A interacting zinc finger protein 1	chr9q34.1	213976_at	NM_001131015 /// NM_001131016 /// NM_001131017 /// NM_001131018 /// NM_012127																				
4.45	4.61	0.16	6.78E-01	8.88E-01	DPT	dermatopontin	chr1q12-q23	207977_s_at	NM_001937																				
3.22	3.28	0.06	6.78E-01	8.88E-01	---	---	---	244343_at	---																				
5.59	5.69	0.10	6.78E-01	8.88E-01	---	---	---	235837_at	---																				
5.61	5.70	0.09	6.78E-01	8.88E-01	UBOX5	U-box domain containing 5	chr20p13	204598_at	NM_014948 /// NM_199415																				
4.41	4.49	0.08	6.78E-01	8.88E-01	GKAP1	G kinase anchoring protein 1	chr9q21.32	229312_s_at	NM_025211																				
4.22	4.27	0.05	6.78E-01	8.88E-01	---	---	---	1560908_at	---																				
5.74	5.84	0.10	6.78E-01	8.88E-01	41335	membrane-associated ring finger (C3HC4) 2	chr19p13.2	210075_at	NM_001005415 /// NM_001005416 /// NM_016496																				
5.48	5.61	0.13	6.78E-01	8.88E-01	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	chr18q11.2	226866_at	NM_052911																				
2.07	2.12	0.05	6.78E-01	8.88E-01	---	---	---	1556287_a_at	---																				
5.48	5.64	0.16	6.78E-01	8.88E-01	PPP4R2	protein phosphatase 4, regulatory subunit 2	chr3p13	226317_at	NM_174907																				
5.89	6.07	0.18	6.79E-01	8.88E-01	---	---	---	229434_at	---																				
5.55	5.70	0.16	6.79E-01	8.88E-01	IGF1R	insulin-like growth factor 1 receptor	chr15q26.3	225330_at	NM_000875																				
3.50	3.62	0.13	6.79E-01	8.88E-01	LOC387723	similar to hCG1648656	chr10q26.3	229323_at	XM_001724717 /// XM_001726551 /// XM_370586																				
3.79	3.90	0.11	6.79E-01	8.88E-01	---	---	---	229417_at	---																				
3.42	3.51	0.09	6.79E-01	8.88E-01	CREB1	cAMP responsive element binding protein 1	chr2q34	237289_at	NM_004379 /// NM_134442																				
3.84	3.93	0.09	6.79E-01	8.88E-01	KPNB1	karyopherin (importin) beta 1	chr17q21.32	217027_x_at	NM_002265																				
4.03	4.12	0.09	6.79E-01	8.88E-01	ATPBD4	ATP binding domain 4	chr15q14	238662_at	NM_080650																				
5.90	5.98	0.08	6.79E-01	8.88E-01	MED9	mediator complex subunit 9	chr17p11.2	218372_at	NM_018019																				
2.40	2.47	0.07	6.79E-01	8.88E-01	FGFR2	fibroblast growth factor receptor 2	chr10q26	211400_at	NM_000141 /// NM_022970																				
2.76	2.83	0.07	6.79E-01	8.88E-01	---	---	---	230184_at	---																				
2.18	2.25	0.07	6.79E-01	8.88E-01	DGKG	diacylglycerol kinase, gamma 90kDa	chr3q27.2-q27.3	242319_at	NM_001080744 /// NM_001080745 /// NM_001346																				
2.54	2.60	0.06	6.79E-01	8.88E-01	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	chr20q13.2-q13.3	224542_s_at	NM_012340 /// NM_173091																				
2.33	2.38	0.06	6.79E-01	8.88E-01	ZFP37	zinc finger protein 37 homolog (mouse)	chr9q32	207068_at	NM_003408																				
2.16	2.22	0.06	6.79E-01	8.88E-01	TRA@	T cell receptor alpha locus	chr14q11.2	217412_at	---																				
2.48	2.53	0.05	6.79E-01	8.88E-01	CXorf1	chromosome X open reading frame 1	chrXq27.3	206711_at	NM_004709																				
1.83	1.88	0.05	6.79E-01	8.88E-01	---	---	---	234641_at	---																				
2.11	2.15	0.04	6.79E-01	8.88E-01	DLX6	distal-less homeobox 6	chr7q22	239309_at	NM_005222																				
1.99	2.03	0.04	6.79E-01	8.88E-01	---	---	---	233875_at	---																				
3.12	3.17	0.06	6.79E-01	8.88E-01	GALK2	galactokinase 2	chr15q21.1	216411_s_at	NM_001001556 /// NM_002044																				
2.85	2.93	0.07	6.79E-01	8.88E-01	---	---	---	243322_at	---																				

3.10	3.19	0.09	6.79E-01	8.88E-01	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	chr19p13.3	216010_x_at	NM_000149 /// NM_001097639 /// NM_001097640 /// NM_001097641
2.34	2.39	0.05	6.79E-01	8.88E-01	LOC257358	hypothetical protein LOC257358	chr5q35.1	1559488_at	XR_017851 /// XR_017954 /// XR_040392
2.58	2.64	0.06	6.79E-01	8.88E-01	CECR3	cat eye syndrome chromosome region, candidate 3	---	1564352_at	---
2.43	2.49	0.06	6.79E-01	8.88E-01	---	---	---	238113_at	---
2.36	2.43	0.06	6.80E-01	8.88E-01	CUL3	cullin 3	chr2q36.2	201372_s_at	NM_003590
2.02	2.07	0.05	6.80E-01	8.88E-01	WISP3	WNT1 inducible signaling pathway protein 3	chr6q21	210861_s_at	NM_003880 /// NM_130396 /// NM_198239
3.70	3.75	0.05	6.80E-01	8.88E-01	---	---	---	232880_at	---
2.87	2.96	0.09	6.80E-01	8.88E-01	---	---	---	231924_at	---
4.06	4.13	0.07	6.80E-01	8.88E-01	MUC2	mucin 2, oligomeric mucus/gel-forming	chr11p15.5	204673_at	NM_002457
3.12	3.17	0.05	6.80E-01	8.88E-01	PDZD3	PDZ domain containing 3	chr11q23.3	1555490_s_at	NM_024791
1.94	1.99	0.05	6.80E-01	8.88E-01	MGC39545	hypothetical protein LOC403312	chr11q24.2	1555002_at	XR_017796 /// XR_017799 /// XR_041651
1.87	1.93	0.06	6.80E-01	8.88E-01	---	---	---	238555_at	---
2.83	2.89	0.06	6.80E-01	8.89E-01	---	---	---	1561829_at	---
2.58	2.67	0.09	6.80E-01	8.89E-01	---	---	---	243707_at	---
4.56	4.81	0.25	6.80E-01	8.89E-01	PPAT	phosphoribosyl pyrophosphate amidotransferase	chr4q12	209433_s_at	NM_002703
2.63	2.69	0.06	6.80E-01	8.89E-01	---	---	---	244243_at	---
5.79	5.98	0.19	6.80E-01	8.89E-01	GPR89A /// GPR89B /// GPR89C	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	chr1q21.1	222140_s_at	NM_001097612 /// NM_001097613 /// NM_001097616 /// NM_016334
4.54	4.72	0.18	6.80E-01	8.89E-01	SCAMP1	secretory carrier membrane protein 1	chr5q13.3-q14.1	206668_s_at	NM_004866
3.98	4.07	0.09	6.80E-01	8.89E-01	---	---	---	227615_at	---
5.92	6.06	0.14	6.80E-01	8.89E-01	THNSL1	threonine synthase-like 1 (S. cerevisiae)	chr10p12.1	222931_s_at	NM_024838
2.30	2.40	0.10	6.80E-01	8.89E-01	---	---	---	242642_at	---
4.92	4.98	0.06	6.80E-01	8.89E-01	E2F3	E2F transcription factor 3	chr6p22	203692_s_at	NM_001949
3.27	3.33	0.06	6.80E-01	8.89E-01	---	---	---	242869_at	---
1.94	1.99	0.05	6.80E-01	8.89E-01	---	---	---	238634_x_at	---
6.05	6.17	0.12	6.81E-01	8.89E-01	RWDD2B	RWD domain containing 2B	chr21q22.11	218377_s_at	NM_016940
10.78	10.86	0.08	6.81E-01	8.89E-01	HLA-B /// HLA-C /// MICA /// XXbac-BPG181B23.1	major histocompatibility complex, class I, B /// major histocompatibility complex, class I, C /// MHC class I polypeptide-related sequence A /// MHC class I polypeptide-related sequence A	chr6p21.3 /// chr6p21.33	209140_x_at	NM_000247 /// NM_002117 /// NM_005514 /// XM_001713607 /// XM_001715881 /// XM_001717045 /// XM_001719879
4.17	4.24	0.07	6.81E-01	8.89E-01	WDR62	WD repeat domain 62	chr19q13.12	215218_s_at	NM_001083961 /// NM_173636
2.12	2.18	0.06	6.81E-01	8.89E-01	ARHGAP29	Rho GTPase activating protein 29	chr1p22.1	1560318_at	NM_004815
4.91	5.18	0.27	6.81E-01	8.89E-01	FIGN	fidgetin	chr2q24.3	242828_at	NM_018086
1.86	1.91	0.05	6.81E-01	8.89E-01	LOC338579	hypothetical protein LOC338579	chr10q11.21	1570473_at	XM_936973
2.39	2.45	0.06	6.81E-01	8.89E-01	---	---	---	241080_at	---
1.93	1.98	0.05	6.81E-01	8.89E-01	DSG3	desmoglein 3 (pemphigus vulgaris antigen)	chr18q12.1-q12.2	235075_at	NM_001944
3.58	3.66	0.09	6.81E-01	8.89E-01	NUDT10	nudix (nucleoside diphosphate linked moiety X)-type motif 10	chrXp11.23	241596_at	NM_153183
3.20	3.27	0.07	6.81E-01	8.89E-01	C9orf89	chromosome 9 open reading frame 89	chr9q22.31	1562559_at	NM_032310
2.93	3.01	0.08	6.81E-01	8.89E-01	ODF2L	outer dense fiber of sperm tails 2-like	chr1p22.3	230926_s_at	NM_001007022 /// NM_020729
3.96	4.05	0.09	6.81E-01	8.89E-01	SERPINA4	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4	chr14q31-q32.1	213874_at	NM_006215
6.15	6.22	0.08	6.81E-01	8.89E-01	SAFB2	scaffold attachment factor B2	chr19p13.3	203280_at	NM_014649
4.13	4.20	0.07	6.81E-01	8.89E-01	ACAN	aggrecan	chr15q26.1	207692_s_at	NM_001135 /// NM_013227
2.02	2.07	0.05	6.81E-01	8.89E-01	C18orf24	chromosome 18 open reading frame 24	chr18q21.1	217640_x_at	NM_001039535 /// NM_145060

1.94	1.99	0.05	6.81E-01	8.89E-01	---	---	---	234139_s_at	---
2.90	2.97	0.07	6.81E-01	8.89E-01	---	---	---	243222_at	---
2.67	2.72	0.05	6.81E-01	8.89E-01	---	---	---	233733_at	---
2.74	2.82	0.09	6.81E-01	8.89E-01	---	---	---	1557477_at	---
2.05	2.10	0.05	6.81E-01	8.89E-01	---	---	---	1559762_at	---
7.33	7.52	0.19	6.82E-01	8.89E-01	MAOA	monoamine oxidase A	chrXp11.3	212741_at	NM_000240
5.89	6.05	0.16	6.82E-01	8.89E-01	LOC642236	similar to FRG1 protein (FSHD region gene 1 protein)	chr9q12	215160_x_at	XR_041084 /// XR_041085 /// XR_041086 /// XR_041087
5.77	5.93	0.16	6.82E-01	8.89E-01	ELF1	E74-like factor 1 (ets domain transcription factor)	chr13q13	212420_at	NM_172373
3.64	3.80	0.16	6.82E-01	8.89E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	227346_at	NM_006060
4.22	4.33	0.11	6.82E-01	8.89E-01	GPR4	G protein-coupled receptor 4	chr19q13.3	211266_s_at	NM_005282
2.78	2.87	0.09	6.82E-01	8.89E-01	---	---	---	244536_at	---
3.65	3.73	0.08	6.82E-01	8.89E-01	---	---	---	237345_at	---
6.99	7.07	0.08	6.82E-01	8.89E-01	TEAD2	TEA domain family member 2	chr19q13.3	243766_s_at	NM_003598
3.18	3.25	0.07	6.82E-01	8.89E-01	C15orf60	chromosome 15 open reading frame 60	chr15q22	240689_at	NM_001042367
3.61	3.68	0.07	6.82E-01	8.89E-01	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	chr5q32	1567627_at	NM_001025158 /// NM_001025159 /// NM_004355
3.05	3.12	0.07	6.82E-01	8.89E-01	---	---	---	214821_at	---
5.22	5.28	0.07	6.81E-01	8.89E-01	LIMD1	LIM domains containing 1	chr3p21.3	234687_x_at	NM_014240
2.18	2.25	0.06	6.82E-01	8.89E-01	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	chr7p15.3	1569072_s_at	NM_178559
2.13	2.18	0.06	6.82E-01	8.89E-01	TLX2	T-cell leukemia homeobox 2	chr2p13.1-p12	207410_s_at	NM_016170
2.06	2.12	0.05	6.82E-01	8.89E-01	---	---	---	1567304_at	---
2.55	2.60	0.05	6.82E-01	8.89E-01	---	---	---	235321_at	---
2.14	2.19	0.05	6.82E-01	8.89E-01	RAC1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	chr7p22	1567457_at	NM_006908 /// NM_018890 /// NM_198829
2.01	2.06	0.05	6.82E-01	8.89E-01	CFHR5	complement factor H-related 5	chr1q22-q23	208088_s_at	NM_030787
2.21	2.26	0.04	6.82E-01	8.89E-01	---	---	---	239420_at	---
12.69	12.74	0.04	6.82E-01	8.89E-01	HUWE1	HECT, UBA and WWE domain containing 1	chrXp11.22	207783_x_at	NM_031407
1.74	1.78	0.04	6.81E-01	8.89E-01	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4	deleted in azoospermia 1 /// deleted in azoospermia 2 /// deleted in azoospermia 3 /// deleted in azoospermia 4	chrYq11.223	207912_s_at	NM_001005375 /// NM_001005785 /// NM_001005786 /// NM_004081 /// NM_020363 /// NM_020364 /// NM_020420 /// XM_001718583
3.49	3.70	0.22	6.82E-01	8.89E-01	SUCNR1	succinate receptor 1	chr3q24-q25.1	223939_at	NM_033050
3.66	3.73	0.07	6.82E-01	8.89E-01	---	---	---	216499_at	---
3.77	3.87	0.10	6.82E-01	8.89E-01	REPIN1	Replication initiator 1	chr7q36.1	228815_s_at	NM_001099695 /// NM_001099696 /// NM_013400 /// NM_014374
5.72	5.81	0.08	6.82E-01	8.89E-01	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	chr12q24.31	232950_s_at	NM_020845
4.59	4.67	0.08	6.82E-01	8.89E-01	---	---	---	235483_at	---
2.78	2.85	0.07	6.82E-01	8.89E-01	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	chrXp11.21	207537_at	NM_002625
3.46	3.53	0.06	6.82E-01	8.89E-01	---	---	---	1565697_at	---
2.33	2.39	0.06	6.82E-01	8.89E-01	---	---	---	233725_at	---
2.32	2.38	0.06	6.82E-01	8.89E-01	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	chr8q22.2	1553852_at	NM_015243 /// NM_017890 /// NM_152564 /// NM_181661
2.70	2.77	0.07	6.82E-01	8.90E-01	CASP4	caspase 4, apoptosis-related cysteine peptidase	chr11q22.2-q22.3	213596_at	NM_001225 /// NM_033306
4.27	4.41	0.14	6.83E-01	8.90E-01	UBE2Z	ubiquitin-conjugating enzyme E2Z	chr17q21.32	236107_at	NM_023079
4.27	4.35	0.09	6.83E-01	8.90E-01	---	---	---	241756_at	---
8.32	8.41	0.09	6.83E-01	8.90E-01	OLA1	Obg-like ATPase 1	chr2q31.1	219293_s_at	NM_001011708 /// NM_013341
2.31	2.37	0.07	6.83E-01	8.90E-01	---	---	---	241026_at	---
3.35	3.41	0.06	6.82E-01	8.90E-01	MMP28	matrix metallopeptidase 28	chr17q11-q21.1	239273_s_at	NM_001032278 /// NM_024302

1.98	2.03	0.05	6.83E-01	8.90E-01	ZMYND11	zinc finger, MYND domain containing 11	chr10p14	1554158_at	NM_006624 /// NM_212479																				
4.16	4.24	0.08	6.83E-01	8.90E-01	LOC728142	hypothetical LOC728142	chrXp11.4	231226_at	XM_001126676 /// XM_001126695																				
4.87	4.95	0.08	6.83E-01	8.90E-01	FRAP1	FK506 binding protein 12-rapamycin associated protein 1	chr1p36.2	202288_at	NM_004958																				
7.60	7.91	0.32	6.83E-01	8.90E-01	CD46	CD46 molecule, complement regulatory protein	chr1q32	207549_x_at	NM_002389 /// NM_153826 /// NM_172350 /// NM_172351 /// NM_172352 /// NM_172353 /// NM_172354 /// NM_172355 /// NM_172356 /// NM_172357 /// NM_172358 /// NM_172359 /// NM_172360 /// NM_172361																		
3.61	3.70	0.09	6.83E-01	8.90E-01	LOC100129633	similar to hCG1651427	chr9q32	231203_at	XM_001715082 /// XM_001717108 /// XM_001718491																				
3.16	3.21	0.06	6.83E-01	8.90E-01	FAM82A1	family with sequence similarity 82, member A1	chr2p22.2	1553232_at	NM_144713																				
3.60	3.65	0.05	6.83E-01	8.90E-01	SIPA1L2	signal-induced proliferation-associated 1 like 2	chr1q42.2	1559469_s_at	NM_020808																				
1.84	1.88	0.05	6.83E-01	8.90E-01	UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	chr4q13	206505_at	NM_021139																				
2.43	2.49	0.06	6.83E-01	8.90E-01	---	---	---	231327_at	---																				
3.09	3.18	0.09	6.83E-01	8.90E-01	SFN	stratifin	chr1p36.11	33323_r_at	NM_006142																				
2.53	2.57	0.05	6.83E-01	8.90E-01	SPAG11B	sperm associated antigen 11B	chr8p23-p22	207271_x_at	NM_016512 /// NM_058200 /// NM_058201 /// NM_058202 /// NM_058203 /// NM_058206 /// NM_058207																				
7.40	7.59	0.19	6.83E-01	8.90E-01	FOXN3	forkhead box N3	chr14q31.3	218031_s_at	NM_001085471 /// NM_005197																				
3.75	3.91	0.16	6.84E-01	8.90E-01	RNGTT	RNA guanylyltransferase and 5'-phosphatase	chr6q16	204207_s_at	NM_003800																				
7.29	7.62	0.33	6.84E-01	8.90E-01	---	---	---	242277_at	---																				
3.88	3.95	0.07	6.84E-01	8.90E-01	---	---	---	1558102_at	---																				
2.11	2.18	0.07	6.84E-01	8.90E-01	C1QTNF9	C1q and tumor necrosis factor related protein 9	chr13q12.12	1554233_at	NM_178540																				
6.16	6.28	0.12	6.84E-01	8.90E-01	UMPS	uridine monophosphate synthetase	chr3q13	215165_x_at	NM_000373																				
2.25	2.30	0.05	6.84E-01	8.90E-01	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	chr3q12.1	213335_s_at	NM_006100																				
1.92	1.98	0.05	6.84E-01	8.90E-01	LOC339862	hypothetical protein LOC339862	chr3p24.3	1557534_at	XM_376212 /// XM_939806																				
3.91	4.11	0.20	6.84E-01	8.90E-01	MBNL1	muscleblind-like (Drosophila)	chr3q25	1555594_a_at	NM_021038 /// NM_207292 /// NM_207293 /// NM_207294 /// NM_207295 /// NM_207296 /// NM_207297																				
6.40	6.59	0.19	6.84E-01	8.90E-01	ZNF12	zinc finger protein 12	chr7p22.1	226015_at	NM_006956 /// NM_016265																				
5.11	5.17	0.06	6.84E-01	8.90E-01	MFSD11	major facilitator superfamily domain containing 11	chr17q25	221192_x_at	NM_024311																				
2.77	2.83	0.06	6.84E-01	8.90E-01	---	---	---	1562455_at	---																				
2.19	2.24	0.05	6.84E-01	8.91E-01	PLCE1	Phospholipase C, epsilon 1	chr10q23	214159_at	NM_016341																				
2.77	2.83	0.05	6.84E-01	8.91E-01	LOC90834	hypothetical protein BC001742	chr22q13.33	233321_x_at	---																				
2.04	2.08	0.05	6.84E-01	8.91E-01	---	---	---	1559879_a_at	---																				
2.46	2.56	0.10	6.84E-01	8.91E-01	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	chr16q13	204762_s_at	NM_020988 /// NM_138736																				
6.04	6.18	0.15	6.84E-01	8.91E-01	---	---	---	238431_at	---																				
4.18	4.26	0.08	6.84E-01	8.91E-01	L2HGDH	L-2-hydroxyglutarate dehydrogenase	chr14q22.1	224460_s_at	NM_024884																				
9.46	9.53	0.07	6.84E-01	8.91E-01	CHMP2A	chromatin modifying protein 2A	chr19q	202121_s_at	NM_014453 /// NM_198426																				
2.02	2.07	0.05	6.84E-01	8.91E-01	---	---	---	234235_at	---																				
2.62	2.68	0.05	6.85E-01	8.91E-01	---	---	---	238157_at	---																				

2.38	2.43	0.05	6.85E-01	8.91E-01	LOC100130353	Hypothetical protein LOC100130353	chr11q23.3	1564449_at	XM_001718382 /// XM_001719137 /// XM_001719182																				
2.63	2.70	0.07	6.85E-01	8.91E-01	---	---	---	210491_at	---																				
3.94	4.01	0.06	6.85E-01	8.91E-01	VNN2	vanin 2	chr6q23-q24	205922_at	NM_004665 /// NM_078488																				
2.30	2.36	0.06	6.85E-01	8.91E-01	ATXN3	Ataxin 3	chr14q24.3-q32.2	217321_x_at	NM_001127696 /// NM_001127697 /// NM_004993 /// NM_030660																				
2.85	2.92	0.07	6.85E-01	8.91E-01	---	---	---	1559148_at	---																				
2.15	2.21	0.06	6.85E-01	8.91E-01	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)	chr5q31.2	1564906_at	NR_003141																				
10.87	10.93	0.06	6.85E-01	8.91E-01	OAZ1	ornithine decarboxylase antizyme 1	chr19p13.3	215952_s_at	NM_004152																				
1.93	1.98	0.05	6.85E-01	8.91E-01	BAGE	B melanoma antigen	chr21p11.1	207712_at	NM_001187																				
3.76	3.81	0.05	6.85E-01	8.91E-01	---	---	---	240247_at	---																				
4.17	4.33	0.16	6.85E-01	8.91E-01	ZCCHC10	zinc finger, CCHC domain containing 10	chr5q31.1	223803_s_at	NM_017665																				
2.37	2.42	0.06	6.85E-01	8.91E-01	---	---	---	1562509_at	---																				
2.04	2.09	0.04	6.85E-01	8.91E-01	---	---	---	232804_at	---																				
6.59	6.74	0.14	6.85E-01	8.91E-01	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	chr6q25.1-q25.3	212184_s_at	NM_015093																				
2.20	2.24	0.04	6.85E-01	8.91E-01	NRAP	nebulin-related anchoring protein	chr10q24-q26	207089_at	NM_006175 /// NM_198060																				
3.61	3.72	0.10	6.86E-01	8.91E-01	SLC22A8	solute carrier family 22 (organic anion transporter), member 8	chr11q11	231352_at	NM_004254																				
2.72	2.79	0.07	6.86E-01	8.91E-01	SCUBE3	Signal peptide, CUB domain, EGF-like 3	chr6p21.3	217600_at	NM_152753																				
2.14	2.19	0.05	6.86E-01	8.92E-01	---	---	---	1564878_at	---																				
6.49	6.80	0.31	6.86E-01	8.92E-01	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	chr8q22.1	218273_s_at	NM_018444																				
2.92	2.99	0.07	6.86E-01	8.92E-01	CKAP2	Cytoskeleton associated protein 2	chr13q14	216708_x_at	NM_001098525 /// NM_018204																				
4.82	4.89	0.07	6.86E-01	8.92E-01	PRODH2	proline dehydrogenase (oxidase) 2	chr19q13.1	243614_s_at	NM_021232																				
2.40	2.45	0.06	6.86E-01	8.92E-01	SCN8A	sodium channel, voltage gated, type VIII, alpha subunit	chr12q13	1561820_at	NM_014191																				
2.14	2.19	0.06	6.86E-01	8.92E-01	LOC133874	hypothetical gene LOC133874	chr5q35.1	237955_at	NM_001102609																				
3.07	3.12	0.05	6.86E-01	8.92E-01	---	---	---	1569767_at	---																				
2.10	2.15	0.05	6.86E-01	8.92E-01	C13orf31	chromosome 13 open reading frame 31	chr13q14.11	1553142_at	NM_001128303 /// NM_153218																				
2.02	2.06	0.04	6.86E-01	8.92E-01	ETV7	ets variant gene 7 (TEL2 oncogene)	chr6p21	224225_s_at	NM_016135																				
1.98	2.02	0.04	6.86E-01	8.92E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	240915_at	---																				
2.18	2.22	0.05	6.86E-01	8.92E-01	OCLN	occludin	chr5q13.1	209925_at	NM_002538																				
2.63	2.73	0.10	6.86E-01	8.92E-01	FBXL17	F-box and leucine-rich repeat protein 17	chr5q21.3	233087_at	NM_022824																				
2.94	3.01	0.07	6.86E-01	8.92E-01	TSSK2	testis-specific serine kinase 2	chr22q11.21	214371_at	NM_053006																				
2.55	2.60	0.06	6.86E-01	8.92E-01	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	chr7q22.1	1564166_s_at	NM_024653																				
2.07	2.12	0.05	6.86E-01	8.92E-01	NKAPL	NFKB activating protein-like	chr6p22.1	230804_at	NM_001007531																				
2.32	2.38	0.05	6.86E-01	8.92E-01	---	---	---	1561665_at	---																				
6.44	6.53	0.09	6.86E-01	8.92E-01	CORO1B	coronin, actin binding protein, 1B	chr11q13.1	221754_s_at	NM_001018070 /// NM_020441																				
2.35	2.42	0.07	6.86E-01	8.92E-01	---	---	---	1558787_a_at	---																				
2.64	2.69	0.05	6.86E-01	8.92E-01	TMEM62	transmembrane protein 62	chr15q15.2	222739_at	NM_024956																				
5.70	5.77	0.06	6.86E-01	8.92E-01	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	chr7q21.1	205998_x_at	NM_017460																				
3.10	3.16	0.05	6.86E-01	8.92E-01	SLC30A6	solute carrier family 30 (zinc transporter), member 6	chr2p22.3	226162_at	NM_017964																				
1.84	1.89	0.05	6.86E-01	8.92E-01	---	---	---	240688_at	---																				
2.95	2.99	0.05	6.86E-01	8.92E-01	---	---	---	224246_at	---																				
2.19	2.25	0.05	6.86E-01	8.92E-01	KRT27	keratin 27	chr17q21.2	240388_at	NM_181537																				
1.82	1.87	0.05	6.87E-01	8.92E-01	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	chr1p33-p32	207793_s_at	NM_004437 /// NM_203342 /// NM_203343																				
5.96	6.18	0.22	6.87E-01	8.92E-01	C19orf2	chromosome 19 open reading frame 2	chr19q12	211563_s_at	NM_003796 /// NM_134447																				
3.00	3.09	0.09	6.87E-01	8.92E-01	---	---	---	239376_at	---																				
3.21	3.30	0.09	6.87E-01	8.92E-01	PLA2G5	phospholipase A2, group V	chr1p36-p34	206178_at	NM_000929																				
2.10	2.14	0.04	6.87E-01	8.92E-01	---	---	---	213580_at	---																				
6.34	6.41	0.07	6.87E-01	8.92E-01	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	chr2p13	216835_s_at	NM_001381																				
5.58	5.68	0.10	6.87E-01	8.92E-01	EXOSC7	exosome component 7	chr3p21.31	213648_at	NM_015004 /// NR_023353																				

2.00	2.07	0.07	6.87E-01	8.92E-01	TEX9	testis expressed 9	chr15q21.3	243198_at	NM_198524
1.87	1.92	0.06	6.87E-01	8.92E-01	---	---	---	234739_at	---
2.01	2.06	0.05	6.87E-01	8.92E-01	---	---	---	240961_at	---
2.84	2.94	0.09	6.87E-01	8.92E-01	PRSS35	protease, serine, 35	chr6q14.2	235874_at	NM_153362
4.20	4.28	0.08	6.87E-01	8.92E-01	CCNJL	cyclin J-like	chr5q33.3	219227_at	NM_024565
2.10	2.16	0.05	6.87E-01	8.92E-01	ZNF192	zinc finger protein 192	chr6p21.3	206579_at	NM_006298
3.14	3.26	0.12	6.87E-01	8.92E-01	BRWD1	bromodomain and WD repeat domain containing 1	chr21q22.2	219280_at	NM_001007246 /// NM_018963 /// NM_033656
2.65	2.72	0.07	6.87E-01	8.92E-01	---	---	---	240240_at	---
2.75	2.82	0.07	6.87E-01	8.92E-01	---	---	---	232503_at	---
4.34	4.41	0.07	6.87E-01	8.92E-01	PRRT2	proline-rich transmembrane protein 2	chr16p11.2	227192_at	NM_145239
2.15	2.19	0.04	6.87E-01	8.92E-01	ST7OT2	ST7 overlapping transcript 2 (antisense non-coding RNA)	chr7q31.1-q31.2	1564790_at	NR_002331
2.55	2.60	0.05	6.87E-01	8.92E-01	GLP1R	glucagon-like peptide 1 receptor	chr6p21	208391_s_at	NM_002062
6.79	6.93	0.14	6.87E-01	8.92E-01	FBXW2	F-box and WD repeat domain containing 2	chr9q34	209630_s_at	NM_012164
3.10	3.21	0.11	6.88E-01	8.92E-01	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	chr19p13.2	227746_at	NM_001419
6.75	6.83	0.09	6.87E-01	8.92E-01	---	---	---	227770_at	---
2.77	2.85	0.08	6.87E-01	8.92E-01	---	---	---	240139_at	---
7.69	7.76	0.07	6.87E-01	8.92E-01	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	chr17q25.3	211716_x_at	NM_004309
2.47	2.53	0.06	6.87E-01	8.92E-01	GGN	gametogenetin	chr19q13.2	231420_at	NM_152657
2.35	2.40	0.05	6.88E-01	8.92E-01	STARD13	StAR-related lipid transfer (START) domain containing 13	chr13q12-q13	233159_at	NM_052851 /// NM_178006 /// NM_178007
3.35	3.44	0.09	6.88E-01	8.92E-01	---	---	---	244215_at	---
5.41	5.48	0.07	6.88E-01	8.92E-01	E2F3	E2F transcription factor 3	chr6p22	203693_s_at	NM_001949
2.51	2.58	0.07	6.88E-01	8.92E-01	PRSS8	protease, serine, 8	chr16p11.2	202525_at	NM_002773
2.84	2.89	0.05	6.88E-01	8.92E-01	---	---	---	239638_at	---
2.08	2.14	0.05	6.88E-01	8.92E-01	---	---	---	1563217_at	---
2.05	2.10	0.05	6.88E-01	8.92E-01	PEX5L	peroxisomal biogenesis factor 5-like	chr3q26.33	222910_s_at	NM_016559
6.45	6.60	0.15	6.88E-01	8.92E-01	LARP4	La ribonucleoprotein domain family, member 4	chr12q13.13	212714_at	NM_052879 /// NM_199188 /// NM_199190
1.95	2.01	0.06	6.88E-01	8.92E-01	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	chr18q21.3-q22	216258_s_at	NM_012397
2.31	2.35	0.04	6.88E-01	8.92E-01	---	---	---	242113_at	---
2.94	3.02	0.07	6.88E-01	8.93E-01	EPB41L5	erythrocyte membrane protein band 4.1 like 5	chr2q14.2	220977_x_at	NM_020909
3.15	3.21	0.06	6.88E-01	8.93E-01	---	---	---	214848_at	---
7.35	7.47	0.12	6.88E-01	8.93E-01	DPP7	dipeptidyl-peptidase 7	chr9q34.3	224814_at	NM_013379
3.61	3.68	0.07	6.88E-01	8.93E-01	TFR2	transferrin receptor 2	chr7q22	207883_s_at	NM_003227
4.33	4.60	0.26	6.88E-01	8.93E-01	FERMT2	fermitin family homolog 2 (Drosophila)	chr14q22.2	209209_s_at	NM_006832
6.08	6.22	0.13	6.88E-01	8.93E-01	C20orf111	chromosome 20 open reading frame 111	chr20q13.11	209020_at	NM_016470
2.96	3.07	0.11	6.88E-01	8.93E-01	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	chr9q32	214697_s_at	NM_005156
2.49	2.58	0.08	6.88E-01	8.93E-01	LHFPL5	lipoma HMGIC fusion partner-like 5	chr6p21.31	1555043_at	NM_182548
2.85	2.91	0.06	6.88E-01	8.93E-01	MYOZ3	myozenin 3	chr5q33.1	1553071_a_at	NM_001122853 /// NM_133371
2.61	2.67	0.06	6.88E-01	8.93E-01	---	---	---	243096_at	---
2.14	2.20	0.06	6.88E-01	8.93E-01	---	---	---	1570234_at	---
2.85	2.90	0.05	6.88E-01	8.93E-01	LOC619207	scavenger receptor protein family member	chr10q26.3	1569212_at	NR_002934
2.20	2.25	0.05	6.88E-01	8.93E-01	---	---	---	1561105_at	---
1.90	1.94	0.04	6.88E-01	8.93E-01	---	---	---	240026_x_at	---
3.03	3.09	0.06	6.88E-01	8.93E-01	KCTD1	Potassium channel tetramerisation domain containing 1	chr18q11.2	229183_at	NM_198991
5.98	6.13	0.15	6.88E-01	8.93E-01	TPM4	tropomyosin 4	chr19p13.1	212481_s_at	NM_003290
4.57	4.68	0.11	6.89E-01	8.93E-01	SDC2	syndecan 2	chr8q22-q23	212158_at	NM_002998
2.26	2.32	0.06	6.88E-01	8.93E-01	---	---	---	240523_at	---
1.98	2.03	0.05	6.89E-01	8.93E-01	ODAM	odontogenic, ameloblast asssociated	chr4q13.3	220133_at	NM_017855
2.34	2.39	0.05	6.89E-01	8.93E-01	---	---	---	244204_at	---
1.89	1.93	0.04	6.89E-01	8.93E-01	C21orf130	chromosome 21 open reading frame 130	chr21q22.3	240068_at	NR_024100
4.50	4.62	0.12	6.89E-01	8.93E-01	MBOAT7	membrane bound O-acyltransferase domain containing 7	chr19q13.4	211037_s_at	NM_024298
2.45	2.55	0.10	6.89E-01	8.93E-01	EWSR1	Ewing sarcoma breakpoint region 1	chr22q12.2	210012_s_at	NM_005243 /// NM_013986
3.24	3.32	0.08	6.89E-01	8.93E-01	FLJ10490	hypothetical protein FLJ10490	chr19q13.33	220151_at	NM_018111
3.09	3.16	0.07	6.89E-01	8.93E-01	LOC100126784	Hypothetical LOC100126784	chr11p15.1	236102_at	XR_040478 /// XR_040479 /// XR_040480
2.65	2.71	0.06	6.89E-01	8.93E-01	---	---	---	242867_x_at	---
2.57	2.63	0.06	6.89E-01	8.93E-01	---	---	---	243882_at	---
6.78	6.88	0.10	6.89E-01	8.93E-01	C16orf57	chromosome 16 open reading frame 57	chr16q13	218060_s_at	NM_024598
3.10	3.19	0.09	6.89E-01	8.93E-01	---	---	---	1563828_at	---
3.27	3.33	0.06	6.89E-01	8.93E-01	---	---	---	241229_at	---
6.25	6.38	0.13	6.89E-01	8.93E-01	NMI	N-myc (and STAT) interactor	chr2q23	203964_at	NM_004688
3.33	3.41	0.08	6.89E-01	8.93E-01	OR2H2	olfactory receptor, family 2, subfamily H, member 2	chr6p21.3	208573_s_at	NM_007160
3.05	3.16	0.11	6.89E-01	8.93E-01	DOCK5	dedicator of cytokinesis 5	chr8p21.2	219921_s_at	NM_024940
2.77	2.86	0.10	6.89E-01	8.93E-01	KIAA1853	KIAA1853	chr12q24.23	236151_at	NM_194286
2.53	2.60	0.07	6.89E-01	8.93E-01	ITGB6	Integrin, beta 6	chr2q24.2	239517_at	NM_000888
2.91	2.97	0.06	6.89E-01	8.93E-01	---	---	---	1566228_at	---

2.10	2.16	0.06	6.89E-01	8.93E-01	C2orf67	chromosome 2 open reading frame 67	chr2q34	215046_at	NM_152519
2.41	2.46	0.06	6.89E-01	8.93E-01	---	---	---	1558320_at	---
2.02	2.07	0.05	6.89E-01	8.93E-01	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	chr5q12	237411_at	NM_197941
2.32	2.36	0.04	6.89E-01	8.93E-01	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	chr11p15.2	1553322_s_at	NM_021961
2.44	2.50	0.06	6.89E-01	8.93E-01	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	chr1p13.2	207464_at	NM_006621
3.47	3.65	0.17	6.90E-01	8.93E-01	CCL5	chemokine (C-C motif) ligand 5	chr17q11.2-q12	204655_at	NM_002985
3.39	3.50	0.11	6.89E-01	8.93E-01	PLS1	plastin 1 (I isoform)	chr3q23	205190_at	NM_002670
2.69	2.76	0.07	6.90E-01	8.93E-01	---	---	---	239521_at	---
4.34	4.40	0.06	6.90E-01	8.93E-01	C8orf56	chromosome 8 open reading frame 56	chr8q22.3	232326_at	---
4.81	4.97	0.16	6.90E-01	8.93E-01	CCDC90B	coiled-coil domain containing 90B	chr11q14.1	1568834_s_at	NM_021825
5.64	5.72	0.08	6.90E-01	8.93E-01	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	chr17p13.1	214792_x_at	NM_014232
5.23	5.41	0.18	6.90E-01	8.93E-01	VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)	chr2p13-p14	233656_s_at	NM_001005739 /// NM_016516
4.73	4.87	0.14	6.90E-01	8.93E-01	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	chr7q21	209737_at	NM_012301
4.72	4.84	0.12	6.90E-01	8.93E-01	DAPK1	death-associated protein kinase 1	chr9q34.1	203139_at	NM_004938
2.48	2.57	0.09	6.90E-01	8.93E-01	LOC153682	Hypothetical protein LOC153682	chr5p13.1	232794_at	---
5.58	5.66	0.08	6.90E-01	8.93E-01	TNK2	tyrosine kinase, non-receptor, 2	chr3q29	203839_s_at	NM_001010938 /// NM_005781
2.56	2.64	0.08	6.90E-01	8.93E-01	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	chr4q12	206310_at	NM_021114
2.43	2.49	0.06	6.90E-01	8.93E-01	PHF12	PHD finger protein 12	chr17q11.2	234939_s_at	NM_001033561 /// NM_020889
2.17	2.23	0.06	6.90E-01	8.93E-01	TDRKH	tudor and KH domain containing	chr1q21	221053_s_at	NM_001083963 /// NM_001083964 /// NM_001083965 /// NM_006862
1.99	2.05	0.06	6.90E-01	8.93E-01	---	---	---	1562596_at	---
2.22	2.28	0.06	6.90E-01	8.93E-01	LOC283674	hypothetical protein LOC283674	chr15q22.32	1566840_at	---
2.14	2.20	0.06	6.90E-01	8.93E-01	---	---	---	1566158_at	---
6.55	6.61	0.06	6.90E-01	8.93E-01	ZNF544	zinc finger protein 544	chr19q13.43	218735_s_at	NM_014480
2.85	2.90	0.05	6.90E-01	8.93E-01	---	---	---	217018_at	---
1.85	1.90	0.05	6.90E-01	8.93E-01	EFCAB6	EF-hand calcium binding domain 6	chr22q13.1-q13.33	233839_at	NM_022785 /// NM_198856
2.44	2.51	0.07	6.90E-01	8.93E-01	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	chr12q12-q13	1563035_x_at	NM_005276
1.93	1.98	0.05	6.90E-01	8.93E-01	---	---	---	236433_at	---
2.13	2.18	0.05	6.90E-01	8.93E-01	---	---	---	208340_at	---
6.38	6.50	0.12	6.90E-01	8.94E-01	KRCC1	lysine-rich coiled-coil 1	chr2p11.2	218303_x_at	NM_016618
3.11	3.21	0.10	6.90E-01	8.94E-01	LOC100131170	hypothetical LOC100131170	chr17q25.3	1556145_a_at	XM_001716812 /// XM_001721745 /// XM_001732862
4.30	4.50	0.20	6.91E-01	8.94E-01	RRAS2	related RAS viral (r-ras) oncogene homolog 2	chr11p15.2	208456_s_at	NM_001102669 /// NM_012250
4.07	4.20	0.12	6.91E-01	8.94E-01	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	chr8q22.3	202873_at	NM_001695
7.42	7.53	0.11	6.91E-01	8.94E-01	FAF2	Fas associated factor family member 2	chr5q35.2	212108_at	NM_014613
3.02	3.10	0.09	6.91E-01	8.94E-01	---	---	---	232959_at	---
7.73	7.81	0.08	6.91E-01	8.94E-01	JMJD8	jumonji domain containing 8	chr16p13.3	224886_at	NM_001005920
2.99	3.07	0.08	6.91E-01	8.94E-01	---	---	---	236149_at	---
3.72	3.79	0.08	6.91E-01	8.94E-01	ALMS1P	Alstrom syndrome 1 pseudogene	chr2p13.2	1552576_at	NR_003683
3.24	3.31	0.07	6.91E-01	8.94E-01	LOC100129098	hypothetical protein LOC100129098	chr8q11.23	1569361_a_at	XM_001714756 /// XM_001714829 /// XM_001714893
3.22	3.28	0.06	6.91E-01	8.94E-01	POLH	polymerase (DNA directed), eta	chr6p21.1	222879_s_at	NM_006502
2.43	2.49	0.06	6.91E-01	8.94E-01	LOC221442	hypothetical LOC221442	chr6p21.1	233959_at	XR_039837 /// XR_039838 /// XR_039839
2.04	2.10	0.06	6.91E-01	8.94E-01	ATM	ataxia telangiectasia mutated	chr11q22-q23	1570352_at	NM_000051 /// NM_138292
2.11	2.16	0.05	6.91E-01	8.94E-01	MAGOH2	mago-nashi homolog 2, proliferation-associated (Drosophila)	chr17p13.1	217692_at	---

1.98	2.03	0.05	6.91E-01	8.94E-01	ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide	chr4q21-q24|4q22	231678_s_at	NM_000670
2.96	3.01	0.05	6.91E-01	8.94E-01	LY6G6E	lymphocyte antigen 6 complex, locus G6E	chr6p21.3	221338_at	NR_003673
5.88	6.04	0.15	6.91E-01	8.94E-01	HTATSF1	HIV-1 Tat specific factor 1	chrXq26.1-q27.2	202602_s_at	NM_014500
6.10	6.23	0.13	6.91E-01	8.94E-01	KIAA0494	KIAA0494	chr1pter-p22.1	201776_s_at	NM_014774
2.19	2.26	0.07	6.91E-01	8.94E-01	---	---	---	1557297_at	---
7.22	7.28	0.06	6.91E-01	8.94E-01	SLC35E1	solute carrier family 35, member E1	chr19p13.11	220796_x_at	NM_024881
3.69	3.78	0.09	6.91E-01	8.94E-01	RFPL1S	ret finger protein-like 1 antisense	chr22q12	214120_at	NR_002727
2.30	2.36	0.06	6.91E-01	8.94E-01	ANXA1	Annexin A1	chr9q12-q21.2|9q12-q21.2	233011_at	NM_000700
5.12	5.21	0.09	6.91E-01	8.94E-01	---	---	---	227851_s_at	---
4.85	5.07	0.21	6.91E-01	8.94E-01	GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide	chr9q21	224862_at	NM_002072
4.96	5.19	0.23	6.91E-01	8.94E-01	AGPS	alkylglycerone phosphate synthase	chr2q31.2	205401_at	NM_003659
2.72	2.82	0.10	6.91E-01	8.94E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	1565483_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284
2.24	2.29	0.06	6.91E-01	8.94E-01	SDR-O	orphan short-chain dehydrogenase / reductase	chr12q13.3	1553077_at	NM_148897
2.33	2.40	0.07	6.91E-01	8.94E-01	---	---	---	238881_at	---
2.55	2.60	0.06	6.91E-01	8.94E-01	LOC100131031	Similar to hCG2041190	chr6p21.2	232992_at	XM_001722443 /// XM_001722513 /// XM_001725253
2.66	2.71	0.04	6.91E-01	8.94E-01	---	---	---	1560109_s_at	---
5.36	5.51	0.15	6.92E-01	8.94E-01	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	chr4p14	212350_at	NM_015173
6.03	6.15	0.13	6.92E-01	8.94E-01	SRD5A3	steroid 5 alpha-reductase 3	chr4q12	222750_s_at	NM_024592
2.10	2.18	0.07	6.92E-01	8.94E-01	C8orf48	chromosome 8 open reading frame 48	chr8p22	236634_at	XR_017857 /// XR_017961 /// XR_042053
2.00	2.04	0.04	6.92E-01	8.94E-01	ZIC1	Zic family member 1 (odd-paired homolog, Drosophila)	chr3q24	236896_at	NM_003412
2.50	2.56	0.06	6.92E-01	8.94E-01	DOCK6	dedicator of cytokinesis 6	chr19p13.2	221793_at	NM_020812
6.76	6.92	0.16	6.92E-01	8.94E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	212263_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855
3.70	3.79	0.10	6.92E-01	8.94E-01	CST7	cystatin F (leukocystatin)	chr20p11.21	210140_at	NM_003650
3.66	3.73	0.07	6.92E-01	8.94E-01	CEP164	centrosomal protein 164kDa	chr11q23.3	204250_s_at	NM_014956
6.24	6.30	0.06	6.92E-01	8.94E-01	ZCCHC17	zinc finger, CCHC domain containing 17	chr1p35.2	223107_s_at	NM_016505
2.88	2.93	0.06	6.92E-01	8.94E-01	CLEC4F	C-type lectin domain family 4, member F	chr2p13.3	1552410_at	NM_173535
5.71	5.82	0.11	6.92E-01	8.94E-01	ADAM15	ADAM metallopeptidase domain 15	chr1q21.3	1555896_a_at	NM_003815 /// NM_207191 /// NM_207194 /// NM_207195 /// NM_207196 /// NM_207197
3.88	3.96	0.07	6.92E-01	8.94E-01	TCF19	transcription factor 19 (SC1)	chr6p21.3	223274_at	NM_001077511 /// NM_007109
4.34	4.39	0.05	6.92E-01	8.94E-01	SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	chr16q22.1	211112_at	NM_005072
3.14	3.23	0.09	6.92E-01	8.94E-01	---	---	---	237652_at	---
1.89	1.94	0.05	6.92E-01	8.94E-01	---	---	---	1558048_x_at	---
2.66	2.72	0.07	6.92E-01	8.94E-01	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	chr8p21	210654_at	NM_003840
5.93	6.08	0.15	6.92E-01	8.94E-01	CRYZL1	crystallin, zeta (quinone reductase)-like 1	chr21q21.3	226151_x_at	NM_145858
5.28	5.35	0.06	6.92E-01	8.94E-01	---	---	---	238473_at	---
3.24	3.33	0.08	6.92E-01	8.94E-01	CD7	CD7 molecule	chr17q25.2-q25.3	214551_s_at	NM_006137
2.73	2.79	0.07	6.92E-01	8.94E-01	FAM129C	family with sequence similarity 129, member C	chr19p13.11	230983_at	NM_001098524 /// NM_173544
2.39	2.44	0.05	6.92E-01	8.94E-01	---	---	---	1563540_at	---
2.15	2.20	0.05	6.92E-01	8.94E-01	---	---	---	1567280_at	---
3.77	3.85	0.08	6.92E-01	8.94E-01	NOS1AP	nitric oxide synthase 1 (neuronal) adaptor protein	chr1q23.3	215153_at	NM_001126060 /// NM_014697
3.73	3.79	0.06	6.92E-01	8.94E-01	GGT1	Gamma-glutamyltransferase 1	chr22q11.23	233837_at	NM_001032364 /// NM_001032365 /// NM_005265 /// NM_013430

1.92	1.97	0.05	6.92E-01	8.94E-01	LOC642236	similar to FRG1 protein (FSHD region gene 1 protein)	chr9q12	242331_x_at	XR_041084 /// XR_041085 /// XR_041086 /// XR_041087
2.15	2.22	0.06	6.93E-01	8.94E-01	CNTN4	contactin 4	chr3p26-p25	237177_at	NM_175607 /// NM_175612 /// NM_175613
2.26	2.32	0.06	6.93E-01	8.95E-01	AEBP2	AE binding protein 2	chr12p12.3	235184_at	NM_001114176 /// NM_153207
2.25	2.31	0.06	6.93E-01	8.95E-01	---	---	---	216978_x_at	---
2.37	2.43	0.06	6.93E-01	8.95E-01	---	---	---	241513_at	---
2.43	2.48	0.05	6.93E-01	8.95E-01	TPPP2	Tubulin polymerization-promoting protein family member 2	chr14q11.2	1559785_at	NM_173846
5.03	5.16	0.13	6.93E-01	8.95E-01	GDF15	growth differentiation factor 15	chr19p13.11	221577_x_at	NM_004864
6.57	6.76	0.19	6.93E-01	8.95E-01	LOC144438	hypothetical LOC144438	chr12q13.12	225493_at	---
3.26	3.36	0.10	6.93E-01	8.95E-01	LOC285620	hypothetical protein LOC285620	chr5q14.3	239395_at	XM_001721126
2.92	3.00	0.08	6.93E-01	8.95E-01	---	---	---	237226_at	---
9.23	9.30	0.07	6.93E-01	8.95E-01	GHITM	growth hormone inducible transmembrane protein	chr10q23.1	209249_s_at	NM_014394
6.72	6.79	0.07	6.93E-01	8.95E-01	---	---	---	221937_at	---
2.92	2.99	0.07	6.93E-01	8.95E-01	CDKL5	cyclin-dependent kinase-like 5	chrXp22	206575_at	NM_001037343 /// NM_003159
2.26	2.32	0.07	6.93E-01	8.95E-01	---	---	---	241175_at	---
2.28	2.34	0.06	6.93E-01	8.95E-01	BMX	BMX non-receptor tyrosine kinase	chrXp22.2	206464_at	NM_001721 /// NM_203281
2.18	2.23	0.05	6.93E-01	8.95E-01	CROT	carnitine O-octanoyltransferase	chr7q21.1	231102_at	NM_021151
6.75	6.86	0.11	6.93E-01	8.95E-01	MANBA	mannosidase, beta A, lysosomal	chr4q22-q25	203778_at	NM_005908
2.49	2.57	0.08	6.93E-01	8.95E-01	TPR	translocated promoter region (to activated MET oncogene)	chr1q25	228709_at	NM_003292
1.82	1.86	0.04	6.93E-01	8.95E-01	DIRC1	disrupted in renal carcinoma 1	chr2q33	1552674_at	NM_052952
2.31	2.40	0.09	6.93E-01	8.95E-01	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	chr1q32	220083_x_at	NM_015984
3.54	3.60	0.06	6.93E-01	8.95E-01	---	---	---	235558_at	---
2.42	2.48	0.06	6.93E-01	8.95E-01	---	---	---	236704_at	---
5.39	5.93	0.55	6.93E-01	8.95E-01	IGH@ /// IGHA1 /// IGHA2 /// IGHV3OR16-13 /// LOC100126583	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// immunoglobulin heavy variable 3/OR16-13 /// hypothetical LOC100126583	chr14q32.33 /// chr16p11.2	217022_s_at	---
2.67	2.72	0.05	6.94E-01	8.95E-01	---	---	---	1562010_x_at	---
2.14	2.20	0.06	6.94E-01	8.95E-01	---	---	---	1559344_at	---
3.02	3.08	0.06	6.94E-01	8.95E-01	C20orf12	chromosome 20 open reading frame 12	chr20p11.23	219951_s_at	NM_001099407
2.01	2.05	0.05	6.94E-01	8.95E-01	---	---	---	216796_s_at	---
3.93	4.04	0.11	6.94E-01	8.95E-01	ELMO1	engulfment and cell motility 1	chr7p14.2	204513_s_at	NM_001039459 /// NM_014800 /// NM_130442
4.21	4.32	0.11	6.94E-01	8.95E-01	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	chr10q23-q25	217502_at	NM_001547
7.13	7.24	0.11	6.94E-01	8.95E-01	RPL38	Ribosomal protein L38	chr17q23-q25	221943_x_at	NM_000999 /// NM_001035258
2.28	2.36	0.08	6.94E-01	8.95E-01	TRA2A	Transformer-2 alpha	chr7p15.3	227939_s_at	NM_013293
3.57	3.65	0.07	6.94E-01	8.95E-01	PRODH	proline dehydrogenase (oxidase) 1	chr22q11.21	214203_s_at	NM_016335
2.99	3.05	0.06	6.94E-01	8.95E-01	MMP11	Matrix metallopeptidase 11 (stromelysin 3)	chr22q11.2|22q11.23	213602_s_at	NM_005940
3.00	3.05	0.05	6.94E-01	8.95E-01	ZNF708	zinc finger protein 708	chr19p12	239482_x_at	NM_021269
2.21	2.25	0.04	6.94E-01	8.95E-01	STXBP6	syntaxin binding protein 6 (amisyn)	chr14q12	220995_at	NM_014178
2.42	2.50	0.08	6.94E-01	8.95E-01	LOC283535	hypothetical protein LOC283535	chr13q12.2	1559603_at	---
5.53	5.60	0.06	6.94E-01	8.95E-01	CCDC9	coiled-coil domain containing 9	chr19q13.32	206257_at	NM_015603
4.18	4.26	0.08	6.94E-01	8.95E-01	YY1	YY1 transcription factor	chr14q	213494_s_at	NM_003403
2.36	2.42	0.06	6.94E-01	8.95E-01	---	---	---	1566787_at	---
2.37	2.43	0.06	6.94E-01	8.95E-01	CG030	hypothetical gene CG030	chr13q12-q13	215105_at	---
2.52	2.57	0.05	6.94E-01	8.95E-01	---	---	---	234179_at	---
4.74	4.80	0.06	6.94E-01	8.95E-01	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	chr1p36.22	212324_s_at	NM_015378 /// NM_018156
3.02	3.09	0.07	6.95E-01	8.95E-01	IREB2	iron-responsive element binding protein 2	chr15q25.1	214666_x_at	NM_004136
2.03	2.08	0.05	6.95E-01	8.95E-01	A26B3	ANKRD26-like family B, member 3	chr21q11.2	1553474_at	NM_174981
2.13	2.18	0.05	6.95E-01	8.95E-01	---	---	---	1559152_at	---
1.86	1.91	0.05	6.95E-01	8.95E-01	LOC100130958	hypothetical protein LOC100130958	chr16q23.1	215301_at	NM_001129979 /// XM_001717986 /// XM_001718777 /// XM_001719609
8.03	8.13	0.10	6.95E-01	8.95E-01	RAB2A	RAB2A, member RAS oncogene family	chr8q12.1	208731_at	NM_002865

1.87	1.93	0.06	6.95E-01	8.95E-01	---	---	---	1560997_at	---
2.58	2.65	0.07	6.95E-01	8.96E-01	FREQ	Frequenin homolog (Drosophila)	chr9q34	230138_at	NM_001128826 /// NM_014286
3.90	4.05	0.15	6.95E-01	8.96E-01	INHBA	inhibin, beta A	chr7p15-p13	210511_s_at	NM_002192
2.87	2.94	0.07	6.95E-01	8.96E-01	ANKMY1	ankyrin repeat and MYND domain containing 1	chr2q37.3	220280_s_at	NM_016552 /// NM_017844
2.53	2.60	0.07	6.95E-01	8.96E-01	---	---	---	1565669_at	---
1.98	2.04	0.06	6.95E-01	8.96E-01	---	---	---	1559804_at	---
4.44	4.50	0.06	6.95E-01	8.96E-01	C19orf47	chromosome 19 open reading frame 47	chr19q13.2	234999_at	NM_178830
3.30	3.35	0.05	6.95E-01	8.96E-01	C21orf104	chromosome 21 open reading frame 104	---	1566927_at	---
2.75	2.82	0.07	6.95E-01	8.96E-01	---	---	---	233690_at	---
1.98	2.03	0.05	6.95E-01	8.96E-01	---	---	---	241088_at	---
6.46	6.58	0.12	6.95E-01	8.96E-01	FCHO2	FCH domain only 2	chr5q13.2	228220_at	NM_138782
2.81	2.86	0.06	6.95E-01	8.96E-01	C10orf85	chromosome 10 open reading frame 85	chr10q26.12	236855_at	XR_041622 /// XR_041623 /// XR_041624
1.86	1.90	0.04	6.95E-01	8.96E-01	---	---	---	1561902_at	---
1.85	1.89	0.04	6.95E-01	8.96E-01	LOC388458	hypothetical gene supported by BC040718	chr18p11.31	1560773_at	XM_371106
3.29	3.37	0.08	6.95E-01	8.96E-01	RAB3IP	RAB3A interacting protein (rabin3)	chr12q14.3	238526_at	NM_001024647 /// NM_022456 /// NM_175623 /// NM_175624 /// NM_175625
2.88	2.95	0.08	6.96E-01	8.96E-01	PLEKHM1	pleckstrin homology domain containing, family M (with RUN domain) member 1	chr17q21.31	216200_at	NM_014798
2.53	2.58	0.05	6.96E-01	8.96E-01	TP63	tumor protein p63	chr3q28	209863_s_at	NM_001114978 /// NM_001114979 /// NM_001114980 /// NM_001114981 /// NM_001114982 /// NM_003722
2.44	2.49	0.06	6.96E-01	8.96E-01	C11orf38	chromosome 11 open reading frame 38	chr11q24.2	243268_at	NM_212555
6.36	6.57	0.21	6.96E-01	8.96E-01	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	chr3q24-q25	232122_s_at	NM_024621
5.81	5.88	0.07	6.96E-01	8.96E-01	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	chr20p12	201203_s_at	NM_001042576 /// NM_004587
2.19	2.25	0.06	6.96E-01	8.96E-01	ANKRD31	ankyrin repeat domain 31	chr5q13.3	1564000_at	XM_001714469 /// XM_927671 /// XM_937397
5.13	5.21	0.08	6.96E-01	8.96E-01	RAI1	retinoic acid induced 1	chr17p11.2	1552558_a_at	NM_030665
2.47	2.53	0.06	6.96E-01	8.96E-01	IFNA6	interferon, alpha 6	chr9p22	208548_at	NM_021002
2.56	2.66	0.11	6.96E-01	8.96E-01	PRLR	Prolactin receptor	chr5p14-p13	231981_at	NM_000949
8.21	8.35	0.13	6.96E-01	8.96E-01	EPS15	epidermal growth factor receptor pathway substrate 15	chr1p32	217887_s_at	NM_001981
1.90	1.94	0.04	6.96E-01	8.96E-01	---	---	---	241479_at	---
3.38	3.50	0.12	6.96E-01	8.96E-01	CHML	choroideremia-like (Rab escort protein 2)	chr1q42-qter	226350_at	NM_001821
2.76	2.83	0.08	6.96E-01	8.96E-01	PSG9	pregnancy specific beta-1-glycoprotein 9	chr19q13.2	207733_x_at	NM_002784
5.07	5.14	0.07	6.96E-01	8.96E-01	SAMD10	sterile alpha motif domain containing 10	chr20q13.33	227773_at	NM_080621
4.08	4.16	0.07	6.96E-01	8.96E-01	BDKRB2	bradykinin receptor B2	chr14q32.1-q32.2	205870_at	NM_000623
3.28	3.34	0.06	6.96E-01	8.96E-01	MFAP3	Microfibrillar-associated protein 3	chr5q32-q33.2	214588_s_at	NM_005927
3.71	3.78	0.07	6.96E-01	8.96E-01	---	---	---	215651_at	---
2.40	2.46	0.06	6.96E-01	8.96E-01	MYNN	Myoneurin	chr3q26.2	237510_at	NM_018657
3.51	3.59	0.08	6.97E-01	8.96E-01	---	---	---	238668_at	---
1.88	1.93	0.05	6.97E-01	8.96E-01	---	---	---	1564405_at	---
1.98	2.03	0.05	6.97E-01	8.96E-01	LOC152118	hypothetical protein LOC152118	chr3q25.2	1555839_a_at	NM_001101337
5.21	5.28	0.07	6.97E-01	8.96E-01	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	chr19q13.43	219733_s_at	NM_012254
4.52	4.62	0.10	6.97E-01	8.96E-01	FGD5	FYVE, RhoGEF and PH domain containing 5	chr3p24.3	226985_at	NM_152536
3.51	3.59	0.07	6.97E-01	8.96E-01	TMEM95	transmembrane protein 95	chr17p13.1	1560281_a_at	NM_198154
4.95	5.02	0.07	6.97E-01	8.96E-01	LOC100130227 /// TMSB4Y	hypothetical protein LOC100130227 /// thymosin beta 4, Y-linked	chrYq11.221	206769_at	NM_004202 /// XM_001713694
7.68	7.81	0.13	6.97E-01	8.97E-01	CSRP1	cysteine and glycine-rich protein 1	chr1q32	200621_at	NM_004078
2.39	2.45	0.06	6.97E-01	8.97E-01	---	---	---	242897_at	---
2.00	2.06	0.06	6.97E-01	8.97E-01	RUFY2	RUN and FYVE domain containing 2	chr10q21.3	238550_at	NM_001042417 /// NM_017987

3.84	3.94	0.09	6.97E-01	8.97E-01	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	chr6q24	210870_s_at	NM_001018041 /// NM_005670																				
3.23	3.32	0.09	6.97E-01	8.97E-01	PNMA2	paraneoplastic antigen MA2	chr8p21.2	209597_s_at	NM_007257																				
5.98	6.10	0.12	6.97E-01	8.97E-01	FAM92A1	family with sequence similarity 92, member A1	chr8q22.1	228011_at	NM_145269																				
2.76	2.87	0.11	6.98E-01	8.97E-01	SLC25A36	Solute carrier family 25, member 36	chr3q23	237741_at	NM_001104647 /// NM_018155																				
2.43	2.50	0.06	6.98E-01	8.97E-01	---	---	---	230499_at	---																				
6.93	6.99	0.06	6.98E-01	8.97E-01	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	chr3p21.3	202681_at	NM_003363 /// NM_199443																				
4.16	4.21	0.05	6.98E-01	8.97E-01	IHH	Indian hedgehog homolog (Drosophila)	chr2q33-q35	215420_at	NM_002181																				
4.45	4.64	0.19	6.98E-01	8.97E-01	ANK2	ankyrin 2, neuronal	chr4q25-q27	202921_s_at	NM_001127493 /// NM_001148 /// NM_020977																				
6.67	6.81	0.14	6.98E-01	8.97E-01	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	chr11q13.1	206580_s_at	NM_016938																				
2.19	2.25	0.06	6.98E-01	8.97E-01	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	chrXp11.21	240883_at	NM_002625																				
2.66	2.71	0.05	6.98E-01	8.97E-01	PCDHB1	protocadherin beta 1	chr5q31	221303_at	NM_013340																				
1.89	1.94	0.04	6.98E-01	8.97E-01	LOC283665	hypothetical protein LOC283665	chr15q21.2	1557328_at	---																				
7.12	7.46	0.34	6.98E-01	8.97E-01	PDGFD	platelet derived growth factor D	chr11q22.3	222860_s_at	NM_025208 /// NM_033135																				
5.98	6.15	0.16	6.98E-01	8.97E-01	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	chr7q21-q22	210962_s_at	NM_005751 /// NM_147166 /// NM_147171 /// NM_147185																				
4.78	4.92	0.13	6.98E-01	8.97E-01	OSBPL11	oxysterol binding protein-like 11	chr3q21	218304_s_at	NM_022776																				
6.36	6.49	0.13	6.98E-01	8.97E-01	KIF1B	kinesin family member 1B	chr1p36.2	209234_at	NM_015074 /// NM_183416																				
6.60	6.68	0.08	6.98E-01	8.97E-01	LOC100133585 /// RABEP2	similar to RABEP2 protein /// rabaptin, RAB GTPase binding effector protein 2	chr16p11.2	219057_at	NM_024816 /// XM_001717918																				
2.52	2.60	0.07	6.98E-01	8.97E-01	---	---	---	244259_s_at	---																				
3.27	3.33	0.06	6.98E-01	8.97E-01	PSMG4	proteasome (prosome, macropain) assembly chaperone 4	chr6p25.2	233447_at	NM_001128591 /// NM_001128592 /// XR_017743 /// XR_017905 /// XR_041314																				
5.19	5.25	0.06	6.98E-01	8.97E-01	LOC338758	hypothetical protein LOC338758	chr12q21.33	238893_at	XM_001718140 /// XM_931359 /// XM_944677																				
2.43	2.49	0.06	6.98E-01	8.97E-01	RNF17	ring finger protein 17	chr13q12.12	221033_s_at	NM_031277																				
2.52	2.58	0.06	6.98E-01	8.97E-01	TAS2R38	taste receptor, type 2, member 38	chr7q34	1553555_at	NM_176817																				
2.14	2.19	0.05	6.98E-01	8.97E-01	MYO1B	myosin IB	chr2q12-q34	215074_at	NM_001130158 /// NM_012223																				
1.94	1.98	0.04	6.98E-01	8.97E-01	LOC729725	hypothetical LOC729725	chr4q32.2	1569712_at	XM_001131898 /// XM_001133787 /// XM_001722327																				
5.55	5.62	0.07	6.98E-01	8.97E-01	UQCR	ubiquinol-cytochrome c reductase, 6.4kDa subunit	chr19p13.3	223613_at	NM_006830																				
2.01	2.06	0.05	6.98E-01	8.97E-01	AKAP14	A kinase (PRKA) anchor protein 14	chrXq24	237282_s_at	NM_001008534 /// NM_001008535 /// NM_178813																				
5.71	5.92	0.21	6.98E-01	8.97E-01	ANAPC4	anaphase promoting complex subunit 4	chr4p15.2	232524_x_at	NM_013367																				
2.39	2.47	0.08	6.98E-01	8.97E-01	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	chr17q21.32	210718_s_at	NM_001113738 /// NM_016632																				
2.22	2.27	0.05	6.98E-01	8.97E-01	---	---	---	1568655_a_at	---																				
2.18	2.24	0.06	6.98E-01	8.97E-01	LOC100133555	similar to LOC440570	---	235284_s_at	XR_038272																				
2.07	2.13	0.07	6.99E-01	8.97E-01	WDR67	WD repeat domain 67	chr8q24.13	1556429_a_at	NM_145647																				
4.42	4.54	0.12	6.99E-01	8.97E-01	ERLIN2	ER lipid raft associated 2	chr8p11.2	221542_s_at	NM_001003790 /// NM_001003791 /// NM_007175																				
4.93	5.05	0.12	6.99E-01	8.97E-01	THUMPD3	THUMP domain containing 3	chr3p25.3	225741_at	NM_001114092 /// NM_015453																				
7.52	7.62	0.10	6.99E-01	8.97E-01	EIF1AP1 /// EIF1AX	eukaryotic translation initiation factor 1A pseudogene 1 /// eukaryotic translation initiation factor 1A, X-linked	chr1p36.13 /// chrXp22.12	201019_s_at	NM_001412																				
5.95	6.05	0.10	6.99E-01	8.97E-01	HEATR1	HEAT repeat containing 1	chr1q43	218595_s_at	NM_018072																				
2.19	2.24	0.05	6.99E-01	8.97E-01	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	chr12p12.1	208462_s_at	NM_005691 /// NM_020297 /// NM_020298																				

2.65	2.70	0.05	6.99E-01	8.97E-01	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	chr19p13.2	244660_at	NM_001419
2.01	2.04	0.04	6.99E-01	8.97E-01	LIN9	lin-9 homolog (C. elegans)	chr1q42.12	230365_at	NM_173083
1.69	1.74	0.04	6.99E-01	8.97E-01	---	---	---	1569810_at	---
1.95	1.99	0.04	6.99E-01	8.97E-01	---	---	---	1562049_at	---
2.58	2.66	0.08	6.99E-01	8.97E-01	PCDHGA3	protocadherin gamma subfamily A, 3	chr5q31	216352_x_at	NM_018916 /// NM_032011
10.04	10.13	0.09	6.99E-01	8.97E-01	MORF4L2	mortality factor 4 like 2	chrXq22	201994_at	NM_012286
3.18	3.26	0.08	6.99E-01	8.97E-01	SLFNL1	schlafen-like 1	chr1p34.2	1554074_s_at	NM_144990
2.91	2.97	0.06	6.99E-01	8.97E-01	HAS3	hyaluronan synthase 3	chr16q22.1	228179_at	NM_005329 /// NM_138612
1.93	1.99	0.06	6.99E-01	8.97E-01	CSN1S2A	casein alpha s2-like A	chr4q13.3	1553080_at	NR_003720
2.23	2.28	0.05	6.99E-01	8.97E-01	ERAP2	endoplasmic reticulum aminopeptidase 2	chr5q15	1554273_a_at	NM_001130140 /// NM_022350
2.43	2.50	0.07	6.99E-01	8.97E-01	LOC100128974	similar to RNA binding motif protein 17	chr15q14	240694_at	XR_037045 /// XR_037834 /// XR_038065
4.53	4.60	0.07	6.99E-01	8.97E-01	USP31	ubiquitin specific peptidase 31	chr16p12.1	226033_at	NM_020718
3.00	3.07	0.07	6.99E-01	8.97E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	210831_s_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719
1.96	2.01	0.04	6.99E-01	8.97E-01	---	---	---	239672_at	---
4.52	4.83	0.31	6.99E-01	8.97E-01	DARC	Duffy blood group, chemokine receptor	chr1q21-q22	208335_s_at	NM_001122951 /// NM_002036
2.16	2.20	0.05	6.99E-01	8.97E-01	---	---	---	230585_at	---
2.91	2.99	0.08	6.99E-01	8.97E-01	KIAA1109	KIAA1109	chr4q27	214929_s_at	NM_015312
2.15	2.21	0.06	6.99E-01	8.97E-01	UBE2U	ubiquitin-conjugating enzyme E2U (putative)	chr1p31.3	242392_at	NM_152489
2.16	2.22	0.06	6.99E-01	8.97E-01	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	chr19p13.11	231478_at	NM_000923 /// NM_001098818 /// NM_001098819
3.68	3.76	0.08	6.99E-01	8.97E-01	---	---	---	216586_at	---
2.40	2.44	0.04	7.00E-01	8.97E-01	LOC729291	Hypothetical protein LOC729291	chr12p11.22	240518_at	XR_041492 /// XR_041493 /// XR_041494
2.52	2.58	0.06	7.00E-01	8.97E-01	---	---	---	222281_s_at	---
2.38	2.43	0.04	7.00E-01	8.97E-01	FAM54A	family with sequence similarity 54, member A	chr6q23.3	234944_s_at	NM_001099286 /// NM_138419
7.15	7.21	0.06	7.00E-01	8.98E-01	LYRM4	LYR motif containing 4	chr6p25.1	218561_s_at	NM_020408
4.05	4.10	0.05	7.00E-01	8.98E-01	C9orf80	chromosome 9 open reading frame 80	chr9q32	223558_at	NM_021218
4.40	4.48	0.08	7.00E-01	8.98E-01	NOD1	nucleotide-binding oligomerization domain containing 1	chr7p15-p14	221073_s_at	NM_006092
2.23	2.30	0.06	7.00E-01	8.98E-01	MFSD4	major facilitator superfamily domain containing 4	chr1q32.1	229254_at	NM_181644
2.17	2.23	0.06	7.00E-01	8.98E-01	---	---	---	236385_at	---
3.51	3.59	0.08	7.00E-01	8.98E-01	HEL308	DNA helicase HEL308	chr4q21.23	241784_x_at	NM_133636
2.82	2.88	0.06	7.00E-01	8.98E-01	---	---	---	217638_at	---
2.59	2.65	0.06	7.00E-01	8.98E-01	---	---	---	1556663_s_at	---
4.32	4.38	0.06	7.00E-01	8.98E-01	PPP1R3F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	chrXp11.23	232211_at	NM_033215
5.36	5.54	0.18	7.00E-01	8.98E-01	THBS1	thrombospondin 1	chr15q15	201108_s_at	NM_003246
6.44	6.53	0.09	7.00E-01	8.98E-01	SATB1	SATB homeobox 1	chr3p23	203408_s_at	NM_001131010 /// NM_002971
3.35	3.41	0.06	7.00E-01	8.98E-01	---	---	---	234012_at	---
2.95	3.01	0.06	7.00E-01	8.98E-01	FSD1L	fibronectin type III and SPRY domain containing 1-like	chr9q31	242807_at	NM_031919 /// NM_207647
7.01	7.13	0.12	7.01E-01	8.98E-01	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	chr18q11.1	213044_at	NM_005406 /// XM_001713904 /// XM_001722015 /// XM_001723570
2.00	2.08	0.08	7.01E-01	8.98E-01	---	---	---	1561030_at	---
2.27	2.32	0.05	7.01E-01	8.98E-01	---	---	---	1556651_at	---
2.04	2.08	0.04	7.01E-01	8.98E-01	LRRC3B	leucine rich repeat containing 3B	chr3p24	229085_at	NM_052953

4.08	4.19	0.11	7.01E-01	8.98E-01	MYO1E	myosin IE	chr15q21-q22	203072_at	NM_004998
3.51	3.59	0.08	7.01E-01	8.98E-01	PCDHB12	protocadherin beta 12	chr5q31	221408_x_at	NM_018932
2.25	2.29	0.04	7.01E-01	8.98E-01	LL22NC03-75B3.6	KIAA1644 protein	---	52837_at	NM_001099294
3.86	3.94	0.09	7.01E-01	8.98E-01	PRCD	progressive rod-cone degeneration	chr17q25.1	230015_at	NM_001077620
9.09	9.21	0.12	7.01E-01	8.98E-01	ADIPOR2	adiponectin receptor 2	chr12p13.31	201346_at	NM_024551
2.16	2.21	0.06	7.01E-01	8.98E-01	---	---	---	1561461_at	---
2.07	2.13	0.06	7.01E-01	8.98E-01	---	---	---	1559914_at	---
2.28	2.33	0.06	7.01E-01	8.98E-01	---	---	---	1565748_at	---
2.89	2.94	0.05	7.01E-01	8.98E-01	TRIM2	tripartite motif-containing 2	chr4q31.3	214249_at	NM_001130067 /// NM_015271
5.13	5.35	0.22	7.01E-01	8.98E-01	HSPA4L	heat shock 70kDa protein 4-like	chr4q28	205543_at	NM_014278
5.18	5.30	0.13	7.01E-01	8.98E-01	KTELC1	KTEL (Lys-Tyr-Glu-Leu) containing 1	chr3q13.33	218587_s_at	NM_020231 /// NM_152305
2.88	2.95	0.07	7.01E-01	8.98E-01	---	---	---	217464_at	---
4.39	4.50	0.12	7.01E-01	8.98E-01	NFYB	nuclear transcription factor Y, beta	chr12q22-q23	218128_at	NM_006166
3.10	3.23	0.13	7.01E-01	8.98E-01	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	chrXq28	231913_s_at	NM_001018055 /// NM_024332
5.28	5.47	0.19	7.01E-01	8.98E-01	ARHGAP12	Rho GTPase activating protein 12	chr10pter-cen	207606_s_at	NM_018287
2.58	2.68	0.10	7.01E-01	8.98E-01	---	---	---	241970_at	---
2.42	2.50	0.07	7.01E-01	8.98E-01	MAGI2	Membrane associated guanylate kinase, WW and PDZ domain containing 2	chr7q21	237786_at	NM_012301
3.18	3.28	0.10	7.01E-01	8.98E-01	TRIP13	thyroid hormone receptor interactor 13	chr5p15.33	204033_at	NM_004237
6.88	7.05	0.17	7.01E-01	8.98E-01	FERMT2	fermitin family homolog 2 (Drosophila)	chr14q22.2	209210_s_at	NM_006832
2.14	2.20	0.06	7.01E-01	8.98E-01	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	chr16q22-q23	1566324_a_at	NM_001031804 /// NM_005360
2.30	2.35	0.05	7.02E-01	8.98E-01	LOC255480	hypothetical protein LOC255480	chr12q24.21	233948_at	XM_001134335 /// XM_001719855 /// XM_001723369
2.33	2.38	0.05	7.02E-01	8.98E-01	RGS17	regulator of G-protein signaling 17	chr6q25.3	220334_at	NM_012419
2.56	2.64	0.09	7.02E-01	8.98E-01	ASCL3	achaete-scute complex homolog 3 (Drosophila)	chr11p15.3	221161_at	NM_020646
4.93	5.05	0.12	7.02E-01	8.98E-01	---	---	---	231296_at	---
7.32	7.46	0.14	7.02E-01	8.99E-01	TMEM106B	transmembrane protein 106B	chr7p21.3	218930_s_at	NM_001134232 /// NM_018374
2.91	3.02	0.11	7.02E-01	8.99E-01	SMC3	structural maintenance of chromosomes 3	chr10q25	209258_s_at	NM_005445
3.65	3.72	0.08	7.02E-01	8.99E-01	---	---	---	240097_at	---
3.66	3.73	0.07	7.02E-01	8.99E-01	---	---	---	239833_at	---
2.27	2.33	0.05	7.02E-01	8.99E-01	TAS2R14	taste receptor, type 2, member 14	chr12p13	221391_at	NM_023922
5.19	5.50	0.31	7.02E-01	8.99E-01	MBNL2	muscleblind-like 2 (Drosophila)	chr13q32.1	205018_s_at	NM_144778 /// NM_207304
2.38	2.44	0.07	7.02E-01	8.99E-01	C16orf87	chromosome 16 open reading frame 87	chr16q11.2	226608_at	NM_001001436
2.09	2.15	0.05	7.02E-01	8.99E-01	COL8A1	collagen, type VIII, alpha 1	chr3q12.3	214587_at	NM_001850 /// NM_020351
3.48	3.56	0.08	7.02E-01	8.99E-01	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	chr19p13.3	207907_at	NM_003807 /// NM_172014
3.62	3.68	0.06	7.02E-01	8.99E-01	TRIM15	tripartite motif-containing 15	chr6p21.3	36742_at	NM_033229
4.16	4.28	0.12	7.02E-01	8.99E-01	USP8	ubiquitin specific peptidase 8	chr15q21.2	229501_s_at	NM_001128610 /// NM_001128611 /// NM_005154
2.57	2.63	0.05	7.02E-01	8.99E-01	ABCG5	ATP-binding cassette, sub-family G (WHITE), member 5	chr2p21	220383_at	NM_022436
3.91	3.96	0.05	7.02E-01	8.99E-01	WFDC2	WAP four-disulfide core domain 2	chr20q12-q13.2	203892_at	NM_006103
4.20	4.36	0.17	7.02E-01	8.99E-01	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	chr11q23	211367_s_at	NM_001223 /// NM_033292 /// NM_033293 /// NM_033294 /// NM_033295
4.36	4.43	0.07	7.02E-01	8.99E-01	C19orf29	chromosome 19 open reading frame 29	chr19p13.3	240373_at	NM_001080543 /// NM_021231
2.68	2.74	0.06	7.02E-01	8.99E-01	LOC646482	hypothetical LOC646482	chr13q12.13	1569517_at	XR_040959 /// XR_040960 /// XR_040961
2.22	2.27	0.04	7.02E-01	8.99E-01	---	---	---	233786_at	---
2.36	2.46	0.09	7.03E-01	8.99E-01	SLAIN2	SLAIN motif family, member 2	chr4p12	233230_s_at	NM_020846

1.88	1.92	0.05	7.03E-01	8.99E-01	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	chr15q11.2-q12	206456_at	NM_000810																					
2.12	2.18	0.06	7.03E-01	8.99E-01	---	---	---	236799_at	---																					
2.07	2.13	0.06	7.03E-01	8.99E-01	FLJ40176	hypothetical LOC121951	chr13q33.1	1561846_s_at	XM_926977 /// XM_937542																					
5.87	6.05	0.18	7.03E-01	8.99E-01	MYH11	myosin, heavy chain 11, smooth muscle	chr16p13.11	207961_x_at	NM_001040113 /// NM_001040114 /// NM_002474 /// NM_022844																					
4.61	4.69	0.08	7.03E-01	8.99E-01	DUSP3	dual specificity phosphatase 3	chr17q21	201538_s_at	NM_004090																					
5.67	5.74	0.07	7.03E-01	8.99E-01	---	---	---	243603_at	---																					
5.07	5.13	0.07	7.03E-01	8.99E-01	TARSL2	threonyl-tRNA synthetase-like 2	chr15q26.3	244615_x_at	NM_152334																					
2.20	2.25	0.06	7.03E-01	8.99E-01	OR5J2	olfactory receptor, family 5, subfamily J, member 2	chr11q12.3	1567244_at	NM_001005492																					
1.89	1.94	0.05	7.03E-01	8.99E-01	---	---	---	1559353_at	---																					
2.88	2.96	0.09	7.03E-01	8.99E-01	CDON	Cdon homolog (mouse)	chr11q23-q24	207230_at	NM_016952																					
2.50	2.56	0.06	7.03E-01	8.99E-01	---	---	---	228371_s_at	---																					
4.46	4.59	0.13	7.03E-01	8.99E-01	PTPRB	protein tyrosine phosphatase, receptor type, B	chr12q15-q21	205846_at	NM_001109754 /// NM_002837																					
4.36	4.46	0.10	7.03E-01	8.99E-01	---	---	---	1558236_at	---																					
1.89	1.93	0.05	7.03E-01	8.99E-01	LOC645478	Hypothetical LOC645478	chr16q22.3	1558724_at	XM_001724615 /// XM_932922 /// XM_942909																					
6.78	6.94	0.16	7.03E-01	8.99E-01	ZNF189	zinc finger protein 189	chr9q22-q31	207513_s_at	NM_003452 /// NM_197977																					
2.88	2.94	0.07	7.03E-01	8.99E-01	TUBB1	tubulin, beta 1	chr20q13.32	208601_s_at	NM_030773																					
2.18	2.25	0.08	7.03E-01	8.99E-01	---	---	---	1555974_a_at	---																					
5.28	5.36	0.08	7.03E-01	8.99E-01	ZNF226	zinc finger protein 226	chr19q13.2	219603_s_at	NM_001032372 /// NM_001032373 /// NM_001032374 /// NM_001032375 /// NM_015919																					
5.43	5.50	0.07	7.03E-01	8.99E-01	---	---	---	225778_at	---																					
5.06	5.12	0.06	7.03E-01	8.99E-01	DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	chr17q21.31	227079_at	NM_004941																					
2.36	2.41	0.05	7.03E-01	8.99E-01	---	---	---	243333_at	---																					
1.96	2.00	0.04	7.03E-01	8.99E-01	HECTD2	HECT domain containing 2	chr10q23.32	1565698_at	NM_173497 /// NM_182765																					
2.01	2.06	0.05	7.03E-01	8.99E-01	---	---	---	231208_at	---																					
2.50	2.54	0.05	7.03E-01	8.99E-01	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	chr10p12	1555098_a_at	NM_000724 /// NM_201570 /// NM_201571 /// NM_201572 /// NM_201590 /// NM_201593 /// NM_201596 /// NM_201597																					
7.05	7.22	0.17	7.04E-01	8.99E-01	H3F3A /// H3F3B	H3 histone, family 3A /// H3 histone, family 3B (H3.3B)	chr17q25 /// chr1q41	211998_at	NM_002107 /// NM_005324																					
3.01	3.06	0.05	7.04E-01	8.99E-01	PTPRF	protein tyrosine phosphatase, receptor type, F	chr1p34	215066_at	NM_002840 /// NM_130440																					
3.42	3.49	0.07	7.04E-01	8.99E-01	CX3CR1	chemokine (C-X3-C motif) receptor 1	chr3p21|3p21.3	1568934_at	NM_001337																					
2.40	2.46	0.06	7.04E-01	8.99E-01	LOC728723	hypothetical LOC728723	chr5q14.1	1564474_at	XR_042120 /// XR_042121 /// XR_042122																					
3.09	3.15	0.05	7.04E-01	8.99E-01	---	---	---	231541_s_at	---																					
2.14	2.18	0.04	7.04E-01	8.99E-01	CADM2	cell adhesion molecule 2	chr3p12.1	1552752_a_at	NM_153184																					
3.12	3.19	0.08	7.04E-01	8.99E-01	WWP2	WW domain containing E3 ubiquitin protein ligase 2	chr16q22.1	1552737_s_at	NM_007014 /// NM_199423 /// NM_199424																					
2.29	2.35	0.06	7.04E-01	8.99E-01	LRRTM2	leucine rich repeat transmembrane neuronal 2	chr5q31.2	206408_at	NM_015564																					
3.16	3.26	0.09	7.04E-01	8.99E-01	TGIF2	TGFB-induced factor homeobox 2	chr20q11.2-q12	218724_s_at	NM_021809																					
2.00	2.05	0.05	7.04E-01	8.99E-01	FLJ11292	hypothetical protein FLJ11292	chr5q14.3	215187_at	NM_018382																					
2.10	2.14	0.04	7.04E-01	8.99E-01	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)	chr7q31.3	216972_at	NM_003117 /// NM_153189																					
6.67	6.76	0.10	7.04E-01	9.00E-01	---	---	---	244197_x_at	---																					
2.18	2.22	0.04	7.04E-01	9.00E-01	---	---	---	1556394_a_at	---																					

4.06	4.14	0.08	7.04E-01	9.00E-01	ICA1	islet cell autoantigen 1, 69kDa	chr7p22	214191_at	NM_004968 /// NM_022307
2.88	2.93	0.06	7.04E-01	9.00E-01	---	---	---	216848_at	---
2.84	2.90	0.06	7.04E-01	9.00E-01	---	---	---	239211_at	---
5.18	5.37	0.19	7.04E-01	9.00E-01	KPNA5	karyopherin alpha 5 (importin alpha 6)	chr6q22.2	227934_at	NM_002269
2.87	2.95	0.08	7.04E-01	9.00E-01	DPF3	D4, zinc and double PHD fingers, family 3	chr14q24.3-q31.1	219746_at	NM_012074
3.06	3.10	0.04	7.04E-01	9.00E-01	ZXDB	zinc finger, X-linked, duplicated B	chrXp11.21	228005_at	NM_007157
6.73	6.87	0.14	7.04E-01	9.00E-01	CYYR1	cysteine/tyrosine-rich 1	chr21q21.2	235044_at	NM_052954
2.53	2.58	0.05	7.04E-01	9.00E-01	LOC100129476	Hypothetical protein LOC100129476	chr1p36.31	1561602_at	XM_001718470 /// XM_001719425 /// XM_001720143
3.43	3.49	0.06	7.05E-01	9.00E-01	ZBTB7A	Zinc finger and BTB domain containing 7A	chr19p13.3	230709_x_at	NM_015898
2.45	2.51	0.06	7.05E-01	9.00E-01	---	---	---	240530_at	---
2.72	2.77	0.05	7.05E-01	9.00E-01	FLJ34651	hypothetical protein LOC646023	chr22q11.23	237447_at	XR_041159 /// XR_041160 /// XR_041161
2.15	2.19	0.04	7.05E-01	9.00E-01	CLSPN	claspin homolog (Xenopus laevis)	chr1p34.2	1553120_at	NM_022111
3.75	3.87	0.12	7.05E-01	9.00E-01	USP48	ubiquitin specific peptidase 48	chr1p36.12	232621_at	NM_001032730 /// NM_032236
2.33	2.40	0.06	7.05E-01	9.00E-01	---	---	---	1570490_at	---
2.15	2.20	0.05	7.05E-01	9.00E-01	---	---	---	231964_at	---
2.66	2.72	0.06	7.05E-01	9.00E-01	---	---	---	236787_at	---
2.12	2.17	0.05	7.05E-01	9.00E-01	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	chr2q32.3	219334_s_at	NM_001031716
2.58	2.64	0.06	7.05E-01	9.00E-01	HIST1H2AM	histone cluster 1, H2am	chr6p22-p21.3	214481_at	NM_003514
5.91	5.96	0.05	7.05E-01	9.00E-01	SENP5	SUMO1/sentrin specific peptidase 5	chr3q29	213184_at	NM_152699
10.79	10.85	0.06	7.05E-01	9.00E-01	ALDOA	aldolase A, fructose-bisphosphate	chr16p11.2	200966_x_at	NM_000034 /// NM_001127617 /// NM_184041 /// NM_184043
5.74	5.84	0.11	7.05E-01	9.00E-01	FOXN2	forkhead box N2	chr2p22-p16	226711_at	NM_002158
4.51	4.64	0.13	7.06E-01	9.00E-01	LOC100133859	hypothetical protein LOC100133859	---	236841_at	XM_001714909
2.69	2.79	0.10	7.06E-01	9.01E-01	---	---	---	233614_at	---
2.77	2.83	0.06	7.06E-01	9.01E-01	MAPK15	mitogen-activated protein kinase 15	---	241528_at	NM_139021
4.05	4.15	0.10	7.06E-01	9.01E-01	TTF1	transcription termination factor, RNA polymerase I	chr9q34.13	204772_s_at	NM_007344
4.53	4.71	0.18	7.06E-01	9.01E-01	MRVI1	murine retrovirus integration site 1 homolog	chr11p15	224550_s_at	NM_001098579 /// NM_001100163 /// NM_001100167 /// NM_130385
4.68	4.75	0.07	7.06E-01	9.01E-01	---	---	---	215387_x_at	---
5.69	5.80	0.11	7.06E-01	9.01E-01	SOCS5	suppressor of cytokine signaling 5	chr2p21	208127_s_at	NM_014011 /// NM_144949
2.07	2.11	0.05	7.06E-01	9.01E-01	SYCE1	synaptonemal complex central element protein 1	chr10q26.3	233084_s_at	NM_130784 /// NM_201564
2.19	2.23	0.04	7.06E-01	9.01E-01	KIAA1655	KIAA1655 protein	---	215673_at	---
2.64	2.73	0.10	7.06E-01	9.01E-01	MYSM1	myb-like, SWIRM and MPN domains 1	chr1p32.1	238644_at	NM_001085487
6.34	6.54	0.20	7.06E-01	9.01E-01	CCNH	cyclin H	chr5q13.3-q14	204093_at	NM_001239
2.62	2.72	0.10	7.06E-01	9.01E-01	SULF1	sulfatase 1	chr8q13.2-q13.3	212353_at	NM_001128204 /// NM_001128205 /// NM_001128206 /// NM_015170
1.98	2.03	0.05	7.06E-01	9.01E-01	PDXDC1 /// PDXDC2	pyridoxal-dependent decarboxylase domain containing 1 /// pyridoxal-dependent decarboxylase domain containing 2	chr16p13.11 /// chr16q22.1	232288_at	NM_015027 /// NR_003610
5.27	5.45	0.18	7.06E-01	9.01E-01	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	chr6p25-p24	202149_at	NM_006403 /// NM_182966
2.43	2.48	0.05	7.07E-01	9.01E-01	---	---	---	1562332_at	---
1.93	1.97	0.04	7.07E-01	9.01E-01	---	---	---	221145_at	---
2.13	2.20	0.07	7.07E-01	9.01E-01	---	---	---	1570302_at	---
2.17	2.22	0.05	7.07E-01	9.01E-01	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	chr15q11.2-q12	227690_at	NM_000814 /// NM_021912
2.52	2.57	0.05	7.07E-01	9.01E-01	---	---	---	1561139_at	---
2.14	2.19	0.05	7.07E-01	9.01E-01	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	chr1q21.2-q21.3	216951_at	NM_000566

2.48	2.52	0.04	7.07E-01	9.01E-01	ELP2P	endozepine-like peptide 2 pseudogene	chr17p13.3	223783_s_at	XM_001714860 /// XM_001723226 /// XM_001725019
1.96	2.01	0.05	7.07E-01	9.01E-01	---	---	---	AFFX-r2-Bs-phe-5_at	---
3.57	3.66	0.09	7.07E-01	9.01E-01	FAM110B	family with sequence similarity 110, member B	chr8q12.1	221959_at	NM_147189
5.10	5.21	0.11	7.07E-01	9.02E-01	MAPK14	mitogen-activated protein kinase 14	chr6p21.3-p21.2	211561_x_at	NM_001315 /// NM_139012 /// NM_139013 /// NM_139014
2.16	2.21	0.06	7.07E-01	9.02E-01	DR1	Down-regulator of transcription 1, TBP-binding (negative cofactor 2)	chr1p22.1	216653_at	NM_001938
2.16	2.20	0.04	7.07E-01	9.02E-01	APIP	APAF1 interacting protein	chr11p13	232630_at	NM_015957
2.24	2.31	0.07	7.08E-01	9.02E-01	---	---	---	241272_at	---
5.07	5.17	0.09	7.08E-01	9.02E-01	DPH1 /// OVCA2	DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor in ovarian cancer 2	chr17p13.3	222041_at	NM_001383 /// NM_080822
2.06	2.10	0.05	7.08E-01	9.02E-01	LOC374443	CLR pseudogene	chr12p13.31	240573_at	NR_002814
7.15	7.29	0.14	7.08E-01	9.02E-01	PTEN	phosphatase and tensin homolog	chr10q23.3	204053_x_at	NM_000314
3.47	3.55	0.08	7.08E-01	9.02E-01	ANKRD19	ankyrin repeat domain 19	chr9q22.31	232926_x_at	XR_040005 /// XR_040006 /// XR_040007
2.15	2.21	0.05	7.08E-01	9.02E-01	RP11-138L21.1	similar to cell recognition molecule CASPR3	chr9p24.3	220436_at	XM_927067
1.90	1.95	0.05	7.08E-01	9.02E-01	---	---	---	231558_at	---
3.26	3.31	0.05	7.08E-01	9.02E-01	---	---	---	244394_at	---
2.08	2.12	0.04	7.08E-01	9.02E-01	---	---	---	228985_at	---
2.13	2.17	0.04	7.08E-01	9.02E-01	ZADH2	Zinc binding alcohol dehydrogenase domain containing 2	chr18q22.3	237776_at	NM_175907
3.23	3.27	0.04	7.08E-01	9.02E-01	---	---	---	237598_at	---
1.89	1.93	0.04	7.08E-01	9.02E-01	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	chr13q12.3	1554634_at	NM_015032
2.24	2.28	0.04	7.08E-01	9.02E-01	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	chr10q11.21-q11.23	224038_at	NM_006327
2.77	2.84	0.07	7.08E-01	9.02E-01	MEPE	matrix extracellular phosphoglycoprotein	chr4q21.1	221150_at	NM_020203
4.91	4.98	0.07	7.08E-01	9.02E-01	CROCCL2	ciliary rootlet coiled-coil, rootletin-like 2	chr1p36.13	215827_x_at	NR_023386 /// XM_001129099 /// XM_001130544 /// XM_001714120
4.27	4.32	0.05	7.08E-01	9.02E-01	---	---	---	242371_x_at	---
1.99	2.04	0.05	7.08E-01	9.02E-01	C6orf150	chromosome 6 open reading frame 150	chr6q13	1561708_at	NM_138441
2.05	2.10	0.05	7.08E-01	9.02E-01	MLANA	melan-A	chr9p24.1	206426_at	NM_005511
2.03	2.09	0.06	7.08E-01	9.02E-01	FRK	fyn-related kinase	chr6q21-q22.3	207178_s_at	NM_002031
4.20	4.26	0.06	7.08E-01	9.02E-01	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	chr17p13.1	220566_at	NM_014308
3.09	3.15	0.06	7.09E-01	9.02E-01	USH1C	Usher syndrome 1C (autosomal recessive, severe)	chr11p15.1-p14	205137_x_at	NM_005709 /// NM_153676
6.05	6.22	0.17	7.09E-01	9.02E-01	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	chr16q13	225106_s_at	NM_018233
2.15	2.19	0.04	7.09E-01	9.02E-01	ZNF257	zinc finger protein 257	chr19q13	210697_at	NM_033468
1.90	1.93	0.04	7.09E-01	9.02E-01	---	---	---	235617_x_at	---
3.74	3.80	0.06	7.09E-01	9.02E-01	DHDH	dihydrodiol dehydrogenase (dimeric)	chr19q13.3	231416_at	NM_014475
4.16	4.24	0.08	7.09E-01	9.02E-01	CLDN9	claudin 9	chr16p13.3	214635_at	NM_020982
5.53	5.67	0.14	7.09E-01	9.02E-01	RSBN1	round spermatid basic protein 1	chr1p13.2	213694_at	NM_018364
7.83	7.96	0.13	7.09E-01	9.02E-01	ETF1	eukaryotic translation termination factor 1	chr5q31.1	201574_at	NM_004730
6.03	6.15	0.13	7.09E-01	9.02E-01	KIAA0494	KIAA0494	chr1pter-p22.1	201775_s_at	NM_014774
3.03	3.13	0.10	7.09E-01	9.02E-01	STOX2	storkhead box 2	chr4q35.1	226822_at	NM_020225
6.94	7.03	0.09	7.09E-01	9.02E-01	CIC	capicua homolog (Drosophila)	chr19q13.2	212784_at	NM_015125
2.17	2.24	0.07	7.09E-01	9.02E-01	GADL1	glutamate decarboxylase-like 1	chr3p24.1-p23	1563533_at	NM_207359
2.60	2.67	0.06	7.09E-01	9.02E-01	---	---	---	1556259_at	---
2.09	2.14	0.05	7.09E-01	9.02E-01	---	---	---	234136_at	---
2.18	2.23	0.05	7.09E-01	9.02E-01	CSN1S1	casein alpha s1	chr4q21.1	208350_at	NM_001025104 /// NM_001890
4.51	4.71	0.20	7.09E-01	9.02E-01	---	---	---	1561167_at	---
4.12	4.26	0.14	7.10E-01	9.02E-01	PLRG1	Pleiotropic regulator 1 (PRL1 homolog, Arabidopsis)	chr4q31.2-q32.1	227246_at	NM_002669
4.71	4.82	0.11	7.10E-01	9.02E-01	UBE2K	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	chr4p14	202346_at	NM_001111112 /// NM_001111113 /// NM_005339
7.61	7.71	0.10	7.09E-01	9.02E-01	EBAG9	estrogen receptor binding site associated, antigen, 9	chr8q23	204274_at	NM_004215 /// NM_198120
3.32	3.40	0.08	7.09E-01	9.02E-01	MTNR1B	melatonin receptor 1B	chr11q21-q22	208516_at	NM_005959

3.22	3.30	0.08	7.10E-01	9.02E-01	41519	Septin 2	chr2q37	232637_at	NM_001008491 /// NM_001008492 /// NM_004404 /// NM_006155																				
3.40	3.48	0.08	7.10E-01	9.02E-01	MRPL52	Mitochondrial ribosomal protein L52	chr14q11.2	221997_s_at	NM_178336 /// NM_180982 /// NM_181304 /// NM_181305 /// NM_181306 /// NM_181307																				
3.34	3.42	0.08	7.10E-01	9.02E-01	ASXL2	additional sex combs like 2 (Drosophila)	chr2p24.1	1555266_a_at	NM_018263																				
2.93	3.01	0.08	7.09E-01	9.02E-01	---	---	---	240077_at	---																				
2.41	2.48	0.07	7.09E-01	9.02E-01	---	---	---	236936_at	---																				
3.39	3.46	0.07	7.10E-01	9.02E-01	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	chr16q22.1	203784_s_at	NM_018380																				
2.63	2.69	0.06	7.09E-01	9.02E-01	LHX3	LIM homeobox 3	chr9q34.3	221670_s_at	NM_014564 /// NM_178138																				
2.41	2.47	0.06	7.09E-01	9.02E-01	GTSE1	G-2 and S-phase expressed 1	chr22q13.2-q13.3	215942_s_at	NM_016426																				
2.35	2.41	0.06	7.09E-01	9.02E-01	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	chr1q42-q44	205307_s_at	NM_003679																				
2.12	2.18	0.05	7.09E-01	9.02E-01	KIAA1109	KIAA1109	chr4q27	233096_at	NM_015312																				
2.89	2.95	0.05	7.09E-01	9.02E-01	MYH3	myosin, heavy chain 3, skeletal muscle, embryonic	chr17p13.1	205940_at	NM_002470																				
2.04	2.09	0.05	7.09E-01	9.02E-01	TMEM27	transmembrane protein 27	chrXp22	223784_at	NM_020665																				
1.83	1.87	0.05	7.09E-01	9.02E-01	PCDH8	protocadherin 8	chr13q14.3-q21.1	206935_at	NM_002590 /// NM_032949																				
1.96	2.00	0.05	7.09E-01	9.02E-01	CCDC82	coiled-coil domain containing 82	chr11q21	1554785_at	NM_024725																				
1.87	1.92	0.04	7.10E-01	9.02E-01	BAI3	brain-specific angiogenesis inhibitor 3	chr6q12	211568_at	NM_001704																				
2.48	2.53	0.05	7.10E-01	9.03E-01	---	---	---	231563_at	---																				
5.24	5.32	0.08	7.10E-01	9.03E-01	RBM8A	RNA binding motif protein 8A	chr1q12	217857_s_at	NM_005105																				
2.70	2.78	0.08	7.10E-01	9.03E-01	ABHD11	abhydrolase domain containing 11	chr7q11.23	1552470_a_at	NM_148912																				
2.74	2.85	0.11	7.10E-01	9.03E-01	DYNLRB2	dynein, light chain, roadblock-type 2	chr16q23.3	238116_at	NM_130897																				
2.96	3.04	0.08	7.10E-01	9.03E-01	---	---	---	1570182_at	---																				
2.26	2.31	0.05	7.10E-01	9.03E-01	SPATA17	spermatogenesis associated 17	chr1q41	230763_at	NM_138796																				
5.38	5.44	0.06	7.10E-01	9.03E-01	---	---	---	208185_x_at	---																				
3.47	3.56	0.08	7.10E-01	9.03E-01	TBX1	T-box 1	chr22q11.21	242941_x_at	NM_005992 /// NM_080646 /// NM_080647																				
2.28	2.35	0.07	7.10E-01	9.03E-01	OSBPL6	oxysterol binding protein-like 6	chr2q31-q32.1	238575_at	NM_032523 /// NM_145739																				
3.89	3.95	0.06	7.10E-01	9.03E-01	---	---	---	234573_at	---																				
4.62	4.74	0.12	7.11E-01	9.03E-01	FREQ	frequenin homolog (Drosophila)	chr9q34	218266_s_at	NM_001128826 /// NM_014286																				

6.00	6.09	0.09	7.11E-01	9.03E-01	PDE9A	phosphodiesterase 9A	chr21q22.3	205593_s_at	NM_001001567 /// NM_001001568 /// NM_001001569 /// NM_001001570 /// NM_001001571 /// NM_001001572 /// NM_001001573 /// NM_001001574 /// NM_001001575 /// NM_001001576 /// NM_001001577 /// NM_001001578 /// NM_001001579 /// NM_001001580 /// NM_001001581 /// NM_001001582 /// NM_001001583 /// NM_001001584 /// NM_001001585 /// NM_002606																				
5.24	5.30	0.06	7.11E-01	9.03E-01	PDCL	phosducin-like	chr9q12-q13	204449_at	NM_005388																				
2.60	2.66	0.07	7.11E-01	9.03E-01	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	chr2q13	1557331_at	NM_019014																				
2.69	2.75	0.06	7.11E-01	9.03E-01	PMPCB	peptidase (mitochondrial processing) beta	chr7q22.1	1570542_a_at	NM_004279																				
2.33	2.39	0.06	7.11E-01	9.03E-01	---	---	---	242182_x_at	---																				
2.87	2.92	0.05	7.11E-01	9.03E-01	---	---	---	236380_at	---																				
4.76	4.84	0.08	7.11E-01	9.03E-01	TOM1L2	target of myb1-like 2 (chicken)	chr17p11.2	214840_at	NM_001033551 /// NM_001082968																				
4.62	4.67	0.06	7.11E-01	9.03E-01	TF	transferrin	chr3q22.1	214064_at	NM_001063																				
2.01	2.05	0.04	7.11E-01	9.03E-01	---	---	---	241238_at	---																				
2.23	2.29	0.06	7.11E-01	9.03E-01	LOC100130357	similar to hCG2038897	chr6p24.1	1559507_at	XM_001720695 /// XM_001725119 /// XM_001725455																				
2.14	2.20	0.05	7.11E-01	9.03E-01	---	---	---	1555135_at	---																				
9.15	9.22	0.07	7.11E-01	9.04E-01	41526	septin 9	chr17q25	41220_at	NM_001113491 /// NM_001113492 /// NM_001113493 /// NM_001113494 /// NM_001113495 /// NM_001113496 /// NM_006640																				
2.06	2.12	0.06	7.11E-01	9.04E-01	---	---	---	216437_at	---																				
3.60	3.66	0.05	7.11E-01	9.04E-01	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	chr1q42.13	229854_at	NM_001098623 /// NM_052843																				
1.86	1.90	0.04	7.11E-01	9.04E-01	---	---	---	243159_x_at	---																				
2.20	2.25	0.05	7.11E-01	9.04E-01	SNTG2	syntrophin, gamma 2	chr2p25.3	1570422_at	NM_018968																				
4.17	4.29	0.12	7.12E-01	9.04E-01	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	chr11q21	205395_s_at	NM_005590 /// NM_005591																				

3.19	3.29	0.11	7.12E-01	9.04E-01	LIN7B	lin-7 homolog B (C. elegans)	chr19q13.3	241957_x_at	NM_022165
2.99	3.09	0.10	7.11E-01	9.04E-01	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	chr6p25-p24	1569020_at	NM_006403 /// NM_182966
3.01	3.10	0.09	7.12E-01	9.04E-01	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	chr15q23-q25	236481_at	NM_000137
4.12	4.21	0.08	7.12E-01	9.04E-01	BANK1	B-cell scaffold protein with ankyrin repeats 1	chr4q24	219667_s_at	NM_001083907 /// NM_001127507 /// NM_017935
3.01	3.09	0.08	7.12E-01	9.04E-01	---	---	---	243948_at	---
2.95	3.03	0.07	7.12E-01	9.04E-01	---	---	---	1556947_at	---
2.80	2.86	0.07	7.12E-01	9.04E-01	ASB1	Ankyrin repeat and SOCS box-containing 1	chr2q37	228895_s_at	NM_001040445
3.05	3.12	0.06	7.12E-01	9.04E-01	LOC727748 /// SCRT1	similar to scratch homolog 1, zinc finger protein (Drosophila) /// scratch homolog 1, zinc finger protein (Drosophila)	chr8q24.3	228761_at	NM_031309 /// XM_001719366
2.63	2.69	0.06	7.12E-01	9.04E-01	---	---	---	1562984_at	---
3.10	3.15	0.06	7.12E-01	9.04E-01	---	---	---	1561667_at	---
2.04	2.09	0.05	7.12E-01	9.04E-01	LOC285224	hypothetical protein LOC285224	chr3q21.3	1562740_at	---
3.40	3.45	0.05	7.12E-01	9.04E-01	LNX1	ligand of numb-protein X 1	chr4q12	223611_s_at	NM_001126328 /// NM_032622
3.59	3.64	0.05	7.12E-01	9.04E-01	ARL5C	ADP-ribosylation factor-like 5C	chr17q12	1560136_at	XM_001720152 /// XM_001722887 /// XM_001725609 /// XM_372668 /// XM_936698
2.39	2.44	0.05	7.12E-01	9.04E-01	---	---	---	1563076_x_at	---
1.92	1.97	0.05	7.12E-01	9.04E-01	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	chr22q13.32	229459_at	NM_001082967 /// NM_015381
1.92	1.97	0.04	7.12E-01	9.04E-01	C9orf93	chromosome 9 open reading frame 93	chr9p22.3	239712_at	NM_173550
2.17	2.21	0.04	7.12E-01	9.04E-01	---	---	---	241097_at	---
3.74	3.82	0.08	7.12E-01	9.04E-01	CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6	chr19q13.2	211295_x_at	NM_000762
2.40	2.46	0.06	7.12E-01	9.04E-01	AKNA	AT-hook transcription factor	chr9q32	1558565_at	NM_030767
2.82	2.87	0.05	7.12E-01	9.04E-01	---	---	---	241210_at	---
5.93	6.02	0.09	7.12E-01	9.04E-01	ZNF787	zinc finger protein 787	chr19q13.42	213402_at	NM_001002836
6.18	6.28	0.10	7.12E-01	9.04E-01	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	chr17q21-q23	202629_at	NM_006380
3.05	3.18	0.12	7.12E-01	9.04E-01	C21orf121	chromosome 21 open reading frame 121	chr21q22.3	240809_at	XR_040349 /// XR_040350 /// XR_040351
3.48	3.57	0.09	7.12E-01	9.04E-01	LOC144571	hypothetical protein LOC144571	chr12p13.31	1564139_at	---
6.53	6.61	0.09	7.12E-01	9.04E-01	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	chr10p12.31	222621_at	NM_022365
2.02	2.07	0.04	7.12E-01	9.04E-01	BPTF	bromodomain PHD finger transcription factor	chr17q24.3	230056_at	NM_004459 /// NM_182641
2.17	2.21	0.04	7.12E-01	9.04E-01	---	---	---	1560758_at	---
6.20	6.35	0.16	7.13E-01	9.04E-01	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	chr4q26	225019_at	NM_001221 /// NM_172115 /// NM_172127 /// NM_172128
3.33	3.46	0.13	7.12E-01	9.04E-01	---	---	---	242846_at	---
7.02	7.11	0.09	7.12E-01	9.04E-01	BAG3	BCL2-associated athanogene 3	chr10q25.2-q26.2	217911_s_at	NM_004281
3.94	4.03	0.09	7.12E-01	9.04E-01	MTMR8	myotubularin related protein 8	chrXq11.1	221390_s_at	NM_017677
2.64	2.69	0.05	7.13E-01	9.04E-01	---	---	---	1555931_at	---
2.30	2.34	0.05	7.13E-01	9.04E-01	---	---	---	237549_at	---
2.36	2.40	0.05	7.12E-01	9.04E-01	RFESD	Rieske (Fe-S) domain containing	chr5q15	236305_at	NM_001131065 /// NM_001131066 /// NM_173362
4.02	4.12	0.11	7.13E-01	9.04E-01	ATXN3	ataxin 3	chr14q24.3-q32.2	205415_s_at	NM_001127696 /// NM_001127697 /// NM_004993 /// NM_030660
2.50	2.57	0.07	7.13E-01	9.04E-01	MOV10L1	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)	chr22q13.33	224385_s_at	NM_018995
2.36	2.42	0.06	7.13E-01	9.04E-01	FAM182A	family with sequence similarity 182, member A	chr20p11.1	230539_at	XR_041125 /// XR_041127

2.51	2.57	0.05	7.13E-01	9.04E-01	OR2L2	olfactory receptor, family 2, subfamily L, member 2	chr1q44	1567240_x_at	NM_001004686
2.26	2.30	0.04	7.13E-01	9.04E-01	PAH	phenylalanine hydroxylase	chr12q22-q24.2	217583_at	NM_000277
7.48	7.62	0.14	7.13E-01	9.04E-01	C5orf43	chromosome 5 open reading frame 43	chr5q12.1	224740_at	NM_001048249
4.18	4.28	0.09	7.13E-01	9.04E-01	RAB15	RAB15, member RAS onocogene family	chr14q23.3	59697_at	NM_198686
2.59	2.63	0.04	7.13E-01	9.04E-01	---	---	---	AFFX-LysX-M_at	---
2.71	2.78	0.06	7.13E-01	9.04E-01	OR5P3	olfactory receptor, family 5, subfamily P, member 3	chr11p15.4	1553078_at	NM_153445
2.25	2.32	0.06	7.13E-01	9.04E-01	SIM2	single-minded homolog 2 (Drosophila)	chr21q22.2|21q22.13	1557900_at	NM_005069 /// NM_009586
1.96	2.01	0.05	7.13E-01	9.04E-01	---	---	---	242755_at	---
2.04	2.08	0.04	7.13E-01	9.04E-01	---	---	---	236714_at	---
2.17	2.22	0.05	7.13E-01	9.04E-01	TEX11	testis expressed 11	chrXq13.1	233514_x_at	NM_001003811 /// NM_031276
4.34	4.44	0.10	7.13E-01	9.04E-01	---	---	---	230590_at	---
3.43	3.51	0.08	7.13E-01	9.04E-01	TREML1	triggering receptor expressed on myeloid cells-like 1	chr6p21.1	1555659_a_at	NM_178174
2.71	2.77	0.06	7.13E-01	9.04E-01	CHRM3	cholinergic receptor, muscarinic 3	chr1q43	214596_at	NM_000740
4.97	5.15	0.19	7.13E-01	9.04E-01	CXorf26	chromosome X open reading frame 26	chrXq13.3	224177_s_at	NM_016500
6.29	6.38	0.09	7.13E-01	9.04E-01	ZNF827	Zinc finger protein 827	chr4q31.22	243618_s_at	NM_178835
5.00	5.12	0.12	7.14E-01	9.04E-01	ATM	ataxia telangiectasia mutated	chr11q22-q23	212672_at	NM_000051 /// NM_138292
5.39	5.49	0.11	7.14E-01	9.04E-01	TLK2	tousled-like kinase 2	chr17q23	212986_s_at	NM_001112707 /// NM_006852
2.75	2.81	0.06	7.14E-01	9.04E-01	GRIPAP1	GRIP1 associated protein 1	chrXp11	1557562_at	NM_020137 /// NM_207672
2.41	2.47	0.06	7.14E-01	9.04E-01	---	---	---	234592_at	---
2.22	2.28	0.05	7.14E-01	9.04E-01	PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	chr12p12.1	231173_at	NM_024854
6.51	6.60	0.08	7.14E-01	9.04E-01	IL17RA	interleukin 17 receptor A	chr22q11.1	205707_at	NM_014339
2.41	2.47	0.06	7.14E-01	9.04E-01	---	---	---	1561420_a_at	---
2.37	2.42	0.05	7.14E-01	9.04E-01	SOX11	SRY (sex determining region Y)-box 11	chr2p25	204915_s_at	NM_003108
10.14	10.19	0.05	7.14E-01	9.04E-01	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	chr16p12.1	202077_at	NM_005003
2.15	2.19	0.05	7.14E-01	9.04E-01	AGR3	anterior gradient homolog 3 (Xenopus laevis)	chr7p21.1	228241_at	NM_176813
2.05	2.09	0.04	7.14E-01	9.04E-01	RGL3	ral guanine nucleotide dissociation stimulator-like 3	chr19p13.2	1556354_s_at	NM_001035223
4.26	4.43	0.17	7.14E-01	9.04E-01	POLI	polymerase (DNA directed) iota	chr18q21.1	219317_at	NM_007195
2.19	2.29	0.10	7.14E-01	9.04E-01	LOC100129482 /// ZNF37A /// ZNF37B	similar to zinc finger protein 37a (KOX 21) /// zinc finger protein 37A /// zinc finger protein 37B	chr10p11.2 /// chr10q11.21	214878_at	NM_001007094 /// NM_003421 /// XR_037028 /// XR_037227 /// XR_039227 /// XR_040507 /// XR_040508 /// XR_040509 /// XR_040510 /// XR_040511 /// XR_040512
7.70	7.79	0.09	7.14E-01	9.04E-01	SORBS3	sorbin and SH3 domain containing 3	chr8p21.3	209253_at	NM_001018003 /// NM_005775
8.31	8.37	0.07	7.14E-01	9.04E-01	TPP1	tripeptidyl peptidase I	chr11p15	200742_s_at	NM_000391
3.26	3.31	0.05	7.14E-01	9.04E-01	AP3M2	adaptor-related protein complex 3, mu 2 subunit	chr8p11.2	1569053_at	NM_001134296 /// NM_006803
2.13	2.18	0.05	7.14E-01	9.04E-01	MSX2	msh homeobox 2	chr5q34-q35	210319_x_at	NM_002449
2.02	2.06	0.04	7.14E-01	9.04E-01	---	---	---	1561021_at	---
2.00	2.05	0.04	7.14E-01	9.04E-01	SLC39A12	solute carrier family 39 (zinc transporter), member 12	chr10p12.33	1553126_a_at	NM_152725
4.51	4.59	0.07	7.14E-01	9.04E-01	---	---	---	229968_at	---
2.36	2.43	0.07	7.14E-01	9.05E-01	---	---	---	1566476_at	---
3.20	3.26	0.07	7.14E-01	9.05E-01	---	---	---	242177_at	---
2.02	2.07	0.05	7.14E-01	9.05E-01	---	---	---	240802_at	---
2.22	2.29	0.07	7.14E-01	9.05E-01	---	---	---	1570049_at	---
6.59	6.65	0.06	7.14E-01	9.05E-01	BTN3A1	butyrophilin, subfamily 3, member A1	chr6p22.1	209770_at	NM_007048
2.68	2.76	0.08	7.14E-01	9.05E-01	LMCD1	LIM and cysteine-rich domains 1	chr3p26-p24	227317_at	NM_014583
2.63	2.70	0.07	7.14E-01	9.05E-01	---	---	---	1561596_at	---
2.06	2.11	0.05	7.14E-01	9.05E-01	---	---	---	244558_at	---
2.27	2.31	0.04	7.14E-01	9.05E-01	GPR180	G protein-coupled receptor 180	chr13q32.1	231871_at	NM_180989
7.75	7.87	0.12	7.14E-01	9.05E-01	INMT	indolethylamine N-methyltransferase	chr7p15.3-p15.2	224061_at	NM_006774
7.32	7.46	0.14	7.15E-01	9.05E-01	IER3IP1	immediate early response 3 interacting protein 1	chr18q12	223071_at	NM_016097
2.77	2.90	0.13	7.15E-01	9.05E-01	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	chr15q11.2-q12	229724_at	NM_000814 /// NM_021912

5.83	5.94	0.11	7.15E-01	9.05E-01	TNPO1	transportin 1	chr5q13.2	212635_at	NM_002270 /// NM_153188
2.88	2.98	0.10	7.15E-01	9.05E-01	LAYN	layilin	chr11q23.1	228080_at	NM_178834
5.39	5.46	0.08	7.15E-01	9.05E-01	ENSA	endosulfine alpha	chr1q21.2	228852_at	NM_004436 /// NM_207042 /// NM_207043 /// NM_207044 /// NM_207045 /// NM_207046 /// NM_207047 /// NM_207168
4.03	4.09	0.06	7.15E-01	9.05E-01	ZNF18	zinc finger protein 18	chr17p11.2	226787_at	NM_144680
2.88	2.94	0.05	7.15E-01	9.05E-01	---	---	---	216738_at	---
9.39	9.54	0.15	7.15E-01	9.05E-01	TINP1	TGF beta-inducible nuclear protein 1	chr5q13.3	201922_at	NM_014886
2.83	2.96	0.13	7.15E-01	9.05E-01	---	---	---	243929_at	---
4.11	4.23	0.12	7.15E-01	9.05E-01	AKAP10	A kinase (PRKA) anchor protein 10	chr17p11.1	236006_s_at	NM_007202
2.81	2.91	0.10	7.15E-01	9.05E-01	CLEC1A	C-type lectin domain family 1, member A	chr12p13.2	219761_at	NM_016511
4.50	4.58	0.08	7.15E-01	9.05E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	1555436_a_at	NM_014423
2.42	2.48	0.06	7.15E-01	9.05E-01	CATSPER2	cation channel, sperm associated 2	chr15q15.3	1553323_a_at	NM_054020 /// NM_172095 /// NM_172096 /// NM_172097
4.42	4.48	0.06	7.15E-01	9.05E-01	ATOH8	Atonal homolog 8 (Drosophila)	chr2p11.2	1558705_at	NM_032827
2.81	2.87	0.06	7.15E-01	9.05E-01	LOC100130328 /// LOC650686 /// NXF2 /// NXF2B	similar to hCG2045904 /// similar to nuclear RNA export factor 2 /// nuclear RNA export factor 2 /// nuclear RNA export factor 2B	chrXq22.1	234173_s_at	NM_001099686 /// NM_017809 /// NM_022053 /// XM_001713916 /// XM_001713918 /// XM_001713996 /// XM_001714190
3.48	3.53	0.05	7.15E-01	9.05E-01	C20orf117	chromosome 20 open reading frame 117	chr20q11.23	215852_x_at	NM_199181
1.91	1.95	0.04	7.15E-01	9.05E-01	---	---	---	243262_at	---
1.84	1.88	0.04	7.15E-01	9.05E-01	---	---	---	237651_x_at	---
2.88	2.95	0.07	7.15E-01	9.05E-01	FLJ31485	hypothetical gene supported by AK056047; AK056281; AK123838	chr12q24.33	239569_at	XM_001128937 /// XM_001133168 /// XM_001715676
2.62	2.70	0.09	7.15E-01	9.05E-01	AP1GBP1	AP1 gamma subunit binding protein 1	chr17q12	1553165_at	NM_007247 /// NM_080550
2.24	2.28	0.05	7.15E-01	9.05E-01	KRTAP4-3	keratin associated protein 4-3	chr17q12-q21	234678_at	NM_033187
3.78	3.95	0.17	7.16E-01	9.05E-01	---	---	---	241036_at	---
4.82	4.95	0.13	7.16E-01	9.05E-01	FAAH	fatty acid amide hydrolase	chr1p35-p34	204231_s_at	NM_001441
5.04	5.16	0.13	7.15E-01	9.05E-01	ANKRD13D	ankyrin repeat domain 13 family, member D	chr11q13.1	238642_at	NM_207354
4.77	4.89	0.12	7.15E-01	9.05E-01	VPS37A	Vacuolar protein sorting 37 homolog A (S. cerevisiae)	chr8p22	228024_at	NM_152415
7.54	7.65	0.11	7.16E-01	9.05E-01	MIRN21 /// TMEM49	microRNA 21 /// transmembrane protein 49	chr17q23.1	220990_s_at	NM_030938
3.13	3.24	0.11	7.16E-01	9.05E-01	MFAP5	microfibrillar associated protein 5	chr12p13.1-p12.3	213765_at	NM_003480
6.92	7.01	0.09	7.16E-01	9.05E-01	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	chr2q37.3	202143_s_at	NM_006710 /// NM_198189
3.70	3.78	0.08	7.16E-01	9.05E-01	TBX1	T-box 1	chr22q11.21	236926_at	NM_005992 /// NM_080646 /// NM_080647
3.60	3.67	0.08	7.16E-01	9.05E-01	---	---	---	236411_at	---
5.01	5.09	0.07	7.16E-01	9.05E-01	TUBA3C /// TUBA3D	tubulin, alpha 3c /// tubulin, alpha 3d	chr13q11 /// chr2q21.1	216323_x_at	NM_006001 /// NM_080386
4.19	4.25	0.07	7.15E-01	9.05E-01	---	---	---	238629_x_at	---
3.07	3.13	0.06	7.16E-01	9.05E-01	---	---	---	233940_at	---
2.65	2.71	0.06	7.16E-01	9.05E-01	SMC1A	structural maintenance of chromosomes 1A	chrXp11.22-p11.21	239688_at	NM_006306
2.25	2.31	0.06	7.16E-01	9.05E-01	MAB21L1	mab-21-like 1 (C. elegans)	chr13q13	206163_at	NM_005584

2.67	2.73	0.06	7.16E-01	9.05E-01	RUNX2	runt-related transcription factor 2	chr6p21	236859_at	NM_001015051 /// NM_001024630 /// NM_004348
2.62	2.68	0.05	7.16E-01	9.05E-01	LYST	lysosomal trafficking regulator	chr1q42.1-q42.2	215415_s_at	NM_000081
2.50	2.55	0.05	7.16E-01	9.05E-01	ZNF17	zinc finger protein 17	chr19q13.4	1558184_s_at	NM_006959
1.97	2.02	0.05	7.16E-01	9.05E-01	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	chr9p21.1	1559042_at	NM_002493 /// NM_182739
4.13	4.18	0.05	7.16E-01	9.05E-01	SAMD4B	sterile alpha motif domain containing 4B	chr19q13.2	220457_at	NM_018028
3.08	3.14	0.05	7.16E-01	9.05E-01	---	---	---	238278_at	---
2.78	2.83	0.05	7.16E-01	9.05E-01	---	---	---	239202_at	---
2.18	2.23	0.05	7.16E-01	9.05E-01	---	---	---	237582_at	---
2.02	2.06	0.04	7.16E-01	9.05E-01	---	---	---	1566459_at	---
2.19	2.24	0.06	7.16E-01	9.05E-01	LOC389043	hypothetical gene supported by AK125982; BC042817	chr2q21.1	1560912_at	XM_001724474 /// XM_374012 /// XM_943029
2.92	2.98	0.05	7.16E-01	9.05E-01	hCG_1795091	hCG1795091	chr10q26.3	234053_at	XR_041016 /// XR_041017 /// XR_041018
3.21	3.25	0.04	7.16E-01	9.05E-01	CHRND	cholinergic receptor, nicotinic, delta	chr2q33-q34	207024_at	NM_000751
1.89	1.93	0.04	7.16E-01	9.05E-01	---	---	---	1561550_at	---
9.80	9.89	0.09	7.16E-01	9.05E-01	UQCRB	ubiquinol-cytochrome c reductase binding protein	chr8q22	209066_x_at	NM_006294
2.37	2.45	0.08	7.16E-01	9.05E-01	CHIC1	cysteine-rich hydrophobic domain 1	chrXq13-q21	1559481_at	NM_001039840
3.26	3.33	0.07	7.16E-01	9.05E-01	---	---	---	1562327_at	---
1.90	1.94	0.04	7.16E-01	9.05E-01	---	---	---	241676_x_at	---
4.03	4.10	0.07	7.16E-01	9.05E-01	C20orf141	chromosome 20 open reading frame 141	chr20p13	231360_at	NM_080739
7.24	7.30	0.06	7.16E-01	9.05E-01	TWF2	twinfilin, actin-binding protein, homolog 2 (Drosophila)	chr3p21.1	202009_at	NM_007284
2.30	2.36	0.05	7.16E-01	9.05E-01	---	---	---	241452_at	---
2.86	2.91	0.05	7.16E-01	9.05E-01	---	---	---	242199_at	---
3.14	3.19	0.05	7.16E-01	9.05E-01	---	---	---	236279_at	---
2.14	2.18	0.05	7.17E-01	9.05E-01	KIAA1239	KIAA1239	chr4p14	230765_at	XM_001713967 /// XM_049078 /// XM_940885
2.85	2.95	0.09	7.17E-01	9.05E-01	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	chr21q22.12	213167_s_at	NM_006933
3.81	3.97	0.16	7.17E-01	9.05E-01	RUFY3	RUN and FYVE domain containing 3	chr4q13.3	203724_s_at	NM_001037442 /// NM_001130709 /// NM_014961
5.18	5.25	0.07	7.17E-01	9.05E-01	EXOSC2	exosome component 2	chr9q34	214507_s_at	NM_014285
4.34	4.40	0.06	7.17E-01	9.05E-01	---	---	---	211374_x_at	---
2.29	2.35	0.06	7.17E-01	9.05E-01	LOC651198	similar to hCG2036706	---	211455_at	XM_001715717 /// XM_001732838
2.73	2.78	0.06	7.17E-01	9.05E-01	MCHR1	melanin-concentrating hormone receptor 1	chr22q13.2	230498_at	NM_005297
2.44	2.49	0.05	7.17E-01	9.05E-01	---	---	---	243781_at	---
2.11	2.17	0.05	7.17E-01	9.05E-01	FGB	fibrinogen beta chain	chr4q28	216238_s_at	NM_005141
2.39	2.44	0.05	7.17E-01	9.05E-01	EGO	eosinophil granule ontogeny	---	240475_at	NR_004428
3.78	3.87	0.09	7.17E-01	9.05E-01	FAM169A	family with sequence similarity 169, member A	chr5q13.3	235048_at	NM_015566
5.92	6.04	0.11	7.17E-01	9.05E-01	FLJ20323	hypothetical protein FLJ20323	chr7p22-p21	211724_x_at	NM_019005
6.13	6.25	0.12	7.17E-01	9.05E-01	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	chr5p13	240873_x_at	NM_001343
3.63	3.81	0.18	7.17E-01	9.05E-01	FAM175B	family with sequence similarity 175, member B	chr10q26.13	212835_at	NM_032182
2.13	2.18	0.05	7.17E-01	9.05E-01	XCL1	chemokine (C motif) ligand 1	chr1q23	206365_at	NM_002995
1.95	1.99	0.05	7.17E-01	9.05E-01	ATOH7	atonal homolog 7 (Drosophila)	chr10q21.3|10q21.3-q22.1	1552878_at	NM_145178
2.71	2.78	0.07	7.17E-01	9.05E-01	RNF217	ring finger protein 217	chr6q22.31	235492_at	NM_152553
3.58	3.66	0.08	7.17E-01	9.05E-01	ZNF677	zinc finger protein 677	chr19q13.41	1560562_a_at	NM_182609
2.09	2.14	0.04	7.17E-01	9.05E-01	KLB	klotho beta	chr4p14	235708_at	NM_175737
2.59	2.65	0.06	7.17E-01	9.05E-01	FLJ21075	hypothetical protein FLJ21075	chr7p12.3	221172_at	NM_025031
2.26	2.32	0.05	7.17E-01	9.05E-01	LOC339505	hypothetical protein LOC339505	chr1p36.12	1557373_at	---
2.46	2.51	0.05	7.17E-01	9.05E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	1559928_at	NM_002581
2.56	2.61	0.04	7.17E-01	9.05E-01	ZNF778	zinc finger protein 778	chr16q24.3	1556581_at	NM_182531
3.42	3.48	0.07	7.18E-01	9.06E-01	NLRC4	NLR family, CARD domain containing 4	chr2p22-p21	1552553_a_at	NM_021209
2.69	2.75	0.07	7.18E-01	9.06E-01	---	---	---	240693_at	---
2.80	2.84	0.04	7.18E-01	9.06E-01	---	---	---	236969_at	---
5.10	5.16	0.06	7.18E-01	9.06E-01	KRTAP5-8	keratin associated protein 5-8	chr11q13.4	208532_x_at	NM_021046
2.49	2.54	0.05	7.18E-01	9.06E-01	PTGDR	prostaglandin D2 receptor (DP)	chr14q22.1	234165_at	NM_000953
2.33	2.38	0.05	7.18E-01	9.06E-01	---	---	---	242231_at	---

2.89	2.94	0.04	7.18E-01	9.06E-01	SLC47A2	solute carrier family 47, member 2	chr17p11.2	231068_at	NM_001099646 /// NM_152908
2.14	2.20	0.06	7.18E-01	9.06E-01	P2RY10	purinergic receptor P2Y, G-protein coupled, 10	chrXq21.1	214615_at	NM_014499 /// NM_198333
3.15	3.22	0.07	7.18E-01	9.06E-01	SH2D1A	SH2 domain protein 1A	chrXq25-q26	210116_at	NM_001114937 /// NM_002351
4.85	5.00	0.15	7.18E-01	9.06E-01	NCF4	neutrophil cytosolic factor 4, 40kDa	chr22q13.1	207677_s_at	NM_000631 /// NM_013416
3.91	4.03	0.11	7.18E-01	9.06E-01	SOCS6	suppressor of cytokine signaling 6	chr18q22.2	227542_at	NM_004232
6.85	6.96	0.11	7.18E-01	9.06E-01	LYPLAL1	lysophospholipase-like 1	chr1q41	226851_at	NM_138794
2.76	2.82	0.06	7.18E-01	9.06E-01	---	---	---	1555206_at	---
1.98	2.02	0.04	7.18E-01	9.06E-01	TBL1XR1	Transducin (beta)-like 1 X-linked receptor 1	chr3q26.32	233633_at	NM_024665
2.28	2.32	0.04	7.18E-01	9.06E-01	---	---	---	241886_x_at	---
7.03	7.13	0.10	7.18E-01	9.06E-01	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	chr7q35-q36	204099_at	NM_001003801 /// NM_001003802 /// NM_003078
2.29	2.34	0.05	7.18E-01	9.06E-01	ROPN1	Ropporin, rhophilin associated protein 1	chr3q21.1	233203_at	NM_017578
2.27	2.32	0.05	7.18E-01	9.06E-01	SNORA74A	small nucleolar RNA, H/ACA box 74A	chr5q31.2	1567679_at	NR_002915
2.07	2.11	0.04	7.18E-01	9.06E-01	LIPG	lipase, endothelial	chr18q21.1	219181_at	NM_006033
3.08	3.14	0.06	7.19E-01	9.06E-01	FAM122C	Family with sequence similarity 122C	chrXq26.3	239047_at	NM_138819
2.73	2.78	0.05	7.19E-01	9.06E-01	PPY2	pancreatic polypeptide 2	chr17q11	220654_at	NR_002181
2.01	2.06	0.04	7.19E-01	9.06E-01	VGLL3	vestigial like 3 (Drosophila)	chr3p12.1	220327_at	NM_016206
2.66	2.74	0.08	7.19E-01	9.06E-01	PDP2	pyruvate dehydrogenase phosphatase isoenzyme 2	chr16q22.1	232861_at	NM_020786
2.12	2.17	0.05	7.19E-01	9.06E-01	LOC399875	hypothetical gene supported by BC040220	chr11p15.1	1562320_at	---
4.82	5.01	0.19	7.19E-01	9.06E-01	ATP9A	ATPase, class II, type 9A	chr20q13.2	212062_at	NM_006045
3.28	3.34	0.05	7.19E-01	9.06E-01	TRAF3IP1	TNF receptor-associated factor 3 interacting protein 1	chr2q37.3	214458_at	NM_015650
5.74	5.79	0.05	7.19E-01	9.06E-01	WDR48	WD repeat domain 48	chr3p21.33	56919_at	NM_020839
2.06	2.11	0.04	7.19E-01	9.06E-01	STON2	Stonin 2	chr14q31.1	235852_at	NM_033104
7.09	7.26	0.17	7.19E-01	9.06E-01	SERBP1	SERPINE1 mRNA binding protein 1	chr1p31	217725_x_at	NM_001018067 /// NM_001018068 /// NM_001018069 /// NM_015640
5.69	5.76	0.08	7.19E-01	9.06E-01	C20orf111	Chromosome 20 open reading frame 111	chr20q13.11	221954_at	NM_016470
3.18	3.24	0.06	7.19E-01	9.06E-01	MYEOV	myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas)	chr11q13	227342_s_at	NM_138768
2.64	2.70	0.06	7.19E-01	9.06E-01	MAPKBP1	mitogen-activated protein kinase binding protein 1	chr15q15.1	1558839_at	NM_001128608 /// NM_014994
2.85	2.91	0.05	7.19E-01	9.06E-01	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	chr17q24.2	242541_at	NM_080283
2.32	2.38	0.05	7.19E-01	9.06E-01	---	---	---	1560240_at	---
7.13	7.18	0.05	7.19E-01	9.06E-01	FKSG49	FKSG49	chr5q13.3	208120_x_at	XR_041698
2.82	2.86	0.04	7.19E-01	9.06E-01	FLJ44653	FLJ44653 protein	chr10q26.3	235715_at	XR_040356 /// XR_040357 /// XR_040358
2.10	2.15	0.04	7.19E-01	9.06E-01	---	---	---	215736_at	---
2.68	2.74	0.06	7.19E-01	9.06E-01	C1orf128	Chromosome 1 open reading frame 128	chr1p36.11	229856_s_at	NM_020362
2.48	2.53	0.05	7.19E-01	9.06E-01	IL20RB	interleukin 20 receptor beta	chr3q22.3	228575_at	NM_144717
2.62	2.67	0.04	7.19E-01	9.06E-01	SPRYD5	SPRY domain containing 5	chr11q11	223975_at	NM_032681
2.06	2.11	0.05	7.19E-01	9.06E-01	---	---	---	1555854_at	---
2.17	2.26	0.09	7.19E-01	9.06E-01	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	chr2q31.3	205885_s_at	NM_000885
3.98	4.05	0.07	7.19E-01	9.06E-01	CASP2	caspase 2, apoptosis-related cysteine peptidase	chr7q34-q35	208050_s_at	NM_032982 /// NM_032983
2.03	2.07	0.04	7.19E-01	9.06E-01	---	---	---	1561562_at	---
4.56	4.67	0.11	7.19E-01	9.06E-01	---	---	---	1566471_at	---
2.53	2.61	0.07	7.19E-01	9.06E-01	MCPH1	microcephalin 1	chr8p23.1	1554155_at	NM_024596
2.64	2.71	0.07	7.20E-01	9.06E-01	LOX	lysyl oxidase	chr5q23.2	204298_s_at	NM_002317
2.76	2.83	0.07	7.20E-01	9.06E-01	CUGBP2	CUG triplet repeat, RNA binding protein 2	chr10p13	1554569_a_at	NM_001025076 /// NM_001025077 /// NM_001083591 /// NM_006561
3.34	3.39	0.05	7.19E-01	9.06E-01	---	---	---	244028_at	---
6.30	6.39	0.09	7.20E-01	9.06E-01	KLHL12	kelch-like 12 (Drosophila)	chr1q32.1	225068_at	NM_021633
7.86	7.95	0.09	7.20E-01	9.06E-01	LAMP2	lysosomal-associated membrane protein 2	chrXq24	203041_s_at	NM_001122606 /// NM_002294 /// NM_013995

2.45	2.53	0.08	7.20E-01	9.06E-01	---	---	---	231061_at	---
2.78	2.85	0.07	7.20E-01	9.06E-01	ZNF462	zinc finger protein 462	chr9q31.2	232393_at	NM_021224
2.66	2.71	0.05	7.20E-01	9.06E-01	ITK	IL2-inducible T-cell kinase	chr5q31-q32	211339_s_at	NM_005546
2.25	2.33	0.07	7.20E-01	9.06E-01	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	chr11q12.3	222053_at	NM_006473
3.07	3.13	0.06	7.20E-01	9.06E-01	---	---	---	216175_at	---
3.36	3.42	0.06	7.20E-01	9.07E-01	PPP4R1L	protein phosphatase 4, regulatory subunit 1-like	chr20q13.32	1560176_s_at	NR_003505
4.95	5.07	0.12	7.20E-01	9.07E-01	C20orf19	chromosome 20 open reading frame 19	chr20pter-q11.23	228291_s_at	NM_018474
2.12	2.17	0.05	7.20E-01	9.07E-01	RG9MTD3	RNA (guanine-9-) methyltransferase domain containing 3	chr9p13.2	235303_at	NM_144964
6.64	6.74	0.10	7.20E-01	9.07E-01	MUTED	muted homolog (mouse)	chr6p25.1-p24.3	226544_x_at	NM_201280
2.65	2.70	0.04	7.20E-01	9.07E-01	DCLK2	Doublecortin-like kinase 2	chr4q31.3	216724_at	NM_001040260 /// NM_001040261
3.42	3.48	0.06	7.21E-01	9.07E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	214361_s_at	NM_002926 /// NM_198227 /// NM_198229
2.39	2.47	0.08	7.21E-01	9.07E-01	QKI	Quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	236154_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855
3.91	3.98	0.07	7.21E-01	9.07E-01	NADK	NAD kinase	chr1p36.33-p36.21	213613_s_at	NM_023018
2.24	2.29	0.06	7.21E-01	9.07E-01	---	---	---	1562121_at	---
2.53	2.59	0.06	7.21E-01	9.07E-01	IKZF1	IKAROS family zinc finger 1 (Ikaros)	chr7p13-p11.1	205038_at	NM_006060
5.41	5.55	0.14	7.21E-01	9.07E-01	GFM1	G elongation factor, mitochondrial 1	chr3q25.1-q26.2	232296_s_at	NM_024996
5.12	5.19	0.07	7.21E-01	9.07E-01	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	chr7q36	209246_at	NM_005692 /// NM_007189
2.48	2.53	0.05	7.21E-01	9.07E-01	MPHOSPH8	M-phase phosphoprotein 8	chr13q12.11	240942_at	NM_017520
3.52	3.66	0.14	7.21E-01	9.07E-01	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	chrXp11.4	238699_s_at	NM_001126054 /// NM_001126055 /// NM_003688
3.90	4.11	0.21	7.21E-01	9.07E-01	---	---	---	234034_at	---
2.57	2.66	0.08	7.21E-01	9.07E-01	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	chr2q36.3	222379_at	NM_080671
5.98	6.06	0.08	7.21E-01	9.07E-01	---	---	---	226391_at	---
4.04	4.10	0.06	7.21E-01	9.07E-01	LIG3	ligase III, DNA, ATP-dependent	chr17q11.2-q12	207348_s_at	NM_002311 /// NM_013975
2.60	2.65	0.05	7.21E-01	9.07E-01	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	chr18q21.3-q22	215817_at	NM_012397
3.11	3.16	0.05	7.21E-01	9.07E-01	C21orf15	chromosome 21 open reading frame 15	chr21q11	1559028_at	---
2.96	3.02	0.06	7.21E-01	9.07E-01	ZNF292	zinc finger protein 292	chr6q15	212366_at	NM_015021
2.86	2.91	0.04	7.21E-01	9.07E-01	TFAP2D	transcription factor AP-2 delta (activating enhancer binding protein 2 delta)	chr6p12.1	233987_at	NM_172238
2.06	2.10	0.04	7.21E-01	9.07E-01	---	---	---	1557758_at	---
2.39	2.45	0.05	7.21E-01	9.07E-01	---	---	---	233928_at	---
2.92	2.98	0.05	7.21E-01	9.07E-01	WNT7A	wingless-type MMTV integration site family, member 7A	chr3p25	210248_at	NM_004625
2.17	2.22	0.05	7.21E-01	9.07E-01	---	---	---	1566727_at	---
2.12	2.18	0.05	7.21E-01	9.07E-01	---	---	---	1555221_at	---
8.15	8.23	0.08	7.21E-01	9.07E-01	CNOT1	CCR4-NOT transcription complex, subunit 1	chr16q21	200860_s_at	NM_016284 /// NM_206999
3.88	3.97	0.09	7.21E-01	9.07E-01	---	---	---	231972_at	---
2.63	2.69	0.06	7.21E-01	9.07E-01	HOXD10	homeobox D10	chr2q31.1	229400_at	NM_002148
2.65	2.71	0.06	7.21E-01	9.07E-01	LOC340544	hypothetical protein LOC340544	chrXq22.2	1559002_at	---
7.13	7.17	0.04	7.21E-01	9.07E-01	LOC100130233 /// LOC399804	similar to NPM1 protein /// similar to nucleophosmin (nucleolar phosphoprotein B23, numatrin)	chr10q23.33 /// chrXp21.1	216387_x_at	XR_016532 /// XR_019618 /// XR_037881 /// XR_038429 /// XR_038579 /// XR_038856
3.26	3.35	0.09	7.22E-01	9.07E-01	---	---	---	225193_at	---
5.65	5.79	0.13	7.22E-01	9.07E-01	JAG1	jagged 1 (Alagille syndrome)	chr20p12.1-p11.23	216268_s_at	NM_000214
2.13	2.20	0.07	7.22E-01	9.07E-01	EFHB	EF-hand domain family, member B	chr3p24.3	239477_at	NM_144715
2.13	2.17	0.04	7.22E-01	9.07E-01	LOC283403	hypothetical protein LOC283403	chr12q13.13	1560276_at	---
2.92	3.01	0.08	7.22E-01	9.07E-01	---	---	---	244049_at	---
2.50	2.55	0.05	7.22E-01	9.07E-01	GLP1R	glucagon-like peptide 1 receptor	chr6p21	208400_at	NM_002062
2.96	3.03	0.07	7.22E-01	9.08E-01	ZNF789	zinc finger protein 789	chr7q22.1	1558762_a_at	NM_001013258 /// NM_213603
3.78	3.95	0.17	7.22E-01	9.08E-01	---	---	---	1557543_at	---
2.41	2.47	0.07	7.22E-01	9.08E-01	---	---	---	1556385_at	---

2.56	2.62	0.06	7.22E-01	9.08E-01	C8A	complement component 8, alpha polypeptide	chr1p32	206305_s_at	NM_000562																				
5.17	5.31	0.15	7.22E-01	9.08E-01	MRPL19	mitochondrial ribosomal protein L19	chr2q11.1-q11.2	203465_at	NM_014763																				
4.37	4.47	0.10	7.22E-01	9.08E-01	TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	chr1q23.3	226059_at	NM_032174																				
2.03	2.08	0.06	7.22E-01	9.08E-01	---	---	---	233162_at	---																				
2.07	2.12	0.05	7.22E-01	9.08E-01	---	---	---	1561417_x_at	---																				
2.03	2.07	0.04	7.22E-01	9.08E-01	CT45-4 /// CT45-6 /// LOC100133581 /// RP13-36C9.1 /// RP13-36C9.3 /// RP13-36C9.6 /// XX-FW88277B6.1	cancer/testis antigen CT45-4 /// cancer/testis antigen CT45-6 /// hypothetical protein LOC100133581 /// cancer/testis antigen CT45 /// cancer/testis antigen CT45-3 /// cancer/testis antigen CT45-5 /// cancer/testis antigen CT45-1	chrXq26.3	1567912_s_at	NM_001007551 /// NM_001017417 /// NM_001017435 /// NM_001017436 /// NM_001017438 /// NM_152582 /// XM_001716002 /// XM_001716054																			
4.80	4.99	0.19	7.22E-01	9.08E-01	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	chr3q13.12	222519_s_at	NM_018010																				
3.32	3.39	0.07	7.22E-01	9.08E-01	---	---	---	239496_at	---																				
4.83	4.89	0.07	7.22E-01	9.08E-01	ABLIM2	actin binding LIM protein family, member 2	chr4p16-p15	236087_at	NM_001130083 /// NM_001130084 /// NM_001130085 /// NM_001130086 /// NM_001130087 /// NM_001130088 /// NM_032432																				
4.02	4.08	0.06	7.22E-01	9.08E-01	KCNK7	potassium channel, subfamily K, member 7	chr11q13	224055_x_at	NM_005714 /// NM_033347 /// NM_033348 /// NM_033455																				
2.58	2.65	0.06	7.22E-01	9.08E-01	---	---	---	1554374_at	---																				
2.78	2.84	0.06	7.23E-01	9.08E-01	PRO1880	PRO1880 protein	chr11q13.1	207743_at	XR_041826 /// XR_041827 /// XR_041828																				
2.25	2.31	0.06	7.22E-01	9.08E-01	SMAD4	SMAD family member 4	chr18q21.1	202526_at	NM_005359																				
3.74	3.79	0.06	7.22E-01	9.08E-01	---	---	---	216631_s_at	---																				
2.03	2.07	0.05	7.23E-01	9.08E-01	---	---	---	1560743_a_at	---																				
1.79	1.83	0.04	7.23E-01	9.08E-01	---	---	---	1562997_a_at	---																				
2.62	2.69	0.07	7.23E-01	9.08E-01	C18orf22	Chromosome 18 open reading frame 22	chr18q23	243001_at	NM_024805																				
3.05	3.11	0.06	7.23E-01	9.08E-01	SMCP	sperm mitochondria-associated cysteine-rich protein	chr1q21.3	206406_at	NM_030663																				
2.46	2.50	0.05	7.23E-01	9.08E-01	---	---	---	242322_at	---																				
2.02	2.06	0.04	7.23E-01	9.08E-01	---	---	---	215763_at	---																				
6.29	6.37	0.08	7.23E-01	9.08E-01	---	---	---	213675_at	---																				
2.14	2.18	0.05	7.23E-01	9.08E-01	ESRRB	Estrogen-related receptor beta	chr14q24.3	1556156_at	NM_004452																				
2.81	2.91	0.10	7.23E-01	9.08E-01	LOC100129932	hypothetical protein LOC100129932	chr11q21	1556409_a_at	XM_001725148 /// XM_001725210 /// XM_001726277																				
7.79	7.92	0.13	7.23E-01	9.08E-01	SBDS /// SBDSP	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	chr7q11.21 /// chr7q11.23	222669_s_at	NM_016038 /// NR_001588 /// NR_024109 /// NR_024110 /// NR_024111																				
4.66	4.75	0.09	7.23E-01	9.08E-01	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	chr2q31	1567014_s_at	NM_006164																				
3.30	3.36	0.07	7.23E-01	9.08E-01	---	---	---	230812_at	---																				
2.31	2.35	0.04	7.23E-01	9.08E-01	TTTY9A /// TTTY9B	testis-specific transcript, Y-linked 9A /// testis-specific transcript, Y-linked 9B	chrYq11.221 /// chrYq11.222	211460_at	NR_001530 /// NR_002159																				
4.09	4.19	0.10	7.23E-01	9.08E-01	LRTM2	leucine-rich repeats and transmembrane domains 2	chr12p13.33	1558530_at	NM_001039029																				
2.09	2.14	0.04	7.23E-01	9.08E-01	NPAS3	neuronal PAS domain protein 3	chr14q12-q13	222172_at	NM_022123 /// NM_173159																				
2.03	2.07	0.04	7.23E-01	9.08E-01	ATXN3L	ataxin 3-like	chrXp22.2	216539_at	NR_003585																				

2.23	2.27	0.04	7.23E-01	9.08E-01	NT5DC4	5'-nucleotidase domain containing 4	chr2q13	1562020_s_at	XM_001715677 /// XM_001716359 /// XM_001716541																				
2.47	2.53	0.05	7.23E-01	9.08E-01	TSPY1	testis specific protein, Y-linked 1	chrYp11.2	217160_at	NM_003308																				
5.85	6.05	0.20	7.23E-01	9.08E-01	LOC100134440 /// PGBD5	similar to PGBD5 protein /// piggyBac transposable element derived 5	chr1q42.13	219225_at	NM_024554 /// XM_001716103																				
2.00	2.05	0.05	7.23E-01	9.08E-01	PCDH20	Protocadherin 20	chr13q21	1560566_at	NM_022843																				
5.09	5.18	0.10	7.23E-01	9.08E-01	B3GALT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	chr1p36.33	225733_at	NM_080605																				
2.43	2.51	0.07	7.23E-01	9.08E-01	SERP2	Stress-associated endoplasmic reticulum protein family member 2	chr13q14.11	239889_at	NM_001010897																				
2.62	2.66	0.05	7.23E-01	9.08E-01	---	---	---	1563553_at	---																				
2.05	2.11	0.06	7.23E-01	9.08E-01	TMOD2	tropomodulin 2 (neuronal)	chr15q21.1-q21.2	219701_at	NM_014548																				
2.57	2.65	0.08	7.23E-01	9.08E-01	HELLS	helicase, lymphoid-specific	chr10q24.2	220085_at	NM_018063																				
1.92	1.97	0.04	7.23E-01	9.08E-01	C1orf62	chromosome 1 open reading frame 62	chr1p13.3	1563834_a_at	NM_152763																				
1.91	1.94	0.03	7.23E-01	9.08E-01	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	chr1p36.21	1564635_a_at	NM_052929 /// XM_001714211 /// XM_934889 /// XM_946265																				
5.24	5.52	0.28	7.24E-01	9.08E-01	---	---	---	232541_at	---																				
10.15	10.24	0.09	7.24E-01	9.08E-01	RBP1	retinol binding protein 1, cellular	chr3q23	203423_at	NM_001130992 /// NM_001130993 /// NM_002899																				
7.49	7.58	0.09	7.24E-01	9.08E-01	VEZF1	vascular endothelial zinc finger 1	chr17q22	202172_at	NM_007146																				
1.81	1.85	0.04	7.24E-01	9.08E-01	---	---	---	1561653_at	---																				
2.09	2.12	0.04	7.24E-01	9.08E-01	HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	chrXq24	211479_s_at	NM_000868																				
2.61	2.66	0.05	7.24E-01	9.08E-01	KRT5	keratin 5	chr12q12-q13	201820_at	NM_000424																				
5.88	5.97	0.10	7.24E-01	9.08E-01	YIPF6	Yip1 domain family, member 6	chrXq12	212343_at	NM_173834																				
3.31	3.38	0.07	7.24E-01	9.08E-01	CDC42BPG	CDC42 binding protein kinase gamma (DMPK-like)	chr11q13.1	1569044_at	NM_017525																				
2.31	2.37	0.06	7.24E-01	9.08E-01	---	---	---	1562895_at	---																				
3.14	3.19	0.06	7.24E-01	9.08E-01	LOC339539	hypothetical protein LOC339539	chr1p34.2	1562496_at	---																				
2.23	2.27	0.04	7.24E-01	9.08E-01	---	---	---	222341_x_at	---																				
5.05	5.13	0.07	7.24E-01	9.08E-01	ZFP161	zinc finger protein 161 homolog (mouse)	chr18pter-p11.2	209724_s_at	NM_003409																				
2.73	2.79	0.06	7.24E-01	9.08E-01	KY	kyphoscoliosis peptidase	chr3q22.2	1556411_s_at	NM_178554																				
2.29	2.33	0.05	7.24E-01	9.08E-01	---	---	---	242570_at	---																				
1.96	2.02	0.06	7.24E-01	9.09E-01	C14orf106	chromosome 14 open reading frame 106	chr14q21.3	244173_at	NM_018353																				
2.04	2.09	0.04	7.24E-01	9.09E-01	---	---	---	237259_at	---																				
2.69	2.73	0.04	7.24E-01	9.09E-01	---	---	---	239880_at	---																				
1.92	1.96	0.04	7.24E-01	9.09E-01	LOC641515	hypothetical protein LOC641515	chr1q31	1570023_at	XR_041508 /// XR_041509 /// XR_041510																				
3.75	3.82	0.08	7.24E-01	9.09E-01	FGF4	fibroblast growth factor 4	chr11q13.3	206783_at	NM_002007																				
4.82	4.99	0.17	7.25E-01	9.09E-01	HSPA13	heat shock protein 70kDa family, member 13	chr21q11.1|21q11	202558_s_at	NM_006948																				
2.87	2.95	0.08	7.25E-01	9.09E-01	MTAP	methylthioadenosine phosphorylase	chr9p21	211363_s_at	NM_002451																				
2.64	2.70	0.06	7.25E-01	9.09E-01	LOC203547	Hypothetical protein LOC203547	chrXq28	235237_at	NM_001017980																				
2.28	2.33	0.05	7.25E-01	9.09E-01	---	---	---	237015_at	---																				
3.47	3.55	0.08	7.25E-01	9.09E-01	C20orf135	chromosome 20 open reading frame 135	chr20q13.33	234002_at	NM_080622																				
6.02	6.20	0.18	7.25E-01	9.09E-01	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	chr4q21.1	208840_s_at	NM_012297 /// NM_203504 /// NM_203505																				
3.95	4.00	0.05	7.25E-01	9.09E-01	RASL11B	RAS-like, family 11, member B	chr4q12	234102_at	NM_023940																				
4.68	4.79	0.10	7.25E-01	9.09E-01	KIAA0090	KIAA0090	chr1p36.13	1556186_s_at	NM_015047																				
2.29	2.35	0.06	7.25E-01	9.09E-01	SPATA5L1	spermatogenesis associated 5-like 1	chr15q21.1	215694_at	NM_024063																				
2.63	2.70	0.07	7.25E-01	9.09E-01	ZNF484	zinc finger protein 484	chr9q22.31	214922_at	NM_001007101 /// NM_031486																				
2.19	2.23	0.04	7.25E-01	9.09E-01	MAGEA11	melanoma antigen family A, 11	chrXq28	210503_at	NM_001011544 /// NM_005366																				
5.07	5.18	0.11	7.25E-01	9.09E-01	DNAJC24	DnaJ (Hsp40) homolog, subfamily C, member 24	chr11p13	213853_at	NM_181706																				
2.85	2.96	0.11	7.25E-01	9.09E-01	BST1	bone marrow stromal cell antigen 1	chr4p15	205715_at	NM_004334																				
3.81	3.91	0.10	7.25E-01	9.09E-01	SCARNA2	small Cajal body-specific RNA 2	chr1q13.1	237137_at	NR_003023																				
6.33	6.41	0.09	7.25E-01	9.09E-01	MRPL35	mitochondrial ribosomal protein L35	chr2p11.2	218890_x_at	NM_016622 /// NM_145644																				
2.80	2.86	0.06	7.25E-01	9.09E-01	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	chr8p22-p21	211163_s_at	NM_003841																				
3.67	3.79	0.12	7.25E-01	9.09E-01	GPBP1L1	GC-rich promoter binding protein 1-like 1	chr1p34.1	1569320_at	NM_021639																				

2.17	2.22	0.06	7.25E-01	9.09E-01	DDAH1	dimethylarginine dimethylaminohydrolase 1	chr1p22	243711_at	NM_001134445 /// NM_012137
2.16	2.20	0.04	7.25E-01	9.09E-01	---	---	---	241590_at	---
5.33	5.44	0.11	7.25E-01	9.09E-01	VEZT	vezatin, adherens junctions transmembrane protein	chr12q22	223675_s_at	NM_017599
3.44	3.49	0.05	7.26E-01	9.09E-01	---	---	---	1569276_at	---
1.91	1.96	0.04	7.26E-01	9.09E-01	---	---	---	240073_at	---
4.22	4.32	0.10	7.26E-01	9.09E-01	BCL2L1	BCL2-like 1	chr20q11.21	206665_s_at	NM_001191 /// NM_138578
2.32	2.41	0.08	7.26E-01	9.09E-01	EFCAB1	EF-hand calcium binding domain 1	chr8q11.21	1568930_at	NM_024593
4.19	4.26	0.08	7.26E-01	9.09E-01	AMPD3	adenosine monophosphate deaminase (isoform E)	chr11p15	209491_s_at	NM_000480 /// NM_001025389 /// NM_001025390
2.28	2.36	0.07	7.26E-01	9.09E-01	---	---	---	231227_at	---
3.18	3.27	0.09	7.26E-01	9.09E-01	EXT1	exostoses (multiple) 1	chr8q24.11-q24.13	230183_at	NM_000127
3.18	3.25	0.07	7.26E-01	9.09E-01	HTR1A	5-hydroxytryptamine (serotonin) receptor 1A	chr5q11.2-q13	221351_at	NM_000524
2.62	2.67	0.06	7.26E-01	9.09E-01	SNTB2	Syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	chr16q22-q23	214350_at	NM_006750
2.14	2.19	0.05	7.26E-01	9.09E-01	---	---	---	1569641_at	---
3.63	3.71	0.08	7.26E-01	9.09E-01	---	---	---	236282_at	---
4.74	4.81	0.06	7.26E-01	9.09E-01	LDLR	low density lipoprotein receptor	chr19p13.3	217183_at	NM_000527
2.97	3.02	0.05	7.26E-01	9.09E-01	---	---	---	1568853_at	---
4.88	5.02	0.14	7.26E-01	9.10E-01	SETD5	SET domain containing 5	chr3p25.3	1569106_s_at	NM_001080517
3.16	3.22	0.06	7.26E-01	9.10E-01	---	---	---	1564620_at	---
1.88	1.91	0.04	7.26E-01	9.10E-01	---	---	---	1563133_at	---
8.28	8.34	0.06	7.26E-01	9.10E-01	GHITM	growth hormone inducible transmembrane protein	chr10q23.1	1554510_s_at	NM_014394
2.07	2.12	0.05	7.26E-01	9.10E-01	---	---	---	244288_s_at	---
2.56	2.62	0.06	7.26E-01	9.10E-01	---	---	---	243718_at	---
5.78	5.86	0.08	7.26E-01	9.10E-01	DLL4	delta-like 4 (Drosophila)	chr15q14	223525_at	NM_019074
2.21	2.26	0.05	7.27E-01	9.10E-01	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	chr3q22.1	1564627_at	NM_015268
3.28	3.34	0.06	7.27E-01	9.10E-01	LOC100133772 /// SLC16A5	similar to MCT /// solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	chr17q25.1	206600_s_at	NM_004695 /// XM_001715145
2.70	2.82	0.12	7.27E-01	9.10E-01	NNMT	Nicotinamide N-methyltransferase	chr11q23.1	231559_at	NM_006169
5.88	5.98	0.11	7.27E-01	9.10E-01	---	---	---	212867_at	---
2.59	2.66	0.06	7.27E-01	9.10E-01	ARHGAP1	Rho GTPase activating protein 1	chr11p12-q12	241419_at	NM_004308
3.05	3.11	0.06	7.27E-01	9.10E-01	ZNRD1	zinc ribbon domain containing 1	chr6p21.3	227673_at	NM_014596 /// NM_170783
6.34	6.40	0.06	7.27E-01	9.10E-01	SNX9	sorting nexin 9	chr6q25.1-q26	223027_at	NM_016224
2.79	2.85	0.06	7.27E-01	9.10E-01	NUP160	nucleoporin 160kDa	chr11p11.2	214963_at	NM_015231
2.15	2.20	0.05	7.27E-01	9.10E-01	FLJ37201	hypothetical protein FLJ37201	chr10q23.31	1560654_at	XR_041091 /// XR_041092 /// XR_041093
2.48	2.52	0.04	7.27E-01	9.10E-01	GAL	galanin prepropeptide	chr11q13.2	207466_at	NM_015973
3.27	3.33	0.06	7.27E-01	9.10E-01	KIAA1394	KIAA1394 protein	chr11q13.1	228984_at	NM_020811
3.32	3.39	0.08	7.27E-01	9.10E-01	LOC440900	hypothetical LOC440900	chr2q14.1	230796_at	XR_041709 /// XR_041710 /// XR_041711
2.43	2.49	0.06	7.27E-01	9.10E-01	---	---	---	240190_at	---
2.12	2.18	0.06	7.27E-01	9.10E-01	---	---	---	237169_at	---
2.70	2.76	0.06	7.27E-01	9.10E-01	---	---	---	1570171_at	---
3.26	3.30	0.05	7.27E-01	9.10E-01	C6orf54	chromosome 6 open reading frame 54	chr6q27	211350_s_at	NM_014354
5.09	5.20	0.11	7.27E-01	9.10E-01	---	---	---	228120_at	---
2.21	2.26	0.05	7.27E-01	9.10E-01	CPNE4	copine IV	chr3q22.1	228796_at	NM_130808
2.28	2.39	0.12	7.27E-01	9.10E-01	PDE5A	phosphodiesterase 5A, cGMP-specific	chr4q25-q27	206757_at	NM_001083 /// NM_033430 /// NM_033437
3.41	3.49	0.08	7.28E-01	9.10E-01	SLC35F1	solute carrier family 35, member F1	chr6q22.2-q22.31	228060_at	NM_001029858
3.27	3.33	0.06	7.28E-01	9.10E-01	ZBTB46	Zinc finger and BTB domain containing 46	chr20q13.33	243214_at	NM_025224
2.62	2.67	0.05	7.28E-01	9.10E-01	LOC145474	hypothetical protein LOC145474	chr14q24.1	230505_at	---
2.25	2.29	0.04	7.27E-01	9.10E-01	---	---	---	229314_at	---
3.63	3.71	0.09	7.28E-01	9.10E-01	TMCC3	transmembrane and coiled-coil domain family 3	chr12q22	226489_at	NM_020698
2.33	2.36	0.04	7.28E-01	9.10E-01	SNX25	sorting nexin 25	chr4q35.1	230066_at	NM_031953
2.18	2.22	0.05	7.28E-01	9.10E-01	---	---	---	1564721_at	---
8.13	8.26	0.13	7.28E-01	9.10E-01	GNG12	guanine nucleotide binding protein (G protein), gamma 12	chr1p31.3	212294_at	NM_018841
1.99	2.03	0.04	7.28E-01	9.10E-01	---	---	---	216613_at	---
2.46	2.50	0.04	7.28E-01	9.10E-01	---	---	---	234347_s_at	---
10.71	10.82	0.11	7.28E-01	9.10E-01	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	chr5q32	209619_at	NM_001025158 /// NM_001025159 /// NM_004355

2.83	2.89	0.06	7.28E-01	9.10E-01	---	---	---	230515_at	---
2.14	2.19	0.06	7.28E-01	9.10E-01	---	---	---	1566898_at	---
2.60	2.65	0.05	7.28E-01	9.10E-01	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	chr9q22.33	211347_at	NM_001077181 /// NM_003671 /// NM_033331
2.68	2.73	0.05	7.28E-01	9.10E-01	LARP2	La ribonucleoprotein domain family, member 2	chr4q28.2	1554038_at	NM_018078 /// NM_032239 /// NM_178043
2.33	2.39	0.05	7.28E-01	9.10E-01	IGSF9B	immunoglobulin superfamily, member 9B	chr11q25	215166_at	NM_014987
4.16	4.33	0.17	7.28E-01	9.10E-01	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	chr1q44	235603_at	NM_004501 /// NM_031844
6.95	7.04	0.09	7.28E-01	9.10E-01	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	chr1p31.3	225475_at	NM_001077700 /// NM_001077701 /// NM_001077702 /// NM_001077703 /// NM_001077704 /// NM_020948
5.33	5.41	0.08	7.28E-01	9.10E-01	CC2D1A	coiled-coil and C2 domain containing 1A	chr19p13.12	221888_at	NM_017721
2.85	2.92	0.06	7.28E-01	9.10E-01	ELOVL3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	chr10q24.32	234513_at	NM_152310
2.28	2.34	0.06	7.28E-01	9.10E-01	---	---	---	231282_at	---
3.00	3.06	0.06	7.28E-01	9.10E-01	---	---	---	242213_at	---
2.94	3.00	0.06	7.28E-01	9.11E-01	STEAP3	STEAP family member 3	chr2q14.2	1554830_a_at	NM_001008410 /// NM_018234 /// NM_182915
2.87	2.94	0.07	7.29E-01	9.11E-01	CN5H6.4	hypothetical protein LOC150384	chr22q13.31	1556661_at	NR_024009 /// XM_001719125 /// XM_001724897 /// XM_001725965
8.88	8.93	0.05	7.29E-01	9.11E-01	EIF3I	eukaryotic translation initiation factor 3, subunit I	chr1p34.1	208756_at	NM_003757
7.96	8.02	0.06	7.29E-01	9.11E-01	C11orf73	chromosome 11 open reading frame 73	chr11q14.2	230326_s_at	NM_016401
7.53	7.73	0.21	7.29E-01	9.11E-01	FBLN1	fibulin 1	chr22q13.31	202995_s_at	NM_001996 /// NM_006485 /// NM_006486 /// NM_006487
5.04	5.20	0.16	7.29E-01	9.11E-01	CCBL2	cysteine conjugate-beta lyase 2	chr1p22.2	227748_at	NM_001008661 /// NM_001008662 /// NM_019610
3.20	3.27	0.07	7.29E-01	9.11E-01	KRT16	keratin 16	chr17q12-q21	209800_at	NM_005557
2.78	2.83	0.05	7.29E-01	9.11E-01	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	chr1q32	205724_at	NM_000299 /// NM_001005337
7.15	7.31	0.16	7.29E-01	9.11E-01	FAM35A	family with sequence similarity 35, member A	chr10q23.2	220547_s_at	NM_019054
2.92	2.99	0.07	7.29E-01	9.11E-01	---	---	---	239235_at	---
3.90	3.96	0.06	7.29E-01	9.11E-01	PSPN	persephin	chr19p13.3	221373_x_at	NM_004158
1.82	1.86	0.05	7.29E-01	9.11E-01	---	---	---	1563546_at	---
1.94	1.98	0.04	7.29E-01	9.11E-01	---	---	---	244247_at	---
2.86	2.96	0.10	7.29E-01	9.11E-01	---	---	---	242806_at	---
7.40	7.47	0.07	7.29E-01	9.11E-01	RNF167	ring finger protein 167	chr17p13.2	212047_s_at	NM_015528
5.98	6.10	0.12	7.29E-01	9.11E-01	FHIT	fragile histidine triad gene	chr3p14.2	206492_at	NM_002012
4.08	4.15	0.07	7.29E-01	9.11E-01	COMMD6	COMM domain containing 6	---	240030_at	NM_203495 /// NM_203497
2.57	2.66	0.09	7.29E-01	9.11E-01	KIAA1199	KIAA1199	chr15q24	212942_s_at	NM_018689
7.06	7.14	0.08	7.29E-01	9.11E-01	STX12	syntaxin 12	chr1p35-p34.1	212112_s_at	NM_177424
3.13	3.20	0.07	7.29E-01	9.11E-01	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	chr1p33	211231_x_at	NM_000778
4.93	4.99	0.06	7.29E-01	9.11E-01	PEX7	peroxisomal biogenesis factor 7	chr6q23.3	205420_at	NM_000288
2.37	2.41	0.04	7.29E-01	9.11E-01	LOC100133899	hypothetical protein LOC100133899	---	1562974_at	XM_001720686
3.21	3.27	0.06	7.30E-01	9.11E-01	---	---	---	240345_x_at	---
2.58	2.63	0.05	7.30E-01	9.11E-01	---	---	---	1569911_at	---

2.85	2.88	0.04	7.30E-01	9.11E-01	KCNT1	potassium channel, subfamily T, member 1	chr9q34.3	1569462_x_at	NM_020822 /// XM_001719828 /// XM_001722509 /// XM_001723196
5.92	6.02	0.09	7.30E-01	9.11E-01	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	chr19q13.11	221522_at	NM_032139
4.42	4.51	0.09	7.30E-01	9.11E-01	LRRC8E	leucine rich repeat containing 8 family, member E	chr19p13.2	220174_at	NM_025061
3.05	3.11	0.06	7.30E-01	9.11E-01	---	---	---	243699_at	---
3.68	3.74	0.05	7.30E-01	9.11E-01	APOB48R	apolipoprotein B48 receptor	chr16p11	220023_at	NM_018690
3.50	3.56	0.07	7.30E-01	9.11E-01	ITSN1	intersectin 1 (SH3 domain protein)	chr21q22.1-q22.2	209298_s_at	NM_001001132 /// NM_003024
2.22	2.27	0.05	7.30E-01	9.11E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	217056_at	---
2.09	2.13	0.04	7.30E-01	9.11E-01	CAPN9	calpain 9	chr1q42.11-q42.3	210641_at	NM_006615 /// NM_016452
4.32	4.40	0.08	7.30E-01	9.11E-01	INTS7	integrator complex subunit 7	chr1p36.13-q42.3	222250_s_at	NM_015434
4.81	4.88	0.08	7.30E-01	9.11E-01	H2AFY	H2A histone family, member Y	chr5q31.3-q32	226840_at	NM_001040158 /// NM_004893 /// NM_138609 /// NM_138610
2.60	2.67	0.07	7.30E-01	9.11E-01	CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	chr3p26.1	204591_at	NM_006614
2.35	2.41	0.06	7.30E-01	9.11E-01	NELL1	NEL-like 1 (chicken)	chr11p15.2-p15.1	1554394_at	NM_006157
3.12	3.18	0.06	7.30E-01	9.11E-01	TBC1D27	TBC1 domain family, member 27	chr17p11.2	233483_at	XR_040581 /// XR_040582 /// XR_040583
3.43	3.49	0.06	7.30E-01	9.11E-01	---	---	---	201205_at	---
2.47	2.52	0.06	7.30E-01	9.11E-01	MYO5A	myosin VA (heavy chain 12, myoxin)	chr15q21	217409_at	NM_000259
2.75	2.80	0.05	7.30E-01	9.11E-01	---	---	---	216170_at	---
3.31	3.36	0.05	7.30E-01	9.11E-01	---	---	---	237082_at	---
2.14	2.19	0.05	7.30E-01	9.11E-01	---	---	---	1566222_at	---
4.75	4.79	0.05	7.30E-01	9.11E-01	PHF21A	PHD finger protein 21A	chr11p11.2	227090_at	NM_001101802 /// NM_016621
2.50	2.54	0.05	7.30E-01	9.11E-01	ELF5	E74-like factor 5 (ets domain transcription factor)	chr11p13-p12	220624_s_at	NM_001422 /// NM_198381
2.59	2.63	0.05	7.30E-01	9.11E-01	SNX13	sorting nexin 13	chr7p21.1	215366_at	NM_015132
2.89	2.94	0.05	7.30E-01	9.11E-01	MGC33556	Hypothetical LOC339541	chr1p34.1	238367_s_at	XR_039961 /// XR_039962 /// XR_039963
2.49	2.53	0.04	7.30E-01	9.11E-01	SCAND3	SCAN domain containing 3	chr6p22.1	244758_at	NM_052923
2.34	2.38	0.04	7.30E-01	9.11E-01	RABL4	RAB, member of RAS oncogene family-like 4	chr22q13.1	243812_at	NM_006860
8.00	8.16	0.16	7.30E-01	9.11E-01	CPNE3	copine III	chr8q21.3	202119_s_at	NM_003909
2.65	2.74	0.09	7.30E-01	9.11E-01	---	---	---	235385_at	---
3.00	3.05	0.05	7.30E-01	9.11E-01	TGFA	transforming growth factor, alpha	chr2p13	205015_s_at	NM_001099691 /// NM_003236
7.42	7.58	0.16	7.30E-01	9.11E-01	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	chr8p11.23	202381_at	NM_001005845 /// NM_003816
6.26	6.34	0.08	7.30E-01	9.11E-01	IVD	isovaleryl Coenzyme A dehydrogenase	chr15q14-q15	203682_s_at	NM_002225
6.38	6.54	0.15	7.31E-01	9.11E-01	SLC25A46	solute carrier family 25, member 46	chr5q22.1	212833_at	NM_138773
4.48	4.60	0.12	7.31E-01	9.11E-01	---	---	---	227539_at	---
2.31	2.37	0.06	7.31E-01	9.11E-01	RGS10	Regulator of G-protein signaling 10	chr10q25	214000_s_at	NM_001005339 /// NM_002925
1.93	1.98	0.05	7.31E-01	9.11E-01	---	---	---	243028_x_at	---
2.85	2.89	0.04	7.31E-01	9.11E-01	RTDR1	rhabdoid tumor deletion region gene 1	chr22q11.2	220105_at	NM_014433
3.22	3.25	0.04	7.31E-01	9.11E-01	ASCC3L1	activating signal cointegrator 1 complex subunit 3-like 1	chr2q11.2	232931_at	NM_014014
5.95	6.12	0.17	7.31E-01	9.11E-01	KLHL8	kelch-like 8 (Drosophila)	chr4q22.1	226874_at	NM_020803
2.36	2.46	0.11	7.31E-01	9.11E-01	---	---	---	1557459_at	---
7.72	7.80	0.08	7.31E-01	9.11E-01	TMEM189-UBE2V1 /// UBE2V1	TMEM189-UBE2V1 /// ubiquitin-conjugating enzyme E2 variant 1	chr20q13.2	201002_s_at	NM_001032288 /// NM_003349 /// NM_021988 /// NM_022442 /// NM_199144 /// NM_199203
4.08	4.15	0.07	7.31E-01	9.11E-01	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	chr14q31	217710_x_at	NM_014216
3.52	3.59	0.07	7.31E-01	9.11E-01	NKAPL	NFKB activating protein-like	chr6p22.1	229340_at	NM_001007531
2.34	2.40	0.06	7.31E-01	9.11E-01	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	chr4q28.1	205515_at	NM_003619
2.48	2.54	0.06	7.31E-01	9.11E-01	UBASH3B	ubiquitin associated and SH3 domain containing, B	chr11q24.1	228359_at	NM_032873

1.89	1.93	0.04	7.31E-01	9.11E-01	PCDHB3	protocadherin beta 3	chr5q31	244183_x_at	NM_018937
2.27	2.32	0.05	7.31E-01	9.11E-01	GCG	glucagon	chr2q36-q37	206422_at	NM_002054
2.10	2.15	0.05	7.31E-01	9.12E-01	---	---	---	1569344_a_at	---
1.86	1.90	0.05	7.31E-01	9.12E-01	LOC100127980	Hypothetical protein LOC100127980	chr19q13.12	1557044_at	XM_001720119 /// XM_001722650
2.23	2.27	0.04	7.31E-01	9.12E-01	---	---	---	234190_at	---
2.05	2.11	0.06	7.31E-01	9.12E-01	EBF3	early B-cell factor 3	chr10q26.3	227242_s_at	NM_001005463
3.64	3.68	0.04	7.31E-01	9.12E-01	---	---	---	234557_at	---
2.57	2.63	0.06	7.32E-01	9.12E-01	GNLY	granulysin	chr2p11.2	37145_at	NM_006433 /// NM_012483
2.71	2.76	0.05	7.32E-01	9.12E-01	C18orf19	chromosome 18 open reading frame 19	chr18p11.21	242149_at	NM_001098801 /// NM_152352
3.66	3.85	0.19	7.32E-01	9.12E-01	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	chr2q32.1	221781_s_at	NM_018981
2.36	2.41	0.06	7.32E-01	9.12E-01	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	chr6p12.2	1553003_at	NM_138694 /// NM_170724
2.88	2.93	0.06	7.32E-01	9.12E-01	GUCY1A2	guanylate cyclase 1, soluble, alpha 2	chr11q21-q22	206927_s_at	NM_000855
3.81	3.86	0.06	7.32E-01	9.12E-01	---	---	---	243314_at	---
3.30	3.35	0.05	7.32E-01	9.12E-01	TRPV2	transient receptor potential cation channel, subfamily V, member 2	chr17p11.2	222855_s_at	NM_016113
4.97	5.02	0.05	7.32E-01	9.12E-01	---	---	---	217664_at	---
5.23	5.37	0.14	7.32E-01	9.12E-01	STARD13	StAR-related lipid transfer (START) domain containing 13	chr13q12-q13	213103_at	NM_052851 /// NM_178006 /// NM_178007
7.57	7.68	0.12	7.32E-01	9.12E-01	ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	chrXp11.4	201444_s_at	NM_005765
5.80	5.91	0.11	7.32E-01	9.12E-01	RBM39	RNA binding motif protein 39	chr20q11.22	227223_at	NM_004902 /// NM_184234
6.34	6.45	0.11	7.32E-01	9.12E-01	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	chr3p21.3	202797_at	NM_014016
3.13	3.22	0.08	7.32E-01	9.12E-01	RIC3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	chr11p15.4	220282_at	NM_024557
7.56	7.63	0.07	7.32E-01	9.12E-01	WNK1	WNK lysine deficient protein kinase 1	chr12p13.3	211994_at	NM_018979
2.64	2.71	0.07	7.32E-01	9.12E-01	MUCL1	mucin-like 1	chr12q	1553602_at	NM_058173
2.27	2.32	0.04	7.32E-01	9.12E-01	---	---	---	237480_at	---
2.01	2.06	0.05	7.32E-01	9.12E-01	---	---	---	1558786_at	---
3.75	3.89	0.15	7.32E-01	9.12E-01	ZNF227	zinc finger protein 227	---	217403_s_at	NM_182490
7.73	7.85	0.12	7.33E-01	9.12E-01	PELO	Pelota homolog (Drosophila)	chr5q11.2	226731_at	NM_015946
9.09	9.17	0.07	7.32E-01	9.12E-01	---	---	---	224597_at	---
4.09	4.15	0.06	7.33E-01	9.12E-01	LOC285033	hypothetical protein LOC285033	chr2q11.2	235584_at	NM_001037228
2.40	2.46	0.05	7.33E-01	9.12E-01	LOC338694	hypothetical protein LOC338694	chr11q13.2	1563042_at	---
2.36	2.41	0.05	7.32E-01	9.12E-01	---	---	---	238502_at	---
2.06	2.11	0.05	7.33E-01	9.12E-01	ZNF321	zinc finger protein 321	chr19q13.41	1558887_at	NM_203307
2.11	2.15	0.04	7.33E-01	9.12E-01	---	---	---	244325_at	---
2.11	2.14	0.04	7.32E-01	9.12E-01	AACSL	acetoacetyl-CoA synthetase-like	chr5q35.3	1570020_at	NR_024035 /// XR_036933 /// XR_037302 /// XR_037666
2.62	2.66	0.04	7.33E-01	9.12E-01	UTF1	undifferentiated embryonic cell transcription factor 1	chr10q26	208275_x_at	NM_003577
4.93	5.03	0.10	7.33E-01	9.12E-01	GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	chr22q11.22	204993_at	NM_002073
2.10	2.15	0.05	7.33E-01	9.12E-01	E2F8	E2F transcription factor 8	chr11p15.1	219990_at	NM_024680
2.13	2.18	0.05	7.33E-01	9.12E-01	GPC5	glypican 5	chr13q32	207174_at	NM_004466
6.63	6.79	0.16	7.33E-01	9.12E-01	N4BP2L2	NEDD4 binding protein 2-like 2	chr13q13.1	202258_s_at	NM_014887 /// NM_033111
8.18	8.27	0.09	7.33E-01	9.12E-01	PHYH	phytanoyl-CoA 2-hydroxylase	chr10p13	203335_at	NM_001037537 /// NM_006214
6.87	6.95	0.08	7.33E-01	9.12E-01	PAK4	p21 protein (Cdc42/Rac)-activated kinase 4	chr19q13.2	33814_at	NM_001014831 /// NM_001014832 /// NM_001014834 /// NM_001014835 /// NM_005884
2.47	2.53	0.06	7.33E-01	9.12E-01	---	---	---	1566884_at	---
1.99	2.03	0.04	7.33E-01	9.12E-01	---	---	---	241482_at	---
2.38	2.42	0.04	7.33E-01	9.12E-01	---	---	---	1562296_at	---
2.03	2.07	0.04	7.33E-01	9.12E-01	LOC400590	hypothetical LOC400590	chr17q11.2	1560994_x_at	XR_042032 /// XR_042033 /// XR_042034
3.32	3.46	0.14	7.34E-01	9.13E-01	TMF1	TATA element modulatory factor 1	chr3p21-p12	213024_at	NM_007114
4.86	4.99	0.13	7.34E-01	9.13E-01	TMEM77	transmembrane protein 77	chr1p13.3	225228_at	NM_178454

3.18	3.25	0.07	7.34E-01	9.13E-01	GDF9	growth differentiation factor 9	chr5q31.1	221314_at	NM_005260
3.49	3.55	0.06	7.34E-01	9.13E-01	ZNF621	zinc finger protein 621	chr3p22.1	230164_at	NM_001098414 /// NM_198484
2.17	2.22	0.05	7.34E-01	9.13E-01	CHL1	Cell adhesion molecule with homology to L1CAM (close homolog of L1)	chr3p26.1	234583_at	NM_006614
2.40	2.44	0.04	7.34E-01	9.13E-01	C8orf83	chromosome 8 open reading frame 83	chr8q22.1	1562066_at	NR_015339 /// XR_041349 /// XR_041350 /// XR_041351
4.75	4.83	0.08	7.34E-01	9.13E-01	WDR5B	WD repeat domain 5B	chr3q21.1	219538_at	NM_019069
2.23	2.27	0.05	7.34E-01	9.13E-01	KIAA1622	KIAA1622	chr14q32.13	220673_s_at	NM_020958 /// NM_058237
2.36	2.40	0.04	7.34E-01	9.13E-01	ZNF471	zinc finger protein 471	chr19q13.43	232117_at	NM_020813
2.49	2.54	0.05	7.34E-01	9.13E-01	TRIM14	tripartite motif-containing 14	chr9q22.33	231934_at	NM_014788 /// NM_033219 /// NM_033220 /// NM_033221
6.05	6.24	0.19	7.34E-01	9.13E-01	---	---	---	229824_at	---
5.72	5.88	0.16	7.34E-01	9.13E-01	SETX	senataxin	chr9q34.13	201964_at	NM_015046
2.27	2.32	0.05	7.34E-01	9.13E-01	---	---	---	232886_at	---
7.18	7.29	0.12	7.34E-01	9.13E-01	SH3D19	SH3 domain containing 19	chr4q31.3	225162_at	NM_001009555 /// NM_001128923 /// NM_001128924
2.48	2.54	0.06	7.35E-01	9.13E-01	G6PC	glucose-6-phosphatase, catalytic subunit	chr17q21	1555612_s_at	NM_000151
6.80	6.86	0.06	7.35E-01	9.13E-01	TFIP11	tuftelin interacting protein 11	chr22q12.1	202750_s_at	NM_001008697 /// NM_012143
2.29	2.34	0.05	7.35E-01	9.13E-01	SALL3	sal-like 3 (Drosophila)	chr18q23	1553411_s_at	NM_171999
2.15	2.19	0.05	7.35E-01	9.13E-01	---	---	---	1563591_at	---
3.15	3.22	0.07	7.35E-01	9.13E-01	---	---	---	236417_at	---
5.83	5.90	0.07	7.35E-01	9.14E-01	C8orf73	chromosome 8 open reading frame 73	chr8q24.3	227672_at	NM_001100878
3.62	3.69	0.07	7.35E-01	9.14E-01	DRD2	dopamine receptor D2	chr11q23	216938_x_at	NM_000795 /// NM_016574
2.08	2.13	0.04	7.35E-01	9.14E-01	LOC100128922	connexin	chr1p33	224362_at	XM_001724838 /// XM_001726126 /// XM_001726266
2.15	2.19	0.04	7.35E-01	9.14E-01	---	---	---	243605_at	---
2.61	2.65	0.04	7.35E-01	9.14E-01	CDC2L5	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	chr7p13	214287_s_at	NM_003718 /// NM_031267
3.38	3.41	0.04	7.35E-01	9.14E-01	---	---	---	1564242_at	---
3.48	3.53	0.04	7.35E-01	9.14E-01	PPP1R3D	protein phosphatase 1, regulatory (inhibitor) subunit 3D	chr20q13.3	204555_s_at	NM_006242
4.19	4.26	0.07	7.35E-01	9.14E-01	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	chr21q22.3	1556127_at	NM_015151 /// NM_206889 /// NM_206890 /// NM_206891
2.19	2.23	0.04	7.35E-01	9.14E-01	IL6R	interleukin 6 receptor	chr1q21	217489_s_at	NM_000565 /// NM_181359
2.66	2.76	0.10	7.35E-01	9.14E-01	SOS2	son of sevenless homolog 2 (Drosophila)	chr14q21	217644_s_at	NM_006939
5.44	5.53	0.09	7.35E-01	9.14E-01	LTBP4	latent transforming growth factor beta binding protein 4	chr19q13.1-q13.2	204442_x_at	NM_001042544 /// NM_001042545 /// NM_003573
2.98	3.04	0.06	7.35E-01	9.14E-01	TM4SF4	transmembrane 4 L six family member 4	chr3q25	209937_at	NM_004617
4.05	4.20	0.15	7.36E-01	9.14E-01	ATF2	activating transcription factor 2	chr2q32	205446_s_at	NM_001880
5.09	5.18	0.08	7.36E-01	9.14E-01	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	chr7q36	203029_s_at	NM_002847 /// NM_130842 /// NM_130843
1.85	1.89	0.03	7.36E-01	9.14E-01	F11	coagulation factor XI	chr4q35	1569592_a_at	NM_000128
1.93	1.96	0.03	7.36E-01	9.14E-01	HIST1H2BA	histone cluster 1, H2ba	chr6p22.2	241519_at	NM_170610
5.92	5.99	0.07	7.36E-01	9.14E-01	ZNF553	zinc finger protein 553	chr16p11.2	227470_at	NM_152652
2.10	2.14	0.04	7.36E-01	9.14E-01	---	---	---	217386_at	---
2.97	3.03	0.06	7.36E-01	9.14E-01	ZFYVE16	zinc finger, FYVE domain containing 16	chr5q14	240859_at	NM_001105251 /// NM_014733
7.41	7.56	0.14	7.36E-01	9.14E-01	CDC42SE2	CDC42 small effector 2	chr5q31.1	224709_s_at	NM_001038702 /// NM_020240
2.56	2.61	0.05	7.36E-01	9.14E-01	---	---	---	234653_at	---

2.66	2.77	0.11	7.36E-01	9.14E-01	DPYSL3	dihydropyrimidinase-like 3	chr5q32	201430_s_at	NM_001387
2.70	2.76	0.06	7.36E-01	9.14E-01	---	---	---	234345_at	---
2.82	2.87	0.05	7.36E-01	9.14E-01	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	chr15q22.31	228252_at	NM_025049
4.08	4.22	0.15	7.36E-01	9.14E-01	SLC2A14 /// SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 14 /// solute carrier family 2 (facilitated glucose transporter), member 3	chr12p13.3 /// chr12p13.31	222088_s_at	NM_006931 /// NM_153449
6.85	6.95	0.10	7.36E-01	9.14E-01	GPBP1L1	GC-rich promoter binding protein 1-like 1	chr1p34.1	222452_s_at	NM_021639
4.61	4.67	0.06	7.36E-01	9.14E-01	PPIL2	Peptidylprolyl isomerase (cyclophilin)-like 2	chr22q11.21	243414_at	NM_014337 /// NM_148175 /// NM_148176
2.49	2.54	0.05	7.36E-01	9.14E-01	LOC154822	hypothetical LOC154822	chr7q36.3	237471_at	---
3.21	3.26	0.06	7.37E-01	9.14E-01	KIF25	kinesin family member 25	chr6q27	207682_s_at	NM_005355 /// NM_030615
3.50	3.57	0.06	7.37E-01	9.14E-01	VSX1	visual system homeobox 1	chr20p11.23-p11.22	221124_s_at	NM_014588 /// NM_199425
5.06	5.35	0.28	7.37E-01	9.14E-01	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	chr16q13-q22.1	209616_s_at	NM_001025194 /// NM_001025195 /// NM_001266
2.86	2.92	0.06	7.37E-01	9.14E-01	---	---	---	231254_at	---
1.83	1.86	0.04	7.37E-01	9.14E-01	BMPER	BMP binding endothelial regulator	chr7p14.3	241986_at	NM_133468
6.12	6.20	0.08	7.37E-01	9.15E-01	TNRC6B	trinucleotide repeat containing 6B	chr22q13.1	1558142_at	NM_001024843 /// NM_015088
5.90	5.97	0.07	7.37E-01	9.15E-01	JRK	jerky homolog (mouse)	chr8q24.3	214692_s_at	NM_001077527 /// NM_003724
3.00	3.06	0.05	7.37E-01	9.15E-01	---	---	---	238726_at	---
2.55	2.59	0.05	7.37E-01	9.15E-01	LOC730631	Hypothetical LOC730631	chr1q21.2	231027_at	XM_001715137 /// XM_001720519 /// XM_001723714
2.55	2.58	0.04	7.37E-01	9.15E-01	MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	chr22q13.33	213395_at	NM_015166 /// NM_139202
3.54	3.66	0.11	7.37E-01	9.15E-01	NUP133	nucleoporin 133kDa	chr1q42.13	233421_s_at	NM_018230
3.61	3.76	0.16	7.37E-01	9.15E-01	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	chr20q13.13	215931_s_at	NM_006420
3.35	3.42	0.07	7.37E-01	9.15E-01	KIAA1704	KIAA1704	chr13q13-q14	229078_s_at	NM_018559
2.70	2.75	0.06	7.37E-01	9.15E-01	---	---	---	241526_at	---
2.29	2.34	0.05	7.37E-01	9.15E-01	NAV2	neuron navigator 2	chr11p15.1	1567358_at	NM_001111018 /// NM_001111019 /// NM_145117 /// NM_182964
2.21	2.26	0.05	7.37E-01	9.15E-01	PCA3	prostate cancer antigen 3 (non-protein coding)	chr9q21-q22	232575_at	NR_015342
3.33	3.41	0.08	7.38E-01	9.15E-01	AZI2	5-azacytidine induced 2	chr3p24.1	227904_at	NM_001134432 /// NM_001134433 /// NM_022461
2.23	2.28	0.06	7.38E-01	9.15E-01	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	chr19p13.12	1554592_a_at	NM_005071
2.41	2.45	0.05	7.38E-01	9.15E-01	HKDC1	hexokinase domain containing 1	chr10q21.3	227614_at	NM_025130
5.30	5.46	0.15	7.38E-01	9.15E-01	EHD3	EH-domain containing 3	chr2p21	218935_at	NM_014600
6.44	6.58	0.15	7.38E-01	9.15E-01	RHOBTB3	Rho-related BTB domain containing 3	chr5q15	216048_s_at	NM_014899
5.64	5.76	0.12	7.38E-01	9.15E-01	KBTBD11	kelch repeat and BTB (POZ) domain containing 11	chr8p23.3	204301_at	NM_014867
4.50	4.61	0.11	7.38E-01	9.15E-01	---	---	---	214896_at	---
3.78	3.84	0.06	7.38E-01	9.15E-01	---	---	---	1561546_at	---
3.84	3.98	0.13	7.38E-01	9.15E-01	ADRBK2	adrenergic, beta, receptor kinase 2	chr22q11|22q12.1	228771_at	NM_005160
2.32	2.37	0.05	7.38E-01	9.15E-01	PDE3B	phosphodiesterase 3B, cGMP-inhibited	chr11p15.1	214582_at	NM_000922
2.40	2.47	0.07	7.38E-01	9.15E-01	DOCK9	dedicator of cytokinesis 9	chr13q32.3	215237_at	NM_001130048 /// NM_001130049 /// NM_001130050 /// NM_015296
2.55	2.61	0.07	7.38E-01	9.15E-01	ZNF496	zinc finger protein 496	chr1q44	1557616_at	NM_032752
1.97	2.02	0.05	7.38E-01	9.15E-01	---	---	---	240137_at	---
2.32	2.36	0.04	7.38E-01	9.15E-01	---	---	---	230336_at	---
4.57	4.78	0.21	7.38E-01	9.15E-01	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	chr2q14.1	205763_s_at	NM_006773
2.44	2.52	0.08	7.38E-01	9.15E-01	FLJ35700	hypothetical protein FLJ35700	chr6q23.2	1559277_at	---
2.41	2.48	0.07	7.38E-01	9.15E-01	CLK4	CDC-like kinase 4	chr5q35	241403_at	NM_020666
2.52	2.59	0.07	7.38E-01	9.15E-01	CCNYL1	cyclin Y-like 1	chr2q33.3	228810_at	NM_152523
2.36	2.42	0.07	7.38E-01	9.15E-01	SH3PXD2A	SH3 and PX domains 2A	chr10q24.33	207661_s_at	NM_014631

2.61	2.67	0.06	7.38E-01	9.15E-01	CXorf31	chromosome X open reading frame 31	chrXp11.3	1563327_a_at	XM_001127244 /// XM_001127284																					
2.39	2.45	0.06	7.38E-01	9.15E-01	KALRN	kalirin, RhoGEF kinase	chr3q21.1-q21.2	205635_at	NM_001024660 /// NM_003947 /// NM_007064																					
3.16	3.22	0.06	7.38E-01	9.15E-01	LOC440366	hect domain and RLD 2 pseudogene	chr16p11.2	216193_at	NR_002828 /// XR_042154																					
2.28	2.33	0.05	7.38E-01	9.15E-01	---	---	---	232826_at	---																					
3.08	3.14	0.05	7.38E-01	9.15E-01	---	---	---	1561497_at	---																					
3.47	3.52	0.05	7.38E-01	9.15E-01	GPRC5B	G protein-coupled receptor, family C, group 5, member B	chr16p12	228313_at	NM_016235																					
2.42	2.47	0.05	7.38E-01	9.15E-01	LOC100131096	hypothetical protein LOC100131096	chr17q25.3	239062_at	XM_001720907 /// XM_001726205 /// XM_001726705																					
2.32	2.36	0.04	7.38E-01	9.15E-01	TRAF3IP2	TRAF3 interacting protein 2	chr6q21	202987_at	NM_147200 /// NM_147686																					
2.91	2.95	0.03	7.38E-01	9.15E-01	---	---	---	232831_at	---																					
6.27	6.45	0.18	7.39E-01	9.15E-01	GFM2	G elongation factor, mitochondrial 2	chr5q13	225392_at	NM_032380 /// NM_170681 /// NM_170691																					
5.32	5.42	0.10	7.39E-01	9.15E-01	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	chr12q12-q13.11	232597_x_at	NM_004719																					
2.85	2.90	0.05	7.39E-01	9.15E-01	---	---	---	230409_at	---																					
2.45	2.50	0.05	7.39E-01	9.15E-01	---	---	---	241524_at	---																					
4.98	5.12	0.14	7.39E-01	9.15E-01	RERG	RAS-like, estrogen-regulated, growth inhibitor	chr12p12.3	244745_at	NM_032918																					
2.70	2.76	0.06	7.39E-01	9.15E-01	GP2	glycoprotein 2 (zymogen granule membrane)	chr16p12	208473_s_at	NM_001007240 /// NM_001007241 /// NM_001007242 /// NM_001502																					
2.73	2.79	0.05	7.39E-01	9.15E-01	---	---	---	235788_at	---																					
2.44	2.49	0.05	7.39E-01	9.15E-01	---	---	---	1561408_at	---																					
1.95	1.98	0.04	7.39E-01	9.15E-01	---	---	---	244295_at	---																					
5.94	6.02	0.08	7.39E-01	9.15E-01	OR7E104P	olfactory receptor, family 7, subfamily E, member 104 pseudogene	chr13q21.31	1566956_at	---																					
2.75	2.80	0.05	7.39E-01	9.15E-01	---	---	---	230578_at	---																					
1.97	2.00	0.04	7.39E-01	9.15E-01	---	---	---	232905_at	---																					
2.99	3.05	0.06	7.39E-01	9.15E-01	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	chr12q24.2|12q24.2	224344_at	NM_004373																					
4.67	4.85	0.18	7.40E-01	9.15E-01	COPA	coatomer protein complex, subunit alpha	chr1q23-q25	214336_s_at	NM_001098398 /// NM_004371																					
4.10	4.26	0.17	7.40E-01	9.15E-01	WBP4	WW domain binding protein 4 (formin binding protein 21)	chr13q14.11	203598_s_at	NM_007187																					
6.58	6.72	0.14	7.40E-01	9.15E-01	PAPOLA	poly(A) polymerase alpha	chr14q32.31	222035_s_at	NM_032632																					
4.68	4.81	0.13	7.40E-01	9.15E-01	TMED5	transmembrane emp24 protein transport domain containing 5	chr1pter-q31.3	202195_s_at	NM_016040																					
6.06	6.17	0.11	7.40E-01	9.15E-01	41340	membrane-associated ring finger (C3HC4) 7	chr2q24.2	202653_s_at	NM_022826																					
5.29	5.40	0.11	7.40E-01	9.15E-01	PLXDC2	plexin domain containing 2	chr10p12.32-p12.31	227276_at	NM_032812																					
5.15	5.25	0.10	7.40E-01	9.15E-01	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	chr8p11.2	224076_s_at	NM_017778 /// NM_023034																					
4.93	4.99	0.06	7.40E-01	9.15E-01	CARD11	caspase recruitment domain family, member 11	chr7p22	223514_at	NM_032415																					
2.34	2.40	0.06	7.40E-01	9.15E-01	AFF2	AF4/FMR2 family, member 2	chrXq28	206105_at	NM_002025																					
3.42	3.47	0.05	7.40E-01	9.15E-01	SEC14L2	SEC14-like 2 (S. cerevisiae)	chr22q12.2	232894_at	NM_012429																					
3.27	3.32	0.05	7.39E-01	9.15E-01	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	chr15q22	210420_at	NM_004727																					
2.40	2.45	0.05	7.40E-01	9.15E-01	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	chr4p16.1	223573_s_at	NM_020416 /// NM_181876																					
2.67	2.72	0.05	7.40E-01	9.15E-01	---	---	---	243566_at	---																					
1.99	2.04	0.05	7.40E-01	9.15E-01	ENTHD1	ENTH domain containing 1	chr22q13.1	1552393_at	NM_152512																					
2.21	2.26	0.05	7.40E-01	9.15E-01	SEZ6L	seizure related 6 homolog (mouse)-like	chr22q12.1	213609_s_at	NM_021115																					
2.12	2.17	0.05	7.39E-01	9.15E-01	---	---	---	1561134_at	---																					
2.69	2.74	0.05	7.40E-01	9.15E-01	---	---	---	1563079_at	---																					
2.73	2.78	0.05	7.39E-01	9.15E-01	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	chr10q21.3	214140_at	NM_152707																					

1.84	1.89	0.05	7.40E-01	9.15E-01	ANKRD20A1 /// ANKRD20A2 /// ANKRD20A3 /// ANKRD20A4 /// ANKRD20B /// CCDC29 /// LOC375010 /// LOC647595 /// LOC728371	ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family, member A2 /// ankyrin repeat domain 20 family, member A3 /// ankyrin repeat domain 20 family, member A4 /// ankyrin repeat domain 20B /// coiled-coil domain containing 29 /// hypothetical LOC375010 /// similar to ankyrin repeat domain 20A /// similar to ankyrin repeat domain 20A	chr1q12 /// chr2q11.1 /// chr4p11 /// chr9p11.2 /// chr9p12-p11.2 /// chr9q12	1570255_s_at	NM_001012419 /// NM_001012421 /// NM_001098805 /// NM_001098806 /// NM_032250 /// NR_003366 /// XR_018156 /// XR_038389 /// XR_041271
2.17	2.22	0.04	7.40E-01	9.15E-01	C21orf58	chromosome 21 open reading frame 58	chr21q22.3	1559439_s_at	NM_058180
2.74	2.78	0.04	7.40E-01	9.15E-01	ZNF398	zinc finger protein 398	chr7q36.1	1555015_a_at	NM_020781 /// NM_170686
1.86	1.90	0.04	7.40E-01	9.15E-01	RUFY2	RUN and FYVE domain containing 2	chr10q21.3	1554133_at	NM_001042417 /// NM_017987
2.01	2.05	0.04	7.40E-01	9.15E-01	---	---	---	242118_x_at	---
2.43	2.47	0.04	7.40E-01	9.15E-01	TYMS	thymidylate synthetase	chr18p11.32	217684_at	NM_001071
5.71	5.83	0.12	7.40E-01	9.15E-01	---	---	---	226280_at	---
2.48	2.53	0.05	7.40E-01	9.15E-01	---	---	---	1561688_at	---
2.07	2.11	0.04	7.40E-01	9.15E-01	MAGEE2	melanoma antigen family E, 2	chrXq13.3	1553254_at	NM_138703
2.75	2.81	0.05	7.40E-01	9.15E-01	---	---	---	237093_at	---
2.57	2.62	0.05	7.40E-01	9.15E-01	MATN1	matrilin 1, cartilage matrix protein	chr1p35	206904_at	NM_002379
2.58	2.65	0.08	7.40E-01	9.15E-01	---	---	---	242845_at	---
2.41	2.47	0.06	7.40E-01	9.15E-01	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	chr12q13.11-q13.3	234708_at	NM_014311
2.10	2.15	0.05	7.40E-01	9.15E-01	ANKRD30A	ankyrin repeat domain 30A	chr10p11.21	223864_at	NM_052997
3.92	3.99	0.08	7.40E-01	9.15E-01	CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21	chr19q13.2	214907_at	NM_001098506 /// NM_033543
2.04	2.08	0.04	7.40E-01	9.15E-01	---	---	---	234170_at	---
7.16	7.28	0.12	7.40E-01	9.15E-01	---	---	---	202603_at	---
2.52	2.55	0.04	7.40E-01	9.15E-01	LEMD1	LEM domain containing 1	chr1q32.1	229927_at	NM_001001552
2.60	2.64	0.05	7.40E-01	9.15E-01	AFF3	AF4/FMR2 family, member 3	chr2q11.2-q12	205734_s_at	NM_001025108 /// NM_002285
9.13	9.23	0.10	7.41E-01	9.16E-01	C7orf28A /// C7orf28B /// LOC100133775	chromosome 7 open reading frame 28A /// chromosome 7 open reading frame 28B /// similar to Chromosome 7 open reading frame 28B	chr7p22.1	201973_s_at	NM_015622 /// NM_198097 /// XM_001719869 /// XM_001719961 /// XM_001720226
7.50	7.60	0.10	7.41E-01	9.16E-01	RPS11	Ribosomal protein S11	chr19q13.3	213350_at	NM_001015
2.88	2.96	0.07	7.41E-01	9.16E-01	---	---	---	215484_at	---
3.18	3.24	0.06	7.41E-01	9.16E-01	---	---	---	238396_at	---
2.26	2.31	0.05	7.41E-01	9.16E-01	COBLL1	COBL-like 1	chr2q24.3	211032_at	NM_014900
2.22	2.26	0.04	7.41E-01	9.16E-01	DCHS2	dachsous 2 (Drosophila)	chr4q32.1	242764_at	NM_017639
2.59	2.66	0.08	7.41E-01	9.16E-01	PALM2	paralemmin 2	chr9q31-q33	1554640_at	NM_001037293 /// NM_053016
11.59	11.67	0.08	7.41E-01	9.16E-01	RPS6	ribosomal protein S6	chr9p21	200081_s_at	NM_001010
5.90	5.96	0.07	7.41E-01	9.16E-01	LOC646044 /// SSBP4	similar to single stranded DNA binding protein 4 /// single stranded DNA binding protein 4	chr18p11.21 /// chr19p13.1	229270_x_at	NM_001009998 /// NM_032627 /// XR_017055 /// XR_018999 /// XR_037328
2.99	3.03	0.04	7.41E-01	9.16E-01	---	---	---	244596_at	---
1.84	1.88	0.04	7.41E-01	9.16E-01	---	---	---	1560104_at	---
4.56	4.73	0.17	7.41E-01	9.16E-01	ZHX1	zinc fingers and homeoboxes 1	chr8q24.13	223213_s_at	NM_001017926 /// NM_007222

7.24	7.33	0.10	7.41E-01	9.16E-01	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily C, 5	chr5q31	205717_x_at	NM_002588 /// NM_003735 /// NM_003736 /// NM_014004 /// NM_018912 /// NM_018913 /// NM_018914 /// NM_018915 /// NM_018916 /// NM_018917 /// NM_018918 /// NM_018919 /// NM_018920 /// NM_018921 /// NM_018922 /// NM_018923 /// NM_018924 /// NM_018925 /// NM_018926 /// NM_018927 /// NM_018928 /// NM_018929 /// NM_031993 /// NM_032009 /// NM_032011 /// NM_032053 /// NM_032054 /// NM_032086 /// NM_032087 /// NM_032088 /// NM_032089 /// NM_032090 /// NM_032091 /// NM_032092 /// NM_032094 /// NM_032095 /// NM_032096 /// NM_032097 /// NM_032098 /// NM_032099 /// NM_032100 /// NM_032101 /// NM_032402 /// NM_032403 /// NM_032406 /// NM_032407
8.12	8.22	0.10	7.41E-01	9.16E-01	RAP1GAP	RAP1 GTPase activating protein	chr1p36.1-p35	203911_at	NM_002885
7.43	7.55	0.12	7.41E-01	9.16E-01	C15orf15	chromosome 15 open reading frame 15	chr15q21	222465_at	NM_016304
2.76	2.82	0.06	7.41E-01	9.16E-01	ANKRD22	ankyrin repeat domain 22	chr10q23.31	239196_at	NM_144590
3.77	3.84	0.06	7.41E-01	9.16E-01	SBF2	SET binding factor 2	chr11p15.4	242935_at	NM_030962
2.08	2.11	0.04	7.41E-01	9.16E-01	---	---	---	216746_at	---
2.39	2.45	0.05	7.42E-01	9.16E-01	VAV3	vav 3 guanine nucleotide exchange factor	chr1p13.3	218806_s_at	NM_001079874 /// NM_006113
2.27	2.31	0.04	7.42E-01	9.16E-01	BLVRA	biliverdin reductase A	chr7p14-cen	203772_at	NM_000712
2.30	2.36	0.06	7.42E-01	9.16E-01	HFE2	hemochromatosis type 2 (juvenile)	chr1q21.1	228621_at	NM_145277 /// NM_202004 /// NM_213652 /// NM_213653
4.39	4.44	0.06	7.42E-01	9.16E-01	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	chr9p22.3	212258_s_at	NM_003070 /// NM_139045
2.88	2.92	0.04	7.42E-01	9.16E-01	ITGA10	integrin, alpha 10	chr1q21	206766_at	NM_003637
4.42	4.52	0.10	7.42E-01	9.16E-01	---	---	---	227115_at	---
2.03	2.08	0.05	7.42E-01	9.16E-01	---	---	---	1568936_a_at	---
5.13	5.18	0.04	7.42E-01	9.16E-01	MR1	major histocompatibility complex, class I-related	chr1q25.3	210224_at	NM_001531
2.24	2.29	0.04	7.42E-01	9.16E-01	LOC650392	Hypothetical protein LOC650392	---	227984_at	XM_944170
4.69	4.75	0.06	7.42E-01	9.16E-01	SIX1	SIX homeobox 1	chr14q23.1	205817_at	NM_005982
2.28	2.33	0.06	7.42E-01	9.16E-01	CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9q34.3	244682_at	NM_015447
4.41	4.52	0.11	7.42E-01	9.16E-01	AKAP11	A kinase (PRKA) anchor protein 11	chr13q14.11	215336_at	NM_016248
2.07	2.12	0.04	7.42E-01	9.16E-01	ISL1	ISL LIM homeobox 1	chr5q11.2	206104_at	NM_002202
2.13	2.18	0.05	7.42E-01	9.16E-01	---	---	---	215969_at	---

3.29	3.35	0.06	7.43E-01	9.17E-01	BTBD7	BTB (POZ) domain containing 7	chr14q32.12-q32.13	220297_at	NM_001002860 /// NM_018167
3.90	4.00	0.10	7.43E-01	9.17E-01	DDAH1	Dimethylarginine dimethylaminohydrolase 1	chr1p22	229456_s_at	NM_001134445 /// NM_012137
2.70	2.76	0.06	7.43E-01	9.17E-01	FOXJ3	forkhead box J3	chr1pter-q31.3	217310_s_at	NM_014947
3.67	3.73	0.06	7.43E-01	9.17E-01	ARHGAP23	Rho GTPase activating protein 23	chr17q12	230013_s_at	XM_001714948 /// XM_001716606 /// XM_290799
1.93	1.97	0.04	7.43E-01	9.17E-01	---	---	---	222966_at	---
2.72	2.78	0.05	7.43E-01	9.17E-01	PRR10	proline rich 10	chr11q24.2	1553478_at	XR_039964 /// XR_039965 /// XR_039966
2.13	2.18	0.05	7.43E-01	9.17E-01	ZNF771	zinc finger protein 771	chr16p11.2	219780_at	NM_016643 /// XM_001721231 /// XM_001721234
2.61	2.65	0.04	7.43E-01	9.17E-01	NLRC3	NLR family, CARD domain containing 3	chr16p13.3	236295_s_at	NM_178844
8.97	9.10	0.13	7.43E-01	9.17E-01	C2orf25	chromosome 2 open reading frame 25	chr2q23.2	217883_at	NM_015702
6.52	6.60	0.08	7.43E-01	9.17E-01	MATN2	matrilin 2	chr8q22	202350_s_at	NM_002380 /// NM_030583
2.10	2.14	0.04	7.43E-01	9.17E-01	NUPL1	nucleoporin like 1	chr13q12.13	223984_s_at	NM_001008564 /// NM_001008565 /// NM_014089
1.85	1.89	0.04	7.43E-01	9.17E-01	---	---	---	1557301_a_at	---
7.35	7.42	0.08	7.43E-01	9.17E-01	LAMC1	laminin, gamma 1 (formerly LAMB2)	chr1q31	200771_at	NM_002293
2.07	2.12	0.06	7.43E-01	9.17E-01	---	---	---	238378_at	---
2.34	2.38	0.05	7.43E-01	9.17E-01	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	chr13q13.3	220129_at	NM_017826
2.13	2.18	0.04	7.43E-01	9.17E-01	PRO1848	PRO1848 protein	---	211218_at	---
2.33	2.38	0.05	7.43E-01	9.17E-01	FAM124A	family with sequence similarity 124A	chr13q14.3	241013_at	NM_145019
3.37	3.48	0.11	7.44E-01	9.17E-01	---	---	---	230661_at	---
2.26	2.32	0.06	7.44E-01	9.17E-01	---	---	---	231331_at	---
3.47	3.54	0.06	7.43E-01	9.17E-01	ARHGEF4	Rho guanine nucleotide exchange factor (GEF) 4	chr2q22	211891_s_at	NM_015320 /// NM_032995
2.31	2.37	0.06	7.44E-01	9.17E-01	SFRS2IP	Splicing factor, arginine/serine-rich 2, interacting protein	chr12q12-q13.11	1570507_at	NM_004719
2.45	2.50	0.05	7.44E-01	9.17E-01	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	chr2q33.1	232184_at	NM_020919
1.94	1.98	0.04	7.44E-01	9.17E-01	C18orf16	chromosome 18 open reading frame 16	chr18q11.2	1553440_at	XR_040524 /// XR_040525 /// XR_040526
1.86	1.89	0.03	7.44E-01	9.17E-01	DKFZp761D1918	hypothetical protein DKFZp761D1918	chr19q13.12	1555798_at	---
5.15	5.25	0.09	7.44E-01	9.17E-01	SAMD4B	Sterile alpha motif domain containing 4B	chr19q13.2	227511_at	NM_018028
2.04	2.10	0.06	7.44E-01	9.17E-01	CD80	CD80 molecule	chr3q13.3-q21	1555689_at	NM_005191
3.11	3.16	0.06	7.44E-01	9.17E-01	MIB2	Mindbomb homolog 2 (Drosophila)	chr1p36.33	241377_s_at	NM_080875
3.35	3.40	0.06	7.44E-01	9.17E-01	TET3	tet oncogene family member 3	chr2p13.1	214754_at	NM_144993
1.94	1.97	0.03	7.44E-01	9.17E-01	OR2H1	olfactory receptor, family 2, subfamily H, member 1	chr6p21.3	1567657_at	NM_030883
9.64	9.67	0.03	7.44E-01	9.17E-01	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	chr5q35.2	201172_x_at	NM_003945
4.67	4.76	0.09	7.44E-01	9.17E-01	MAP7	microtubule-associated protein 7	chr6q23.3	202890_at	NM_003980
2.00	2.04	0.04	7.44E-01	9.17E-01	NT5C1B	5'-nucleotidase, cytosolic IB	chr2p24.2	1554368_at	NM_001002006 /// NM_033253
2.97	3.03	0.06	7.44E-01	9.17E-01	AFF2	AF4/FMR2 family, member 2	chrXq28	210957_s_at	NM_002025
2.37	2.43	0.06	7.44E-01	9.17E-01	CD1B	CD1b molecule	chr1q22-q23	206749_at	NM_001764
2.36	2.41	0.06	7.44E-01	9.17E-01	NR5A2	nuclear receptor subfamily 5, group A, member 2	chr1q32.1	208337_s_at	NM_003822 /// NM_205860
2.36	2.41	0.05	7.44E-01	9.17E-01	LOC100101116 /// TTTY1	testis-specific transcript, Y-linked 1-like /// testis-specific transcript, Y-linked 1	chrYp11.2	216673_at	NR_001538 /// NR_003589
2.53	2.59	0.05	7.44E-01	9.17E-01	KRT19P2	keratin 19 pseudogene 2	chr12q22	217350_at	---
3.77	3.82	0.05	7.44E-01	9.17E-01	---	---	---	243394_at	---
3.39	3.44	0.05	7.44E-01	9.17E-01	---	---	---	234200_at	---
1.82	1.85	0.04	7.44E-01	9.17E-01	---	---	---	1565819_at	---
6.76	6.84	0.08	7.44E-01	9.17E-01	XIAP	X-linked inhibitor of apoptosis	chrXq25	225858_s_at	NM_001167
2.00	2.04	0.04	7.44E-01	9.17E-01	CALML4	Calmodulin-like 4	chr15q23	1566150_at	NM_001031733 /// NM_033429
1.94	1.97	0.04	7.44E-01	9.17E-01	---	---	---	241390_at	---
1.95	1.98	0.04	7.44E-01	9.17E-01	C6orf168	chromosome 6 open reading frame 168	chr6q16.2-q16.3	230447_at	NM_032511
2.12	2.15	0.04	7.44E-01	9.17E-01	RIPK2	receptor-interacting serine-threonine kinase 2	chr8q21	209544_at	NM_003821

2.43	2.50	0.07	7.45E-01	9.17E-01	---	---	---	240998_at	---
2.68	2.76	0.08	7.45E-01	9.17E-01	---	---	---	236589_at	---
3.78	3.85	0.07	7.45E-01	9.17E-01	---	---	---	239484_at	---
3.19	3.24	0.05	7.45E-01	9.17E-01	TMEM108	transmembrane protein 108	chr3q21	234818_at	NM_023943
4.79	4.85	0.06	7.45E-01	9.17E-01	---	---	---	226232_at	---
4.05	4.11	0.06	7.45E-01	9.17E-01	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	chr19p13.12	216271_x_at	NM_033025
3.54	3.59	0.05	7.45E-01	9.17E-01	DLGAP2	discs, large (Drosophila) homolog-associated protein 2	chr8p23	216916_s_at	NM_004745
2.41	2.46	0.05	7.45E-01	9.17E-01	---	---	---	221720_s_at	---
2.15	2.19	0.04	7.45E-01	9.17E-01	---	---	---	1557787_at	---
1.93	1.96	0.03	7.45E-01	9.17E-01	BTC	betacellulin	chr4q13-q21	207326_at	NM_001729
4.88	4.93	0.05	7.45E-01	9.17E-01	HSD11B1L	hydroxysteroid (11-beta) dehydrogenase 1-like	chr19p13.3	1569905_at	NM_198533 /// NM_198704 /// NM_198705 /// NM_198706 /// NM_198707 /// NM_198708
2.81	2.86	0.05	7.45E-01	9.17E-01	---	---	---	241324_at	---
2.54	2.60	0.05	7.45E-01	9.17E-01	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	chr2q24.1	207141_s_at	NM_002239
5.00	5.07	0.07	7.45E-01	9.17E-01	MEF2B	myocyte enhancer factor 2B	chr19p12	209926_at	NM_005919
2.94	3.00	0.07	7.45E-01	9.17E-01	LOC100131419	hypothetical protein LOC100131419	chr17q25.3	1563226_at	XM_001717284 /// XM_001721800 /// XM_001726788
5.27	5.33	0.06	7.45E-01	9.17E-01	RBM22	RNA binding motif protein 22	chr5q33.1	222527_s_at	NM_018047
1.91	1.96	0.04	7.45E-01	9.17E-01	---	---	---	216104_at	---
2.30	2.36	0.06	7.46E-01	9.18E-01	GPR115	G protein-coupled receptor 115	chr6p12.3	1553031_at	NM_153838
2.13	2.19	0.06	7.46E-01	9.18E-01	CCDC129	coiled-coil domain containing 129	chr7p15.1	231653_at	NM_194300
2.77	2.82	0.05	7.46E-01	9.18E-01	USP22	ubiquitin specific peptidase 22	chr17p11.2	216957_at	NM_015276
5.87	5.99	0.12	7.46E-01	9.18E-01	NNT	nicotinamide nucleotide transhydrogenase	chr5p13.1-cen	202783_at	NM_012343 /// NM_182977
4.09	4.18	0.08	7.46E-01	9.18E-01	SLC19A1	Solute carrier family 19 (folate transporter), member 1	chr21q22.3	1555952_at	NM_194255
2.51	2.57	0.06	7.46E-01	9.18E-01	PALM2 /// PALM2-AKAP2	paralemmin 2 /// PALM2-AKAP2	chr9q31-q33	1553502_a_at	NM_001037293 /// NM_007203 /// NM_053016 /// NM_147150
3.45	3.50	0.06	7.46E-01	9.18E-01	NEDD1	neural precursor cell expressed, developmentally down-regulated 1	chr12q23.1	1560116_a_at	NM_152905
4.05	4.09	0.04	7.46E-01	9.18E-01	CCDC93	coiled-coil domain containing 93	chr2q14.1	243282_at	NM_019044
2.03	2.07	0.04	7.46E-01	9.18E-01	---	---	---	1561205_at	---
3.11	3.18	0.07	7.46E-01	9.18E-01	GRM2	glutamate receptor, metabotropic 2	chr3p21.1	208465_at	NM_000839 /// NM_001130063
4.80	4.87	0.06	7.46E-01	9.18E-01	C2orf72	chromosome 2 open reading frame 72	chr2q37.1	1556464_a_at	XM_001129456 /// XM_001132119 /// XM_001715135
3.09	3.14	0.05	7.46E-01	9.18E-01	---	---	---	235999_at	---
6.53	6.69	0.16	7.46E-01	9.18E-01	CTSO	cathepsin O	chr4q31-q32	203758_at	NM_001334
2.59	2.66	0.06	7.46E-01	9.18E-01	C14orf1	chromosome 14 open reading frame 1	chr14q24.3	202563_at	NM_007176
2.07	2.12	0.04	7.46E-01	9.18E-01	PRG4	proteoglycan 4	chr1q25-q31	206007_at	NM_001127708 /// NM_001127709 /// NM_001127710 /// NM_005807
2.50	2.54	0.04	7.46E-01	9.18E-01	EVC2	Ellis van Creveld syndrome 2	chr4p16.2-p16.1	229974_at	NM_147127
2.60	2.64	0.04	7.47E-01	9.18E-01	NPY2R	neuropeptide Y receptor Y2	chr4q31	210730_s_at	NM_000910
2.41	2.47	0.06	7.47E-01	9.18E-01	---	---	---	244805_at	---
2.46	2.51	0.05	7.47E-01	9.18E-01	---	---	---	236938_at	---
4.14	4.24	0.09	7.47E-01	9.18E-01	FECH	ferrochelatase (protoporphyria)	chr18q21.3	229696_at	NM_000140 /// NM_001012515
10.06	10.10	0.04	7.47E-01	9.18E-01	PRDX1	peroxiredoxin 1	chr1p34.1	208680_at	NM_002574 /// NM_181696 /// NM_181697
2.38	2.43	0.05	7.47E-01	9.18E-01	---	---	---	241253_at	---
2.51	2.56	0.05	7.47E-01	9.18E-01	BAG1	BCL2-associated athanogene	chr9p12	229720_at	NM_004323
2.24	2.29	0.04	7.47E-01	9.18E-01	VSIG1	V-set and immunoglobulin domain containing 1	chrXq22.3	234370_at	NM_182607
2.50	2.55	0.05	7.47E-01	9.18E-01	SLC30A8	solute carrier family 30 (zinc transporter), member 8	chr8q24.11	239983_at	NM_173851
1.86	1.90	0.04	7.47E-01	9.18E-01	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	chr7q31	214586_at	NM_005302
2.45	2.49	0.04	7.47E-01	9.18E-01	LOC283278	hypothetical protein LOC283278	chr11p15.1	242417_at	XM_495868

2.41	2.45	0.04	7.47E-01	9.18E-01	RRAD	Ras-related associated with diabetes	chr16q22	231100_at	NM_001128850 /// NM_004165
4.25	4.33	0.08	7.47E-01	9.18E-01	RAVER2	ribonucleoprotein, PTB-binding 2	chr1p31.3	231851_at	NM_018211
2.65	2.70	0.05	7.47E-01	9.18E-01	---	---	---	1563320_at	---
2.85	2.96	0.11	7.47E-01	9.18E-01	C21orf7	chromosome 21 open reading frame 7	chr21q22.3	221211_s_at	NM_020152
2.09	2.14	0.04	7.47E-01	9.18E-01	LAMA4	Laminin, alpha 4	chr6q21	210989_at	NM_001105206 /// NM_001105207 /// NM_001105208 /// NM_001105209 /// NM_002290
2.77	2.83	0.06	7.47E-01	9.19E-01	FREM1	FRAS1 related extracellular matrix 1	chr9p22.3	228233_at	NM_144966
2.14	2.19	0.05	7.47E-01	9.19E-01	---	---	---	241330_x_at	---
2.15	2.19	0.04	7.47E-01	9.19E-01	---	---	---	1560523_at	---
2.21	2.25	0.04	7.47E-01	9.19E-01	---	---	---	237071_at	---
2.52	2.57	0.05	7.47E-01	9.19E-01	C2orf65	Chromosome 2 open reading frame 65	chr2p13.1	234498_at	NM_138804
3.17	3.23	0.06	7.48E-01	9.19E-01	ILVBL	ilvB (bacterial acetolactate synthase)-like	chr19p13.1	216270_at	NM_006844
2.68	2.73	0.05	7.48E-01	9.19E-01	NEK1	NIMA (never in mitosis gene a)-related kinase 1	chr4q33	211086_x_at	NM_012224
6.57	6.72	0.15	7.48E-01	9.19E-01	ZNF638	zinc finger protein 638	chr2p13.2-p13.1	213775_x_at	NM_001014972 /// NM_014497
2.94	3.01	0.07	7.48E-01	9.19E-01	KIAA1704	KIAA1704	chr13q13-q14	220171_x_at	NM_018559
5.74	5.80	0.06	7.48E-01	9.19E-01	SH3GLB2	SH3-domain GRB2-like endophilin B2	chr9q34	224907_s_at	NM_020145
2.73	2.77	0.04	7.48E-01	9.19E-01	HERC2P7	hect domain and RLD 2 pseudogene 7	chr15q11-q13	232900_at	---
3.59	3.66	0.08	7.48E-01	9.19E-01	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	chr1p12	202235_at	NM_003051
2.18	2.23	0.05	7.48E-01	9.19E-01	---	---	---	1560903_at	---
2.37	2.41	0.04	7.48E-01	9.19E-01	CAPRIN1	Cell cycle associated protein 1	chr11p13	236850_at	NM_005898 /// NM_203364
2.28	2.32	0.04	7.48E-01	9.19E-01	PTPRE	protein tyrosine phosphatase, receptor type, E	chr10q26	1559018_at	NM_006504 /// NM_130435
3.65	3.72	0.07	7.48E-01	9.19E-01	---	---	---	1566973_at	---
2.16	2.20	0.04	7.48E-01	9.19E-01	LOC440896	hypothetical gene LOC440896	chr9q12	1570388_a_at	NM_001039940 /// NR_015361
2.92	2.99	0.07	7.48E-01	9.19E-01	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	chr22q12|7p14.3-p14.1	211483_x_at	NM_001220 /// NM_172078 /// NM_172079 /// NM_172080 /// NM_172081 /// NM_172082 /// NM_172083 /// NM_172084
1.96	1.99	0.04	7.48E-01	9.19E-01	PF4V1	platelet factor 4 variant 1	chr4q12-q21	207815_at	NM_002620
7.95	8.03	0.08	7.48E-01	9.19E-01	TTC3	tetratricopeptide repeat domain 3	chr21q22.2	208073_x_at	NM_001001894 /// NM_003316
4.33	4.39	0.06	7.48E-01	9.19E-01	FLCN	folliculin	chr17p11.2	243062_at	NM_144606 /// NM_144997
6.75	6.80	0.05	7.48E-01	9.19E-01	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	chr11q13	232169_x_at	NM_002496
4.70	4.75	0.05	7.48E-01	9.19E-01	KCNH4	potassium voltage-gated channel, subfamily H (eag-related), member 4	chr17q21.2	220802_at	NM_012285
2.48	2.53	0.05	7.48E-01	9.19E-01	FGD3	FYVE, RhoGEF and PH domain containing 3	---	1555407_s_at	NM_001083536 /// NM_033086
3.77	3.82	0.05	7.48E-01	9.19E-01	FOXP4	forkhead box P4	chr6p21.1	229763_at	NM_001012426 /// NM_001012427 /// NM_138457
2.61	2.66	0.05	7.49E-01	9.19E-01	LOXHD1	lipoxygenase homology domains 1	chr18q21.1	241117_at	XM_001713754 /// XM_001713755 /// XM_001713756
1.76	1.79	0.03	7.48E-01	9.19E-01	FCRL5	Fc receptor-like 5	chr1q21	231647_s_at	NM_031281
3.20	3.29	0.09	7.49E-01	9.19E-01	---	---	---	215322_at	---
3.58	3.64	0.06	7.49E-01	9.19E-01	ALX4	aristaless-like homeobox 4	chr11p11.2	208330_at	NM_021926
2.14	2.18	0.05	7.49E-01	9.19E-01	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	chr13q12.3	1570119_at	NM_015032
3.49	3.55	0.06	7.49E-01	9.19E-01	---	---	---	239755_at	---

2.72	2.81	0.09	7.49E-01	9.19E-01	PGK1	Phosphoglycerate kinase 1	chrXq13	217383_at	NM_000291
2.25	2.30	0.04	7.49E-01	9.19E-01	---	---	---	217582_at	---
4.68	4.77	0.08	7.49E-01	9.19E-01	---	---	---	231005_at	---
2.80	2.84	0.03	7.49E-01	9.19E-01	CARD14	caspase recruitment domain family, member 14	chr17q25	232608_x_at	NM_024110 /// NM_052819
4.38	4.49	0.11	7.49E-01	9.19E-01	---	---	---	244826_at	---
3.58	3.62	0.05	7.49E-01	9.19E-01	TADA2L	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	chr17q12-q21	209938_at	NM_001488 /// NM_133439
2.85	2.92	0.07	7.49E-01	9.20E-01	---	---	---	233224_at	---
2.27	2.31	0.05	7.49E-01	9.20E-01	RPL5	ribosomal protein L5	chr1p22.1	1556498_at	NM_000969
2.04	2.08	0.04	7.49E-01	9.20E-01	CEP135	centrosomal protein 135kDa	chr4q12	207286_at	NM_025009
2.54	2.61	0.07	7.49E-01	9.20E-01	KCNH5	potassium voltage-gated channel, subfamily H (eag-related), member 5	chr14q23.1	1555304_a_at	NM_139318 /// NM_172375 /// NM_172376
2.99	3.04	0.05	7.49E-01	9.20E-01	---	---	---	234063_at	---
4.84	4.94	0.10	7.49E-01	9.20E-01	LOC648998 /// NCF1 /// NCF1B /// NCF1C	similar to Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH oxidase factor 1) (47 kDa neutrophil oxidase factor) (p47-phox) (NCF-47K) (47 kDa autosomal chronic granulomatous disease protein) (NOXO2) /// neutrophil cytosolic factor 1 /// neutrophil cytosolic factor 1B pseudogene /// neutrophil cytosolic factor 1C pseudogene	chr7q11.23	204961_s_at	NM_000265 /// NR_003186 /// NR_003187 /// XM_001723264 /// XM_001725090
2.43	2.50	0.07	7.49E-01	9.20E-01	EID3	EP300 interacting inhibitor of differentiation 3	chr12q23-q24.1	231292_at	NM_001008394
2.35	2.40	0.04	7.49E-01	9.20E-01	---	---	---	215079_at	---
4.98	5.02	0.04	7.49E-01	9.20E-01	---	---	---	237080_at	---
1.71	1.74	0.03	7.49E-01	9.20E-01	---	---	---	1560385_x_at	---
6.66	6.74	0.08	7.49E-01	9.20E-01	NCKAP1	NCK-associated protein 1	chr2q32	207738_s_at	NM_013436 /// NM_205842
4.50	4.58	0.07	7.50E-01	9.20E-01	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	chr9q34	210100_s_at	NM_001606 /// NM_212533
3.68	3.73	0.05	7.50E-01	9.20E-01	ATP11B	ATPase, class VI, type 11B	chr3q27	1564063_a_at	NM_014616
7.07	7.15	0.08	7.50E-01	9.20E-01	PHPT1	phosphohistidine phosphatase 1	chr9q34.3	225683_x_at	NM_014172
3.85	3.91	0.06	7.50E-01	9.20E-01	CCDC37	coiled-coil domain containing 37	chr3q21.2	242615_at	NM_182628
4.26	4.32	0.06	7.50E-01	9.20E-01	EXOC7	exocyst complex component 7	chr17q25.1	214802_at	NM_001013839 /// NM_015219
2.03	2.07	0.04	7.50E-01	9.20E-01	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	chr9q31-q32	233098_s_at	NM_018424 /// NM_019114
5.43	5.67	0.25	7.50E-01	9.20E-01	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	chr1p31.1	203811_s_at	NM_007034
2.89	2.95	0.06	7.50E-01	9.20E-01	---	---	---	238707_at	---
2.48	2.53	0.05	7.50E-01	9.20E-01	TANK	TRAF family member-associated NFKB activator	chr2q24-q31	243376_at	NM_004180 /// NM_133484
7.07	7.13	0.05	7.50E-01	9.20E-01	FBXW12	F-box and WD repeat domain containing 12	chr3p21.31	215600_x_at	NM_207102
2.82	2.91	0.09	7.50E-01	9.20E-01	SCRN3	secernin 3	chr2q31.1	219234_x_at	NM_024583
2.80	2.85	0.05	7.50E-01	9.20E-01	KIAA0892	KIAA0892	chr19p13.11	216926_s_at	NM_015329
6.28	6.37	0.09	7.50E-01	9.20E-01	---	---	---	244697_at	---
5.43	5.51	0.07	7.50E-01	9.20E-01	SP110	SP110 nuclear body protein	chr2q37.1	208392_x_at	NM_004509 /// NM_004510 /// NM_080424
4.23	4.29	0.07	7.50E-01	9.20E-01	PTK2B	PTK2B protein tyrosine kinase 2 beta	chr8p21.1	203110_at	NM_004103 /// NM_173174 /// NM_173175 /// NM_173176
5.49	5.55	0.06	7.50E-01	9.20E-01	LOC126661	Hypothetical protein LOC126661	chr1p34.1	236900_x_at	NM_001102601
3.05	3.09	0.04	7.50E-01	9.20E-01	CALHM1	calcium homeostasis modulator 1	chr10q24.33	1554367_at	NM_001001412
3.45	3.52	0.07	7.50E-01	9.20E-01	---	---	---	1562624_at	---
3.90	4.01	0.12	7.50E-01	9.20E-01	ANG	angiogenin, ribonuclease, RNase A family, 5	chr14q11.1-q11.2	205141_at	NM_001097577 /// NM_001145
2.63	2.68	0.04	7.50E-01	9.20E-01	FDPSL2A	MGC44478	chr7q11.23	231366_at	NR_003262
2.84	2.87	0.04	7.50E-01	9.20E-01	NEBL	nebulette	chr10p12	207279_s_at	NM_006393 /// NM_213569
2.00	2.04	0.04	7.50E-01	9.20E-01	---	---	---	1560288_at	---
4.96	5.02	0.05	7.50E-01	9.20E-01	ZNF395	zinc finger protein 395	chr8p21.1	222536_s_at	NM_018660
4.17	4.22	0.05	7.50E-01	9.20E-01	SMG7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr1q25	201793_x_at	NM_173156 /// NM_201568 /// NM_201569
1.84	1.88	0.04	7.50E-01	9.20E-01	MAGEB6	melanoma antigen family B, 6	chrXp21.3	1552858_at	NM_173523
2.20	2.26	0.05	7.50E-01	9.20E-01	---	---	---	234896_at	---
2.24	2.32	0.08	7.51E-01	9.20E-01	---	---	---	205764_at	---
3.10	3.15	0.05	7.51E-01	9.20E-01	---	---	---	230094_at	---
2.46	2.50	0.04	7.51E-01	9.20E-01	VPRBP	Vpr (HIV-1) binding protein	chr3p21.2	204376_at	NM_014703
2.32	2.37	0.05	7.51E-01	9.20E-01	---	---	---	1569346_a_at	---

2.50	2.57	0.08	7.51E-01	9.20E-01	YTHDC1	YTH domain containing 1	chr4q13.2	214814_at	NM_001031732 /// NM_133370
2.38	2.43	0.05	7.51E-01	9.20E-01	---	---	---	1566446_at	---
3.48	3.54	0.06	7.51E-01	9.20E-01	---	---	---	241493_at	---
2.53	2.59	0.06	7.51E-01	9.20E-01	FAM169A	family with sequence similarity 169, member A	chr5q13.3	213954_at	NM_015566
2.42	2.46	0.04	7.51E-01	9.20E-01	---	---	---	231458_at	---
10.17	10.24	0.06	7.51E-01	9.20E-01	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	chr11q13	203190_at	NM_002496
4.92	4.98	0.06	7.51E-01	9.20E-01	FGD2	FYVE, RhoGEF and PH domain containing 2	chr6p21.2	1565752_at	NM_173558
3.50	3.56	0.06	7.51E-01	9.20E-01	---	---	---	1569745_at	---
2.50	2.53	0.03	7.51E-01	9.20E-01	---	---	---	1559053_at	---
4.84	4.98	0.15	7.51E-01	9.20E-01	---	---	---	215479_at	---
4.00	4.12	0.11	7.51E-01	9.20E-01	---	---	---	243388_at	---
2.27	2.32	0.05	7.51E-01	9.20E-01	---	---	---	232538_at	---
2.43	2.47	0.04	7.51E-01	9.20E-01	WNT3	wingless-type MMTV integration site family, member 3	chr17q21	229103_at	NM_030753
5.66	5.84	0.18	7.51E-01	9.20E-01	CD58	CD58 molecule	chr1p13	205173_x_at	NM_001779
3.54	3.64	0.10	7.52E-01	9.20E-01	FIGN	fidgetin	chr2q24.3	238964_at	NM_018086
3.32	3.37	0.05	7.51E-01	9.20E-01	SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	chr16q22.1	1559092_at	NM_004594
2.58	2.63	0.05	7.52E-01	9.20E-01	EFCAB1	EF-hand calcium binding domain 1	chr8q11.21	220156_at	NM_024593
1.94	1.99	0.05	7.52E-01	9.20E-01	---	---	---	1565924_a_at	---
2.32	2.36	0.04	7.52E-01	9.20E-01	---	---	---	240953_at	---
7.33	7.39	0.06	7.52E-01	9.20E-01	ALG3	asparagine-linked glycosylation 3 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)	chr3q27.1	207396_s_at	NM_005787
9.79	9.85	0.06	7.52E-01	9.20E-01	ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	chr16p13.3	36994_at	NM_001694
2.27	2.31	0.05	7.52E-01	9.20E-01	---	---	---	240438_at	---
2.07	2.12	0.05	7.52E-01	9.20E-01	---	---	---	1564965_at	---
7.13	7.26	0.14	7.52E-01	9.20E-01	PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	chrXq22.3	1554577_a_at	NM_002814 /// NM_170750
2.99	3.07	0.08	7.52E-01	9.20E-01	ZFR	zinc finger RNA binding protein	chr5p13.3	33148_at	NM_016107
2.85	2.92	0.07	7.52E-01	9.20E-01	LPXN	leupaxin	chr11q12.1	242778_at	NM_004811
4.22	4.28	0.06	7.52E-01	9.20E-01	---	---	---	235586_at	---
2.36	2.41	0.05	7.52E-01	9.20E-01	JAG1	Jagged 1 (Alagille syndrome)	chr20p12.1-p11.23	231183_s_at	NM_000214
4.03	4.07	0.04	7.52E-01	9.20E-01	C10orf95	chromosome 10 open reading frame 95	chr10q24.32	220152_at	NM_024886
3.04	3.08	0.04	7.52E-01	9.20E-01	---	---	---	1557539_at	---
2.35	2.38	0.04	7.52E-01	9.20E-01	---	---	---	217663_at	---
2.00	2.04	0.03	7.52E-01	9.20E-01	---	---	---	234248_at	---
2.04	2.08	0.04	7.52E-01	9.20E-01	C9orf68	chromosome 9 open reading frame 68	chr9p24.2-p24.1	1555079_at	NM_001039395
2.03	2.07	0.03	7.52E-01	9.20E-01	---	---	---	241278_at	---
1.86	1.89	0.03	7.52E-01	9.20E-01	MYLK	myosin light chain kinase	chr3q21	1569956_at	NM_053025 /// NM_053026 /// NM_053027 /// NM_053028 /// NM_053031 /// NM_053032
3.84	3.94	0.10	7.52E-01	9.21E-01	PHKA1	phosphorylase kinase, alpha 1 (muscle)	chrXq12-q13	229876_at	NM_001122670 /// NM_002637
2.97	3.04	0.07	7.52E-01	9.21E-01	LOC151657	hypothetical protein LOC151657	chr3q13.12	1560928_at	---
2.71	2.77	0.06	7.52E-01	9.21E-01	ATN1	Atrophin 1	chr12p13.31	211076_x_at	NM_001007026 /// NM_001940
2.05	2.10	0.05	7.52E-01	9.21E-01	LOC100131819	Similar to hCG1778814	chr8q13.3	1558819_at	XM_001715525 /// XM_001715618 /// XM_001715673
2.25	2.30	0.05	7.52E-01	9.21E-01	---	---	---	237688_at	---
2.74	2.79	0.05	7.52E-01	9.21E-01	---	---	---	244073_at	---
2.13	2.17	0.04	7.52E-01	9.21E-01	GPRIN3	GPRIN family member 3	chr4q22.1	1556698_a_at	NM_198281
2.01	2.05	0.04	7.52E-01	9.21E-01	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	chr2q31.3	1555462_at	NM_001080545
1.83	1.87	0.04	7.52E-01	9.21E-01	C11orf47	chromosome 11 open reading frame 47	chr11p15.4	1560781_at	NM_173589
4.51	4.67	0.16	7.52E-01	9.21E-01	LMAN1	lectin, mannose-binding, 1	chr18q21.3-q22	203293_s_at	NM_005570
1.68	1.71	0.03	7.52E-01	9.21E-01	---	---	---	1559103_s_at	---
2.08	2.13	0.05	7.52E-01	9.21E-01	---	---	---	1570596_at	---
3.13	3.18	0.04	7.52E-01	9.21E-01	SNX26	sorting nexin 26	chr19q13.12	233885_at	NM_052948
2.86	2.90	0.04	7.52E-01	9.21E-01	PNLIPRP1	pancreatic lipase-related protein 1	chr10q25.3	210722_at	NM_006229
5.55	5.65	0.10	7.53E-01	9.21E-01	FAM18B	family with sequence similarity 18, member B	chr17p11.2	218446_s_at	NM_016078
2.91	2.96	0.05	7.53E-01	9.21E-01	C9orf100	chromosome 9 open reading frame 100	chr9p13.3	231892_at	NM_032818

2.73	2.77	0.05	7.53E-01	9.21E-01	LOC100131781	similar to hCG1815045	chr14q11.2	240320_at	XM_001714931 /// XM_001716883 /// XM_001717132																				
2.65	2.70	0.04	7.53E-01	9.21E-01	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	chr9q31-q32	220524_at	NM_018424 /// NM_019114																				
2.69	2.72	0.04	7.53E-01	9.21E-01	RAP1A	RAP1A, member of RAS oncogene family	chr1p13.3	1555339_at	NM_001010935 /// NM_002884																				
3.39	3.50	0.11	7.53E-01	9.21E-01	LOC541469	hypothetical protein LOC541469	chr19q13.2	231211_s_at	XR_039882 /// XR_039883 /// XR_039884																				
6.61	6.70	0.09	7.53E-01	9.21E-01	C5orf51	chromosome 5 open reading frame 51	chr5p13.1	226159_at	NM_175921																				
5.32	5.41	0.08	7.53E-01	9.21E-01	SP110	SP110 nuclear body protein	chr2q37.1	223980_s_at	NM_004509 /// NM_004510 /// NM_080424																				
4.92	4.98	0.06	7.53E-01	9.21E-01	KLC1	kinesin light chain 1	chr14q32.3	212877_at	NM_001130107 /// NM_005552 /// NM_182923																				
2.76	2.82	0.05	7.53E-01	9.21E-01	SLC1A7	solute carrier family 1 (glutamate transporter), member 7	chr1p32.3	210923_at	NM_006671																				
2.42	2.47	0.06	7.53E-01	9.21E-01	RBMXL2	RNA binding motif protein, X-linked-like 2	chr11p15	207207_at	NM_014469																				
3.42	3.52	0.10	7.53E-01	9.21E-01	ZDHHC17	zinc finger, DHHC-type containing 17	chr12q21.2	217486_s_at	NM_015336																				
3.20	3.25	0.06	7.53E-01	9.21E-01	LOC283693	Actin, gamma pseudogene	chr15q25.2	1565911_at	---																				
2.09	2.14	0.05	7.53E-01	9.21E-01	C4orf36	chromosome 4 open reading frame 36	chr4q21.3	1552919_at	NM_144645																				
8.08	8.21	0.13	7.53E-01	9.21E-01	IGFBP4	insulin-like growth factor binding protein 4	chr17q12-q21.1	201508_at	NM_001552																				
6.60	6.68	0.08	7.53E-01	9.21E-01	CDV3	CDV3 homolog (mouse)	chr3q22.1	213554_s_at	NM_001134422 /// NM_001134423 /// NM_017548																				
2.03	2.07	0.04	7.53E-01	9.21E-01	PREPL	prolyl endopeptidase-like	chr2p21	243542_at	NM_001042385 /// NM_001042386 /// NM_006036																				
2.13	2.16	0.04	7.53E-01	9.21E-01	KCNE1	potassium voltage-gated channel, Isk-related family, member 1	chr21q22.1-q22.2|21q22.12	236407_at	NM_000219 /// NM_001127668 /// NM_001127669 /// NM_001127670																				
2.06	2.10	0.04	7.54E-01	9.21E-01	C2orf34	chromosome 2 open reading frame 34	chr2p21	1554875_at	NM_024766																				
5.89	5.95	0.06	7.54E-01	9.21E-01	POLR1E	polymerase (RNA) I polypeptide E, 53kDa	chr9p13.2	218997_at	NM_022490																				
3.01	3.10	0.10	7.54E-01	9.21E-01	LOC606495	hypothetical protein LOC606495	chr1p32.3	235992_s_at	NM_001031672																				
4.06	4.13	0.07	7.54E-01	9.21E-01	SFXN1	sideroflexin 1	---	230069_at	NM_022754																				
2.34	2.39	0.05	7.54E-01	9.21E-01	ZNF568	zinc finger protein 568	chr19q13.12	1568900_a_at	NM_198539																				
2.38	2.43	0.04	7.54E-01	9.21E-01	---	---	---	241264_at	---																				
2.21	2.26	0.04	7.54E-01	9.21E-01	---	---	---	236408_at	---																				
3.58	3.67	0.10	7.54E-01	9.21E-01	SAA1 /// SAA2	serum amyloid A1 /// serum amyloid A2	chr11p15.1 /// chr11p15.1-p14	214456_x_at	NM_000331 /// NM_001127380 /// NM_030754 /// NM_199161																				
5.66	5.80	0.14	7.54E-01	9.21E-01	---	---	---	239600_at	---																				
7.71	7.85	0.14	7.54E-01	9.21E-01	HNRNPR	heterogeneous nuclear ribonucleoprotein R	chr1p36.12	208765_s_at	NM_001102397 /// NM_001102398 /// NM_001102399 /// NM_005826																				
2.85	2.93	0.08	7.54E-01	9.21E-01	CCDC91	Coiled-coil domain containing 91	chr12p11.22	1570571_at	NM_018318																				
3.89	4.02	0.13	7.54E-01	9.21E-01	CNOT7	CCR4-NOT transcription complex, subunit 7	chr8p22-p21.3	1552344_s_at	NM_013354 /// NM_054026																				
4.38	4.50	0.12	7.54E-01	9.21E-01	C5orf41	chromosome 5 open reading frame 41	chr5q35.2	1554229_at	NM_153607																				
11.86	11.96	0.10	7.54E-01	9.21E-01	RPL17	ribosomal protein L17	chr18q21	212537_x_at	NM_000985 /// NM_001035006																				
3.46	3.55	0.10	7.54E-01	9.21E-01	DDHD1	DDHD domain containing 1	chr14q21	225971_at	NM_030637																				
9.06	9.12	0.06	7.54E-01	9.21E-01	C10orf104	chromosome 10 open reading frame 104	chr10q22.1	224664_at	NM_173473																				

2.56	2.61	0.05	7.55E-01	9.21E-01	LOC100130950	similar to hCG1991536	chr17p13.2	1554666_at	XM_001720180 /// XM_001724243 /// XM_001725608
2.16	2.20	0.05	7.54E-01	9.21E-01	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	chr13q32.1	235749_at	NM_020121
2.00	2.05	0.04	7.54E-01	9.21E-01	---	---	---	243958_at	---
2.27	2.31	0.04	7.54E-01	9.21E-01	LOC283731	hypothetical protein LOC283731	chr15q22.33	1560723_at	---
3.91	3.95	0.04	7.55E-01	9.21E-01	---	---	---	231401_s_at	---
4.68	4.73	0.04	7.55E-01	9.21E-01	HOXC13	homeobox C13	chr12q13.3	219832_s_at	NM_017410
2.23	2.26	0.04	7.54E-01	9.21E-01	---	---	---	1562157_at	---
2.03	2.07	0.04	7.55E-01	9.21E-01	LRCH3	Leucine-rich repeats and calponin homology (CH) domain containing 3	chr3q29	229387_at	NM_032773
2.03	2.07	0.04	7.54E-01	9.21E-01	PSG1	pregnancy specific beta-1-glycoprotein 1	chr19q13.2	210196_s_at	NM_006905
1.99	2.02	0.03	7.54E-01	9.21E-01	MTIF3	mitochondrial translational initiation factor 3	chr13q12.2	223357_s_at	NM_152912
2.04	2.07	0.03	7.54E-01	9.21E-01	WDR21B	WD repeat domain 21B	chr4p13	1562209_at	NM_001029955
3.63	3.72	0.09	7.55E-01	9.21E-01	RAB2A	RAB2A, member RAS oncogene family	chr8q12.1	221960_s_at	NM_002865
6.30	6.40	0.10	7.55E-01	9.21E-01	RAB22A	RAB22A, member RAS oncogene family	chr20q13.32	218360_at	NM_020673
2.61	2.65	0.04	7.55E-01	9.21E-01	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	chr1p36	207536_s_at	NM_001561
4.50	4.68	0.18	7.55E-01	9.21E-01	ZNF146	zinc finger protein 146	chr19q13.1	1554433_a_at	NM_001099638 /// NM_001099639 /// NM_007145
7.46	7.58	0.12	7.55E-01	9.21E-01	STAB1	stabilin 1	chr3p21.1	38487_at	NM_015136
3.23	3.35	0.12	7.55E-01	9.21E-01	EMP1	epithelial membrane protein 1	chr12p12.3	1564796_at	NM_001423
5.51	5.62	0.11	7.55E-01	9.21E-01	SOX6	SRY (sex determining region Y)-box 6	chr11p15.3	235526_at	NM_017508 /// NM_033326
4.69	4.79	0.10	7.55E-01	9.21E-01	USP47	ubiquitin specific peptidase 47	chr11p15.3	223118_s_at	NM_017944
5.13	5.19	0.07	7.55E-01	9.21E-01	IL6R	interleukin 6 receptor	chr1q21	226333_at	NM_000565 /// NM_181359
2.42	2.48	0.06	7.55E-01	9.21E-01	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	chr17q21.32	204627_s_at	NM_000212
3.48	3.54	0.06	7.55E-01	9.21E-01	DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	chrXq13.1	207732_s_at	NM_020730 /// NM_021120
2.74	2.80	0.06	7.55E-01	9.21E-01	KRT19P2	keratin 19 pseudogene 2	chr12q22	217338_at	---
2.24	2.29	0.05	7.55E-01	9.21E-01	ZNF663	zinc finger protein 663	chr20q13.12	1553911_at	XM_001715904 /// XM_001716205 /// XM_001716314
3.77	3.82	0.05	7.55E-01	9.21E-01	DGCR2	DiGeorge syndrome critical region gene 2	chr22q11.21	227028_s_at	NM_005137
3.90	3.94	0.04	7.55E-01	9.21E-01	C6orf162	chromosome 6 open reading frame 162	chr6q15-q16.1	213314_at	NM_001042493 /// NM_020425
2.70	2.74	0.04	7.55E-01	9.21E-01	ESR1	estrogen receptor 1	chr6q25.1	217163_at	NM_000125 /// NM_001122740 /// NM_001122741 /// NM_001122742
2.52	2.56	0.04	7.55E-01	9.21E-01	---	---	---	240090_at	---
3.38	3.42	0.04	7.55E-01	9.21E-01	---	---	---	1560214_at	---
2.37	2.41	0.04	7.55E-01	9.21E-01	SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	chr1p35.3	205309_at	NM_001009568 /// NM_014474
2.25	2.29	0.04	7.55E-01	9.21E-01	LOC100129289 /// PFTK1	similar to rCG41102 /// PFTAIRE protein kinase 1	chr7q21-q22 /// chr7q21.13	243761_at	NM_012395 /// XM_001717002 /// XM_001717218 /// XM_001717785
3.59	3.63	0.04	7.55E-01	9.21E-01	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	chr5qter	214535_s_at	NM_014244 /// NM_021599
1.87	1.91	0.04	7.55E-01	9.21E-01	POF1B	premature ovarian failure, 1B	chrXq21.1-q21.2	1555382_at	NM_024921
2.32	2.37	0.05	7.55E-01	9.21E-01	---	---	---	243913_at	---
2.59	2.63	0.04	7.55E-01	9.21E-01	---	---	---	243107_at	---
3.31	3.35	0.04	7.56E-01	9.22E-01	TADA3L	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	chr3p25.3	215272_at	NM_006354 /// NM_133480
8.62	8.85	0.23	7.56E-01	9.22E-01	SGK1	serum/glucocorticoid regulated kinase 1	chr6q23	201739_at	NM_005627
2.35	2.40	0.05	7.56E-01	9.22E-01	OR51E1	olfactory receptor, family 51, subfamily E, member 1	chr11p15.4	229768_at	NM_152430
3.99	4.05	0.06	7.56E-01	9.22E-01	S100A1	S100 calcium binding protein A1	chr1q21	205334_at	NM_006271
2.60	2.64	0.04	7.56E-01	9.22E-01	---	---	---	234500_at	---

2.23	2.31	0.08	7.56E-01	9.22E-01	ARMC8	armadillo repeat containing 8	chr3q22.3	1555279_at	NM_014154 /// NM_015396 /// NM_213654
5.26	5.34	0.09	7.56E-01	9.22E-01	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	chr1p31.1	227639_at	NM_005482
1.86	1.90	0.04	7.56E-01	9.22E-01	SPATA1	spermatogenesis associated 1	chr1p22.3	221057_at	NM_001081472
2.41	2.46	0.05	7.56E-01	9.22E-01	---	---	---	244736_at	---
2.62	2.68	0.06	7.56E-01	9.22E-01	NCK1	NCK adaptor protein 1	chr3q21	229895_s_at	NM_006153
1.72	1.76	0.04	7.56E-01	9.22E-01	---	---	---	1560372_at	---
2.20	2.25	0.04	7.56E-01	9.22E-01	C3orf70	chromosome 3 open reading frame 70	chr3q27.2	235562_at	NM_001025266
2.32	2.36	0.04	7.56E-01	9.22E-01	CATSPER2	cation channel, sperm associated 2	chr15q15.3	1561405_s_at	NM_054020 /// NM_172095 /// NM_172096 /// NM_172097
9.12	9.18	0.06	7.56E-01	9.22E-01	C14orf166	chromosome 14 open reading frame 166	chr14q22.1	217768_at	NM_016039
3.14	3.19	0.05	7.56E-01	9.22E-01	---	---	---	237872_at	---
3.94	4.05	0.12	7.56E-01	9.22E-01	---	---	---	232174_at	---
3.80	3.87	0.06	7.56E-01	9.22E-01	MGC39584	Hypothetical gene supported by BC029568	chr4q35.2	242822_at	XR_017735 /// XR_017787 /// XR_041937
3.15	3.20	0.05	7.56E-01	9.22E-01	FLJ21408	hypothetical gene supported by AK025061	chr16p12.1	234216_at	---
3.59	3.81	0.21	7.56E-01	9.22E-01	CALN1	calneuron 1	chr7q11	223885_at	NM_001017440 /// NM_031468
5.11	5.26	0.15	7.56E-01	9.22E-01	---	---	---	228562_at	---
6.05	6.14	0.09	7.56E-01	9.22E-01	RPL37A	Ribosomal protein L37a	chr2q35	214041_x_at	NM_000998
2.62	2.75	0.12	7.57E-01	9.22E-01	PRIMA1	proline rich membrane anchor 1	chr14q32.13	230087_at	NM_178013
7.87	7.96	0.09	7.57E-01	9.22E-01	DCTN6	dynactin 6	chr8p12-p11	203261_at	NM_006571
2.61	2.69	0.08	7.57E-01	9.22E-01	IPO11	importin 11	chr5q12.1	238488_at	NM_016338
2.47	2.53	0.06	7.57E-01	9.22E-01	ACOT11	acyl-CoA thioesterase 11	chr1p32.3	216103_at	NM_015547 /// NM_147161
2.84	2.90	0.06	7.57E-01	9.22E-01	---	---	---	239760_at	---
5.90	5.96	0.05	7.57E-01	9.22E-01	TMEM192	transmembrane protein 192	chr4q32.3	226589_at	NM_001100389
3.26	3.31	0.05	7.57E-01	9.22E-01	---	---	---	240092_at	---
4.34	4.48	0.14	7.57E-01	9.22E-01	---	---	---	241956_at	---
1.92	1.96	0.04	7.57E-01	9.22E-01	C21orf109	chromosome 21 open reading frame 109	chr21q22.11	1553607_at	---
2.08	2.11	0.03	7.57E-01	9.22E-01	YTHDC1	YTH domain containing 1	chr4q13.2	240459_at	NM_001031732 /// NM_133370
3.60	3.70	0.09	7.57E-01	9.22E-01	PLD4	phospholipase D family, member 4	chr14q32.33	235802_at	NM_138790
3.19	3.23	0.04	7.57E-01	9.22E-01	KLHDC7B	kelch domain containing 7B	chr22q13.33	1552639_at	NM_138433
1.90	1.94	0.04	7.57E-01	9.22E-01	---	---	---	239621_at	---
4.01	4.05	0.04	7.57E-01	9.22E-01	UNQ2963	hypothetical protein LOC283314	chr12p13.31	1564224_x_at	XR_039860 /// XR_039861 /// XR_039862
4.98	5.08	0.10	7.57E-01	9.22E-01	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	chr21q22.3	223183_at	NM_001037553 /// NM_020132
3.10	3.16	0.06	7.57E-01	9.22E-01	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	chr10q21	209442_x_at	NM_001149 /// NM_020987
3.32	3.38	0.06	7.57E-01	9.22E-01	FAM100A	family with sequence similarity 100, member A	chr16p13.3	1558976_x_at	NM_145253
2.54	2.60	0.06	7.57E-01	9.22E-01	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	chr3q26.1	1564231_at	NM_020800
2.80	2.86	0.05	7.57E-01	9.22E-01	ZSCAN18	zinc finger and SCAN domain containing 18	chr19q13.43	232866_at	NM_023926
2.07	2.10	0.04	7.57E-01	9.22E-01	LOC255025	hypothetical LOC255025	chr3q11.2	1556406_at	XM_173083 /// XM_943241
2.91	2.96	0.05	7.57E-01	9.22E-01	---	---	---	1560724_at	---
8.28	8.41	0.12	7.57E-01	9.22E-01	EIF2A	eukaryotic translation initiation factor 2A, 65kDa	chr3q25.1	223015_at	NM_032025
5.46	5.62	0.16	7.57E-01	9.22E-01	SYTL2	synaptotagmin-like 2	chr11q14	232914_s_at	NM_032379 /// NM_032943 /// NM_206927 /// NM_206928 /// NM_206929 /// NM_206930
2.71	2.76	0.05	7.57E-01	9.22E-01	---	---	---	217471_at	---
3.31	3.35	0.03	7.57E-01	9.22E-01	NOX1	NADPH oxidase 1	chrXq22	207380_x_at	NM_007052 /// NM_013955
2.25	2.30	0.05	7.57E-01	9.22E-01	FUT7	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	chr9q34.3	210506_at	NM_004479
2.24	2.28	0.04	7.57E-01	9.22E-01	KLHL3	kelch-like 3 (Drosophila)	chr5q31	1555110_a_at	NM_017415
3.48	3.54	0.06	7.57E-01	9.22E-01	FBXO18	F-box protein, helicase, 18	chr10p15.1	1559561_at	NM_032807 /// NM_178150

2.61	2.65	0.04	7.57E-01	9.22E-01	PCDHAC1 /// PCDHAC2	protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	chr5q31	224539_s_at	NM_018898 /// NM_018899 /// NM_031882 /// NM_031883																				
2.45	2.51	0.06	7.57E-01	9.22E-01	ARV1	ARV1 homolog (S. cerevisiae)	chr1q42.2	238140_at	NM_022786																				
1.84	1.88	0.04	7.57E-01	9.22E-01	---	---	---	1565788_at	---																				
2.12	2.15	0.03	7.57E-01	9.22E-01	ARMCX4	armadillo repeat containing, X-linked 4	chrXq22.1	1557726_at	NM_152583																				
3.07	3.13	0.06	7.58E-01	9.22E-01	DSG3	desmoglein 3 (pemphigus vulgaris antigen)	chr18q12.1-q12.2	205595_at	NM_001944																				
3.15	3.20	0.05	7.58E-01	9.22E-01	LOC100133229	hypothetical protein LOC100133229	chr12p13.31	238163_at	XM_001721004 /// XM_001722447 /// XM_001722628																				
2.20	2.25	0.05	7.58E-01	9.22E-01	PHF21B	PHD finger protein 21B	chr22q13.31	1560091_a_at	NM_138415																				
2.65	2.70	0.05	7.58E-01	9.22E-01	LOC284788	hypothetical protein LOC284788	chr20p11.21	1557483_at	---																				
2.95	2.98	0.04	7.58E-01	9.22E-01	TMEM182	transmembrane protein 182	chr2q12.1	238867_at	NM_144632																				
2.18	2.21	0.03	7.58E-01	9.22E-01	---	---	---	1560652_at	---																				
6.45	6.60	0.15	7.58E-01	9.22E-01	SSB	Sjogren syndrome antigen B (autoantigen La)	chr2q31.1	201139_s_at	NM_003142																				
3.78	3.92	0.14	7.58E-01	9.22E-01	NXT2	nuclear transport factor 2-like export factor 2	chrXq22.3	209629_s_at	NM_018698																				
2.03	2.07	0.04	7.58E-01	9.22E-01	CCL14 /// CCL15	chemokine (C-C motif) ligand 14 /// chemokine (C-C motif) ligand 15	chr17q11.2	210390_s_at	NM_004166 /// NM_004167 /// NM_032962 /// NM_032963 /// NM_032964 /// NM_032965																				
3.68	3.72	0.04	7.58E-01	9.22E-01	LOC100133686	hypothetical protein LOC100133686	---	237266_at	XM_001718404																				
2.47	2.56	0.10	7.58E-01	9.23E-01	---	---	---	223641_at	---																				
2.31	2.35	0.04	7.58E-01	9.23E-01	---	---	---	1560871_a_at	---																				
1.90	1.93	0.03	7.58E-01	9.23E-01	DKFZp761H2121	hypothetical protein DKFZp761H2121	chr10q26.13	1553864_at	---																				
4.92	5.14	0.21	7.58E-01	9.23E-01	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	chr2p16	201843_s_at	NM_001039348 /// NM_001039349 /// NM_004105																				
4.70	4.78	0.07	7.58E-01	9.23E-01	STARD8	StAR-related lipid transfer (START) domain containing 8	chrXq13.1	206868_at	NM_014725																				
7.73	7.79	0.06	7.58E-01	9.23E-01	PL-5283	PL-5283 protein	chr7q33	224752_at	NM_001130929 /// XM_930101 /// XM_935586 /// XM_938850																				
3.59	3.64	0.05	7.58E-01	9.23E-01	---	---	---	233410_at	---																				
1.84	1.88	0.04	7.58E-01	9.23E-01	PBRM1	polybromo 1	chr3p21	221212_x_at	NM_018165 /// NM_018313 /// NM_181042																				
2.14	2.18	0.04	7.58E-01	9.23E-01	DKFZP761C1711	Hypothetical protein DKFZp761C1711	---	234525_at	---																				
9.08	9.21	0.13	7.58E-01	9.23E-01	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	chr2q14.1	200996_at	NM_005721																				
2.47	2.51	0.04	7.58E-01	9.23E-01	C12orf54	chromosome 12 open reading frame 54	chr12q13.11	240354_at	NM_152319																				
2.93	2.99	0.06	7.58E-01	9.23E-01	SFXN5	sideroflexin 5	---	1563708_at	NM_144579																				
3.67	3.73	0.07	7.58E-01	9.23E-01	TROAP	trophinin associated protein (tastin)	chr12q13.12	1568596_a_at	NM_001100620 /// NM_005480																				
2.58	2.62	0.04	7.59E-01	9.23E-01	ZNF248	zinc finger protein 248	---	1569557_at	NM_021045																				
2.42	2.47	0.05	7.59E-01	9.23E-01	SLC19A1	Solute carrier family 19 (folate transporter), member 1	chr21q22.3	229639_s_at	NM_194255																				
3.39	3.46	0.07	7.59E-01	9.23E-01	FLJ33065	Hypothetical gene supported by AK057627; BC031275; BC045736	chr3p22.1	1556249_a_at	---																				
2.13	2.18	0.05	7.59E-01	9.23E-01	---	---	---	243586_at	---																				
2.15	2.19	0.04	7.59E-01	9.23E-01	ADAM18	ADAM metallopeptidase domain 18	chr8p11.22	207597_at	NM_014237																				
5.02	5.08	0.07	7.59E-01	9.23E-01	---	---	---	227069_at	---																				
3.39	3.45	0.06	7.59E-01	9.23E-01	---	---	---	239005_at	---																				
6.60	6.73	0.13	7.59E-01	9.23E-01	LONP2	lon peptidase 2, peroxisomal	chr16q12.1	223098_s_at	NM_031490																				
3.31	3.40	0.09	7.59E-01	9.23E-01	---	---	---	229284_at	---																				
1.87	1.91	0.04	7.59E-01	9.23E-01	MTMR7	myotubularin related protein 7	chr8p22	217292_at	NM_004686																				
4.98	5.14	0.17	7.59E-01	9.23E-01	MTERFD3	MTERF domain containing 3	chr12q24.1	225341_at	NM_001033050 /// NM_025198																				
1.96	2.00	0.04	7.59E-01	9.23E-01	SLC22A25	solute carrier family 22, member 25	chr11q12.3	1561094_a_at	NM_199352																				
6.74	6.83	0.10	7.59E-01	9.23E-01	FAM73B	family with sequence similarity 73, member B	chr9q34.11	226356_at	NM_032809																				
2.96	3.01	0.05	7.59E-01	9.23E-01	LOC283387	hypothetical protein LOC283387	chr12q13.2	1561233_at	---																				
2.59	2.63	0.05	7.59E-01	9.23E-01	LAMC3	laminin, gamma 3	chr9q31-q34	232558_at	NM_006059																				
7.53	7.61	0.08	7.60E-01	9.23E-01	---	---	---	244661_at	---																				
4.07	4.14	0.07	7.59E-01	9.23E-01	ZNF827	Zinc finger protein 827	chr4q31.22	243617_at	NM_178835																				

2.39	2.46	0.07	7.60E-01	9.23E-01	CC2D1A	coiled-coil and C2 domain containing 1A	chr19p13.12	222137_at	NM_017721
3.48	3.55	0.07	7.59E-01	9.23E-01	LOC100133572 /// LOC442381 /// LOC650293 /// OR7E125P /// OR7E37P /// OR7E87P /// UNC93B2 /// UNC93B4	similar to seven transmembrane helix receptor /// similar to seven transmembrane helix receptor /// seven transmembrane helix receptor /// olfactory receptor, family 7, subfamily E, member 125 pseudogene /// olfactory receptor, family 7, subfamily E, member 37 pseudogene /// olfactory receptor, family 7, subfamily E, member 87 pseudogene /// unc-93 homolog B2 pseudogene (C. elegans) /// unc-93 homolog B4 pseudogene (C. elegans)	chr11q13 /// chr13q14.11 /// chr4p16.2 /// chr7p22.1 /// chr8p23.1	216476_at	NM_001040071 /// NR_002163 /// XM_001716461 /// XM_001719874 /// XR_016363 /// XR_037209 /// XR_037560 /// XR_037638 /// XR_038242 /// XR_042149
2.45	2.50	0.05	7.60E-01	9.23E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	216056_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392
2.10	2.15	0.05	7.60E-01	9.23E-01	---	---	---	1561527_at	---
2.12	2.16	0.04	7.60E-01	9.23E-01	C17orf57	chromosome 17 open reading frame 57	chr17q21.32	1553626_a_at	NM_152347
6.00	6.12	0.13	7.60E-01	9.23E-01	CHMP2B	chromatin modifying protein 2B	chr3p11.2	202536_at	NM_014043
4.09	4.15	0.06	7.60E-01	9.23E-01	LOC159110 /// LOC401629 /// LOC401630	hypothetical protein LOC159110 /// LOC401629 /// LOC401630	chrYq11.221	235941_s_at	NR_002160 /// NR_002161
2.56	2.61	0.05	7.60E-01	9.23E-01	TYRO3P	TYRO3P protein tyrosine kinase pseudogene	chr15q24.2	1566934_at	---
2.80	2.85	0.05	7.60E-01	9.23E-01	IL1RN	interleukin 1 receptor antagonist	chr2q14.2	216243_s_at	NM_000577 /// NM_173841 /// NM_173842 /// NM_173843
2.28	2.32	0.05	7.60E-01	9.23E-01	---	---	---	234087_at	---
2.09	2.12	0.04	7.60E-01	9.23E-01	C12orf48	chromosome 12 open reading frame 48	chr12q23.2	227928_at	NM_017915
2.06	2.09	0.03	7.60E-01	9.23E-01	CCDC148	coiled-coil domain containing 148	chr2q24.1	231504_at	NM_138803
2.77	2.84	0.06	7.60E-01	9.23E-01	SGPP2	sphingosine-1-phosphate phosphotase 2	chr2q36.1	238567_at	NM_152386
5.25	5.30	0.06	7.60E-01	9.23E-01	---	---	---	243724_at	---
2.75	2.81	0.05	7.60E-01	9.23E-01	---	---	---	1561128_at	---
2.26	2.30	0.03	7.60E-01	9.23E-01	---	---	---	1558623_at	---
2.62	2.67	0.05	7.60E-01	9.23E-01	---	---	---	1562970_at	---
2.41	2.45	0.04	7.60E-01	9.23E-01	---	---	---	244319_at	---
2.69	2.73	0.04	7.60E-01	9.23E-01	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	chr17p13.3	239042_at	NM_018128
3.14	3.19	0.05	7.60E-01	9.24E-01	IGSF3	immunoglobulin superfamily, member 3	chr1p13	1552672_a_at	NM_001007237 /// NM_001542
2.19	2.24	0.05	7.60E-01	9.24E-01	RNF180	ring finger protein 180	chr5q12.2	242033_at	NM_001113561 /// NM_178532
2.58	2.62	0.04	7.60E-01	9.24E-01	---	---	---	1560772_a_at	---
3.32	3.37	0.05	7.60E-01	9.24E-01	MGC32805	hypothetical protein MGC32805	chr5q23.2	233475_at	---
4.65	4.72	0.07	7.61E-01	9.24E-01	---	---	---	232841_at	---
3.84	3.89	0.05	7.61E-01	9.24E-01	DLEC1	deleted in lung and esophageal cancer 1	chr3p22-p21.3	207896_s_at	NM_007335 /// NM_007337
2.39	2.44	0.05	7.61E-01	9.24E-01	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	chr10q21	207950_s_at	NM_001149 /// NM_020987
2.13	2.17	0.04	7.61E-01	9.24E-01	PTPRO	protein tyrosine phosphatase, receptor type, O	chr12p13.3-p13.2|12p13-p12	1554199_at	NM_002848 /// NM_030667 /// NM_030668 /// NM_030669 /// NM_030670 /// NM_030671
2.18	2.22	0.04	7.61E-01	9.24E-01	ACOXL	acyl-Coenzyme A oxidase-like	chr2q13	220845_at	NM_001105516
8.81	8.86	0.05	7.61E-01	9.24E-01	DRG1	developmentally regulated GTP binding protein 1	chr22q12.2	202810_at	NM_004147
4.53	4.58	0.05	7.61E-01	9.24E-01	HYPK	Huntingtin interacting protein K	chr15q15.3	233809_at	NM_016400
3.39	3.44	0.05	7.61E-01	9.24E-01	---	---	---	233398_at	---
1.86	1.90	0.04	7.61E-01	9.24E-01	FLJ35848	hypothetical protein FLJ35848	chr17q21.31	1557206_at	NM_001033659
7.65	7.83	0.18	7.61E-01	9.24E-01	IGF2	insulin-like growth factor 2 (somatomedin A)	chr11p15.5	202409_at	NM_000612 /// NM_001007139 /// NM_001127598

5.05	5.17	0.12	7.61E-01	9.24E-01	QKI	quaking homolog, KH domain RNA binding (mouse)	chr6q26|6q26-q27	1555154_a_at	NM_006775 /// NM_206853 /// NM_206854 /// NM_206855																				
7.58	7.67	0.10	7.61E-01	9.24E-01	MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	chr2p13.1	214812_s_at	NM_018221																				
4.82	4.91	0.09	7.61E-01	9.24E-01	BAIAP2L1	BAI1-associated protein 2-like 1	chr7q21.3	227371_at	NM_018842																				
4.08	4.16	0.08	7.61E-01	9.24E-01	GLB1L	galactosidase, beta 1-like	chr2q35	206540_at	NM_024506																				
8.60	8.68	0.07	7.61E-01	9.24E-01	GNS	glucosamine (N-acetyl)-6-sulfatase	chr12q14	212335_at	NM_002076																				
5.52	5.58	0.06	7.61E-01	9.24E-01	DND1	dead end homolog 1 (zebrafish)	chr5q31.3	222070_at	NM_194249																				
3.95	4.01	0.06	7.61E-01	9.24E-01	---	---	---	236372_at	---																				
2.38	2.44	0.06	7.61E-01	9.24E-01	SOCS4	suppressor of cytokine signaling 4	chr14q22.3	1552792_at	NM_080867 /// NM_199421																				
7.38	7.43	0.06	7.61E-01	9.24E-01	FNIP1	folliculin interacting protein 1	chr5q23.3	228768_at	NM_001008738 /// NM_133372																				
2.11	2.15	0.05	7.61E-01	9.24E-01	SHOX2	short stature homeobox 2	chr3q25-q26.1	208443_x_at	NM_003030 /// NM_006884																				
2.71	2.76	0.05	7.61E-01	9.24E-01	C12orf42	chromosome 12 open reading frame 42	chr12q23.2-q23.3	239977_at	NM_001099336 /// NM_198521																				
2.78	2.82	0.05	7.61E-01	9.24E-01	KCNJ9	potassium inwardly-rectifying channel, subfamily J, member 9	chr1q21-q23	207527_at	NM_004983																				
6.35	6.39	0.05	7.61E-01	9.24E-01	C14orf21	chromosome 14 open reading frame 21	chr14q12	225514_at	NM_174913																				
3.40	3.44	0.04	7.61E-01	9.24E-01	TAF3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa	chr10p15.1	235154_at	NM_031923																				
3.58	3.62	0.04	7.61E-01	9.24E-01	LRRC36	leucine rich repeat containing 36	chr16q22.1	220003_at	NM_018296																				
2.61	2.65	0.04	7.61E-01	9.24E-01	---	---	---	1569802_at	---																				
2.05	2.08	0.03	7.61E-01	9.24E-01	FGF14	fibroblast growth factor 14	chr13q34	231523_at	NM_004115 /// NM_175929																				
5.11	5.25	0.14	7.61E-01	9.24E-01	FAM101B	family with sequence similarity 101, member B	chr17p13	226905_at	NM_182705																				
5.89	5.95	0.06	7.61E-01	9.24E-01	DRG2	developmentally regulated GTP binding protein 2	chr17p11.2	203268_s_at	NM_001388																				
7.95	7.99	0.04	7.61E-01	9.24E-01	UFD1L	ubiquitin fusion degradation 1 like (yeast)	chr22q11.21	209103_s_at	NM_001035247 /// NM_005659																				
3.91	4.00	0.10	7.61E-01	9.24E-01	TFRC	transferrin receptor (p90, CD71)	chr3q29	237215_s_at	NM_001128148 /// NM_003234																				
2.03	2.07	0.04	7.61E-01	9.24E-01	MSX2	msh homeobox 2	chr5q34-q35	205556_at	NM_002449																				
2.40	2.45	0.06	7.62E-01	9.24E-01	---	---	---	239797_at	---																				
3.46	3.56	0.10	7.62E-01	9.24E-01	MGC16385	hypothetical protein MGC16385	chr16q24.3	1552330_at	NM_145039																				
2.20	2.24	0.04	7.62E-01	9.24E-01	---	---	---	237712_at	---																				
6.98	7.04	0.06	7.62E-01	9.24E-01	BRSK1	BR serine/threonine kinase 1	chr19q13.4	1552504_a_at	NM_032430																				
5.96	6.10	0.13	7.62E-01	9.24E-01	BRD7	bromodomain containing 7	chr16q12	221776_s_at	NM_013263																				
7.76	7.83	0.07	7.62E-01	9.24E-01	DGAT1 /// LOC727765	diacylglycerol O-acyltransferase homolog 1 (mouse) /// similar to diacylglycerol O-acyltransferase homolog 1 (mouse)	chr8q24.3	203669_s_at	NM_012079 /// XM_001719374																				
12.93	12.99	0.07	7.62E-01	9.24E-01	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	chr6q14.1	206559_x_at	NM_001402																				
3.37	3.43	0.06	7.62E-01	9.24E-01	ZNF70	zinc finger protein 70	chr22q11.2|22q11.23	1554578_at	NM_021916																				
2.42	2.47	0.05	7.62E-01	9.24E-01	NEU3	sialidase 3 (membrane sialidase)	chr11q13.5	206948_at	NM_006656																				
2.44	2.48	0.04	7.62E-01	9.24E-01	---	---	---	237172_at	---																				
1.81	1.84	0.03	7.62E-01	9.24E-01	---	---	---	1563135_at	---																				
2.66	2.70	0.05	7.62E-01	9.24E-01	ACAD9	Acyl-Coenzyme A dehydrogenase family, member 9	chr3q21.3	239976_at	NM_014049																				
3.10	3.17	0.07	7.62E-01	9.24E-01	BRUNOL4	bruno-like 4, RNA binding protein (Drosophila)	chr18q12	223653_x_at	NM_001025087 /// NM_001025088 /// NM_001025089 /// NM_020180																				
2.14	2.18	0.04	7.62E-01	9.24E-01	---	---	---	217151_at	---																				
2.27	2.31	0.04	7.62E-01	9.24E-01	GNAL	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	chr18p11.22-p11.21	206356_s_at	NM_002071 /// NM_182978																				
2.74	2.79	0.05	7.62E-01	9.24E-01	---	---	---	234322_at	---																				
2.59	2.64	0.05	7.62E-01	9.24E-01	KANK1	KN motif and ankyrin repeat domains 1	chr9p24.3	216763_at	NM_015158 /// NM_153186																				
2.08	2.12	0.04	7.62E-01	9.24E-01	---	---	---	216121_at	---																				
2.10	2.13	0.03	7.62E-01	9.24E-01	---	---	---	240636_at	---																				

2.38	2.41	0.03	7.62E-01	9.24E-01	KHDC1 /// RP11-257K9.7	KH homology domain containing 1 /// hypothetical protein LOC100129128	chr6q13	220513_at	NM_001126063 /// NM_030568 /// XM_001716256 /// XM_001718926 /// XM_001725050
6.46	6.56	0.10	7.62E-01	9.24E-01	DCAKD	dephospho-CoA kinase domain containing	chr17q21.31	224522_s_at	NM_001128631 /// NM_024819
6.33	6.43	0.10	7.63E-01	9.24E-01	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	chr11q13	208997_s_at	NM_003355
3.58	3.67	0.09	7.63E-01	9.24E-01	---	---	---	236297_at	---
2.05	2.08	0.04	7.63E-01	9.24E-01	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	chr6q14	223891_at	NM_019842
2.29	2.35	0.06	7.63E-01	9.24E-01	---	---	---	1562891_at	---
8.36	8.42	0.06	7.63E-01	9.24E-01	HLA-G	major histocompatibility complex, class I, G	chr6p21.3	210514_x_at	NM_002127
4.79	4.93	0.13	7.63E-01	9.24E-01	FMO3	flavin containing monooxygenase 3	chr1q23-q25	206496_at	NM_001002294 /// NM_006894
2.95	3.00	0.05	7.63E-01	9.24E-01	---	---	---	238750_at	---
5.27	5.42	0.15	7.63E-01	9.25E-01	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	chr3p21	1554411_at	NM_001098209 /// NM_001098210 /// NM_001904
11.85	11.95	0.10	7.63E-01	9.25E-01	RPL17	ribosomal protein L17	chr18q21	212270_x_at	NM_000985 /// NM_001035006
2.57	2.64	0.06	7.63E-01	9.25E-01	---	---	---	220914_at	---
2.21	2.27	0.06	7.63E-01	9.25E-01	MAGEB3	melanoma antigen family B, 3	chrXp21.3	207579_at	NM_002365
2.53	2.59	0.05	7.63E-01	9.25E-01	---	---	---	234203_at	---
3.06	3.11	0.05	7.63E-01	9.25E-01	---	---	---	241687_at	---
2.50	2.54	0.05	7.63E-01	9.25E-01	---	---	---	232580_x_at	---
2.17	2.22	0.05	7.63E-01	9.25E-01	LOC644135	Hypothetical LOC644135	chr6q23.3	240581_at	XR_039968
2.38	2.42	0.04	7.63E-01	9.25E-01	C12orf69	chromosome 12 open reading frame 69	chr12p12.3	237484_at	NM_001013698
2.03	2.06	0.04	7.63E-01	9.25E-01	RSPO2	R-spondin 2 homolog (Xenopus laevis)	chr8q23.1	1554012_at	NM_178565
2.87	2.92	0.05	7.63E-01	9.25E-01	IQCF2	IQ motif containing F2	chr3p21.1	236767_at	NM_203424
2.75	2.79	0.04	7.63E-01	9.25E-01	---	---	---	1566490_at	---
3.02	3.05	0.04	7.63E-01	9.25E-01	---	---	---	1561223_at	---
1.88	1.92	0.04	7.63E-01	9.25E-01	PYHIN1	pyrin and HIN domain family, member 1	chr1q23.1	240413_at	NM_152501 /// NM_198928 /// NM_198929 /// NM_198930
3.57	3.63	0.06	7.63E-01	9.25E-01	---	---	---	237430_at	---
6.05	6.10	0.05	7.63E-01	9.25E-01	NUTF2	Nuclear transport factor 2	chr16q22.1	228379_at	NM_005796
3.02	3.06	0.04	7.63E-01	9.25E-01	TBC1D28	TBC1 domain family, member 28	chr17p11.2	233462_at	NM_001039397
2.04	2.08	0.04	7.63E-01	9.25E-01	MPZL3	myelin protein zero-like 3	chr11q23.3	1570584_at	NM_198275
3.93	4.11	0.18	7.64E-01	9.25E-01	ADAM10	ADAM metallopeptidase domain 10	chr15q2|15q22	214895_s_at	NM_001110
7.58	7.68	0.10	7.64E-01	9.25E-01	NCOA1	nuclear receptor coactivator 1	chr2p23	209107_x_at	NM_003743 /// NM_147223 /// NM_147233
4.00	4.07	0.08	7.64E-01	9.25E-01	TBX10	T-box 10	chr11q13.2	222377_at	NM_005995
3.48	3.53	0.06	7.64E-01	9.25E-01	---	---	---	1570167_at	---
5.78	5.86	0.09	7.64E-01	9.25E-01	SOCS7	suppressor of cytokine signaling 7	chr17q12	226572_at	NM_014598
2.90	2.97	0.06	7.64E-01	9.25E-01	C1orf187	chromosome 1 open reading frame 187	chr1p36.22	1558368_s_at	NM_198545
7.79	8.00	0.21	7.64E-01	9.25E-01	---	---	---	1559117_at	---
3.62	3.70	0.08	7.64E-01	9.25E-01	LOC100132798	Similar to hCG1774772	chr15q26.2	244655_at	XM_001721122 /// XM_001722414 /// XM_001722478
4.33	4.38	0.05	7.64E-01	9.25E-01	LOC653390	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	chr16p11.2	230952_at	NR_003369
2.82	2.87	0.05	7.64E-01	9.25E-01	RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	chr12q13.1	215027_at	NM_001098531 /// NM_001098532 /// NM_006105
4.32	4.36	0.05	7.64E-01	9.25E-01	---	---	---	1561044_at	---
2.76	2.81	0.04	7.64E-01	9.25E-01	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	chr2p22.1	211439_at	NM_001031684

2.43	2.48	0.04	7.64E-01	9.25E-01	---	---	---	237862_at	---
4.53	4.56	0.04	7.64E-01	9.25E-01	ZNF449	zinc finger protein 449	chrXq26.3	241066_at	NM_152695
2.62	2.66	0.03	7.64E-01	9.25E-01	BSDC1	BSD domain containing 1	chr1p35.1	1559971_at	NM_018045
5.12	5.24	0.12	7.64E-01	9.25E-01	TWISTNB	TWIST neighbor	chr7p15.3	226784_at	NM_001002926
4.00	4.08	0.07	7.64E-01	9.25E-01	ZNF564	zinc finger protein 564	chr19p13.2	1553957_at	NM_144976
4.37	4.44	0.07	7.65E-01	9.25E-01	ANO7	anoctamin 7	chr2q37.3	241918_at	NM_001001666 /// NM_001001891
2.98	3.04	0.07	7.64E-01	9.25E-01	---	---	---	242306_at	---
3.59	3.65	0.06	7.65E-01	9.25E-01	---	---	---	236486_at	---
3.21	3.26	0.05	7.65E-01	9.25E-01	SIPA1L3	signal-induced proliferation-associated 1 like 3	chr19q13.13	236096_at	NM_015073
2.02	2.07	0.05	7.64E-01	9.25E-01	S100A1L	Protein S100-A1-like	chr3p14.2	239150_at	NM_001080537
3.21	3.26	0.05	7.64E-01	9.25E-01	SOX3	SRY (sex determining region Y)-box 3	chrXq27.1	1553802_a_at	NM_005634
7.45	7.50	0.05	7.64E-01	9.25E-01	MRPL30	mitochondrial ribosomal protein L30	chr2q11.2	224971_at	NM_145212 /// NM_145213
2.49	2.53	0.05	7.64E-01	9.25E-01	---	---	---	236010_at	---
2.92	2.97	0.04	7.64E-01	9.25E-01	ZNF395	zinc finger protein 395	chr8p21.1	232694_at	NM_018660
3.28	3.32	0.04	7.64E-01	9.25E-01	---	---	---	243787_at	---
2.53	2.57	0.04	7.65E-01	9.25E-01	CNOT2	CCR4-NOT transcription complex, subunit 2	chr12q15	233054_at	NM_014515
2.57	2.61	0.04	7.64E-01	9.25E-01	---	---	---	236276_at	---
2.06	2.09	0.03	7.64E-01	9.25E-01	NMT2	N-myristoyltransferase 2	chr10p13	215743_at	NM_004808
1.87	1.90	0.03	7.64E-01	9.25E-01	---	---	---	240914_at	---
1.94	1.97	0.03	7.64E-01	9.25E-01	SPOCK3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	chr4q32.3	1554418_s_at	NM_001040159 /// NM_016950
5.39	5.49	0.10	7.65E-01	9.25E-01	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	chr19q13.33	234068_s_at	NM_014203 /// NM_130787
4.19	4.29	0.10	7.65E-01	9.25E-01	NGLY1	N-glycanase 1	chr3p24.2	207492_at	NM_018297
2.12	2.17	0.05	7.65E-01	9.25E-01	C6orf204	chromosome 6 open reading frame 204	chr6q22	232444_at	NM_001042475 /// NM_206921
5.41	5.54	0.13	7.65E-01	9.25E-01	MAN1C1	mannosidase, alpha, class 1C, member 1	chr1p35	218918_at	NM_020379
1.97	2.00	0.04	7.65E-01	9.25E-01	---	---	---	244083_at	---
4.57	4.64	0.07	7.65E-01	9.25E-01	C19orf12	chromosome 19 open reading frame 12	chr19q12	227704_at	NM_001031726 /// NM_031448
2.46	2.50	0.04	7.65E-01	9.25E-01	CBLN2	cerebellin 2 precursor	chr18q22.3	242301_at	NM_182511
2.49	2.53	0.04	7.65E-01	9.25E-01	FAM75A1 /// FAM75A2 /// FAM75A3 /// FAM75A4 /// FAM75A5 /// FAM75A6 /// FAM75A7	family with sequence similarity 75, member A1 /// family with sequence similarity 75, member A2 /// family with sequence similarity 75, member A3 /// family with sequence similarity 75, member A4 /// family with sequence similarity 75, member A5 /// family with sequence similarity 75, member A6 /// family with sequence similarity 75, member A7	chr9p11.2 /// chr9p12 /// chr9p13.1 /// chr9q12	215935_at	NM_001040065 /// NM_001083124 /// NM_001085452 /// NM_001113541 /// NM_015667 /// XM_001714924 /// XM_001714927 /// XM_001714938 /// XM_001715076 /// XM_001715083 /// XM_001715093 /// XR_041504 /// XR_041505 /// XR_041506 /// XR_041507
4.32	4.37	0.04	7.65E-01	9.25E-01	---	---	---	243216_x_at	---
4.49	4.57	0.08	7.65E-01	9.25E-01	LOC92270	hypothetical protein LOC92270	chr5q14.2	228816_at	NM_001017971
2.42	2.49	0.07	7.65E-01	9.25E-01	KLF12	Kruppel-like factor 12	chr13q22	229881_at	NM_007249
2.55	2.61	0.06	7.65E-01	9.25E-01	SLC5A7	solute carrier family 5 (choline transporter), member 7	chr2q12	220722_s_at	NM_021815
3.54	3.58	0.05	7.65E-01	9.25E-01	SPATA16	spermatogenesis associated 16	chr3q26.31	223876_at	NM_031955
2.20	2.24	0.04	7.65E-01	9.25E-01	---	---	---	1556261_a_at	---
2.41	2.46	0.04	7.65E-01	9.25E-01	FAM164B	family with sequence similarity 164, member B	chr6q24.2	237592_at	NM_001013623 /// XM_001723038 /// XM_928657 /// XM_941265
2.00	2.04	0.03	7.65E-01	9.25E-01	RNF141	ring finger protein 141	chr11p15.4	1565546_at	NM_016422
6.48	6.60	0.12	7.65E-01	9.25E-01	KPNB1	karyopherin (importin) beta 1	chr17q21.32	208975_s_at	NM_002265

6.70	6.81	0.11	7.65E-01	9.25E-01	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	chr14q32	1554365_a_at	NM_002719 /// NM_178586 /// NM_178587 /// NM_178588
6.61	6.69	0.08	7.65E-01	9.25E-01	RHOQ	ras homolog gene family, member Q	chr2p21	212120_at	NM_012249
2.71	2.77	0.06	7.65E-01	9.25E-01	CHRNA10	Cholinergic receptor, nicotinic, alpha 10	chr11p15.5	1568675_at	NM_020402
2.94	2.98	0.04	7.65E-01	9.25E-01	FAM169B	family with sequence similarity 169, member B	chr15q26.3	1562319_at	NM_182562
1.99	2.03	0.04	7.65E-01	9.25E-01	---	---	---	238178_at	---
1.96	2.00	0.04	7.65E-01	9.25E-01	MAGEB4	melanoma antigen family B, 4	chrXp21.3	207580_at	NM_002367
3.59	3.89	0.30	7.65E-01	9.25E-01	POSTN	periostin, osteoblast specific factor	chr13q13.3	1555778_a_at	NM_006475
3.51	3.57	0.06	7.66E-01	9.25E-01	---	---	---	1556274_at	---
3.50	3.55	0.05	7.66E-01	9.25E-01	LCN1	lipocalin 1 (tear prealbumin)	chr9q34	207930_at	NM_002297
1.97	2.00	0.04	7.66E-01	9.25E-01	---	---	---	240627_x_at	---
4.41	4.50	0.09	7.66E-01	9.25E-01	MSR1	macrophage scavenger receptor 1	chr8p22	214770_at	NM_002445 /// NM_138715 /// NM_138716
7.08	7.15	0.07	7.66E-01	9.25E-01	UCRC	ubiquinol-cytochrome c reductase complex (7.2 kD)	chr22cen-q12.3	228142_at	NM_001003684 /// NM_013387
2.12	2.16	0.04	7.66E-01	9.25E-01	---	---	---	244793_at	---
2.25	2.28	0.03	7.66E-01	9.25E-01	---	---	---	1570273_at	---
1.98	2.02	0.05	7.66E-01	9.25E-01	VWA3B	von Willebrand factor A domain containing 3B	chr2q11.2	1562371_s_at	NM_144992
2.44	2.48	0.03	7.66E-01	9.25E-01	CLTB	Clathrin, light chain (Lcb)	chr4q2-q3|5q35	221996_s_at	NM_001834 /// NM_007097
3.06	3.12	0.06	7.66E-01	9.25E-01	C6orf174	chromosome 6 open reading frame 174	chr6q22.33	1569146_s_at	NM_001012279
2.76	2.79	0.03	7.66E-01	9.25E-01	---	---	---	1559350_at	---
3.02	3.08	0.06	7.66E-01	9.25E-01	SLC45A2	solute carrier family 45, member 2	chr5p13.3	220245_at	NM_001012509 /// NM_016180
2.02	2.06	0.03	7.66E-01	9.25E-01	LOC339260	Hypothetical gene supported by BC072410	chr17p11.2	1564360_a_at	---
1.73	1.76	0.03	7.66E-01	9.25E-01	---	---	---	1556207_a_at	---
2.78	2.84	0.07	7.66E-01	9.25E-01	PTK2	PTK2 protein tyrosine kinase 2	chr8q24-qter	1559529_at	NM_005607 /// NM_153831
3.82	3.87	0.05	7.66E-01	9.25E-01	TACR2	tachykinin receptor 2	chr10q11-q21	214348_at	NM_001057
5.37	5.42	0.05	7.66E-01	9.25E-01	MAPK11	mitogen-activated protein kinase 11	chr22q13.33	211500_at	NM_002751
2.62	2.67	0.05	7.66E-01	9.25E-01	---	---	---	1568742_at	---
2.05	2.08	0.04	7.66E-01	9.25E-01	---	---	---	217259_at	---
3.25	3.30	0.04	7.67E-01	9.25E-01	KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2	chr8q22	1554212_s_at	NM_020697
2.07	2.10	0.03	7.67E-01	9.25E-01	TXNDC10	thioredoxin domain containing 10	chr18q22	1552822_at	NM_019022
5.36	5.44	0.08	7.67E-01	9.25E-01	PHF19	PHD finger protein 19	chr9q33.2	225533_at	NM_001009936 /// NM_015651
5.47	5.51	0.04	7.67E-01	9.25E-01	---	---	---	232516_x_at	---
6.77	6.84	0.08	7.67E-01	9.26E-01	MRPS18A	mitochondrial ribosomal protein S18A	chr6p21.3	221693_s_at	NM_018135
3.33	3.39	0.06	7.67E-01	9.26E-01	---	---	---	1558890_at	---
7.07	7.12	0.05	7.67E-01	9.26E-01	TRUB2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	chr9q34.11	223109_at	NM_015679
3.40	3.44	0.04	7.67E-01	9.26E-01	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	chr7q22.1	1564165_at	NM_024653
2.52	2.58	0.06	7.67E-01	9.26E-01	ALG10	asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase)	chr12p11.1	1552304_at	NM_032834
6.89	7.00	0.11	7.67E-01	9.26E-01	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	chr4q13.3	226153_s_at	NM_144571
4.31	4.41	0.09	7.67E-01	9.26E-01	STX17	syntaxin 17	chr9q31.1	228091_at	NM_017919
3.12	3.21	0.09	7.67E-01	9.26E-01	---	---	---	242261_at	---
2.61	2.66	0.05	7.67E-01	9.26E-01	KIF13A	kinesin family member 13A	chr6p23	230990_at	NM_001105566 /// NM_001105567 /// NM_001105568 /// NM_022113
3.06	3.11	0.05	7.67E-01	9.26E-01	CECR4	cat eye syndrome chromosome region, candidate 4 (non-protein coding)	chr22q11.1	1559920_a_at	XM_001721039 /// XM_001725494 /// XM_001726306
4.18	4.23	0.05	7.67E-01	9.26E-01	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	chr19q13.2	210789_x_at	NM_001815
4.69	4.80	0.11	7.67E-01	9.26E-01	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	chr17p13.3	218156_s_at	NM_018128
2.00	2.04	0.04	7.67E-01	9.26E-01	---	---	---	224216_at	---
2.39	2.45	0.06	7.67E-01	9.26E-01	LOC100129546	hypothetical protein LOC100129546	chrXq13.1	237219_at	XM_001720535 /// XM_001721140 /// XM_001721946

2.55	2.60	0.05	7.67E-01	9.26E-01	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	chr17q24-q25|17q25.1	207656_s_at	NM_004035 /// NM_007292
5.93	6.04	0.11	7.67E-01	9.26E-01	RP1-27O5.1 /// ZBTB8	zinc finger and BTB domain containing 8-like /// zinc finger and BTB domain containing 8	chr1p35.1	235142_at	NM_001040441 /// XR_040711 /// XR_040712 /// XR_040713
2.95	3.02	0.06	7.67E-01	9.26E-01	---	---	---	230139_at	---
3.46	3.52	0.06	7.67E-01	9.26E-01	PIGQ	phosphatidylinositol glycan anchor biosynthesis, class Q	chr16p13.3	1555359_at	NM_004204 /// NM_148920
7.51	7.57	0.06	7.67E-01	9.26E-01	SQRDL	sulfide quinone reductase-like (yeast)	chr15q15	217995_at	NM_021199
7.29	7.41	0.12	7.68E-01	9.26E-01	SELT	selenoprotein T	chr3q25.1	225561_at	NM_016275
1.90	1.94	0.04	7.67E-01	9.26E-01	GALNTL5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5	chr7q36.1	233150_at	NM_145292
2.12	2.15	0.03	7.68E-01	9.26E-01	---	---	---	241356_at	---
2.10	2.13	0.04	7.68E-01	9.26E-01	---	---	---	1566463_at	---
2.84	2.89	0.05	7.68E-01	9.26E-01	---	---	---	1563283_at	---
3.69	3.79	0.10	7.68E-01	9.26E-01	PPARG	peroxisome proliferator-activated receptor gamma	chr3p25	208510_s_at	NM_005037 /// NM_015869 /// NM_138711 /// NM_138712
2.75	2.81	0.07	7.68E-01	9.26E-01	---	---	---	238289_at	---
5.97	6.02	0.06	7.68E-01	9.26E-01	AQP12A /// AQP12B	aquaporin 12A /// aquaporin 12B	chr2q37.3	1554344_s_at	NM_001102467 /// NM_198998
4.24	4.42	0.18	7.68E-01	9.26E-01	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	chr12q24.2-q24.3	216450_x_at	NM_003299
3.12	3.18	0.06	7.68E-01	9.26E-01	DKFZP547L112	hypothetical protein DKFZp547L112	chr15q11.2	234912_at	XR_041953 /// XR_041954 /// XR_041955
4.97	5.02	0.05	7.68E-01	9.26E-01	BCL6B	B-cell CLL/lymphoma 6, member B (zinc finger protein)	chr17p13.1	228311_at	NM_181844
2.24	2.28	0.05	7.68E-01	9.26E-01	LOC339047	Hypothetical protein LOC339047	chr16p13.11	1558075_at	NM_178541 /// XM_001134445
2.43	2.47	0.04	7.68E-01	9.26E-01	HIF3A	Hypoxia inducible factor 3, alpha subunit	chr19q13.32	232669_at	NM_022462 /// NM_152794 /// NM_152795
6.22	6.32	0.10	7.68E-01	9.26E-01	RNF135	ring finger protein 135	chr17q11.2	223591_at	NM_032322 /// NM_197939
3.11	3.16	0.04	7.68E-01	9.26E-01	TNAP	TRAFs and NIK-associated protein	---	1555707_at	XR_040533 /// XR_040534 /// XR_040535
3.08	3.16	0.08	7.68E-01	9.26E-01	---	---	---	215083_at	---
8.24	8.32	0.09	7.68E-01	9.26E-01	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	chrXq13.3	201312_s_at	NM_003022
1.98	2.01	0.03	7.68E-01	9.26E-01	OR2H1	Olfactory receptor, family 2, subfamily H, member 1	chr6p21.3	1567656_at	NM_030883
2.63	2.68	0.05	7.68E-01	9.26E-01	RABGAP1L	RAB GTPase activating protein 1-like	chr1q24	232702_at	NM_001035230 /// NM_014857
2.02	2.05	0.03	7.68E-01	9.26E-01	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	chr10q21-q24	236281_x_at	NM_000872 /// NM_019859 /// NM_019860
1.82	1.85	0.04	7.69E-01	9.26E-01	UGT2B17	UDP glucuronosyltransferase 2 family, polypeptide B17	chr4q13	207245_at	NM_001077
4.11	4.21	0.09	7.69E-01	9.27E-01	HOPX	HOP homeobox	chr4q11-q12	1566140_at	NM_032495 /// NM_139211 /// NM_139212
2.92	2.98	0.06	7.69E-01	9.27E-01	TLX1	T-cell leukemia homeobox 1	chr10q24	207179_at	NM_005521
2.07	2.11	0.04	7.69E-01	9.27E-01	SPINK1	serine peptidase inhibitor, Kazal type 1	chr5q32	206239_s_at	NM_003122
2.30	2.34	0.04	7.69E-01	9.27E-01	ADAM21 /// ADAM21P	ADAM metallopeptidase domain 21 /// ADAM metallopeptidase domain 21 pseudogene	chr14q24.1 /// chr14q24.2	207665_at	NM_003813 /// NR_003951
6.55	6.63	0.08	7.69E-01	9.27E-01	ACOT8	acyl-CoA thioesterase 8	chr20q13.12	204212_at	NM_005469 /// NM_183386
2.03	2.07	0.04	7.69E-01	9.27E-01	MYNN	myoneurin	chr3q26.2	1566109_at	NM_018657
8.52	8.62	0.10	7.69E-01	9.27E-01	CDV3	CDV3 homolog (mouse)	chr3q22.1	212010_s_at	NM_001134422 /// NM_001134423 /// NM_017548
2.38	2.44	0.06	7.69E-01	9.27E-01	LOC100130809 /// SRY	hypothetical protein LOC100130809 /// sex determining region Y	chrYp11.3	207893_at	NM_003140 /// XM_001713691
2.51	2.56	0.06	7.69E-01	9.27E-01	MYO5B	myosin VB	chr18q21	225299_at	NM_001080467
4.43	4.48	0.05	7.69E-01	9.27E-01	GAS2L2	growth arrest-specific 2 like 2	chr17q12	1552596_at	NM_139285
4.62	4.73	0.12	7.69E-01	9.27E-01	ECSM2	endothelial cell-specific molecule 2	chr5q31.2	227780_s_at	NM_001077693
3.92	4.02	0.10	7.69E-01	9.27E-01	---	---	---	239175_at	---
2.22	2.26	0.04	7.69E-01	9.27E-01	---	---	---	1569585_at	---
5.19	5.29	0.10	7.69E-01	9.27E-01	PTHR1	parathyroid hormone receptor 1	chr3p22-p21.1	205911_at	NM_000316

4.35	4.43	0.09	7.69E-01	9.27E-01	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	chr2q33-q34	210214_s_at	NM_001204
2.93	2.98	0.06	7.69E-01	9.27E-01	---	---	---	241092_at	---
5.11	5.29	0.18	7.69E-01	9.27E-01	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	chr1q23	210889_s_at	NM_001002273 /// NM_001002274 /// NM_001002275 /// NM_004001
3.41	3.46	0.05	7.69E-01	9.27E-01	---	---	---	227509_x_at	---
2.14	2.17	0.03	7.69E-01	9.27E-01	---	---	---	1569927_at	---
2.11	2.15	0.04	7.69E-01	9.27E-01	---	---	---	1562532_at	---
6.18	6.29	0.12	7.69E-01	9.27E-01	NPAL2	NIPA-like domain containing 2	chr8q22.2	227001_at	NM_024759
2.57	2.62	0.05	7.69E-01	9.27E-01	---	---	---	233426_at	---
2.21	2.24	0.04	7.69E-01	9.27E-01	LOC283567	hypothetical protein LOC283567	chr14q24.1	237032_x_at	---
2.65	2.69	0.03	7.69E-01	9.27E-01	RBM43	RNA binding motif protein 43	chr2q23.3	243038_at	NM_198557
2.65	2.69	0.04	7.70E-01	9.27E-01	GABRQ	gamma-aminobutyric acid (GABA) receptor, theta	chrXq28	238123_at	NM_018558
3.51	3.55	0.04	7.70E-01	9.27E-01	ASB7	ankyrin repeat and SOCS box-containing 7	---	233807_at	NM_024708 /// NM_198243
7.41	7.53	0.12	7.70E-01	9.27E-01	PNPLA8	patatin-like phospholipase domain containing 8	chr7q31	223310_x_at	NM_015723
3.00	3.06	0.06	7.70E-01	9.27E-01	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	chr17q25.3	213606_s_at	NM_004309
2.23	2.27	0.04	7.70E-01	9.27E-01	---	---	---	1561767_at	---
2.25	2.28	0.04	7.70E-01	9.27E-01	---	---	---	1559331_x_at	---
2.37	2.40	0.03	7.70E-01	9.27E-01	VIL1	villin 1	chr2q35-q36	1554945_x_at	NM_007127
5.86	5.97	0.11	7.70E-01	9.27E-01	---	---	---	243561_at	---
5.07	5.15	0.09	7.70E-01	9.27E-01	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	chr7p15.1	217785_s_at	NM_006555
2.22	2.26	0.04	7.70E-01	9.27E-01	BBS9	Bardet-Biedl syndrome 9	chr7p14	1555555_at	NM_001033604 /// NM_001033605 /// NM_014451 /// NM_198428
5.05	5.16	0.11	7.70E-01	9.27E-01	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1	chr2p25.1-p24.1	203762_s_at	NM_001012665 /// NM_015522 /// NM_016008
6.25	6.31	0.06	7.70E-01	9.27E-01	H2BFS	H2B histone family, member S	chr21q22.3	208579_x_at	---
2.73	2.79	0.05	7.70E-01	9.27E-01	SNX29	sorting nexin 29	chr16p13.13-p13.12	215500_at	NM_001080530
3.12	3.17	0.05	7.70E-01	9.27E-01	---	---	---	240276_at	---
2.35	2.39	0.04	7.70E-01	9.27E-01	LOC100101118 /// TTTY8	testis-specific transcript, Y-linked 8-like /// testis-specific transcript, Y-linked 8	chrYp11.2	224142_s_at	NR_001533 /// NR_003591
4.02	4.05	0.04	7.70E-01	9.27E-01	IQCK	IQ motif containing K	chr16p12.3	215131_at	NM_153208
3.61	3.71	0.09	7.70E-01	9.27E-01	ZNF432 /// ZNF614	zinc finger protein 432 /// zinc finger protein 614	chr19q13.33	227045_at	NM_014650 /// NM_025040
3.07	3.12	0.05	7.70E-01	9.27E-01	---	---	---	230346_x_at	---
2.36	2.39	0.03	7.70E-01	9.27E-01	ZNF71	zinc finger protein 71	chr19q13.4	234570_at	NM_021216
2.09	2.14	0.05	7.70E-01	9.27E-01	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	chr7p15-p14	236471_at	NM_004289
2.47	2.52	0.05	7.70E-01	9.27E-01	---	---	---	1563063_at	---
2.18	2.21	0.03	7.70E-01	9.27E-01	C4orf26	chromosome 4 open reading frame 26	chr4q21.1	236984_at	NM_178497
3.07	3.12	0.05	7.70E-01	9.27E-01	MGC23284	hypothetical LOC197187	chr16q24.3	1556154_a_at	---
2.21	2.24	0.04	7.70E-01	9.27E-01	EPS8L2	EPS8-like 2	chr11p15.5	229020_x_at	NM_022772
2.85	2.89	0.04	7.71E-01	9.27E-01	FLJ27354	hypothetical gene supported by AK130864	chr1p22.2	231313_at	XM_378874 /// XM_943040
6.51	6.62	0.10	7.71E-01	9.27E-01	---	---	---	234987_at	---
2.76	2.82	0.06	7.71E-01	9.27E-01	OCLM	oculomedin	chr1q25	208274_at	NM_022375
4.00	4.06	0.06	7.71E-01	9.27E-01	OPA3	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	chr19q13.32	206357_at	NM_001017989 /// NM_025136
2.40	2.44	0.04	7.71E-01	9.27E-01	FLJ35390	hypothetical LOC255031	chr7p13	1569089_a_at	---
2.65	2.69	0.04	7.71E-01	9.28E-01	---	---	---	240723_at	---
3.25	3.33	0.07	7.71E-01	9.28E-01	---	---	---	240473_at	---
2.37	2.41	0.04	7.71E-01	9.28E-01	NUMB	numb homolog (Drosophila)	chr14q24.3	230462_at	NM_001005743 /// NM_001005744 /// NM_001005745 /// NM_003744
2.05	2.09	0.04	7.71E-01	9.28E-01	---	---	---	241628_at	---
2.23	2.27	0.04	7.72E-01	9.28E-01	GLRB	glycine receptor, beta	chr4q31.3	244680_at	NM_000824
6.15	6.28	0.13	7.72E-01	9.28E-01	EIF3A	eukaryotic translation initiation factor 3, subunit A	chr10q26	200597_at	NM_003750
3.74	3.79	0.05	7.72E-01	9.28E-01	GRAP	GRB2-related adaptor protein	chr17p11.2	206620_at	NM_006613
6.61	6.71	0.10	7.72E-01	9.28E-01	EPS15	epidermal growth factor receptor pathway substrate 15	chr1p32	217886_at	NM_001981
5.78	5.87	0.09	7.72E-01	9.28E-01	KIAA1219	KIAA1219	chr20q11.23	221736_at	NM_020336
2.10	2.15	0.05	7.72E-01	9.28E-01	---	---	---	1563092_at	---

2.57	2.61	0.04	7.72E-01	9.28E-01	MRPL47	mitochondrial ribosomal protein L47	chr3q26.33	223481_s_at	NM_020409 /// NM_177988
5.93	6.14	0.21	7.72E-01	9.28E-01	LDLR	low density lipoprotein receptor	chr19p13.3	217173_s_at	NM_000527
4.56	4.66	0.10	7.72E-01	9.28E-01	LACTB2	lactamase, beta 2	chr8p22-q22.3	218701_at	NM_016027
4.46	4.55	0.09	7.72E-01	9.28E-01	LOC100132214 /// LOC100134722	similar to HSPC047 protein /// similar to HSPC047 protein	chr7q22.1	220692_at	XM_001725218 /// XM_001725602
2.86	2.93	0.07	7.72E-01	9.28E-01	GRIN2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	chr12p12	210411_s_at	NM_000834
3.67	3.73	0.05	7.72E-01	9.28E-01	TACR1	tachykinin receptor 1	chr2p13.1	210637_at	NM_001058 /// NM_015727
2.32	2.36	0.04	7.72E-01	9.28E-01	---	---	---	234802_at	---
2.45	2.52	0.07	7.72E-01	9.28E-01	HUNK	hormonally up-regulated Neu-associated kinase	chr21q22.1	1555935_s_at	NM_014586
2.89	2.96	0.06	7.72E-01	9.28E-01	---	---	---	238115_at	---
5.66	5.75	0.08	7.72E-01	9.28E-01	DNLZ	DNL-type zinc finger	chr9q34.3	228272_at	NM_001080849
4.32	4.38	0.06	7.72E-01	9.28E-01	ZNF284	zinc finger protein 284	chr19q13.31	239462_at	NM_001037813
2.44	2.48	0.04	7.72E-01	9.28E-01	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	chr2q14	215509_s_at	NM_004336
5.05	5.11	0.06	7.73E-01	9.28E-01	REST	RE1-silencing transcription factor	chr4q12	204535_s_at	NM_005612
2.70	2.75	0.05	7.73E-01	9.28E-01	---	---	---	1555665_at	---
3.03	3.08	0.05	7.73E-01	9.28E-01	C14orf45	chromosome 14 open reading frame 45	chr14q24.3	220173_at	NM_025057
6.14	6.18	0.05	7.73E-01	9.28E-01	CTAGE5	CTAGE family, member 5	chr14q13.3	215930_s_at	NM_005930 /// NM_203354 /// NM_203355 /// NM_203356
2.91	2.96	0.04	7.73E-01	9.28E-01	GRIK4	glutamate receptor, ionotropic, kainate 4	chr11q22.3	208552_at	NM_014619
2.06	2.10	0.03	7.73E-01	9.28E-01	---	---	---	1559709_at	---
5.45	5.55	0.10	7.73E-01	9.28E-01	C9orf3	chromosome 9 open reading frame 3	chr9q22.32	212848_s_at	NM_032823
2.95	2.99	0.04	7.73E-01	9.28E-01	ZNF397	zinc finger protein 397	chr18q12.2	235270_at	NM_032347
2.23	2.27	0.03	7.73E-01	9.28E-01	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	chr3q28	1556134_a_at	NM_032047
2.10	2.13	0.03	7.73E-01	9.29E-01	---	---	---	1561604_at	---
2.84	2.88	0.04	7.73E-01	9.29E-01	---	---	---	240145_at	---
4.68	4.76	0.09	7.73E-01	9.29E-01	C7orf25	chromosome 7 open reading frame 25	chr7p14-p11.2	221573_at	NM_001099858 /// NM_024054
2.48	2.52	0.04	7.73E-01	9.29E-01	KRTAP10-12	keratin associated protein 10-12	chr21q22.3	237853_x_at	NM_198699
2.56	2.60	0.04	7.73E-01	9.29E-01	ZDHHC21	zinc finger, DHHC-type containing 21	chr9p22.3	229923_at	NM_178566
6.75	6.89	0.14	7.73E-01	9.29E-01	CLCN3	chloride channel 3	chr4q33	201735_s_at	NM_001829 /// NM_173872
5.45	5.53	0.08	7.73E-01	9.29E-01	CD22	CD22 molecule	chr19q13.1	38521_at	NM_001771
12.49	12.56	0.07	7.74E-01	9.29E-01	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	chr7q35	201272_at	NM_001628
2.05	2.09	0.04	7.74E-01	9.29E-01	KRTAP19-1	keratin associated protein 19-1	chr21q22.1	1556410_a_at	NM_181607
2.03	2.07	0.04	7.74E-01	9.29E-01	---	---	---	1561914_at	---
2.51	2.56	0.05	7.74E-01	9.29E-01	ASCL1	achaete-scute complex homolog 1 (Drosophila)	chr12q23.2	209985_s_at	NM_004316
2.80	2.85	0.04	7.74E-01	9.29E-01	---	---	---	237397_at	---
2.29	2.33	0.03	7.74E-01	9.29E-01	STXBP5L	syntaxin binding protein 5-like	chr3q13.33	215518_at	NM_014980
2.11	2.15	0.04	7.74E-01	9.29E-01	ACTN2	actinin, alpha 2	chr1q42-q43	203862_s_at	NM_001103
4.11	4.17	0.06	7.74E-01	9.29E-01	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	chr7q36.1	233748_x_at	NM_001040633 /// NM_016203 /// NM_024429
2.45	2.50	0.05	7.74E-01	9.29E-01	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	chr2q37.1	233545_at	NM_001017915 /// NM_005541
2.03	2.06	0.04	7.74E-01	9.29E-01	F9	coagulation factor IX	chrXq27.1-q27.2	207218_at	NM_000133
6.64	6.73	0.09	7.74E-01	9.29E-01	RAD1	RAD1 homolog (S. pombe)	chr5p13.2	204461_x_at	NM_002853 /// NM_133377
2.53	2.61	0.08	7.74E-01	9.29E-01	INADL	InaD-like (Drosophila)	chr1p31.3	223681_s_at	NM_176877
4.92	4.97	0.05	7.74E-01	9.29E-01	ZNF200	zinc finger protein 200	chr16p13.3	207338_s_at	NM_003454 /// NM_198087 /// NM_198088
3.25	3.30	0.05	7.74E-01	9.29E-01	CSMD2	CUB and Sushi multiple domains 2	chr1p35.1-p34.3	1570169_at	NM_052896
2.33	2.37	0.05	7.74E-01	9.29E-01	PER3	Period homolog 3 (Drosophila)	chr1p36.23	1569701_at	NM_016831
2.89	2.93	0.04	7.74E-01	9.29E-01	FLJ11506	hypothetical protein FLJ11506	chr15q22.33-q23	243284_at	NM_024666
2.23	2.27	0.04	7.74E-01	9.29E-01	---	---	---	230278_at	---
2.29	2.32	0.04	7.74E-01	9.29E-01	---	---	---	238786_at	---
3.46	3.52	0.06	7.74E-01	9.29E-01	BSND	Bartter syndrome, infantile, with sensorineural deafness (Barttin)	chr1p32.1	1552549_a_at	NM_057176

5.93	6.03	0.11	7.74E-01	9.29E-01	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	chr1q23.3	211395_x_at	NM_001005410 /// NM_001005411 /// NM_201563
6.90	6.96	0.06	7.74E-01	9.29E-01	RIN2	Ras and Rab interactor 2	chr20p11.22	209684_at	NM_018993
2.97	3.03	0.06	7.74E-01	9.29E-01	LOC728564	Similar to hCG1640714	chr4p16.1	216688_at	XM_001720661 /// XM_001721575 /// XM_001722727
3.48	3.53	0.05	7.74E-01	9.29E-01	---	---	---	217444_at	---
2.52	2.56	0.05	7.74E-01	9.29E-01	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	chr2q32.3-q33	239875_at	NM_005966
2.17	2.21	0.04	7.74E-01	9.29E-01	---	---	---	233927_at	---
3.06	3.12	0.06	7.74E-01	9.29E-01	MCM8	minichromosome maintenance complex component 8	chr20p12.3	233560_x_at	NM_032485 /// NM_182802
6.17	6.23	0.06	7.75E-01	9.29E-01	DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1	chr3p22.3	222479_s_at	NM_016141
2.86	2.90	0.04	7.75E-01	9.29E-01	---	---	---	241424_at	---
2.92	2.97	0.05	7.75E-01	9.29E-01	hCG_17241	flamingo-like	chr22q11.21	1569446_x_at	XM_001126962
6.33	6.45	0.12	7.75E-01	9.29E-01	AACS	acetoacetyl-CoA synthetase	chr12q24.31	218434_s_at	NM_023928
2.29	2.32	0.04	7.75E-01	9.29E-01	---	---	---	217320_at	---
2.14	2.18	0.04	7.75E-01	9.29E-01	---	---	---	240820_at	---
3.93	4.01	0.08	7.75E-01	9.29E-01	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	chr5q33.3	243916_x_at	NM_145049
2.90	2.95	0.05	7.75E-01	9.29E-01	GJB3	gap junction protein, beta 3, 31kDa	chr1p34	215243_s_at	NM_001005752 /// NM_024009
2.47	2.52	0.05	7.75E-01	9.29E-01	LOC728883	Hypothetical LOC728883	chr10q11.22	1563255_at	XM_001127767 /// XM_001128700 /// XM_001715110
3.63	3.67	0.04	7.75E-01	9.29E-01	SPERT	spermatid associated	chr13q14.12	1553846_at	NM_152719
2.13	2.17	0.04	7.75E-01	9.29E-01	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	chr12p12.1	235578_at	NM_005691 /// NM_020297 /// NM_020298
2.33	2.37	0.04	7.75E-01	9.29E-01	POLDIP3 /// RRP7A /// RRP7B	polymerase (DNA-directed), delta interacting protein 3 /// ribosomal RNA processing 7 homolog A (S. cerevisiae) /// ribosomal RNA processing 7 homolog B (S. cerevisiae)	chr22q13.2 /// chr22q13.2-q13.31	210584_s_at	NM_015703 /// NM_032311 /// NM_178136 /// NR_002184
1.93	1.97	0.03	7.75E-01	9.29E-01	---	---	---	1565563_at	---
2.01	2.04	0.03	7.75E-01	9.29E-01	---	---	---	240401_at	---
3.61	3.82	0.21	7.75E-01	9.29E-01	ZNF711	zinc finger protein 711	chrXq21.1-q21.2	207781_s_at	NM_021998
5.59	5.70	0.11	7.75E-01	9.29E-01	CAPN5	calpain 5	chr11q14	226292_at	NM_004055
3.34	3.40	0.06	7.75E-01	9.29E-01	---	---	---	1566512_at	---
3.55	3.61	0.06	7.75E-01	9.29E-01	GLT25D2	glycosyltransferase 25 domain containing 2	chr1q25	237382_at	NM_015101
2.34	2.38	0.04	7.75E-01	9.29E-01	---	---	---	217656_at	---
2.15	2.18	0.03	7.75E-01	9.29E-01	---	---	---	1557885_at	---
3.13	3.16	0.03	7.75E-01	9.29E-01	---	---	---	236452_at	---
2.74	2.79	0.05	7.75E-01	9.29E-01	---	---	---	230431_at	---
4.58	4.71	0.13	7.75E-01	9.29E-01	FRMD5	FERM domain containing 5	chr15q15.3	230831_at	NM_032892
2.31	2.37	0.05	7.75E-01	9.29E-01	SLC19A3	solute carrier family 19, member 3	chr2q37	220736_at	NM_025243
2.40	2.45	0.05	7.75E-01	9.29E-01	CCBP2	Chemokine binding protein 2	chr3p21.3	1568850_at	NM_001296
2.37	2.41	0.04	7.75E-01	9.29E-01	---	---	---	1564905_at	---
5.32	5.42	0.10	7.75E-01	9.29E-01	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	chr14q23	203565_s_at	NM_002431
1.98	2.01	0.03	7.76E-01	9.29E-01	DNAH14	dynein, axonemal, heavy chain 14	chr1q42.12	1567861_at	XM_001721899 /// XM_059166 /// XM_938194
2.65	2.68	0.03	7.76E-01	9.29E-01	---	---	---	244254_at	---
7.74	7.88	0.14	7.76E-01	9.30E-01	TBC1D4	TBC1 domain family, member 4	chr13q22.2	203387_s_at	NM_014832
4.56	4.62	0.07	7.76E-01	9.30E-01	PTPRA	protein tyrosine phosphatase, receptor type, A	chr20p13	213799_s_at	NM_002836 /// NM_080840 /// NM_080841
6.52	6.57	0.05	7.76E-01	9.30E-01	AKAP13	A kinase (PRKA) anchor protein 13	chr15q24-q25	224884_at	NM_006738 /// NM_007200 /// NM_144767
1.98	2.02	0.05	7.76E-01	9.30E-01	OPRK1	opioid receptor, kappa 1	chr8q11.2	229944_at	NM_000912
2.14	2.19	0.05	7.76E-01	9.30E-01	RCBTB1	Regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	chr13q14	237417_at	NM_018191
5.82	5.87	0.04	7.76E-01	9.30E-01	PPIE	peptidylprolyl isomerase E (cyclophilin E)	chr1p32	202494_at	NM_006112 /// NM_203456 /// NM_203457

2.05	2.09	0.04	7.76E-01	9.30E-01	CTCFL	CCCTC-binding factor (zinc finger protein)-like	chr20q13.31	1552368_at	NM_080618
2.81	2.85	0.04	7.76E-01	9.30E-01	CPT1A	carnitine palmitoyltransferase 1A (liver)	chr11q13.1-q13.2	210687_at	NM_001031847 /// NM_001876
1.99	2.03	0.04	7.76E-01	9.30E-01	---	---	---	241016_at	---
1.91	1.94	0.03	7.76E-01	9.30E-01	SLC25A31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	chr4q28.1	221037_s_at	NM_031291
2.05	2.09	0.04	7.76E-01	9.30E-01	---	---	---	1557699_x_at	---
2.27	2.32	0.05	7.76E-01	9.30E-01	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	chr15q22	211842_s_at	NM_004727
2.61	2.64	0.04	7.76E-01	9.30E-01	CORO2A	coronin, actin binding protein, 2A	chr9q22.3	205538_at	NM_003389 /// NM_052820
2.53	2.57	0.04	7.76E-01	9.30E-01	MDM2	Mdm2 p53 binding protein homolog (mouse)	chr12q14.3-q15	211832_s_at	NM_002392 /// NM_006878 /// NM_006879 /// NM_006881 /// NM_006882
2.43	2.47	0.04	7.76E-01	9.30E-01	CSH1 /// CSH2 /// GH1	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// growth hormone 1	chr17q24.2	208341_x_at	NM_000515 /// NM_001317 /// NM_020991 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645
3.92	4.09	0.17	7.76E-01	9.30E-01	---	---	---	242542_at	---
3.99	4.06	0.07	7.76E-01	9.30E-01	KRT86 /// LOC100134394	keratin 86 /// hypothetical protein LOC100134394	chr12q13	215189_at	NM_002284 /// XM_001721084
2.79	2.84	0.05	7.76E-01	9.30E-01	PRSS33	protease, serine, 33	chr16p13.3	1552349_a_at	NM_152891
3.20	3.23	0.03	7.76E-01	9.30E-01	LOC100128093	hypothetical LOC100128093	chr1p34.3	234763_at	XR_037596 /// XR_038001 /// XR_038009
2.20	2.23	0.03	7.76E-01	9.30E-01	---	---	---	220877_at	---
4.42	4.51	0.09	7.76E-01	9.30E-01	---	---	---	236616_at	---
2.27	2.31	0.04	7.76E-01	9.30E-01	---	---	---	1561014_at	---
5.08	5.16	0.08	7.76E-01	9.30E-01	AP3S2	adaptor-related protein complex 3, sigma 2 subunit	chr15q26.1	202398_at	NM_005829 /// NR_023361
3.49	3.61	0.13	7.76E-01	9.30E-01	---	---	---	235919_at	---
2.81	2.85	0.04	7.76E-01	9.30E-01	DAB1	disabled homolog 1 (Drosophila)	chr1p32-p31	220611_at	NM_021080
7.34	7.43	0.08	7.77E-01	9.30E-01	NMD3	NMD3 homolog (S. cerevisiae)	chr3q26.1	231870_s_at	NM_015938
2.63	2.67	0.04	7.76E-01	9.30E-01	DOCK8	dedicator of cytokinesis 8	chr9p24.3	232842_at	NM_203447
2.06	2.10	0.04	7.77E-01	9.30E-01	WDR22	WD repeat domain 22	chr14q23-q24.1	1554558_at	NM_003861
5.91	5.99	0.08	7.77E-01	9.30E-01	ANP32A /// LOC100128146	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A /// hypothetical protein LOC100128146	chr15q22.3-q23 /// chr15q23	201043_s_at	NM_006305 /// XM_001724880 /// XM_001725287 /// XM_001726740
5.69	5.78	0.09	7.77E-01	9.30E-01	PPAPDC3	phosphatidic acid phosphatase type 2 domain containing 3	chr9q34.13	224506_s_at	NM_032728
2.99	3.03	0.04	7.77E-01	9.30E-01	LOC253039	hypothetical LOC253039	chr9q33.2	239958_at	XM_001715306 /// XM_001719409 /// XM_001725827
4.49	4.63	0.14	7.77E-01	9.30E-01	CHAD	chondroadherin	chr17q21.33	206869_at	NM_001267
3.19	3.26	0.07	7.77E-01	9.30E-01	SESTD1	SEC14 and spectrin domains 1	chr2q31.2	227041_at	NM_178123
3.53	3.59	0.06	7.77E-01	9.30E-01	HEATR2	HEAT repeat containing 2	chr7p22.3	1554761_a_at	NM_017802
2.13	2.16	0.04	7.77E-01	9.30E-01	---	---	---	234100_at	---

2.58	2.61	0.03	7.77E-01	9.30E-01	LOC100133558 /// LOC730052 /// TMEM189-UBE2V1 /// UBE2V1	similar to hCG1642170 /// similar to ubiquitin-conjugating enzyme E2 /// TMEM189-UBE2V1 /// ubiquitin-conjugating enzyme E2 variant 1	chr20q13.2 /// chr3q26.31	216315_x_at	NM_001032288 /// NM_003349 /// NM_021988 /// NM_022442 /// NM_199144 /// NM_199203 /// XM_001716419 /// XR_016022 /// XR_016054 /// XR_038933
2.05	2.08	0.03	7.77E-01	9.30E-01	PHACTR3	phosphatase and actin regulator 3	chr20q13.32	227949_at	NM_080672 /// NM_183244 /// NM_183246
6.57	6.67	0.10	7.77E-01	9.30E-01	SLC30A9	solute carrier family 30 (zinc transporter), member 9	chr4p13-p12	202614_at	NM_006345
4.60	4.67	0.06	7.77E-01	9.30E-01	REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	chr19p13.3	226144_at	NM_020695
2.48	2.52	0.04	7.77E-01	9.30E-01	---	---	---	233272_at	---
3.92	3.95	0.03	7.77E-01	9.30E-01	VWA3A	von Willebrand factor A domain containing 3A	chr16p12.1	1553657_at	NM_173615
2.80	2.84	0.04	7.77E-01	9.30E-01	LOC780529	hypothetical LOC780529	chr13q31	231354_at	---
8.42	8.49	0.07	7.77E-01	9.30E-01	ARF3	ADP-ribosylation factor 3	chr12q13	200734_s_at	NM_001659
2.37	2.42	0.05	7.77E-01	9.30E-01	LOC100133946 /// MTCP1	similar to mature T-cell proliferations 1 /// mature T-cell proliferation 1	chrXq28	205106_at	NM_001018024 /// NM_001018025 /// NM_014221 /// XM_001719446
9.79	9.88	0.09	7.77E-01	9.30E-01	MDH1	malate dehydrogenase 1, NAD (soluble)	chr2p13.3	200978_at	NM_005917
1.91	1.95	0.04	7.77E-01	9.30E-01	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	chr2q36.1	1555421_at	NM_001039569
1.99	2.03	0.03	7.77E-01	9.30E-01	CKAP2	cytoskeleton associated protein 2	chr13q14	1554264_at	NM_001098525 /// NM_018204
2.37	2.41	0.04	7.77E-01	9.30E-01	---	---	---	233828_at	---
3.59	3.66	0.06	7.78E-01	9.30E-01	IQCD	IQ motif containing D	chr12q24.13	1552540_s_at	NM_138451
4.93	5.01	0.08	7.78E-01	9.30E-01	---	---	---	239959_x_at	---
4.21	4.25	0.05	7.78E-01	9.30E-01	LOC100133896 /// SEMA4G	hypothetical protein LOC100133896 /// sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	chr10q24.31	203483_at	NM_017893 /// XM_001723682
2.36	2.41	0.05	7.78E-01	9.30E-01	---	---	---	242237_at	---
3.59	3.63	0.04	7.78E-01	9.30E-01	---	---	---	236686_at	---
2.36	2.41	0.05	7.78E-01	9.30E-01	---	---	---	232927_at	---
2.16	2.20	0.03	7.78E-01	9.30E-01	SPAG17	Sperm associated antigen 17	chr1p12	1557593_at	NM_206996
4.37	4.44	0.07	7.78E-01	9.30E-01	PLEKHA8 /// PLEKHA9	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8 /// pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 9	chr12q /// chr7p21-p11.2	220157_x_at	NM_015899 /// NM_032639
2.27	2.33	0.05	7.78E-01	9.30E-01	FAR1	fatty acyl CoA reductase 1	chr11p15.2	1558014_s_at	NM_032228
5.98	6.11	0.12	7.78E-01	9.30E-01	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	chr6q15	217826_s_at	NM_016021
3.27	3.30	0.04	7.78E-01	9.30E-01	---	---	---	234638_at	---
2.14	2.17	0.03	7.78E-01	9.30E-01	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	chr11q22.3	204475_at	NM_002421
6.37	6.44	0.08	7.78E-01	9.30E-01	NRSN2	neurensin 2	chr20p13	218359_at	NM_024958
2.08	2.12	0.04	7.78E-01	9.30E-01	LOC100128329	similar to PRO2958	chr2p24.3	207478_at	XM_001720404 /// XM_001722263 /// XM_001726683
4.22	4.39	0.17	7.78E-01	9.30E-01	KLHL24	kelch-like 24 (Drosophila)	chr3q27.1	221986_s_at	NM_017644
7.31	7.39	0.08	7.78E-01	9.30E-01	SNX6	sorting nexin 6	chr14q13.2	217789_at	NM_021249 /// NM_152233
7.75	7.86	0.11	7.78E-01	9.31E-01	PUM2	pumilio homolog 2 (Drosophila)	chr2p22-p21	216221_s_at	NM_015317
2.03	2.07	0.04	7.78E-01	9.31E-01	TEX12	testis expressed 12	chr11q22	221438_s_at	NM_031275
4.71	4.88	0.17	7.79E-01	9.31E-01	LOC100132181	hypothetical protein LOC100132181	---	225046_at	XM_001722051
3.91	3.97	0.06	7.79E-01	9.31E-01	ZBTB34	zinc finger and BTB domain containing 34	chr9q33.3	227111_at	NM_001099270
2.17	2.21	0.04	7.79E-01	9.31E-01	---	---	---	233680_at	---
4.01	4.10	0.09	7.79E-01	9.31E-01	RGMA	RGM domain family, member A	chr15q26.1	223468_s_at	NM_020211
6.17	6.23	0.06	7.79E-01	9.31E-01	UBR2	ubiquitin protein ligase E3 component n-recognin 2	chr6p21.1	212760_at	NM_015255
2.78	2.83	0.05	7.79E-01	9.31E-01	WDR62	WD repeat domain 62	chr19q13.12	1553125_x_at	NM_001083961 /// NM_173636
2.91	2.95	0.04	7.79E-01	9.31E-01	DNASE1	deoxyribonuclease I	chr16p13.3	210165_at	NM_005223
1.82	1.85	0.03	7.79E-01	9.31E-01	---	---	---	243274_x_at	---

2.01	2.05	0.04	7.79E-01	9.31E-01	---	---	---	242481_at	---
2.92	2.95	0.03	7.79E-01	9.31E-01	ELSPBP1	epididymal sperm binding protein 1	chr19q13.32	220366_at	NM_022142
8.99	9.06	0.07	7.79E-01	9.31E-01	NARS	asparaginyl-tRNA synthetase	chr18q21.2-q21.3	200027_at	NM_004539
2.38	2.43	0.05	7.79E-01	9.31E-01	SLC5A4	solute carrier family 5 (low affinity glucose cotransporter), member 4	chr22q12.2-q12.3	215960_at	NM_014227
1.98	2.01	0.03	7.79E-01	9.31E-01	---	---	---	237615_at	---
2.93	2.96	0.04	7.79E-01	9.31E-01	DNAJC5B	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	chr8q13.1	232798_at	NM_033105
2.01	2.04	0.03	7.79E-01	9.31E-01	---	---	---	234209_at	---
2.94	3.00	0.06	7.79E-01	9.31E-01	PTOV1	Prostate tumor overexpressed gene 1	chr19q13.33	235665_at	NM_017432
5.70	5.81	0.10	7.79E-01	9.31E-01	SFRS4	Splicing factor, arginine/serine-rich 4	chr1p35.3	242837_at	NM_005626
5.64	5.75	0.12	7.80E-01	9.31E-01	RAD17	RAD17 homolog (S. pombe)	chr5q13	211228_s_at	NM_002873 /// NM_133338 /// NM_133339 /// NM_133340 /// NM_133341 /// NM_133342 /// NM_133343 /// NM_133344
2.61	2.69	0.08	7.80E-01	9.31E-01	---	---	---	227769_at	---
2.81	2.88	0.07	7.80E-01	9.31E-01	---	---	---	239245_at	---
6.82	6.89	0.07	7.80E-01	9.31E-01	TMEM33	transmembrane protein 33	chr4p13	225492_at	NM_018126
3.46	3.51	0.05	7.80E-01	9.31E-01	---	---	---	240615_at	---
2.61	2.66	0.05	7.80E-01	9.31E-01	---	---	---	236572_at	---
2.16	2.19	0.04	7.80E-01	9.31E-01	C1orf125	chromosome 1 open reading frame 125	chr1q25.2	1553376_a_at	NM_144696 /// NM_182766
1.89	1.93	0.03	7.80E-01	9.31E-01	KIAA2018	KIAA2018	chr3q13.2	242513_x_at	NM_001009899
2.33	2.37	0.03	7.80E-01	9.31E-01	GNAS	GNAS complex locus	chr20q13.3	239037_at	NM_000516 /// NM_001077488 /// NM_001077489 /// NM_001077490 /// NM_016592 /// NM_080425 /// NM_080426 /// NR_003259
2.43	2.47	0.04	7.80E-01	9.31E-01	---	---	---	220695_at	---
3.98	4.15	0.17	7.80E-01	9.31E-01	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	chr7q21.1	1570505_at	NM_000443 /// NM_018849 /// NM_018850
4.09	4.21	0.12	7.80E-01	9.31E-01	KLF3	Kruppel-like factor 3 (basic)	chr4p14	225140_at	NM_016531
4.04	4.13	0.09	7.80E-01	9.31E-01	MCM8	minichromosome maintenance complex component 8	chr20p12.3	224320_s_at	NM_032485 /// NM_182802
3.91	3.96	0.05	7.80E-01	9.31E-01	CA9	carbonic anhydrase IX	chr9p13-p12	205199_at	NM_001216
3.30	3.34	0.04	7.80E-01	9.31E-01	---	---	---	240372_at	---
2.09	2.13	0.03	7.80E-01	9.31E-01	RNASE7	ribonuclease, RNase A family, 7	chr14q11.2	233488_at	NM_032572
2.30	2.34	0.04	7.80E-01	9.31E-01	---	---	---	222098_s_at	---
4.41	4.56	0.15	7.80E-01	9.31E-01	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	chr6p22-p21	209291_at	NM_001546
2.86	2.91	0.05	7.80E-01	9.31E-01	HSPC105	NAD(P) dependent steroid dehydrogenase-like	chr16q23.3	229522_at	NM_145168
4.12	4.15	0.04	7.80E-01	9.31E-01	NUMB	numb homolog (Drosophila)	chr14q24.3	207545_s_at	NM_001005743 /// NM_001005744 /// NM_001005745 /// NM_003744
6.63	6.72	0.09	7.80E-01	9.31E-01	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	chr19q13.3	209785_s_at	NM_003706
2.25	2.30	0.04	7.80E-01	9.31E-01	TEX10	Testis expressed 10	chr9q31.1	1558702_at	NM_017746
3.32	3.40	0.08	7.81E-01	9.32E-01	---	---	---	240666_at	---
6.50	6.56	0.06	7.81E-01	9.32E-01	SMAD4	SMAD family member 4	chr18q21.1	235725_at	NM_005359
2.55	2.61	0.06	7.81E-01	9.32E-01	---	---	---	1561245_at	---
2.43	2.49	0.05	7.81E-01	9.32E-01	---	---	---	1566033_at	---
3.47	3.52	0.05	7.81E-01	9.32E-01	---	---	---	1563792_at	---
2.64	2.68	0.03	7.81E-01	9.32E-01	TAAR8	trace amine associated receptor 8	chr6q23.2	1553552_at	NM_053278
1.82	1.85	0.03	7.81E-01	9.32E-01	---	---	---	1556624_at	---
2.28	2.31	0.03	7.81E-01	9.32E-01	---	---	---	1555027_at	---
5.46	5.54	0.08	7.81E-01	9.32E-01	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	chr12q22	212751_at	NM_003348
3.65	3.69	0.04	7.81E-01	9.32E-01	---	---	---	228919_at	---
2.21	2.25	0.04	7.81E-01	9.32E-01	CCDC131	coiled-coil domain containing 131	chr12q21.1	1553736_at	NM_144982
2.05	2.08	0.03	7.81E-01	9.32E-01	NXNL2	nucleoredoxin-like 2	chr9q22.1	1552816_at	NM_145283

1.90	1.93	0.03	7.81E-01	9.32E-01	---	---	---	1557698_at	---
6.07	6.13	0.06	7.81E-01	9.32E-01	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	chr11q13.1	203777_s_at	NM_003952
2.24	2.28	0.04	7.81E-01	9.32E-01	---	---	---	1561881_at	---
1.90	1.94	0.04	7.81E-01	9.32E-01	C14orf143	chromosome 14 open reading frame 143	chr14q32.11	210525_x_at	NM_145231
1.89	1.93	0.03	7.81E-01	9.32E-01	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	chr9q31	205122_at	NM_003692
7.51	7.65	0.13	7.82E-01	9.32E-01	DARS	aspartyl-tRNA synthetase	chr2q21.3	201623_s_at	NM_001349
5.90	6.01	0.10	7.81E-01	9.32E-01	C1QTNF5 /// MFRP	C1q and tumor necrosis factor related protein 5 /// membrane frizzled-related protein	chr11q23 /// chr11q23.3	223499_at	NM_015645 /// NM_031433
2.70	2.75	0.05	7.81E-01	9.32E-01	---	---	---	243189_at	---
2.66	2.71	0.05	7.82E-01	9.32E-01	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	chr14q32.12	220369_at	NM_032560
9.91	9.96	0.05	7.82E-01	9.32E-01	UQCRQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	chr5q31.1	201568_at	NM_014402
2.13	2.17	0.04	7.81E-01	9.32E-01	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	chr8q11.23	244706_at	NM_052937
4.37	4.40	0.03	7.82E-01	9.32E-01	MAML3	mastermind-like 3 (Drosophila)	chr4q28	228508_at	NM_018717
1.84	1.87	0.03	7.82E-01	9.32E-01	---	---	---	241814_at	---
5.80	5.88	0.08	7.82E-01	9.32E-01	---	---	---	244043_at	---
4.80	4.86	0.06	7.82E-01	9.32E-01	ARHGAP25	Rho GTPase activating protein 25	chr2p14	38149_at	NM_001007231 /// NM_014882
4.69	4.73	0.04	7.82E-01	9.32E-01	CLDND2	claudin domain containing 2	chr19q13.33	231162_at	NM_152353
2.00	2.03	0.04	7.82E-01	9.32E-01	CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1	chr20q13	206504_at	NM_000782 /// NM_001128915
2.21	2.24	0.03	7.82E-01	9.32E-01	STRBP	Chromosome 9 open reading frame 45	chr9q33.3	233251_at	NM_018387
1.91	1.95	0.03	7.82E-01	9.32E-01	---	---	---	237521_x_at	---
6.23	6.42	0.19	7.82E-01	9.32E-01	---	---	---	1556590_s_at	---
2.07	2.10	0.03	7.82E-01	9.32E-01	---	---	---	243125_x_at	---
5.75	5.84	0.09	7.82E-01	9.32E-01	GATAD2A	GATA zinc finger domain containing 2A	chr19p13.11	222526_at	NM_017660
2.16	2.20	0.04	7.82E-01	9.32E-01	C1QTNF7	C1q and tumor necrosis factor related protein 7	chr4p16-p15	239349_at	NM_031911
2.10	2.13	0.03	7.82E-01	9.32E-01	---	---	---	236065_at	---
5.67	5.78	0.11	7.82E-01	9.32E-01	TNPO1	transportin 1	chr5q13.2	225766_s_at	NM_002270 /// NM_153188
2.88	2.92	0.04	7.82E-01	9.32E-01	ENOX1	ecto-NOX disulfide-thiol exchanger 1	chr13q14.11	219501_at	NM_001127615 /// NM_017993
1.92	1.96	0.04	7.82E-01	9.32E-01	---	---	---	217091_at	---
2.42	2.46	0.04	7.82E-01	9.32E-01	BNC2	basonuclin 2	chr9p22.3-p22.2	243445_at	NM_017637
1.99	2.02	0.03	7.82E-01	9.32E-01	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	chr17q23.1-q24.2	219564_at	NM_018658 /// NM_170741 /// NM_170742
3.16	3.20	0.04	7.82E-01	9.32E-01	KRT33B	keratin 33B	chr17q12-q21	207787_at	NM_002279
2.03	2.06	0.03	7.82E-01	9.32E-01	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	chr6p21.3	214455_at	NM_003518 /// NM_003522 /// NM_003523 /// NM_003525 /// NM_003526
3.51	3.55	0.04	7.82E-01	9.32E-01	PRM2	protamine 2	chr16p13.2	210122_at	NM_002762
3.34	3.40	0.06	7.83E-01	9.32E-01	---	---	---	241104_at	---
5.57	5.72	0.15	7.83E-01	9.32E-01	RSRC2	arginine/serine-rich coiled-coil 2	chr12q24.31	202301_s_at	NM_023012 /// NM_198261 /// NM_198262
5.41	5.52	0.11	7.83E-01	9.32E-01	CUL2	cullin 2	chr10p11.21	203079_s_at	NM_003591
5.71	5.82	0.11	7.83E-01	9.32E-01	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	chr14q32.12	220368_s_at	NM_032560
2.56	2.61	0.05	7.83E-01	9.32E-01	A1CF	APOBEC1 complementation factor	chr10q11.23	220951_s_at	NM_014576 /// NM_138932 /// NM_138933
3.14	3.18	0.04	7.83E-01	9.32E-01	FLJ14213	protor-2	chr11p13-p12	1555486_a_at	NM_024841
6.75	6.79	0.04	7.83E-01	9.32E-01	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	chr7q11.23	208445_s_at	NM_032408
2.20	2.24	0.04	7.83E-01	9.32E-01	---	---	---	1556996_at	---
2.40	2.44	0.03	7.83E-01	9.32E-01	---	---	---	1557564_at	---
7.69	7.78	0.09	7.83E-01	9.32E-01	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	chr11q12.1	219666_at	NM_022349 /// NM_152851 /// NM_152852
2.37	2.41	0.04	7.83E-01	9.32E-01	C9orf97	chromosome 9 open reading frame 97	chr9q22.33	1555430_at	NM_139246
3.65	3.72	0.07	7.83E-01	9.32E-01	---	---	---	230310_at	---
5.72	5.78	0.06	7.83E-01	9.32E-01	RFX1	regulatory factor X, 1 (influences HLA class II expression)	chr19p13.1	226786_at	NM_002918
4.49	4.53	0.04	7.83E-01	9.32E-01	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	chr9q34	223285_s_at	NM_175039 /// NM_175040
2.14	2.17	0.03	7.83E-01	9.32E-01	C15orf41	chromosome 15 open reading frame 41	chr15q14	232507_at	NM_001130010 /// NM_032499
2.67	2.71	0.04	7.83E-01	9.32E-01	WWC2	WW and C2 domain containing 2	chr4q35.1	222738_at	NM_024949
6.46	6.53	0.07	7.83E-01	9.32E-01	RIN3	Ras and Rab interactor 3	chr14q32.12	60471_at	NM_024832

6.88	6.93	0.05	7.83E-01	9.32E-01	FLJ12151	hypothetical protein FLJ12151	chr12q24.31	215373_x_at	XR_040977 /// XR_040978 /// XR_040979
2.61	2.65	0.04	7.83E-01	9.33E-01	---	---	---	214967_at	---
3.10	3.14	0.04	7.83E-01	9.33E-01	---	---	---	231333_at	---
2.86	2.90	0.04	7.83E-01	9.33E-01	C6orf162	chromosome 6 open reading frame 162	chr6q15-q16.1	236178_at	NM_001042493 /// NM_020425
2.36	2.39	0.03	7.83E-01	9.33E-01	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	chr14q24.3-q31	216203_at	NM_004863
2.60	2.64	0.04	7.83E-01	9.33E-01	MMP24	matrix metallopeptidase 24 (membrane-inserted)	chr20q11.2	208387_s_at	NM_006690
5.37	5.49	0.11	7.84E-01	9.33E-01	TTC17	tetratricopeptide repeat domain 17	chr11p12-p11.2	232323_s_at	NM_018259
3.94	4.00	0.06	7.84E-01	9.33E-01	ODF2	outer dense fiber of sperm tails 2	chr9q34.11	210415_s_at	NM_002540 /// NM_153437
4.84	4.90	0.06	7.84E-01	9.33E-01	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	chr17q11.2	204100_at	NM_003250 /// NM_199334
5.31	5.36	0.05	7.84E-01	9.33E-01	PXK	PX domain containing serine/threonine kinase	chr3p14.3	225796_at	NM_017771
2.64	2.68	0.04	7.84E-01	9.33E-01	SLAMF1	signaling lymphocytic activation molecule family member 1	chr1q22-q23	1555626_a_at	NM_003037
2.22	2.25	0.04	7.84E-01	9.33E-01	PLCB4	Phospholipase C, beta 4	chr20p12	240728_at	NM_000933 /// NM_182797
2.27	2.30	0.03	7.84E-01	9.33E-01	---	---	---	233097_x_at	---
2.19	2.22	0.03	7.84E-01	9.33E-01	CCDC54	coiled-coil domain containing 54	chr3q13.12	244735_at	NM_032600
7.85	7.96	0.10	7.84E-01	9.33E-01	41532	15 kDa selenoprotein	chr1p31	200902_at	NM_004261 /// NM_203341
4.99	5.05	0.06	7.84E-01	9.33E-01	LOC286167	hypothetical LOC286167	chr8q24.22	225034_at	---
3.73	3.80	0.06	7.84E-01	9.33E-01	ETV3	ets variant gene 3	chr1q21-q23	1552423_at	NM_005240
3.41	3.45	0.04	7.84E-01	9.33E-01	WFDC12	WAP four-disulfide core domain 12	chr20q12-q13.1	1553081_at	NM_080869
2.31	2.36	0.05	7.84E-01	9.33E-01	---	---	---	237657_at	---
4.08	4.12	0.04	7.84E-01	9.33E-01	C16orf13	Chromosome 16 open reading frame 13	chr16p13.3	228118_x_at	NM_001040160 /// NM_001040161 /// NM_001040162 /// NM_001040165 /// NM_032366
5.13	5.17	0.04	7.84E-01	9.33E-01	SEC22A	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	chr3q21.1	218703_at	NM_012430
7.30	7.37	0.07	7.84E-01	9.33E-01	CD302	CD302 molecule	chr2q24.2	203799_at	NM_014880
2.63	2.70	0.07	7.84E-01	9.33E-01	---	---	---	243527_at	---
2.38	2.43	0.04	7.84E-01	9.33E-01	FLJ32756	hypothetical LOC642757	chr22q13.31	1561099_at	XR_041518 /// XR_041519 /// XR_041520
4.52	4.56	0.04	7.84E-01	9.33E-01	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	chr17q12	201081_s_at	NM_003559
2.94	2.97	0.04	7.84E-01	9.33E-01	---	---	---	230890_at	---
6.19	6.30	0.11	7.84E-01	9.33E-01	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	chr10q26	201456_s_at	NM_001007793 /// NM_004725
4.67	4.74	0.07	7.84E-01	9.33E-01	---	---	---	234111_at	---
2.50	2.54	0.04	7.84E-01	9.33E-01	IGSF2	immunoglobulin superfamily, member 2	chr1p13	207167_at	NM_004258
5.71	5.85	0.13	7.84E-01	9.33E-01	MFAP4	microfibrillar-associated protein 4	chr17p11.2	212713_at	NM_002404
7.33	7.44	0.10	7.84E-01	9.33E-01	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')	chrXq22	201132_at	NM_001032393 /// NM_019597
2.08	2.12	0.04	7.84E-01	9.33E-01	PCDH11Y	protocadherin 11 Y-linked	chrYp11.2	211227_s_at	NM_032971 /// NM_032972 /// NM_032973
2.09	2.12	0.03	7.85E-01	9.33E-01	INHBE	inhibin, beta E	chr12q13.3	210587_at	NM_031479
5.37	5.47	0.10	7.85E-01	9.33E-01	---	---	---	232889_at	---
4.52	4.58	0.06	7.85E-01	9.33E-01	---	---	---	214349_at	---
2.12	2.16	0.04	7.85E-01	9.33E-01	FBXO32	F-box protein 32	chr8q24.13	241762_at	NM_058229 /// NM_148177
7.80	7.92	0.12	7.85E-01	9.33E-01	TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	chr5q31	201023_at	NM_005642
6.31	6.42	0.11	7.85E-01	9.33E-01	PHF16	PHD finger protein 16	chrXp11.3	204866_at	NM_001077445 /// NM_014735
6.93	7.01	0.08	7.85E-01	9.33E-01	UTRN	utrophin	chr6q24	225093_at	NM_007124
2.02	2.06	0.04	7.85E-01	9.33E-01	TMEM45B	transmembrane protein 45B	chr11q24.3	230323_s_at	NM_138788
2.59	2.62	0.04	7.85E-01	9.33E-01	DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	chr22q13.1	208386_x_at	NM_007068
5.29	5.39	0.10	7.85E-01	9.33E-01	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	chr4q31	201873_s_at	NM_001040876 /// NM_002940
3.80	3.94	0.14	7.85E-01	9.33E-01	TIMP4	TIMP metallopeptidase inhibitor 4	chr3p25	206243_at	NM_003256
2.62	2.67	0.04	7.85E-01	9.33E-01	MTAP	methylthioadenosine phosphorylase	chr9p21	217134_at	NM_002451

5.16	5.22	0.06	7.85E-01	9.33E-01	ALPPL2	alkaline phosphatase, placental-like 2	chr2q37	210431_at	NM_031313
1.87	1.91	0.04	7.85E-01	9.33E-01	---	---	---	230874_at	---
2.36	2.39	0.04	7.85E-01	9.33E-01	---	---	---	1562550_at	---
7.61	7.70	0.10	7.85E-01	9.33E-01	MUT	methylmalonyl Coenzyme A mutase	chr6p12.3	202960_s_at	NM_000255
7.27	7.36	0.08	7.85E-01	9.33E-01	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	chr8q13	202626_s_at	NM_001111097 /// NM_002350
6.58	6.65	0.07	7.85E-01	9.33E-01	NUAK1	NUAK family, SNF1-like kinase, 1	chr12q23.3	204589_at	NM_014840
3.02	3.09	0.06	7.85E-01	9.33E-01	---	---	---	226407_at	---
4.18	4.23	0.06	7.85E-01	9.33E-01	MUTED	muted homolog (mouse)	chr6p25.1-p24.3	226543_at	NM_201280
2.60	2.65	0.05	7.85E-01	9.33E-01	---	---	---	240611_at	---
4.97	5.02	0.05	7.85E-01	9.33E-01	FLJ14107	hypothetical protein FLJ14107	chr8p21.3	207287_at	XR_017858 /// XR_017962 /// XR_041874
2.51	2.56	0.05	7.85E-01	9.33E-01	LOC285692	hypothetical protein LOC285692	chr5p15.31	1568739_at	---
2.76	2.80	0.04	7.85E-01	9.33E-01	C20orf107	chromosome 20 open reading frame 107	chr20q13.31	232513_x_at	NM_001013646
3.32	3.35	0.04	7.85E-01	9.33E-01	---	---	---	243960_x_at	---
2.74	2.77	0.03	7.86E-01	9.33E-01	BMP6	Bone morphogenetic protein 6	chr6p24-p23	241141_at	NM_001718
1.89	1.92	0.03	7.85E-01	9.33E-01	---	---	---	1561703_at	---
2.28	2.32	0.03	7.85E-01	9.33E-01	SHMT1	Serine hydroxymethyltransferase 1 (soluble)	chr17p11.2	231701_s_at	NM_004169 /// NM_148918
2.81	2.85	0.04	7.86E-01	9.33E-01	---	---	---	238381_x_at	---
3.36	3.41	0.04	7.86E-01	9.33E-01	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	chr9q22.3	1568779_a_at	NM_001393
3.99	4.02	0.03	7.86E-01	9.33E-01	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	chr10p12	216509_x_at	NM_001009569 /// NM_004641
3.67	3.71	0.04	7.86E-01	9.33E-01	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	chr5p12	225985_at	NM_006251 /// NM_206907
9.68	9.74	0.06	7.86E-01	9.34E-01	RPN2	ribophorin II	chr20q12-q13.1	213491_x_at	NM_002951
7.43	7.52	0.09	7.86E-01	9.34E-01	TMED5	transmembrane emp24 protein transport domain containing 5	chr1pter-q31.3	202194_at	NM_016040
5.49	5.56	0.08	7.86E-01	9.34E-01	EDNRB	endothelin receptor type B	chr13q22	206701_x_at	NM_000115 /// NM_001122659 /// NM_003991
11.03	11.07	0.04	7.86E-01	9.34E-01	ITM2B	integral membrane protein 2B	chr13q14.3	217732_s_at	NM_021999
4.93	5.01	0.08	7.86E-01	9.34E-01	---	---	---	227854_at	---
3.73	3.79	0.06	7.86E-01	9.34E-01	SFRS12	Splicing factor, arginine/serine-rich 12	chr5q12.3	242185_at	NM_001077199 /// NM_139168
6.52	6.58	0.05	7.86E-01	9.34E-01	APOL3	apolipoprotein L, 3	chr22q13.1	221087_s_at	NM_014349 /// NM_030644 /// NM_145639 /// NM_145640 /// NM_145641 /// NM_145642
2.36	2.41	0.04	7.86E-01	9.34E-01	SEC14L3	SEC14-like 3 (S. cerevisiae)	chr22q12.2	216346_at	NM_174975
2.12	2.15	0.03	7.86E-01	9.34E-01	---	---	---	237596_at	---
2.39	2.43	0.04	7.86E-01	9.34E-01	---	---	---	232241_at	---
1.84	1.87	0.03	7.86E-01	9.34E-01	HPRT1	Hypoxanthine phosphoribosyltransferase 1	chrXq26.1	1565446_at	NM_000194
5.57	5.65	0.08	7.86E-01	9.34E-01	KIAA0427	KIAA0427	chr18q21.1	204303_s_at	NM_014772
3.75	3.79	0.05	7.86E-01	9.34E-01	GPR135	G protein-coupled receptor 135	chr14q23.1	211659_at	NM_022571
2.12	2.15	0.04	7.86E-01	9.34E-01	CNTN5	contactin 5	chr11q21-q22.2	207452_s_at	NM_014361 /// NM_175566
1.94	1.97	0.03	7.86E-01	9.34E-01	C9orf72	chromosome 9 open reading frame 72	chr9p21.2	1553134_s_at	NM_018325 /// NM_145005
1.81	1.84	0.03	7.87E-01	9.34E-01	SI	sucrase-isomaltase (alpha-glucosidase)	chr3q25.2-q26.2	206664_at	NM_001041
2.29	2.33	0.04	7.87E-01	9.34E-01	TOP2A	topoisomerase (DNA) II alpha 170kDa	chr17q21-q22	201291_s_at	NM_001067
5.21	5.35	0.14	7.87E-01	9.34E-01	---	---	---	230913_at	---
5.54	5.63	0.09	7.87E-01	9.34E-01	CSNK1A1	Casein kinase 1, alpha 1	chr5q32	240221_at	NM_001025105 /// NM_001892
6.34	6.43	0.09	7.87E-01	9.34E-01	RBM9	RNA binding motif protein 9	chr22q13.1	213901_x_at	NM_001031695 /// NM_001082576 /// NM_001082577 /// NM_001082578 /// NM_001082579 /// NM_014309
4.20	4.27	0.08	7.87E-01	9.34E-01	DNAH9	dynein, axonemal, heavy chain 9	chr17p12	207959_s_at	NM_001372 /// NM_004662

7.01	7.06	0.05	7.87E-01	9.34E-01	IPO9	importin 9	chr1q32.1	217885_at	NM_018085
2.10	2.15	0.05	7.87E-01	9.34E-01	MRGPRX1	MAS-related GPR, member X1	chr11p15.1|11	1553401_at	NM_147199
2.27	2.31	0.04	7.87E-01	9.34E-01	TCHH	trichohyalin	chr1q21.3	213780_at	NM_007113
4.59	4.70	0.11	7.87E-01	9.34E-01	FOXN3	forkhead box N3	chr14q31.3	241984_at	NM_001085471 /// NM_005197
4.19	4.30	0.10	7.87E-01	9.34E-01	---	---	---	240260_at	---
5.89	5.97	0.08	7.87E-01	9.34E-01	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	chr18q11.2	202691_at	NM_006938
1.98	2.03	0.04	7.87E-01	9.34E-01	ITGBL1	Integrin, beta-like 1 (with EGF-like repeat domains)	chr13q33	1557079_at	NM_004791
4.11	4.14	0.04	7.87E-01	9.34E-01	TDRD3	tudor domain containing 3	chr13q21.2	214028_x_at	NM_030794
5.36	5.46	0.11	7.88E-01	9.34E-01	SKAP2	src kinase associated phosphoprotein 2	chr7p21-p15	216899_s_at	NM_003930
3.17	3.24	0.07	7.88E-01	9.34E-01	---	---	---	226885_at	---
3.78	3.84	0.05	7.88E-01	9.34E-01	RAD52	RAD52 homolog (S. cerevisiae)	chr12p13-p12.2	211904_x_at	NM_134424
2.04	2.09	0.05	7.88E-01	9.34E-01	IL5RA	interleukin 5 receptor, alpha	chr3p26-p24	211516_at	NM_000564 /// NM_175724 /// NM_175725 /// NM_175726 /// NM_175727 /// NM_175728
3.03	3.08	0.05	7.88E-01	9.34E-01	LOC728883	hypothetical LOC728883	chr10q11.22	1557660_s_at	XM_001127767 /// XM_001128700 /// XM_001715110
2.16	2.21	0.04	7.88E-01	9.34E-01	---	---	---	237558_at	---
2.71	2.75	0.04	7.87E-01	9.34E-01	RNF185	Ring finger protein 185	chr22q12.2	207280_at	NM_152267
2.43	2.47	0.05	7.88E-01	9.34E-01	FRAS1	Fraser syndrome 1	chr4q21.21	220910_at	NM_025074
1.98	2.01	0.03	7.88E-01	9.34E-01	LOC644620	Similar to hCG2041997	chr9q31.2	1569817_at	XM_001716736 /// XM_001717475 /// XM_001718226
2.41	2.45	0.04	7.88E-01	9.34E-01	---	---	---	230589_at	---
6.73	6.80	0.07	7.88E-01	9.34E-01	SMAP1	stromal membrane-associated GTPase-activating protein 1	chr6q13	218137_s_at	NM_001044305 /// NM_021940
2.09	2.12	0.03	7.88E-01	9.34E-01	FAM71D	family with sequence similarity 71, member D	chr14q23.3	1552839_at	NM_173526
3.23	3.31	0.08	7.88E-01	9.34E-01	WDSOF1	WD repeats and SOF1 domain containing	chr8q22.3	231784_s_at	NM_015420
2.14	2.17	0.03	7.88E-01	9.34E-01	---	---	---	233502_at	---
2.94	2.97	0.03	7.88E-01	9.34E-01	KIAA0146	KIAA0146	chr8q11.21	236284_at	NM_001080394
5.00	5.09	0.09	7.88E-01	9.34E-01	PCDH17	protocadherin 17	chr13q21.1	205656_at	NM_001040429
6.47	6.56	0.09	7.88E-01	9.34E-01	MOBKL2A	MOB1, Mps One Binder kinase activator-like 2A (yeast)	chr19p13.3	225530_at	NM_130807
6.54	6.67	0.13	7.89E-01	9.34E-01	---	---	---	1559776_at	---
5.30	5.43	0.13	7.89E-01	9.34E-01	DOCK7	dedicator of cytokinesis 7	chr1p31.3	225384_at	NM_033407
2.96	3.04	0.09	7.89E-01	9.34E-01	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	chr20p12	215687_x_at	NM_015192 /// NM_182734
5.09	5.18	0.08	7.89E-01	9.34E-01	C5orf37	chromosome 5 open reading frame 37	chr5q13.3	227267_at	NM_001099271 /// NM_152408
5.41	5.49	0.08	7.89E-01	9.34E-01	JARID1A	jumonji, AT rich interactive domain 1A	chr12p11	215698_at	NM_001042603 /// NM_005056
4.06	4.13	0.07	7.89E-01	9.34E-01	COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung)	chr20q11.21	232761_at	NM_032609
3.67	3.72	0.05	7.89E-01	9.34E-01	FBXL18	F-box and leucine-rich repeat protein 18	chr7p22.2	220896_at	NM_024963
2.76	2.81	0.05	7.89E-01	9.34E-01	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	chr5p14-p13	219790_s_at	NM_000908
7.15	7.20	0.05	7.88E-01	9.34E-01	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	chr10p14-p13	223100_s_at	NM_014142
5.90	5.94	0.04	7.88E-01	9.34E-01	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	chr1p34.1	1555181_a_at	NM_006279 /// NM_174963 /// NM_174964 /// NM_174965 /// NM_174966 /// NM_174967 /// NM_174968 /// NM_174969 /// NM_174970 /// NM_174971
2.07	2.11	0.04	7.89E-01	9.34E-01	---	---	---	1563519_at	---
3.03	3.07	0.03	7.89E-01	9.34E-01	---	---	---	232687_at	---
1.87	1.90	0.03	7.89E-01	9.34E-01	---	---	---	234632_x_at	---
1.82	1.84	0.03	7.89E-01	9.34E-01	LOC283112	hypothetical protein LOC283112	chr11p15.1	1562400_at	---
2.27	2.32	0.05	7.89E-01	9.35E-01	KIF6	kinesin family member 6	chr6p21.2	1562639_at	NM_145027
4.02	4.06	0.04	7.89E-01	9.35E-01	VAMP4	vesicle-associated membrane protein 4	chr1q24-q25	211760_s_at	NM_003762
2.79	2.85	0.06	7.89E-01	9.35E-01	---	---	---	216585_at	---

2.13	2.17	0.04	7.89E-01	9.35E-01	ZNF543	Zinc finger protein 543	chr19q13.43	240191_at	NM_213598
4.78	4.91	0.13	7.90E-01	9.35E-01	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	chr1q32.1	212763_at	NM_203459
4.83	4.91	0.08	7.89E-01	9.35E-01	ZNF784	zinc finger protein 784	chr19q13.42	228364_at	NM_203374
5.99	6.06	0.07	7.89E-01	9.35E-01	LOC100131993	Similar to hCG2020760	chr13q14.2	230292_at	XM_001720626 /// XM_001722750 /// XM_001725590
6.15	6.22	0.07	7.89E-01	9.35E-01	CTNNBIP1	catenin, beta interacting protein 1	chr1p36.22	203081_at	NM_001012329 /// NM_020248
2.49	2.53	0.05	7.89E-01	9.35E-01	FOXA1	forkhead box A1	chr14q12-q13	204667_at	NM_004496
2.83	2.87	0.05	7.90E-01	9.35E-01	---	---	---	239505_at	---
2.15	2.18	0.03	7.89E-01	9.35E-01	LOC339593	hypothetical protein LOC339593	chr20p12.2	1564049_at	---
1.91	1.94	0.03	7.89E-01	9.35E-01	LOC401497	similar to PRO2738	chr9p21.1	1561414_at	XM_376822 /// XM_939123
7.23	7.29	0.06	7.90E-01	9.35E-01	IQSEC1	IQ motif and Sec7 domain 1	chr3p25.1	203906_at	NM_001134382 /// NM_014869
2.40	2.45	0.04	7.90E-01	9.35E-01	C10orf128	chromosome 10 open reading frame 128	chr10q11.22	1561890_at	NM_001010863
2.06	2.08	0.03	7.90E-01	9.35E-01	---	---	---	237902_at	---
3.03	3.07	0.04	7.90E-01	9.35E-01	FLJ12595	guanine nucleotide binding protein-like 3 (nucleolar)-like pseudogene	chr5q12.1	220716_at	---
3.60	3.63	0.04	7.90E-01	9.35E-01	---	---	---	238972_at	---
1.90	1.93	0.03	7.90E-01	9.35E-01	FLJ43390	hypothetical LOC646113	chr14q23.2	231186_at	NR_015358 /// XR_041177 /// XR_041178 /// XR_041179
2.78	2.82	0.05	7.90E-01	9.35E-01	C1orf61	chromosome 1 open reading frame 61	chr1q22	1570451_at	NM_006365
2.50	2.55	0.04	7.90E-01	9.35E-01	ARL2BP	ADP-ribosylation factor-like 2 binding protein	chr16q13	202091_at	NM_012106
2.75	2.80	0.05	7.90E-01	9.35E-01	---	---	---	238182_at	---
2.45	2.49	0.05	7.90E-01	9.35E-01	C21orf117	chromosome 21 open reading frame 117	---	1554983_at	---
2.29	2.32	0.03	7.90E-01	9.35E-01	---	---	---	243200_at	---
2.32	2.35	0.03	7.90E-01	9.35E-01	---	---	---	AFFX-ThrX-5_at	---
3.42	3.45	0.03	7.90E-01	9.35E-01	---	---	---	242266_x_at	---
3.12	3.16	0.04	7.90E-01	9.35E-01	TK1	thymidine kinase 1, soluble	chr17q23.2-q25.3	1554408_a_at	NM_003258
6.22	6.38	0.16	7.91E-01	9.35E-01	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	chr1p12	202236_s_at	NM_003051
8.73	8.84	0.11	7.91E-01	9.35E-01	HMGB1	high-mobility group box 1	chr13q12	200679_x_at	NM_002128
3.01	3.06	0.05	7.91E-01	9.35E-01	---	---	---	1570531_at	---
3.43	3.48	0.05	7.90E-01	9.35E-01	SH3RF1	SH3 domain containing ring finger 1	chr4q32.3-q33	225590_at	NM_020870
2.67	2.72	0.04	7.91E-01	9.35E-01	---	---	---	244329_at	---
2.31	2.35	0.04	7.91E-01	9.35E-01	LOC400128	hypothetical gene supported by BC025370	chr13q14.11	1569436_at	---
2.59	2.62	0.03	7.91E-01	9.35E-01	---	---	---	241386_at	---
9.62	9.68	0.07	7.91E-01	9.35E-01	PHPT1	phosphohistidine phosphatase 1	chr9q34.3	223207_x_at	NM_014172
1.96	1.99	0.03	7.91E-01	9.35E-01	LCTL	lactase-like	chr15q22.31	1563899_at	NM_207338
4.69	4.80	0.11	7.91E-01	9.35E-01	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	chr12q24.1	202869_at	NM_001032409 /// NM_002534 /// NM_016816
5.52	5.63	0.11	7.91E-01	9.35E-01	ATF7IP2	activating transcription factor 7 interacting protein 2	chr16p13.13	219870_at	NM_024997
5.90	5.99	0.09	7.91E-01	9.35E-01	SLC19A1	solute carrier family 19 (folate transporter), member 1	chr21q22.3	211576_s_at	NM_194255
5.06	5.14	0.08	7.91E-01	9.35E-01	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	chr12q24.1	205552_s_at	NM_001032409 /// NM_002534 /// NM_016816
4.25	4.32	0.07	7.91E-01	9.35E-01	STK40	serine/threonine kinase 40	chr1p34.3	223852_s_at	NM_032017
4.56	4.62	0.06	7.91E-01	9.35E-01	LOC100132503 /// RNF208	similar to ring finger protein 208 /// ring finger protein 208	chr9q34.3	221273_s_at	NM_031297 /// XM_001721014
6.12	6.18	0.06	7.91E-01	9.35E-01	FAM152A	family with sequence similarity 152, member A	chr1q44	222158_s_at	NM_016076
4.20	4.26	0.06	7.91E-01	9.35E-01	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	chr12q12-q14	216845_x_at	NM_003482
5.28	5.34	0.06	7.91E-01	9.35E-01	POLD3	polymerase (DNA-directed), delta 3, accessory subunit	chr11q14	212836_at	NM_006591
5.07	5.12	0.06	7.91E-01	9.35E-01	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	chr20q11.23	202571_s_at	NM_001042486 /// NM_014902 /// NM_183006
2.95	3.01	0.05	7.91E-01	9.35E-01	---	---	---	1566111_at	---
2.45	2.50	0.05	7.91E-01	9.35E-01	RPGRIP1L	RPGRIP1-like	chr16q12.2	213959_s_at	NM_001127897 /// NM_015272
2.20	2.24	0.05	7.91E-01	9.35E-01	---	---	---	243571_at	---
4.41	4.46	0.05	7.91E-01	9.35E-01	ADAT1	adenosine deaminase, tRNA-specific 1	chr16q23.1	219384_s_at	NM_012091
3.19	3.23	0.05	7.91E-01	9.35E-01	GNLY	granulysin	chr2p11.2	205495_s_at	NM_006433 /// NM_012483

2.61	2.65	0.04	7.91E-01	9.35E-01	MPO	myeloperoxidase	chr17q23.1	203949_at	NM_000250
3.66	3.70	0.04	7.91E-01	9.35E-01	LOC145694	hypothetical protein LOC145694	chr15q22.31	243622_at	---
1.87	1.91	0.04	7.91E-01	9.35E-01	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	chr11q14.3-q21	1554504_at	NM_005467
2.38	2.42	0.04	7.91E-01	9.35E-01	VN1R5	vomeronasal 1 receptor 5	chr1q44	1553550_at	NM_173858
3.05	3.08	0.04	7.91E-01	9.35E-01	MPDU1	mannose-P-dolichol utilization defect 1	chr17p13.1-p12	1557569_at	NM_004870
2.29	2.32	0.04	7.91E-01	9.35E-01	---	---	---	237698_at	---
2.20	2.24	0.04	7.91E-01	9.35E-01	LOC284260	hypothetical gene supported by BC011527; BC021928; BC011527; BC021928	chr18q12.3	1558903_at	XM_001720683 /// XM_001721958 /// XM_001723622
1.91	1.94	0.03	7.91E-01	9.35E-01	---	---	---	210698_at	---
2.79	2.83	0.04	7.91E-01	9.35E-01	CCBP2	chemokine binding protein 2	chr3p21.3	1559432_at	NM_001296
1.93	1.96	0.03	7.92E-01	9.35E-01	LRTM1	leucine-rich repeats and transmembrane domains 1	chr3p14.3	91580_at	NM_020678
2.72	2.77	0.05	7.92E-01	9.35E-01	PPP1R2	Protein phosphatase 1, regulatory (inhibitor) subunit 2	chr3q29	213774_s_at	NM_006241
5.00	5.12	0.12	7.92E-01	9.35E-01	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	chr8p23.1	222662_at	NM_024607
2.11	2.16	0.05	7.92E-01	9.35E-01	LRRIQ3	leucine-rich repeats and IQ motif containing 3	chr1p31.1	235498_at	NM_001105659
2.42	2.46	0.04	7.92E-01	9.35E-01	---	---	---	241548_at	---
3.13	3.17	0.05	7.92E-01	9.35E-01	LOC100130328 /// LOC650686 /// NXF2 /// NXF2B	similar to hCG2045904 /// similar to nuclear RNA export factor 2 /// nuclear RNA export factor 2 /// nuclear RNA export factor 2B	chrXq22.1	220257_x_at	NM_001099686 /// NM_017809 /// NM_022053 /// XM_001713916 /// XM_001713918 /// XM_001713996 /// XM_001714190
1.97	2.01	0.04	7.92E-01	9.35E-01	---	---	---	240734_at	---
5.48	5.58	0.11	7.92E-01	9.35E-01	CCL5	chemokine (C-C motif) ligand 5	chr17q11.2-q12	1555759_a_at	NM_002985
2.04	2.07	0.03	7.92E-01	9.35E-01	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	chr6p21.2	1555186_at	NM_000389 /// NM_078467
2.66	2.71	0.04	7.92E-01	9.35E-01	---	---	---	230450_at	---
5.17	5.24	0.06	7.92E-01	9.36E-01	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	chr20q11.23	202570_s_at	NM_001042486 /// NM_014902 /// NM_183006
2.97	3.01	0.05	7.92E-01	9.36E-01	GARNL4	GTPase activating Rap/RanGAP domain-like 4	chr17p13.3	213280_at	NM_001100398 /// NM_015085
2.17	2.21	0.03	7.92E-01	9.36E-01	---	---	---	220450_at	---
3.32	3.37	0.05	7.92E-01	9.36E-01	LOC338651	hypothetical protein LOC338651	chr11p15.5	1562681_at	NR_021489
3.14	3.19	0.05	7.92E-01	9.36E-01	C20orf165	chromosome 20 open reading frame 165	chr20q13.12	1553752_at	NM_080608
2.50	2.53	0.03	7.92E-01	9.36E-01	---	---	---	238050_at	---
1.94	1.97	0.03	7.92E-01	9.36E-01	---	---	---	1563833_at	---
2.50	2.55	0.04	7.92E-01	9.36E-01	---	---	---	237008_at	---
2.36	2.42	0.06	7.92E-01	9.36E-01	EPHB1	EPH receptor B1	chr3q21-q23	230425_at	NM_004441
8.37	8.42	0.04	7.92E-01	9.36E-01	LMNA	lamin A/C	chr1q21.2-q21.3	203411_s_at	NM_005572 /// NM_170707 /// NM_170708
1.96	1.99	0.03	7.92E-01	9.36E-01	---	---	---	224080_at	---
5.75	5.82	0.07	7.92E-01	9.36E-01	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	chr6q27	204906_at	NM_001006932 /// NM_021135
3.29	3.34	0.05	7.92E-01	9.36E-01	---	---	---	1563273_at	---
3.14	3.18	0.05	7.92E-01	9.36E-01	HIST1H1A	histone cluster 1, H1a	chr6p21.3	208484_at	NM_005325
1.95	1.99	0.04	7.92E-01	9.36E-01	ARL11	ADP-ribosylation factor-like 11	chr13q14.3	1552693_at	NM_138450
2.19	2.23	0.04	7.92E-01	9.36E-01	FAM155A	family with sequence similarity 155, member A	chr13q33.3	230869_at	NM_001080396
2.04	2.07	0.03	7.92E-01	9.36E-01	ENTHD1	ENTH domain containing 1	chr22q13.1	1552394_a_at	NM_152512
2.87	2.92	0.05	7.93E-01	9.36E-01	---	---	---	240697_at	---
2.23	2.27	0.03	7.93E-01	9.36E-01	C1orf187	chromosome 1 open reading frame 187	chr1p36.22	1554340_a_at	NM_198545
2.38	2.41	0.03	7.93E-01	9.36E-01	FLJ10213	Hypothetical protein FLJ10213	chr3p13	231641_at	NM_018029
3.37	3.40	0.03	7.93E-01	9.36E-01	A2LD1	AIG2-like domain 1	chr13q32.3	237869_at	NM_033110 /// XM_001714498 /// XM_001714769 /// XM_001715756
3.38	3.43	0.05	7.93E-01	9.36E-01	SLAIN2	SLAIN motif family, member 2	chr4p12	224853_at	NM_020846
1.98	2.02	0.03	7.93E-01	9.36E-01	---	---	---	244203_at	---
5.00	5.05	0.05	7.93E-01	9.36E-01	C2orf82	chromosome 2 open reading frame 82	chr2q37.1	232299_at	NM_206895
1.88	1.91	0.04	7.93E-01	9.36E-01	---	---	---	1568662_at	---
2.57	2.61	0.04	7.93E-01	9.36E-01	---	---	---	232047_at	---

2.14	2.18	0.04	7.93E-01	9.36E-01	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	chr16q22.1	1570128_at	NM_018332
2.18	2.22	0.04	7.93E-01	9.36E-01	---	---	---	243086_at	---
3.57	3.65	0.08	7.93E-01	9.36E-01	ANPEP	alanyl (membrane) aminopeptidase	chr15q25-q26	202888_s_at	NM_001150
2.38	2.44	0.07	7.93E-01	9.36E-01	ZNF616	zinc finger protein 616	chr19q13.33	239007_at	NM_178523
3.98	4.04	0.06	7.93E-01	9.36E-01	ZDHHC1	zinc finger, DHHC-type containing 1	chr16q22.1	228637_at	NM_013304
3.25	3.30	0.05	7.94E-01	9.36E-01	C4orf46	chromosome 4 open reading frame 46	chr4q32.1	238015_at	NM_001008393
2.39	2.44	0.05	7.94E-01	9.36E-01	OR2L2	olfactory receptor, family 2, subfamily L, member 2	chr1q44	1567237_at	NM_001004686
2.17	2.22	0.05	7.93E-01	9.36E-01	---	---	---	240370_at	---
2.44	2.48	0.05	7.93E-01	9.36E-01	---	---	---	244794_at	---
2.59	2.64	0.04	7.93E-01	9.36E-01	---	---	---	1570160_at	---
2.20	2.24	0.04	7.94E-01	9.36E-01	CENPQ	centromere protein Q	chr6p12.3	219294_at	NM_018132
3.89	3.93	0.03	7.94E-01	9.36E-01	---	---	---	1569601_at	---
2.29	2.34	0.04	7.94E-01	9.36E-01	C12orf32 /// IGHG1	Chromosome 12 open reading frame 32 /// Immunoglobulin heavy constant mu	chr12p13.33 /// chr14q32.33	211642_at	NM_031465
2.41	2.45	0.04	7.94E-01	9.36E-01	---	---	---	1559812_at	---
3.71	3.77	0.05	7.94E-01	9.36E-01	PSD4	pleckstrin and Sec7 domain containing 4	chr2q13	215923_s_at	NM_012455
1.95	1.99	0.04	7.94E-01	9.36E-01	ZNF695	zinc finger protein 695	chr1q44	208273_at	NM_020394
3.74	3.79	0.05	7.94E-01	9.36E-01	NEK11	NIMA (never in mitosis gene a)- related kinase 11	chr3q22.1	1555082_a_at	NM_024800 /// NM_145910
7.68	7.78	0.10	7.94E-01	9.36E-01	ZNF24	zinc finger protein 24	chr18q12	212534_at	NM_006965
4.53	4.62	0.09	7.94E-01	9.36E-01	LRRC8E	leucine rich repeat containing 8 family, member E	chr19p13.2	239433_at	NM_025061
9.23	9.32	0.08	7.94E-01	9.36E-01	EIF5A	eukaryotic translation initiation factor 5A	chr17p13-p12	201123_s_at	NM_001970 /// XM_001724572
3.50	3.55	0.04	7.94E-01	9.36E-01	ART1	ADP-ribosyltransferase 1	chr11p15	207919_at	NM_004314
2.26	2.30	0.04	7.94E-01	9.36E-01	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	chr4q23-q25	237856_at	NM_001100426 /// NM_001100427 /// NM_001100428 /// NM_001100429 /// NM_001100430 /// NM_021159
3.51	3.76	0.25	7.94E-01	9.36E-01	RASGEF1A	RasGEF domain family, member 1A	chr10q11.21	230563_at	NM_145313
7.97	8.03	0.06	7.94E-01	9.36E-01	C17orf79	chromosome 17 open reading frame 79	chr17q11.2	225096_at	NM_018405
2.66	2.71	0.05	7.94E-01	9.36E-01	LOC644090	hypothetical LOC644090	chr7q36.1	238319_at	XM_001719144 /// XM_931994 /// XM_945887
2.12	2.17	0.04	7.94E-01	9.36E-01	---	---	---	1570292_at	---
1.98	2.02	0.04	7.94E-01	9.36E-01	SORBS2	sorbin and SH3 domain containing 2	chr4q35.1	1555472_at	NM_003603 /// NM_021069
3.59	3.64	0.05	7.94E-01	9.36E-01	---	---	---	230672_at	---
2.17	2.21	0.04	7.94E-01	9.36E-01	C6orf218	Chromosome 6 open reading frame 218	chr6p24.3	244829_at	NM_152738
2.16	2.19	0.04	7.94E-01	9.36E-01	FAM38B2	family with sequence similarity 38, member B2	chr18p11.22	1563584_at	XM_001130754
2.20	2.23	0.03	7.94E-01	9.36E-01	---	---	---	237224_at	---
4.45	4.49	0.04	7.94E-01	9.36E-01	ANKRD11	ankyrin repeat domain 11	chr16q24.3	219437_s_at	NM_013275
2.39	2.42	0.03	7.94E-01	9.36E-01	---	---	---	240417_at	---
4.83	5.04	0.21	7.95E-01	9.36E-01	---	---	---	235592_at	---
6.72	6.77	0.05	7.95E-01	9.36E-01	---	---	---	213691_at	---
2.61	2.67	0.06	7.95E-01	9.36E-01	XRCC6BP1	XRCC6 binding protein 1	chr12q14.1	1554349_at	NM_033276
2.43	2.48	0.05	7.95E-01	9.36E-01	GPATCH2	G patch domain containing 2	chr1q41	242224_at	NM_018040
3.93	4.00	0.07	7.95E-01	9.37E-01	ATE1	arginyltransferase 1	chr10q26.13	234584_s_at	NM_001001976 /// NM_007041
2.49	2.56	0.07	7.95E-01	9.37E-01	NUP43	nucleoporin 43kDa	chr6q25.1	238474_at	NM_198887
2.09	2.14	0.05	7.95E-01	9.37E-01	TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	chr10q25.3	235447_at	NM_139169
2.10	2.13	0.03	7.95E-01	9.37E-01	---	---	---	220697_at	---
6.22	6.33	0.12	7.95E-01	9.37E-01	GPR89A /// GPR89B /// GPR89C	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	chr1q21.1	225463_x_at	NM_001097612 /// NM_001097613 /// NM_001097616 /// NM_016334
10.33	10.43	0.10	7.95E-01	9.37E-01	IGFBP7	insulin-like growth factor binding protein 7	chr4q12	201162_at	NM_001553
5.33	5.41	0.09	7.95E-01	9.37E-01	ITGA7	integrin, alpha 7	chr12q13	216331_at	NM_002206
4.01	4.08	0.07	7.95E-01	9.37E-01	ZNF354C	zinc finger protein 354C	chr5q35	228208_x_at	NM_014594
2.93	2.98	0.05	7.95E-01	9.37E-01	EEA1	early endosome antigen 1	chr12q22	204841_s_at	NM_003566
1.89	1.93	0.03	7.95E-01	9.37E-01	RGS1	regulator of G-protein signaling 1	chr1q31	202989_at	NM_002922
1.88	1.91	0.03	7.95E-01	9.37E-01	---	---	---	240713_s_at	---
1.96	2.00	0.03	7.95E-01	9.37E-01	---	---	---	243142_at	---

7.18	7.24	0.06	7.95E-01	9.37E-01	ACTN1	actinin, alpha 1	chr14q24.1-q24.2|14q24|14q22-q24	211160_x_at	NM_001102 /// NM_001130004 /// NM_001130005
2.46	2.50	0.04	7.95E-01	9.37E-01	DKFZp434J0226	hypothetical gene DKFZp434J0226	chr19q13.32	232832_at	---
3.25	3.31	0.06	7.96E-01	9.37E-01	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	chr9q34.13	1553181_at	NM_022779 /// NM_138620
2.28	2.32	0.04	7.96E-01	9.37E-01	LOC338653	hypothetical protein LOC338653	chr11p15.5	1562960_at	---
1.81	1.84	0.03	7.96E-01	9.37E-01	---	---	---	1557599_a_at	---
7.43	7.59	0.15	7.96E-01	9.37E-01	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	chr11p15	220037_s_at	NM_006691
7.36	7.48	0.12	7.96E-01	9.37E-01	LASS6	LAG1 homolog, ceramide synthase 6	chr2q24.3	212442_s_at	NM_203463
3.67	3.78	0.11	7.96E-01	9.37E-01	ITIH4	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	chr3p21-p14	242720_at	NM_002218
3.63	3.71	0.08	7.96E-01	9.37E-01	LOC100128640	Hypothetical protein LOC100128640	chr3p22.2	215590_x_at	XM_001717236 /// XM_001717717 /// XM_001718131
7.52	7.60	0.08	7.96E-01	9.37E-01	RBKS	ribokinase	chr2p23.3	57540_at	NM_022128
3.90	3.96	0.06	7.96E-01	9.37E-01	hCG_1654703	hCG1654703	chr1q23.1	1568745_at	XM_001722850 /// XM_933506 /// XM_943630
2.69	2.75	0.06	7.96E-01	9.37E-01	---	---	---	232775_at	---
4.28	4.33	0.05	7.96E-01	9.37E-01	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	chrXp11.23-p11.22	207440_at	NM_001032289 /// NM_001042498 /// NM_005660
6.33	6.38	0.05	7.96E-01	9.37E-01	GOLGB1	golgin B1, golgi integral membrane protein	chr3q13	201056_at	NM_004487
2.79	2.84	0.05	7.96E-01	9.37E-01	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	chr15q26.1	210045_at	NM_002168
2.44	2.49	0.05	7.96E-01	9.37E-01	---	---	---	234416_at	---
5.49	5.53	0.04	7.96E-01	9.37E-01	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	chr3p23-p21	201075_s_at	NM_003074
2.80	2.84	0.04	7.96E-01	9.37E-01	OPN1SW	opsin 1 (cone pigments), short-wave-sensitive	chr7q32.1	208036_at	NM_001708
2.07	2.10	0.04	7.96E-01	9.37E-01	---	---	---	244260_at	---
3.07	3.13	0.06	7.96E-01	9.37E-01	RIN3	Ras and Rab interactor 3	chr14q32.12	1562005_at	NM_024832
4.34	4.45	0.11	7.96E-01	9.37E-01	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	chr9p12	242961_x_at	NM_014314
3.50	3.53	0.03	7.96E-01	9.37E-01	SILV	silver homolog (mouse)	chr12q13-q14	209848_s_at	NM_006928
8.33	8.45	0.12	7.97E-01	9.37E-01	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	chr17q24	204719_at	NM_007168
9.38	9.48	0.10	7.97E-01	9.37E-01	PON2	paraoxonase 2	chr7q21.3	201876_at	NM_000305 /// NM_001018161
4.74	4.80	0.06	7.97E-01	9.37E-01	ZNF75A	zinc finger protein 75a	chr16p13.11	227670_at	NM_153028
2.57	2.62	0.05	7.96E-01	9.37E-01	---	---	---	241719_at	---
2.21	2.26	0.05	7.96E-01	9.37E-01	---	---	---	1555174_at	---
2.79	2.83	0.05	7.96E-01	9.37E-01	---	---	---	235732_at	---
2.72	2.77	0.05	7.96E-01	9.37E-01	HSPB9	heat shock protein, alpha-crystallin-related, B9	chr17q21.2	230510_at	NM_033194
4.24	4.29	0.05	7.97E-01	9.37E-01	TRIM65	tripartite motif-containing 65	chr17q25.1	235081_x_at	NM_173547
3.13	3.17	0.04	7.97E-01	9.37E-01	---	---	---	230373_at	---
2.16	2.20	0.04	7.97E-01	9.37E-01	TRA@ /// TRD@	T cell receptor alpha locus /// T cell receptor delta locus	chr14q11.2	216191_s_at	---
2.06	2.09	0.03	7.97E-01	9.37E-01	TNPO1	transportin 1	chr5q13.2	243324_x_at	NM_002270 /// NM_153188
2.51	2.54	0.03	7.97E-01	9.37E-01	KIR3DL2 /// LOC727787	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 /// similar to killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I NK cell receptor) (Natural killer-associated transcript 4) (NKAT-4) (p70 natural killer cell receptor clone CL-5) (CD158k antigen)	chr19q13.4	207314_x_at	NM_006737 /// XM_001718625
7.28	7.35	0.07	7.97E-01	9.37E-01	LYPLA1	lysophospholipase I	chr8q11.23	203007_x_at	NM_006330
2.04	2.07	0.03	7.97E-01	9.37E-01	C16orf62	chromosome 16 open reading frame 62	chr16p12.3	1558557_at	NM_020314
4.49	4.56	0.06	7.97E-01	9.37E-01	BMPR1A	bone morphogenetic protein receptor, type IA	chr10q22.3	204832_s_at	NM_004329
4.30	4.37	0.06	7.97E-01	9.37E-01	WDR51A	WD repeat domain 51A	chr3p21.1	226355_at	NM_015426
2.52	2.57	0.05	7.97E-01	9.37E-01	IFNA21	interferon, alpha 21	chr9p22	211145_x_at	NM_002175
2.43	2.48	0.04	7.97E-01	9.37E-01	---	---	---	239402_at	---
2.51	2.55	0.04	7.97E-01	9.37E-01	PCDHGC3	protocadherin gamma subfamily C, 3	chr5q31	214563_at	NM_002588 /// NM_032402 /// NM_032403
2.29	2.33	0.04	7.97E-01	9.37E-01	IL9	interleukin 9	chr5q31.1	208193_at	NM_000590
1.89	1.92	0.03	7.97E-01	9.37E-01	ASB5	ankyrin repeat and SOCS box-containing 5	chr4q34.2	235503_at	NM_080874
4.42	4.47	0.05	7.97E-01	9.37E-01	GRTP1	growth hormone regulated TBC protein 1	chr13q34	206712_at	NM_024719

4.64	4.79	0.15	7.97E-01	9.37E-01	SLC39A6	solute carrier family 39 (zinc transporter), member 6	chr18q12.2	1555460_a_at	NM_001099406 /// NM_012319
5.80	5.86	0.06	7.97E-01	9.37E-01	BAG4	BCL2-associated athanogene 4	chr8p12	228189_at	NM_004874
2.76	2.83	0.06	7.97E-01	9.37E-01	OR2C1	olfactory receptor, family 2, subfamily C, member 1	chr16p13.3	221460_at	NM_012368
8.35	8.41	0.06	7.97E-01	9.37E-01	GYPC	glycophorin C (Gerbich blood group)	chr2q14-q21	202947_s_at	NM_002101 /// NM_016815
3.27	3.32	0.05	7.97E-01	9.37E-01	---	---	---	234044_at	---
3.73	3.78	0.04	7.97E-01	9.37E-01	MSI1	musashi homolog 1 (Drosophila)	chr12q24.1-q24.31	206333_at	NM_002442
3.67	3.71	0.03	7.97E-01	9.37E-01	---	---	---	229621_x_at	---
2.09	2.12	0.03	7.97E-01	9.37E-01	CD96	CD96 molecule	chr3q13.13-q13.2	1555120_at	NM_005816 /// NM_198196
1.69	1.72	0.03	7.97E-01	9.37E-01	---	---	---	1556170_at	---
1.84	1.87	0.03	7.98E-01	9.37E-01	---	---	---	1563000_at	---
3.93	3.98	0.05	7.98E-01	9.37E-01	SMTNL1	smoothelin-like 1	chr11q12.1	230367_at	NM_001105565
2.45	2.49	0.04	7.98E-01	9.37E-01	AJAP1	adherens junctions associated protein 1	chr1p36.32	206460_at	NM_001042478 /// NM_018836
4.06	4.13	0.07	7.98E-01	9.37E-01	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	chr14q32	1557718_at	NM_002719 /// NM_178586 /// NM_178587 /// NM_178588
4.53	4.60	0.07	7.98E-01	9.37E-01	---	---	---	228442_at	---
2.52	2.58	0.06	7.98E-01	9.37E-01	---	---	---	232833_at	---
2.36	2.40	0.05	7.98E-01	9.37E-01	FRAS1	Fraser syndrome 1	chr4q21.21	1560153_at	NM_025074
2.10	2.13	0.03	7.98E-01	9.37E-01	KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	chr1p13.3	207237_at	NM_002232
2.10	2.14	0.03	7.98E-01	9.37E-01	POPDC3	popeye domain containing 3	chr6q21	219926_at	NM_022361
1.87	1.89	0.03	7.98E-01	9.37E-01	---	---	---	237243_at	---
3.13	3.17	0.04	7.98E-01	9.37E-01	AMBP	Alpha-1-microglobulin/bikunin precursor	chr9q32-q33	214425_at	NM_001633
3.22	3.29	0.08	7.98E-01	9.38E-01	hCG_1776259	hypothetical protein FLJ23556	chr10q25.2	206548_at	XR_039606 /// XR_040924 /// XR_040925
4.22	4.28	0.06	7.98E-01	9.38E-01	---	---	---	233440_at	---
2.93	2.97	0.04	7.98E-01	9.38E-01	---	---	---	241431_at	---
3.15	3.20	0.05	7.98E-01	9.38E-01	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17p13.3	235710_at	NM_001128159 /// NM_018289
4.84	5.08	0.24	7.98E-01	9.38E-01	C2orf40	chromosome 2 open reading frame 40	chr2q12.2	223623_at	NM_032411
2.08	2.11	0.03	7.98E-01	9.38E-01	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	chr17q21.1	1570415_at	NM_007010 /// NM_152300
7.35	7.41	0.06	7.98E-01	9.38E-01	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	chr16p13.3	201498_at	NM_003470
1.94	1.97	0.03	7.98E-01	9.38E-01	TTC29	tetratricopeptide repeat domain 29	chr4q31.23	223962_at	NM_031956
3.29	3.41	0.13	7.99E-01	9.38E-01	ZNF644	zinc finger protein 644	chr1p22.2	1553725_s_at	NM_016620 /// NM_032186 /// NM_201269
3.81	3.88	0.06	7.99E-01	9.38E-01	RC3H2	ring finger and CCCH-type zinc finger domains 2	chr9q34	230134_s_at	NM_001100588 /// NM_018835
3.00	3.05	0.05	7.99E-01	9.38E-01	PIGG	Phosphatidylinositol glycan anchor biosynthesis, class G	chr4p16.3	233654_at	NM_001127178 /// NM_017733
2.50	2.55	0.06	7.99E-01	9.38E-01	HECTD1	HECT domain containing 1	chr14q12	241683_at	NM_015382
2.51	2.54	0.03	7.99E-01	9.38E-01	NEB	nebulin	chr2q22	215368_at	NM_004543
2.92	2.95	0.03	7.99E-01	9.38E-01	LPA /// PLG	lipoprotein, Lp(a) /// plasminogen	chr6q26	209978_s_at	NM_000301 /// NM_005577
1.96	1.98	0.03	7.99E-01	9.38E-01	---	---	---	1561680_at	---
2.71	2.76	0.05	7.99E-01	9.38E-01	---	---	---	1566097_at	---
6.50	6.58	0.08	7.99E-01	9.38E-01	WDR3	WD repeat domain 3	chr1p13-p12	218882_s_at	NM_006784
2.20	2.24	0.04	7.99E-01	9.38E-01	ODF2L	outer dense fiber of sperm tails 2-like	chr1p22.3	237420_at	NM_001007022 /// NM_020729
6.61	6.68	0.08	7.99E-01	9.38E-01	C10orf46	chromosome 10 open reading frame 46	chr10q26.11	225192_at	NM_153810
7.21	7.32	0.11	7.99E-01	9.38E-01	CD164	CD164 molecule, sialomucin	chr6q21	208654_s_at	NM_006016
2.47	2.50	0.04	7.99E-01	9.38E-01	LRIG1	Leucine-rich repeats and immunoglobulin-like domains 1	chr3p14	236173_s_at	NM_015541
6.77	6.87	0.10	7.99E-01	9.38E-01	TESC	tescalcin	chr12q24.22	218872_at	NM_017899
3.55	3.64	0.09	7.99E-01	9.38E-01	CD38	CD38 molecule	chr4p15	205692_s_at	NM_001775
4.92	4.98	0.06	7.99E-01	9.38E-01	CXorf39	chromosome X open reading frame 39	chrXq22.2	227133_at	NM_207318
2.36	2.40	0.04	7.99E-01	9.38E-01	---	---	---	1567698_x_at	---
3.03	3.07	0.04	7.99E-01	9.38E-01	---	---	---	238659_at	---
6.92	6.95	0.03	7.99E-01	9.38E-01	KIAA1143	KIAA1143	chr3p21.31	227493_s_at	NM_020696
5.90	5.99	0.09	8.00E-01	9.38E-01	---	---	---	206874_s_at	---
7.86	7.93	0.07	8.00E-01	9.38E-01	ZMYND8	zinc finger, MYND-type containing 8	chr20q13.12	209049_s_at	NM_012408 /// NM_183047 /// NM_183048
7.87	7.92	0.05	8.00E-01	9.38E-01	USF2	upstream transcription factor 2, c-fos interacting	chr19q13	214879_x_at	NM_003367 /// NM_207291
2.78	2.83	0.05	8.00E-01	9.38E-01	---	---	---	236865_at	---

2.50	2.54	0.04	8.00E-01	9.38E-01	---	---	---	241417_at	---
2.25	2.29	0.04	8.00E-01	9.38E-01	SNX5	sorting nexin 5	chr20p11	238433_at	NM_014426 /// NM_152227
2.92	2.97	0.06	8.00E-01	9.38E-01	RAP2C	RAP2C, member of RAS oncogene family	chrXq25	234344_at	NM_021183
2.80	2.85	0.04	8.00E-01	9.38E-01	---	---	---	1565836_at	---
2.26	2.30	0.04	8.00E-01	9.38E-01	BAIAP2L2	BAI1-associated protein 2-like 2	chr22q13.1	221178_at	NM_025045
2.88	2.93	0.06	8.00E-01	9.39E-01	FOXM1	forkhead box M1	chr12p13	202580_x_at	NM_021953 /// NM_202002 /// NM_202003
3.39	3.45	0.06	8.00E-01	9.39E-01	---	---	---	1563031_at	---
2.42	2.47	0.04	8.00E-01	9.39E-01	---	---	---	208324_at	---
2.11	2.14	0.03	8.00E-01	9.39E-01	---	---	---	241887_at	---
1.84	1.86	0.03	8.00E-01	9.39E-01	---	---	---	216068_at	---
2.10	2.13	0.04	8.00E-01	9.39E-01	---	---	---	239140_at	---
2.18	2.21	0.04	8.00E-01	9.39E-01	TRA@	YME1-like 1 (S. cerevisiae)	chr14q11.2	234440_at	---
4.63	4.69	0.06	8.00E-01	9.39E-01	---	---	---	239969_at	---
2.32	2.36	0.04	8.00E-01	9.39E-01	NEIL3	nei endonuclease VIII-like 3 (E. coli)	chr4q34.3	219502_at	NM_018248
6.81	6.87	0.06	8.01E-01	9.39E-01	GAS2L1	growth arrest-specific 2 like 1	chr22q12.2	209729_at	NM_006478 /// NM_152236 /// NM_152237
7.10	7.28	0.18	8.01E-01	9.39E-01	LDLR	low density lipoprotein receptor	chr19p13.3	202067_s_at	NM_000527
3.84	3.92	0.08	8.01E-01	9.39E-01	---	---	---	1557830_at	---
2.52	2.60	0.08	8.01E-01	9.39E-01	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	chr15q14	205590_at	NM_001128602 /// NM_005739
2.72	2.76	0.04	8.01E-01	9.39E-01	---	---	---	240332_at	---
2.32	2.36	0.04	8.01E-01	9.39E-01	LOC283045	hypothetical protein LOC283045	chr10q21.3	1563854_s_at	---
2.01	2.03	0.03	8.01E-01	9.39E-01	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	chr18p11.32	241620_at	NM_015295
6.42	6.52	0.10	8.01E-01	9.39E-01	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	chr11p15.2	224955_at	NM_021961
7.01	7.07	0.06	8.01E-01	9.39E-01	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	chr7q31.2-q31.3	201237_at	NM_006136
2.23	2.26	0.03	8.01E-01	9.39E-01	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	chr13q12.3	242302_at	NM_015032
2.11	2.14	0.03	8.01E-01	9.39E-01	ASTN2	astrotactin 2	chr9q33.1	1554816_at	NM_014010 /// NM_198186 /// NM_198187 /// NM_198188
4.79	4.84	0.04	8.01E-01	9.39E-01	PIM2	pim-2 oncogene	chrXp11.23	204269_at	NM_006875
1.80	1.82	0.02	8.01E-01	9.39E-01	NRXN1	neurexin 1	chr2p16.3	1558708_at	NM_004801 /// NM_138735
8.50	8.57	0.07	8.01E-01	9.39E-01	IMMT	inner membrane protein, mitochondrial (mitofilin)	chr2p11.2|2	200955_at	NM_001100169 /// NM_001100170 /// NM_006839
3.95	4.02	0.07	8.01E-01	9.39E-01	SYT17	synaptotagmin XVII	chr16p12.3	205613_at	NM_016524
9.21	9.26	0.05	8.01E-01	9.39E-01	HDLBP	high density lipoprotein binding protein	chr2q37.3	221767_x_at	NM_005336 /// NM_203346
2.80	2.85	0.04	8.01E-01	9.39E-01	---	---	---	243868_at	---
1.83	1.86	0.03	8.01E-01	9.39E-01	CNTNAP4	contactin associated protein-like 4	chr16q23.1	1553441_at	NM_033401 /// NM_138994
6.77	6.85	0.08	8.01E-01	9.39E-01	---	---	---	217922_at	---
5.00	5.06	0.07	8.02E-01	9.39E-01	NSUN6	NOL1/NOP2/Sun domain family, member 6	chr10p12.33	230200_at	NM_182543
2.93	2.97	0.03	8.02E-01	9.39E-01	ZNF202	zinc finger protein 202	chr11q23.3	204329_s_at	NM_003455
6.33	6.42	0.09	8.02E-01	9.39E-01	DISP1	dispatched homolog 1 (Drosophila)	chr1q41	228184_at	NM_032890
7.53	7.60	0.06	8.02E-01	9.39E-01	ARMCX1	armadillo repeat containing, X-linked 1	chrXq21.33-q22.2	218694_at	NM_016608
2.22	2.26	0.04	8.02E-01	9.39E-01	---	---	---	243959_at	---
6.99	7.05	0.06	8.02E-01	9.40E-01	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	chr2q37.3	202142_at	NM_006710 /// NM_198189
5.90	5.99	0.09	8.02E-01	9.40E-01	GSN	gelsolin (amyloidosis, Finnish type)	chr9q33	214040_s_at	NM_000177 /// NM_001127662 /// NM_001127663 /// NM_001127664 /// NM_001127665 /// NM_001127666 /// NM_001127667 /// NM_198252
4.08	4.22	0.13	8.02E-01	9.40E-01	MT1M	metallothionein 1M	chr16q13	217546_at	NM_176870

3.04	3.11	0.07	8.02E-01	9.40E-01	---	---	---	229123_at	---
4.02	4.08	0.06	8.02E-01	9.40E-01	SLC22A23	solute carrier family 22, member 23	chr6p25.2	1568718_at	NM_015482 /// NM_021945
2.73	2.79	0.06	8.02E-01	9.40E-01	---	---	---	220932_at	---
4.11	4.17	0.06	8.02E-01	9.40E-01	LOC728705	hypothetical protein LOC728705	chr12q23.3	230579_at	XM_001128243
3.56	3.62	0.06	8.02E-01	9.40E-01	LOH12CR2	loss of heterozygosity, 12, chromosomal region 2	chr12p13.2	236311_at	NR_024061
2.59	2.62	0.04	8.02E-01	9.40E-01	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	238840_at	NM_004735
2.17	2.21	0.04	8.02E-01	9.40E-01	---	---	---	238195_at	---
2.34	2.37	0.04	8.02E-01	9.40E-01	HDX	highly divergent homeobox	chrXq21.1	1553646_at	NM_144657
2.36	2.39	0.03	8.02E-01	9.40E-01	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	chr12q13-q14	1555353_at	NM_002332
2.11	2.14	0.03	8.02E-01	9.40E-01	hCG_1731871	hCG1731871	chrXq13.1	242292_at	XR_041247 /// XR_041248 /// XR_041249
2.00	2.03	0.03	8.02E-01	9.40E-01	---	---	---	1569755_at	---
2.61	2.69	0.08	8.02E-01	9.40E-01	---	---	---	243031_at	---
1.99	2.04	0.04	8.02E-01	9.40E-01	AREGB	Amphiregulin B	chr4q13.3	1557285_at	XM_001125684
3.89	3.95	0.06	8.02E-01	9.40E-01	AK2	adenylate kinase 2	chr1p34	205996_s_at	NM_001625 /// NM_013411
4.46	4.54	0.08	8.02E-01	9.40E-01	ZHX1	zinc fingers and homeoboxes 1	chr8q24.13	223214_s_at	NM_001017926 /// NM_007222
7.16	7.30	0.13	8.02E-01	9.40E-01	IFNGR1	interferon gamma receptor 1	chr6q23.3	211676_s_at	NM_000416
2.23	2.32	0.08	8.03E-01	9.40E-01	CLGN	calmegin	chr4q28.3-q31.1	205830_at	NM_001130675 /// NM_004362
4.51	4.57	0.06	8.03E-01	9.40E-01	CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1	chr7q21-q22	207050_at	NM_000722
2.47	2.51	0.04	8.03E-01	9.40E-01	SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1	chr1q23-q25.1	210049_at	NM_000488
6.49	6.62	0.13	8.03E-01	9.40E-01	NUP88	nucleoporin 88kDa	chr17p13.2	202900_s_at	NM_002532
2.74	2.80	0.06	8.03E-01	9.40E-01	DOCK9	dedicator of cytokinesis 9	chr13q32.3	232874_at	NM_001130048 /// NM_001130049 /// NM_001130050 /// NM_015296
3.13	3.19	0.05	8.03E-01	9.40E-01	SETD3	SET domain containing 3	chr14q32.2	229940_at	NM_032233 /// NM_199123
2.64	2.68	0.04	8.03E-01	9.40E-01	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	chr2q24-q31	203398_s_at	NM_004482
3.87	3.92	0.05	8.03E-01	9.40E-01	DKFZp434K191 /// DKFZP434P211	hypothetical locus DKFZp434K191 /// POM121-like protein	chr22q11.2 /// chr22q11.22	232736_s_at	NR_003714 /// XR_040035
3.74	3.79	0.05	8.03E-01	9.40E-01	IL27RA	interleukin 27 receptor, alpha	chr19p13.11	205926_at	NM_004843
3.74	3.79	0.05	8.03E-01	9.40E-01	DHFR	dihydrofolate reductase	chr5q11.2-q13.2	48808_at	NM_000791
2.52	2.57	0.04	8.03E-01	9.40E-01	---	---	---	230168_at	---
1.91	1.94	0.03	8.03E-01	9.40E-01	---	---	---	241255_at	---
5.10	5.19	0.09	8.03E-01	9.40E-01	TOPORS	topoisomerase I binding, arginine/serine-rich	chr9p21	204071_s_at	NM_005802
2.69	2.74	0.05	8.03E-01	9.40E-01	PIPOX	pipecolic acid oxidase	chr17q11.2	221605_s_at	NM_016518
3.86	3.91	0.04	8.03E-01	9.40E-01	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2	chr12q24.31	205704_s_at	NM_012463
2.99	3.03	0.03	8.03E-01	9.40E-01	---	---	---	238232_at	---
1.92	1.95	0.03	8.03E-01	9.40E-01	---	---	---	1562886_at	---
2.56	2.59	0.03	8.03E-01	9.40E-01	LOC100128661	hypothetical LOC100128661	chr1p34.3	230293_at	XR_039097 /// XR_039428 /// XR_039475
2.02	2.05	0.03	8.03E-01	9.40E-01	---	---	---	244331_at	---
2.56	2.60	0.03	8.03E-01	9.40E-01	SPRY4	sprouty homolog 4 (Drosophila)	chr5q31.3	220983_s_at	NM_001127496 /// NM_030964
2.18	2.21	0.03	8.03E-01	9.40E-01	---	---	---	1570163_at	---
2.19	2.21	0.03	8.03E-01	9.40E-01	RCAN3	RCAN family member 3	chr1p35.3-p33	219864_s_at	NM_013441
5.28	5.33	0.05	8.03E-01	9.40E-01	---	---	---	229182_at	---
3.58	3.64	0.06	8.03E-01	9.40E-01	ASXL2	Additional sex combs like 2 (Drosophila)	chr2p24.1	240072_at	NM_018263
4.20	4.26	0.07	8.04E-01	9.40E-01	YLPM1	YLP motif containing 1	chr14q24.3	1557065_at	NM_019589
2.11	2.14	0.03	8.03E-01	9.40E-01	GRIA2	glutamate receptor, ionotropic, AMPA 2	chr4q32-q33	241172_at	NM_000826 /// NM_001083619 /// NM_001083620
3.12	3.18	0.06	8.04E-01	9.40E-01	TMED4	transmembrane emp24 protein transport domain containing 4	chr7p13	1558053_s_at	NM_182547
4.83	4.87	0.05	8.04E-01	9.40E-01	---	---	---	238351_x_at	---

2.29	2.32	0.03	8.04E-01	9.40E-01	ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18	chr16q23	230040_at	NM_199355
7.65	7.71	0.06	8.04E-01	9.40E-01	LEPROTL1	leptin receptor overlapping transcript-like 1	chr8p21.2-p21.1	202594_at	NM_001128208 /// NM_015344
2.94	2.99	0.05	8.04E-01	9.40E-01	---	---	---	227004_at	---
3.78	3.82	0.05	8.04E-01	9.40E-01	KIAA1530	KIAA1530	chr4p16.3	241201_at	NM_020894 /// XM_001720077
3.95	3.99	0.05	8.04E-01	9.40E-01	TMEM68	transmembrane protein 68	chr8q12.1	226483_at	NM_152417
2.14	2.18	0.04	8.04E-01	9.40E-01	---	---	---	244749_at	---
2.41	2.45	0.04	8.04E-01	9.40E-01	PSORS1C1	psoriasis susceptibility 1 candidate 1	chr6p21.3	220362_at	NM_014068
2.05	2.07	0.02	8.04E-01	9.40E-01	LOC727924 /// OR4N4	hypothetical LOC727924 /// olfactory receptor, family 4, subfamily N, member 4	chr15q11.2	1560734_at	NM_001005241 /// XR_039952
3.66	3.70	0.04	8.04E-01	9.40E-01	LOC401312	LOC401318	chr7p15.3	1557605_a_at	---
3.10	3.13	0.04	8.04E-01	9.40E-01	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	chr4p14-p13	212972_x_at	NM_173075
2.20	2.23	0.03	8.04E-01	9.40E-01	SNX29	sorting nexin 29	chr16p13.13-p13.12	1558745_at	NM_001080530
5.95	6.02	0.06	8.04E-01	9.40E-01	MAPK9	mitogen-activated protein kinase 9	chr5q35	203218_at	NM_002752 /// NM_139068 /// NM_139069 /// NM_139070
4.57	4.64	0.07	8.04E-01	9.40E-01	SLC44A1	solute carrier family 44, member 1	chr9q31.2	227620_at	NM_080546
2.40	2.44	0.03	8.04E-01	9.40E-01	LOC440338	hypothetical gene supported by AJ002784	chr16p13.12	229978_at	XR_041913 /// XR_041914 /// XR_041915
3.07	3.11	0.04	8.04E-01	9.40E-01	---	---	---	235786_at	---
6.30	6.35	0.05	8.04E-01	9.40E-01	POLG	polymerase (DNA directed), gamma	chr15q25	217635_s_at	NM_001126131 /// NM_002693
5.28	5.37	0.09	8.04E-01	9.40E-01	RAB11FIP2	RAB11 family interacting protein 2 (class I)	chr10q26.11	203884_s_at	NM_014904
6.42	6.49	0.07	8.04E-01	9.40E-01	MGC3196	hypothetical protein MGC3196	chr11q12.3	220934_s_at	NM_001080501
5.84	5.91	0.08	8.04E-01	9.40E-01	SELPLG	selectin P ligand	chr12q24	209879_at	NM_003006
3.49	3.53	0.04	8.04E-01	9.40E-01	AVPR2	arginine vasopressin receptor 2	chrXq28	208111_at	NM_000054
2.37	2.40	0.04	8.04E-01	9.40E-01	RANBP1	RAN binding protein 1	chr22q11.21	221915_s_at	NM_002882
2.70	2.73	0.03	8.04E-01	9.40E-01	---	---	---	221243_s_at	---
4.30	4.36	0.05	8.05E-01	9.40E-01	EXTL3	exostoses (multiple)-like 3	chr8p21	211051_s_at	NM_001440
2.35	2.39	0.04	8.05E-01	9.41E-01	---	---	---	1569746_s_at	---
5.42	5.51	0.09	8.05E-01	9.41E-01	MAML2	mastermind-like 2 (Drosophila)	chr11q21	235457_at	NM_032427
2.53	2.61	0.08	8.05E-01	9.41E-01	C15orf29	chromosome 15 open reading frame 29	chr15q14	232094_at	NM_024713
2.60	2.67	0.07	8.05E-01	9.41E-01	LOC692247	hypothetical locus LOC692247	chr11p15.5	1569453_a_at	---
5.37	5.43	0.06	8.05E-01	9.41E-01	PEAR1	platelet endothelial aggregation receptor 1	chr1q23.1	228618_at	NM_001080471
4.80	4.84	0.04	8.05E-01	9.41E-01	AGRN	agrin	chr1p36.33	212283_at	NM_198576
1.92	1.94	0.03	8.05E-01	9.41E-01	---	---	---	1559930_at	---
3.07	3.14	0.07	8.05E-01	9.41E-01	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	chr7p13	207319_s_at	NM_003718 /// NM_031267
2.69	2.73	0.05	8.05E-01	9.41E-01	---	---	---	1565577_s_at	---
2.74	2.78	0.03	8.05E-01	9.41E-01	NACA2	nascent polypeptide-associated complex alpha subunit 2	chr17q23.2	222224_at	NM_199290
4.40	4.45	0.05	8.05E-01	9.41E-01	ACOT11	acyl-CoA thioesterase 11	chr1p32.3	214763_at	NM_015547 /// NM_147161
3.21	3.27	0.06	8.05E-01	9.41E-01	---	---	---	231404_at	---
2.29	2.32	0.03	8.05E-01	9.41E-01	---	---	---	240243_at	---
10.91	10.95	0.05	8.05E-01	9.41E-01	GSTA4	glutathione S-transferase A4	chr6p12.1	202967_at	NM_001512
2.43	2.47	0.04	8.05E-01	9.41E-01	MFSD4	major facilitator superfamily domain containing 4	chr1q32.1	242372_s_at	NM_181644
2.00	2.03	0.04	8.05E-01	9.41E-01	---	---	---	239962_at	---
2.31	2.35	0.03	8.05E-01	9.41E-01	ARID5B	AT rich interactive domain 5B (MRF1-like)	chr10q21.2	1558000_at	NM_032199
2.38	2.41	0.03	8.05E-01	9.41E-01	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	chr5q21	242943_at	NM_005668 /// NM_175052
2.03	2.06	0.03	8.05E-01	9.41E-01	---	---	---	1563884_at	---
2.11	2.13	0.03	8.05E-01	9.41E-01	KRTAP1-3 /// LOC728951	keratin associated protein 1-3 /// hypothetical LOC728951	chr17q12-q21	220978_at	NM_030966 /// XM_001128885
1.90	1.92	0.02	8.05E-01	9.41E-01	---	---	---	1559653_at	---
5.46	5.50	0.05	8.06E-01	9.41E-01	MYO1C	myosin IC	chr17p13	32811_at	NM_001080779 /// NM_001080950 /// NM_033375
2.91	2.94	0.03	8.06E-01	9.41E-01	BEST1	bestrophin 1	chr11q13	1554443_s_at	NM_004183
3.31	3.38	0.07	8.06E-01	9.41E-01	ABHD4	Abhydrolase domain containing 4	chr14q11.2	242023_at	NM_022060

2.31	2.35	0.03	8.06E-01	9.41E-01	C6orf163	chromosome 6 open reading frame 163	chr6q15	233787_at	XM_001720089 /// XM_001720635 /// XM_001725542																				
4.37	4.40	0.03	8.06E-01	9.41E-01	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	chr1p36.2	219422_at	NM_001039664 /// NM_003790 /// NM_148965 /// NM_148966 /// NM_148967 /// NM_148970																				
3.76	3.79	0.03	8.06E-01	9.41E-01	OR12D2	olfactory receptor, family 12, subfamily D, member 2	chr6p22.2-p21.31	221344_at	NM_013936																				
6.86	6.96	0.10	8.06E-01	9.41E-01	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	chr5q31-q32	202273_at	NM_002609																				
8.55	8.62	0.07	8.06E-01	9.41E-01	OCIAD1	OCIA domain containing 1	chr4p11	223010_s_at	NM_001079839 /// NM_001079840 /// NM_001079841 /// NM_001079842 /// NM_017830																				
2.88	2.92	0.04	8.06E-01	9.41E-01	---	---	---	243205_at	---																				
2.06	2.09	0.03	8.06E-01	9.41E-01	---	---	---	215958_at	---																				
6.23	6.28	0.05	8.06E-01	9.41E-01	ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2	chr19q13.3	213468_at	NM_000400 /// NM_001130867																				
3.89	3.94	0.05	8.06E-01	9.41E-01	WWP2	WW domain containing E3 ubiquitin protein ligase 2	chr16q22.1	210200_at	NM_007014 /// NM_199423 /// NM_199424																				
3.25	3.29	0.05	8.06E-01	9.41E-01	ACTN2	actinin, alpha 2	chr1q42-q43	203861_s_at	NM_001103																				
5.98	6.06	0.08	8.06E-01	9.41E-01	LOC161527 /// PML	hypothetical protein LOC161527 /// promyelocytic leukemia	chr15q22 /// chr15q25.2	211012_s_at	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246 /// NM_033247 /// NM_033249 /// NM_033250 /// XM_929030																				
5.00	5.07	0.07	8.06E-01	9.41E-01	ATG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae)	chrXq22.1-q22.3	213115_at	NM_052936 /// NM_178270																				
5.29	5.35	0.06	8.06E-01	9.41E-01	LOC339352	similar to hCG1772360	chr19q13.33	231056_at	XR_017668 /// XR_019601 /// XR_038066																				
4.86	4.91	0.05	8.06E-01	9.41E-01	PSPC1	paraspeckle component 1	chr13q12.11	218371_s_at	NM_001042414 /// NR_003272																				
6.81	6.86	0.05	8.06E-01	9.41E-01	FARSB	phenylalanyl-tRNA synthetase, beta subunit	chr2q36.1	223035_s_at	NM_005687																				
2.38	2.43	0.05	8.06E-01	9.41E-01	---	---	---	1565882_at	---																				
2.98	3.02	0.04	8.06E-01	9.41E-01	LOC100133781	hypothetical protein LOC100133781	---	230725_at	XM_001716343																				
2.21	2.25	0.04	8.06E-01	9.41E-01	IFIH1	interferon induced with helicase C domain 1	chr2q24	1555464_at	NM_022168																				
2.64	2.68	0.03	8.06E-01	9.41E-01	SCTR	Secretin receptor	chr2q14.1	1565738_at	NM_002980																				
2.93	2.96	0.03	8.06E-01	9.41E-01	RBM33	RNA binding motif protein 33	chr7q36.3	1554095_at	NM_001008408 /// NM_053043																				
2.13	2.16	0.03	8.06E-01	9.41E-01	NOL4	nucleolar protein 4	chr18q12	238605_at	NM_003787																				
2.54	2.59	0.04	8.06E-01	9.41E-01	SGOL2	shugoshin-like 2 (S. pombe)	chr2q33.1	230165_at	NM_152524																				
3.74	3.84	0.10	8.06E-01	9.41E-01	TRIM23	tripartite motif-containing 23	chr5q12.3	210995_s_at	NM_001656 /// NM_033227 /// NM_033228																				
3.55	3.62	0.07	8.06E-01	9.41E-01	---	---	---	238342_at	---																				

2.28	2.32	0.05	8.07E-01	9.41E-01	NCOA7	nuclear receptor coactivator 7	chr6q22.31-q22.32	1568805_at	NM_001122842 /// NM_181782																					
3.33	3.37	0.04	8.07E-01	9.41E-01	---	---	---	215597_x_at	---																					
2.69	2.72	0.03	8.07E-01	9.41E-01	---	---	---	1562701_at	---																					
2.17	2.20	0.03	8.06E-01	9.41E-01	WDR41	WD repeat domain 41	chr5q14.1	240637_at	NM_018268																					
1.87	1.90	0.03	8.07E-01	9.41E-01	CDH7	cadherin 7, type 2	chr18q22-q23	1554700_at	NM_004361 /// NM_033646																					
8.17	8.22	0.05	8.07E-01	9.41E-01	GRN	granulin	chr17q21.32	211284_s_at	NM_002087																					
2.48	2.53	0.04	8.07E-01	9.41E-01	---	---	---	235456_at	---																					
2.74	2.77	0.03	8.07E-01	9.41E-01	---	---	---	222312_s_at	---																					
5.82	5.86	0.04	8.07E-01	9.41E-01	LILRA6 /// LILRB3	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	chr19q13.4	210784_x_at	NM_001081450 /// NM_006864 /// NM_024318																					
2.82	2.86	0.04	8.07E-01	9.41E-01	GDNF	glial cell derived neurotrophic factor	chr5p13.1-p12	221359_at	NM_000514 /// NM_199231 /// NM_199234																					
1.98	2.01	0.03	8.07E-01	9.41E-01	RUNDC2B	RUN domain containing 2B	chr16p12.2	214712_at	NM_001012391 /// XM_001714307																					
2.10	2.14	0.04	8.07E-01	9.41E-01	---	---	---	1568736_s_at	---																					
2.02	2.05	0.03	8.07E-01	9.41E-01	LIMD1	LIM domains containing 1	chr3p21.3	222353_at	NM_014240																					
2.88	2.91	0.03	8.07E-01	9.41E-01	UBA1	ubiquitin-like modifier activating enzyme 1	chrXp11.23	1555387_at	NM_003334 /// NM_153280																					
4.47	4.52	0.05	8.07E-01	9.41E-01	---	---	---	243178_at	---																					
3.27	3.31	0.04	8.07E-01	9.41E-01	RIN3	Ras and Rab interactor 3	chr14q32.12	220439_at	NM_024832																					
5.63	5.71	0.09	8.08E-01	9.42E-01	TPP2	tripeptidyl peptidase II	chr13q32-q33	203375_s_at	NM_003291																					
4.04	4.10	0.06	8.08E-01	9.42E-01	GIMAP7	GTPase, IMAP family member 7	chr7q36.1	228071_at	NM_153236																					
3.10	3.15	0.05	8.08E-01	9.42E-01	CENTG3	centaurin, gamma 3	chr7q36.1	231299_at	NM_001042535 /// NM_031946																					
2.22	2.27	0.05	8.08E-01	9.42E-01	---	---	---	1556623_at	---																					
2.64	2.68	0.04	8.07E-01	9.42E-01	KCNIP3	Kv channel interacting protein 3, calsenilin	chr2q21.1	1569355_at	NM_001034914 /// NM_013434																					
2.14	2.18	0.04	8.07E-01	9.42E-01	---	---	---	242588_at	---																					
2.02	2.05	0.03	8.08E-01	9.42E-01	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	chr12q21.3	232263_at	NM_018057 /// NM_182767																					
3.45	3.50	0.05	8.08E-01	9.42E-01	P2RY11 /// PPAN	purinergic receptor P2Y, G-protein coupled, 11 /// peter pan homolog (Drosophila)	chr19p13 /// chr19p13.2	214546_s_at	NM_002566 /// NM_020230																					
8.47	8.52	0.05	8.08E-01	9.42E-01	DPY30	dpy-30 homolog (C. elegans)	chr2p22.3	224129_s_at	NM_032574																					
2.36	2.39	0.03	8.08E-01	9.42E-01	TACC1	transforming, acidic coiled-coil containing protein 1	chr8p11	217433_at	NM_001122824 /// NM_006283																					
2.26	2.30	0.04	8.08E-01	9.42E-01	LOC728544	Similar to hCG2017827	chr10p15.1	1558660_at	XM_001127725 /// XM_001127963 /// XM_001720285																					
2.87	2.99	0.12	8.08E-01	9.42E-01	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	chr1q25.2-q25.3	204748_at	NM_000963																					
2.20	2.24	0.04	8.08E-01	9.42E-01	ERC1	ELKS/RAB6-interacting/CAST family member 1	chr12p13.3	216440_at	NM_015064 /// NM_178037 /// NM_178038 /// NM_178039 /// NM_178040																					
2.39	2.41	0.03	8.08E-01	9.42E-01	---	---	---	1569510_at	---																					
6.11	6.17	0.06	8.08E-01	9.42E-01	USP15	ubiquitin specific peptidase 15	chr12q14	209475_at	NM_006313																					
2.49	2.53	0.04	8.08E-01	9.42E-01	MAPT	microtubule-associated protein tau	chr17q21.1	203930_s_at	NM_001123066 /// NM_001123067 /// NM_005910 /// NM_016834 /// NM_016835 /// NM_016841																					
2.60	2.64	0.03	8.08E-01	9.42E-01	NUDT3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	chr6p21.2	1569990_at	NM_006703																					
2.40	2.43	0.03	8.08E-01	9.42E-01	---	---	---	234083_at	---																					
2.12	2.16	0.03	8.08E-01	9.42E-01	---	---	---	243562_at	---																					
2.15	2.18	0.03	8.08E-01	9.42E-01	KLRC3	killer cell lectin-like receptor subfamily C, member 3	chr12p13	207723_s_at	NM_002261 /// NM_007333																					
6.88	6.95	0.07	8.08E-01	9.42E-01	LIN7C	lin-7 homolog C (C. elegans)	chr11p14	223350_x_at	NM_018362																					
6.24	6.37	0.13	8.09E-01	9.42E-01	---	---	---	235242_at	---																					

5.34	5.44	0.10	8.09E-01	9.42E-01	TTC17	tetratricopeptide repeat domain 17	chr11p12-p11.2	218972_at	NM_018259
4.96	5.05	0.09	8.09E-01	9.42E-01	MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	chr1p12-p11.2	226770_at	NM_152900
3.54	3.62	0.08	8.09E-01	9.42E-01	TAGLN3	transgelin 3	chr3q13.2	204743_at	NM_001008272 /// NM_001008273 /// NM_013259
2.71	2.75	0.04	8.09E-01	9.42E-01	MGC15705	hypothetical protein MGC15705	chr22q12.2	1553623_at	XR_040879 /// XR_040880 /// XR_040881
2.19	2.23	0.04	8.09E-01	9.42E-01	SLC4A9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	chr5q31	233183_at	NM_031467
2.00	2.03	0.03	8.09E-01	9.42E-01	LOC643648	hypothetical protein LOC643648	chr9p11.2	1560833_at	XM_926953
2.18	2.21	0.02	8.09E-01	9.42E-01	LOC100131756	hypothetical LOC100131756	chr1p34.2	1564202_at	XM_001725469 /// XM_001725690 /// XM_001725849
5.73	5.78	0.04	8.09E-01	9.42E-01	NPAL3	NIPA-like domain containing 3	chr1p36.12-p35.1	214579_at	NM_020448
2.90	2.94	0.03	8.09E-01	9.42E-01	---	---	---	217129_at	---
5.40	5.45	0.05	8.09E-01	9.42E-01	ATG4D	ATG4 autophagy related 4 homolog D (S. cerevisiae)	chr19p13.2	226871_s_at	NM_032885
5.25	5.38	0.13	8.09E-01	9.42E-01	VLDLR	very low density lipoprotein receptor	chr9p24	209822_s_at	NM_001018056 /// NM_003383
5.70	5.81	0.11	8.09E-01	9.42E-01	---	---	---	224999_at	---
3.75	3.84	0.09	8.09E-01	9.42E-01	LRRC4C	leucine rich repeat containing 4C	chr11p12	232226_at	NM_020929
4.82	4.87	0.05	8.09E-01	9.42E-01	PRRG1	proline rich Gla (G-carboxyglutamic acid) 1	chrXp21.1	205618_at	NM_000950
3.21	3.26	0.05	8.09E-01	9.42E-01	C22orf30	chromosome 22 open reading frame 30	chr22q12.2-q12.3	236941_at	NM_173566
3.66	3.71	0.04	8.09E-01	9.42E-01	SENP1	SUMO1/sentrin specific peptidase 1	chr12q13.1	1552812_a_at	NM_014554
2.74	2.77	0.03	8.09E-01	9.42E-01	PTCD1	pentatricopeptide repeat domain 1	chr7q22.1	222796_at	NM_015545
2.30	2.34	0.03	8.09E-01	9.42E-01	CASP12	caspase 12 (gene/pseudogene)	chr11q22.3	1564736_a_at	NR_000035
7.85	7.89	0.04	8.09E-01	9.42E-01	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	chr10q21-q22	208770_s_at	NM_004096
6.29	6.37	0.08	8.09E-01	9.42E-01	KATNB1	katanin p80 (WD repeat containing) subunit B 1	chr16q13	203162_s_at	NM_005886
3.31	3.35	0.05	8.09E-01	9.42E-01	---	---	---	243501_at	---
2.84	2.87	0.03	8.09E-01	9.42E-01	---	---	---	1557626_at	---
7.00	7.11	0.10	8.09E-01	9.42E-01	FAM82A1	family with sequence similarity 82, member A1	chr2p22.2	235349_at	NM_144713
3.07	3.15	0.08	8.09E-01	9.42E-01	DDEF2	development and differentiation enhancing factor 2	chr2p25|2p24	206414_s_at	NM_003887
3.40	3.45	0.05	8.09E-01	9.42E-01	C19orf51	chromosome 19 open reading frame 51	chr19q13.4	230033_at	NM_178837
3.73	3.77	0.04	8.09E-01	9.42E-01	---	---	---	243976_at	---
2.27	2.32	0.04	8.09E-01	9.42E-01	NCRNA00032	non-protein coding RNA 32	chr9p21	1563728_at	XM_376821 /// XM_938938
2.40	2.44	0.03	8.09E-01	9.42E-01	---	---	---	1570134_at	---
4.63	4.70	0.07	8.10E-01	9.42E-01	NEK8	NIMA (never in mitosis gene a)- related kinase 8	chr17q11.1	1557172_x_at	NM_178170
2.46	2.50	0.05	8.10E-01	9.42E-01	TNR	tenascin R (restrictin, janusin)	chr1q24	206990_at	NM_003285
3.30	3.34	0.04	8.10E-01	9.42E-01	---	---	---	236427_at	---
3.35	3.39	0.04	8.10E-01	9.42E-01	C9orf50	chromosome 9 open reading frame 50	chr9q34.11	230335_at	NM_199350
2.21	2.23	0.02	8.10E-01	9.42E-01	MTTP	microsomal triglyceride transfer protein	chr4q24	205675_at	NM_000253
4.42	4.51	0.09	8.10E-01	9.42E-01	TJP1	tight junction protein 1 (zona occludens 1)	chr15q13	214168_s_at	NM_003257 /// NM_175610
5.35	5.44	0.09	8.10E-01	9.42E-01	SPG20	spastic paraplegia 20 (Troyer syndrome)	chr13q13.3	236600_at	NM_015087
7.48	7.55	0.07	8.10E-01	9.42E-01	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	chr14q23.3	201144_s_at	NM_004094
2.03	2.06	0.02	8.10E-01	9.42E-01	ACPP	Acid phosphatase, prostate	chr3q21-q23	231711_at	NM_001099 /// NM_001134194
6.69	6.78	0.09	8.10E-01	9.42E-01	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	chr10q21.3	221699_s_at	NM_024045
3.24	3.28	0.04	8.10E-01	9.42E-01	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	217377_x_at	NM_001007156 /// NM_001012338 /// NM_002530
1.75	1.77	0.02	8.10E-01	9.42E-01	---	---	---	237422_at	---

3.57	3.62	0.05	8.10E-01	9.43E-01	FLJ36131 /// LOC100131452 /// LOC100132025 /// LOC100132566 /// LOC100132727 /// LOC729272	hypothetical protein FLJ36131 /// hypothetical protein LOC100131452 /// Putative transmembrane domain-containing protein ENSP00000320207 /// hypothetical protein LOC100132566 /// hypothetical protein LOC100132727 /// hypothetical LOC729272	chr15q11.2	1561171_a_at	XM_001129814 /// XM_001722016 /// XM_001722364 /// XM_001722366 /// XM_001722378 /// XM_001723325 /// XM_001723489 /// XM_001723658 /// XM_001723722 /// XM_001725103
3.11	3.16	0.05	8.10E-01	9.43E-01	DHRS7	Dehydrogenase/reductase (SDR family) member 7	chr14q23.1	236332_at	NM_016029
2.78	2.83	0.05	8.10E-01	9.43E-01	CSH1 /// CSH2 /// CSHL1 /// GH1 /// GH2	chorionic somatomammotropin hormone 1 (placental lactogen) /// chorionic somatomammotropin hormone 2 /// chorionic somatomammotropin hormone-like 1 /// growth hormone 1 /// growth hormone 2	chr17q24.2	208069_x_at	NM_000515 /// NM_001317 /// NM_001318 /// NM_002059 /// NM_020991 /// NM_022556 /// NM_022557 /// NM_022558 /// NM_022559 /// NM_022560 /// NM_022561 /// NM_022562 /// NM_022579 /// NM_022580 /// NM_022581 /// NM_022640 /// NM_022641 /// NM_022644 /// NM_022645
2.86	2.89	0.04	8.10E-01	9.43E-01	---	---	---	221130_s_at	---
3.37	3.43	0.06	8.11E-01	9.43E-01	tcag7.1196	similar to GLI-Kruppel family member HKR1	chr7q36.1	225907_at	XR_041712 /// XR_041713 /// XR_041714
3.26	3.30	0.04	8.11E-01	9.43E-01	PRM3	protamine 3	chr16p13.3	231758_at	NM_021247
2.78	2.82	0.03	8.11E-01	9.43E-01	LOC339822	hypothetical protein LOC339822	chr2p25.3	1562844_at	---
6.80	6.83	0.03	8.11E-01	9.43E-01	ATF5	activating transcription factor 5	chr19q13.3	230938_x_at	NM_012068
5.46	5.55	0.10	8.11E-01	9.43E-01	C8orf83	chromosome 8 open reading frame 83	chr8q22.1	225600_at	NR_015339 /// XR_041349 /// XR_041350 /// XR_041351
2.38	2.42	0.04	8.11E-01	9.43E-01	CHI3L2	chitinase 3-like 2	chr1p13.3	213060_s_at	NM_001025197 /// NM_001025199 /// NM_004000
2.20	2.23	0.03	8.11E-01	9.43E-01	LOC643201	hypothetical protein LOC643201	chr5q35.2	1570444_at	XM_001716444 /// XM_001717933 /// XM_932161
2.57	2.61	0.04	8.11E-01	9.43E-01	FCF1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	chr14q24.3	240928_at	NM_015962
4.92	5.01	0.09	8.11E-01	9.43E-01	CNN1	calponin 1, basic, smooth muscle	chr19p13.2-p13.1	203951_at	NM_001299
2.76	2.80	0.03	8.11E-01	9.43E-01	---	---	---	1568635_at	---
6.62	6.66	0.04	8.11E-01	9.43E-01	GALNT2 /// LOC100132910	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) /// PRO1477	chr18q12.2 /// chr1q41-q42	223991_s_at	NM_004481 /// XM_001720527 /// XM_001722059 /// XM_001723529

2.37	2.40	0.03	8.11E-01	9.43E-01	---	---	---	1569987_at	---
3.71	3.76	0.05	8.11E-01	9.43E-01	CRIM2	cysteine rich BMP regulator 2 (chordin-like)	chr7q32.1	1556956_at	XM_001128429 /// XM_001715223 /// XM_001715714
2.84	2.89	0.04	8.11E-01	9.43E-01	CRHR1	corticotropin releasing hormone receptor 1	chr17q12-q22	208593_x_at	NM_004382
2.02	2.05	0.03	8.11E-01	9.43E-01	---	---	---	1569942_at	---
7.11	7.21	0.09	8.11E-01	9.43E-01	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	chr12q14.2	212160_at	NM_007235
5.16	5.23	0.07	8.11E-01	9.43E-01	---	---	---	229031_at	---
2.90	2.96	0.05	8.11E-01	9.43E-01	---	---	---	240746_s_at	---
2.21	2.25	0.04	8.11E-01	9.43E-01	GPR17	G protein-coupled receptor 17	chr2q21	206190_at	NM_005291
3.78	3.86	0.08	8.12E-01	9.43E-01	LPP	LIM domain containing preferred translocation partner in lipoma	chr3q28	202821_s_at	NM_005578
4.11	4.18	0.07	8.12E-01	9.43E-01	SIGLEC8	sialic acid binding Ig-like lectin 8	chr19q13.33-q13.41	208253_at	NM_014442
3.15	3.19	0.04	8.12E-01	9.43E-01	C4orf42	Chromosome 4 open reading frame 42	chr4p16.3	237642_at	NM_052861
2.64	2.68	0.03	8.12E-01	9.43E-01	INO80C	INO80 complex subunit C	chr18q12.2	1559716_at	NM_001098817 /// NM_194281
2.13	2.16	0.03	8.12E-01	9.43E-01	---	---	---	1560222_at	---
1.93	1.96	0.03	8.12E-01	9.43E-01	SLC9A11	solute carrier family 9, member 11	chr1q25.1	1554988_at	NM_178527
5.14	5.22	0.08	8.12E-01	9.43E-01	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	chr1q23.3	210992_x_at	NM_001005410 /// NM_001005411 /// NM_201563
1.87	1.90	0.03	8.12E-01	9.43E-01	GABRA1	gamma-aminobutyric acid (GABA) A receptor, alpha 1	chr5q34-q35	244118_at	NM_000806 /// NM_001127643 /// NM_001127644 /// NM_001127645 /// NM_001127646 /// NM_001127647 /// NM_001127648
2.96	3.02	0.07	8.12E-01	9.43E-01	ZBTB10	zinc finger and BTB domain containing 10	chr8q13-q21.1	222863_at	NM_001105539 /// NM_023929
2.67	2.72	0.05	8.12E-01	9.43E-01	---	---	---	1566002_at	---
2.25	2.28	0.03	8.12E-01	9.44E-01	---	---	---	242130_at	---
2.77	2.80	0.03	8.12E-01	9.44E-01	HCG2P7	HLA complex group 2 pseudogene 7	chr6p21.3	216227_at	NR_001318
2.76	2.83	0.07	8.12E-01	9.44E-01	CD44	CD44 molecule (Indian blood group)	chr11p13	217523_at	NM_000610 /// NM_001001389 /// NM_001001390 /// NM_001001391 /// NM_001001392
10.18	10.25	0.07	8.12E-01	9.44E-01	EID1	EP300 interacting inhibitor of differentiation 1	chr15q21.1-q21.2	208669_s_at	NM_014335
6.05	6.10	0.04	8.12E-01	9.44E-01	---	---	---	222352_at	---
2.66	2.69	0.04	8.12E-01	9.44E-01	OR1J4	olfactory receptor, family 1, subfamily J, member 4	chr9q34.11	1567284_at	NM_001004452
2.74	2.78	0.03	8.12E-01	9.44E-01	C18orf2	chromosome 18 open reading frame 2	---	234712_at	NM_031416 /// NR_023925 /// NR_023926 /// NR_023927 /// NR_023928
5.16	5.35	0.19	8.12E-01	9.44E-01	PCSK6	proprotein convertase subtilisin/kexin type 6	chr15q26.3	207414_s_at	NM_002570 /// NM_138319 /// NM_138320 /// NM_138321 /// NM_138322 /// NM_138323 /// NM_138324 /// NM_138325
6.47	6.56	0.08	8.12E-01	9.44E-01	CENTA2	centaurin, alpha 2	chr17q11.2	219358_s_at	NM_018404
2.99	3.02	0.03	8.12E-01	9.44E-01	XAF1	XIAP associated factor 1	chr17p13.2	242234_at	NM_017523 /// NM_199139
5.28	5.36	0.08	8.13E-01	9.44E-01	FGL2	fibrinogen-like 2	chr7q11.23	204834_at	NM_006682

8.34	8.40	0.06	8.13E-01	9.44E-01	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	chr12p12.3	201288_at	NM_001175
5.30	5.35	0.05	8.13E-01	9.44E-01	C17orf63	chromosome 17 open reading frame 63	chr17q11.2	229418_at	NM_001077498 /// NM_018182
3.39	3.46	0.06	8.13E-01	9.44E-01	GKAP1	G kinase anchoring protein 1	chr9q21.32	234192_s_at	NM_025211
2.79	2.83	0.04	8.13E-01	9.44E-01	WWC1	WW and C2 domain containing 1	chr5q35.1	236725_at	NM_015238
4.30	4.36	0.05	8.13E-01	9.44E-01	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	chr1q24-q25	220926_s_at	NM_025191
2.29	2.32	0.03	8.13E-01	9.44E-01	FAM91A2	family with sequence similarity 91, member A2	chr1q21.1	1563483_at	XR_040635
5.36	5.44	0.07	8.13E-01	9.44E-01	ZNF627	zinc finger protein 627	chr19p13.2	224492_s_at	NM_145295
3.64	3.67	0.03	8.13E-01	9.44E-01	FANCA	Fanconi anemia, complementation group A	chr16q24.3	215530_at	NM_000135 /// NM_001018112
4.43	4.52	0.09	8.13E-01	9.44E-01	GJA4	gap junction protein, alpha 4, 37kDa	chr1p35.1	40687_at	NM_002060
6.40	6.46	0.06	8.14E-01	9.44E-01	STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	chr20q13.1	211505_s_at	NM_001037328 /// NM_004602 /// NM_017452 /// NM_017453 /// NM_017454
2.67	2.71	0.04	8.14E-01	9.44E-01	CCNA2	cyclin A2	chr4q25-q31	213226_at	NM_001237
2.35	2.39	0.04	8.14E-01	9.44E-01	TCEB3C	transcription elongation factor B polypeptide 3C (elongin A3)	chr18q21.1	1552860_at	NM_145653 /// XM_001713655
2.01	2.04	0.03	8.14E-01	9.44E-01	PANX3	pannexin 3	chr11q24.2	240955_at	NM_052959
2.51	2.54	0.03	8.14E-01	9.44E-01	KRT8P12	Keratin 8 pseudogene 12	chr3q26.1	230116_at	---
2.09	2.12	0.04	8.14E-01	9.44E-01	MCM3APAS	minichromosome maintenance complex component 3 associated protein antisense	chr21q22.3	220459_at	NR_002776
2.34	2.38	0.04	8.14E-01	9.45E-01	GPX5	glutathione peroxidase 5 (epididymal androgen-related protein)	chr6p22.1	214648_at	NM_001509 /// NM_003996
1.83	1.85	0.02	8.14E-01	9.45E-01	CCDC144A /// CCDC144B /// CCDC144C /// LOC100134159	coiled-coil domain containing 144A /// coiled-coil domain containing 144B /// coiled-coil domain containing 144C /// similar to Coiled-coil domain containing 144B	chr17p11.2	1557366_at	NM_014695 /// NM_182568 /// NR_023380 /// XM_001718183 /// XM_001718261
2.52	2.56	0.04	8.14E-01	9.45E-01	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	chr8p11.2	218173_s_at	NM_017778 /// NM_023034
3.99	4.02	0.03	8.14E-01	9.45E-01	DOCK6	dedicator of cytokinesis 6	chr19p13.2	222004_s_at	NM_020812
2.54	2.59	0.05	8.14E-01	9.45E-01	TSC22D2	TSC22 domain family, member 2	chr3q25.1	215547_at	NM_014779
2.18	2.22	0.04	8.14E-01	9.45E-01	---	---	---	233174_at	---
2.70	2.73	0.03	8.14E-01	9.45E-01	---	---	---	1556321_a_at	---
2.39	2.42	0.03	8.14E-01	9.45E-01	LOC26010	Viral DNA polymerase-transactivated protein 6	chr2q33.1	232961_at	NM_001100422 /// NM_001100423 /// NM_001100424 /// NM_015535
3.20	3.25	0.05	8.14E-01	9.45E-01	TARP /// TRGC2	TCR gamma alternate reading frame protein /// T cell receptor gamma constant 2	chr7p14 /// chr7p15-p14	211144_x_at	NM_001003799 /// NM_001003806
3.31	3.35	0.04	8.14E-01	9.45E-01	CHRNA10	Cholinergic receptor, nicotinic, alpha 10	chr11p15.5	239717_at	NM_020402
8.14	8.19	0.05	8.14E-01	9.45E-01	KIAA0494	KIAA0494	chr1pter-p22.1	201778_s_at	NM_014774
1.96	1.99	0.03	8.15E-01	9.45E-01	C10orf90	chromosome 10 open reading frame 90	chr10q26.2	1564198_a_at	NM_001004298
3.93	3.98	0.05	8.15E-01	9.45E-01	SIP1	survival of motor neuron protein interacting protein 1	chr14q13	211115_x_at	NM_001009182 /// NM_001009183 /// NM_003616
3.14	3.20	0.05	8.15E-01	9.45E-01	MATR3	Matrin 3	chr5q31.2	242260_at	NM_018834 /// NM_199189
3.63	3.67	0.04	8.15E-01	9.45E-01	BHLHB9	basic helix-loop-helix domain containing, class B, 9	chrXq23	213709_at	NM_030639
3.35	3.41	0.05	8.15E-01	9.45E-01	NSL1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	chr1q41	230592_at	NM_001042549 /// NM_015471
4.04	4.09	0.05	8.15E-01	9.45E-01	---	---	---	1563577_at	---
3.56	3.60	0.05	8.15E-01	9.45E-01	PTPN21	protein tyrosine phosphatase, non-receptor type 21	chr14q31.3	205438_at	NM_007039
5.09	5.17	0.07	8.15E-01	9.45E-01	GPR137B	G protein-coupled receptor 137B	chr1q42-q43	204137_at	NM_003272
3.43	3.51	0.07	8.15E-01	9.45E-01	SLC30A9	solute carrier family 30 (zinc transporter), member 9	chr4p13-p12	229500_at	NM_006345
4.82	4.88	0.06	8.15E-01	9.45E-01	TMEM110	Transmembrane protein 110	chr3p21.1	227127_at	NM_198563
3.39	3.45	0.06	8.15E-01	9.45E-01	---	---	---	240213_at	---
3.76	3.82	0.05	8.15E-01	9.45E-01	LOC100129129	Hypothetical protein LOC100129129	chr8p23.1	1559870_at	XM_001715395 /// XM_001716192 /// XM_001716441

4.84	4.89	0.05	8.15E-01	9.45E-01	ASTN2	astrotactin 2	chr9q33.1	209693_at	NM_014010 /// NM_198186 /// NM_198187 /// NM_198188																				
2.27	2.31	0.04	8.15E-01	9.45E-01	---	---	---	240625_at	---																				
8.42	8.46	0.04	8.15E-01	9.45E-01	OSBP	oxysterol binding protein	chr11q12-q13	201800_s_at	NM_002556																				
2.30	2.35	0.04	8.15E-01	9.45E-01	FLJ20184	hypothetical protein FLJ20184	chr4q24	221119_at	NM_017700																				
2.46	2.51	0.04	8.15E-01	9.45E-01	ADCY1	adenylate cyclase 1 (brain)	chr7p13-p12	213245_at	NM_021116																				
2.61	2.65	0.04	8.15E-01	9.45E-01	CD84	CD84 molecule	chr1q24	211192_s_at	NM_003874																				
2.86	2.89	0.04	8.15E-01	9.45E-01	---	---	---	243480_at	---																				
2.50	2.53	0.03	8.16E-01	9.45E-01	PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	chr10q23-q24	240187_at	NM_005398																				
2.37	2.40	0.03	8.15E-01	9.45E-01	---	---	---	239176_at	---																				
2.25	2.28	0.03	8.15E-01	9.45E-01	---	---	---	1561891_at	---																				
4.42	4.45	0.03	8.15E-01	9.45E-01	C15orf23	chromosome 15 open reading frame 23	chr15q15.1	225300_at	NM_033286																				
2.30	2.33	0.02	8.15E-01	9.45E-01	LOC286177	hypothetical protein LOC286177	chr8q12.1	1562365_at	XM_001714958 /// XM_001715027 /// XM_001715081																				
4.22	4.28	0.06	8.16E-01	9.45E-01	CPNE8	copine VIII	chr12q12	228365_at	NM_153634																				
5.75	5.94	0.19	8.16E-01	9.45E-01	AQP1	aquaporin 1 (Colton blood group)	chr7p14	209047_at	NM_198098																				
2.96	3.01	0.05	8.16E-01	9.45E-01	---	---	---	232939_at	---																				
7.84	7.88	0.04	8.16E-01	9.45E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	201334_s_at	NM_015313																				
2.80	2.85	0.04	8.16E-01	9.45E-01	LOC730733	Similar to zinc finger protein 484	chr19q13.33	1556905_at	XM_001126981 /// XM_001724898 /// XM_001726008																				
2.63	2.67	0.04	8.16E-01	9.45E-01	GPRC5D	G protein-coupled receptor, family C, group 5, member D	chr12p13.3	221297_at	NM_018654																				
2.87	2.91	0.04	8.16E-01	9.45E-01	---	---	---	239602_at	---																				
5.48	5.52	0.04	8.16E-01	9.45E-01	DKFZP434A062	DKFZP434A062 protein	chr9q34.3	217219_at	XM_001719952 /// XM_001722610 /// XM_001723271																				
2.15	2.18	0.03	8.16E-01	9.45E-01	HIP1	huntingtin interacting protein 1	chr7q11.23	1560317_s_at	NM_005338																				
2.71	2.78	0.07	8.16E-01	9.45E-01	PCGF5	polycomb group ring finger 5	chr10q23.32	235331_x_at	NM_032373																				
9.18	9.24	0.07	8.16E-01	9.45E-01	NCL	nucleolin	chr2q12-qter	200610_s_at	NM_005381																				
6.93	6.99	0.06	8.16E-01	9.45E-01	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa	chr8p21-p12	202680_at	NM_002095																				
5.02	5.08	0.06	8.16E-01	9.45E-01	NSUN4	NOL1/NOP2/Sun domain family, member 4	chr1p34	230023_at	NM_199044																				
3.91	3.96	0.05	8.16E-01	9.45E-01	---	---	---	214101_s_at	---																				

2.95	3.00	0.05	8.16E-01	9.45E-01	SNRPN	small nuclear ribonucleoprotein polypeptide N	chr15q11.2	1559545_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																			
2.48	2.51	0.03	8.16E-01	9.45E-01	---	---	---	1559384_at	---																			
2.28	2.31	0.03	8.16E-01	9.45E-01	CDH10	cadherin 10, type 2 (T2-cadherin)	chr5p14-p13	220115_s_at	NM_006727																			
5.62	5.69	0.07	8.16E-01	9.45E-01	HVCN1	hydrogen voltage-gated channel 1	chr12q24.11	226879_at	NM_001040107 /// NM_032369																			
6.26	6.31	0.05	8.16E-01	9.45E-01	---	---	---	1561346_at	---																			
2.21	2.24	0.03	8.16E-01	9.45E-01	---	---	---	1570127_at	---																			
2.12	2.15	0.03	8.16E-01	9.45E-01	VASH2	vasohibin 2	chr1q32.3	235343_at	NM_024749																			
2.15	2.18	0.02	8.16E-01	9.45E-01	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	chr6p12.2	241694_at	NM_138694 /// NM_170724																			
2.24	2.26	0.03	8.16E-01	9.46E-01	ASCC3L1	activating signal cointegrator 1 complex subunit 3-like 1	chr2q11.2	214982_at	NM_014014																			
3.22	3.27	0.06	8.17E-01	9.46E-01	---	---	---	240612_at	---																			
2.35	2.38	0.03	8.17E-01	9.46E-01	---	---	---	237684_at	---																			
2.27	2.30	0.03	8.17E-01	9.46E-01	---	---	---	1557486_at	---																			
2.13	2.16	0.03	8.17E-01	9.46E-01	ZNF226	zinc finger protein 226	chr19q13.2	224004_at	NM_001032372 /// NM_001032373 /// NM_001032374 /// NM_001032375 /// NM_015919																			
2.09	2.12	0.03	8.17E-01	9.46E-01	---	---	---	1566666_at	---																			
8.34	8.41	0.07	8.17E-01	9.46E-01	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	chr3q26.32	223013_at	NM_024665																			
2.54	2.58	0.04	8.17E-01	9.46E-01	SNORA74A	small nucleolar RNA, H/ACA box 74A	chr5q31.2	1567681_at	NR_002915																			

2.55	2.58	0.04	8.17E-01	9.46E-01	DEPDC2	DEP domain containing 2	chr8q13.2	233408_at	NM_024870 /// NM_025170
2.50	2.55	0.04	8.17E-01	9.46E-01	C15orf29	chromosome 15 open reading frame 29	chr15q14	1559658_at	NM_024713
2.03	2.06	0.03	8.17E-01	9.46E-01	ROPN1L	ropporin 1-like	chr5p15.2	233312_at	NM_031916
2.31	2.34	0.03	8.17E-01	9.46E-01	LOC647288	hypothetical LOC647288	chr13q22.2	217332_at	XR_017516 /// XR_038154 /// XR_038777
3.81	3.87	0.07	8.17E-01	9.46E-01	TRIM34 /// TRIM6 /// TRIM6-TRIM34	tripartite motif-containing 34 /// tripartite motif-containing 6 /// TRIM6-TRIM34	chr11p15 /// chr11p15.4	224175_s_at	NM_001003818 /// NM_001003819 /// NM_001003827 /// NM_021616 /// NM_058166 /// NM_130389 /// NM_130390
4.82	4.87	0.04	8.17E-01	9.46E-01	CCDC109B	coiled-coil domain containing 109B	chr4q25	218802_at	NM_017918
4.56	4.64	0.08	8.17E-01	9.46E-01	USP32	ubiquitin specific peptidase 32	chr17q23.2	226505_x_at	NM_032582
2.23	2.26	0.03	8.17E-01	9.46E-01	C5orf44	chromosome 5 open reading frame 44	chr5q12.3	236526_x_at	NM_001093755 /// NM_001093756 /// NM_024941 /// NR_003545
3.24	3.29	0.05	8.17E-01	9.46E-01	RSC1A1	regulatory solute carrier protein, family 1, member 1	chr1p36.1	214583_at	NM_006511
8.70	8.77	0.08	8.17E-01	9.46E-01	---	---	---	227052_at	---
4.09	4.15	0.06	8.17E-01	9.46E-01	NUP210	nucleoporin 210kDa	chr3p25.1	213947_s_at	NM_024923
2.75	2.80	0.05	8.17E-01	9.46E-01	ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	chr4q13.3	214913_at	NM_014243
2.78	2.82	0.04	8.18E-01	9.46E-01	CRABP1	cellular retinoic acid binding protein 1	chr15q24	205350_at	NM_004378
5.86	6.02	0.17	8.18E-01	9.46E-01	---	---	---	232113_at	---
6.67	6.72	0.05	8.18E-01	9.46E-01	TMCO1	transmembrane and coiled-coil domains 1	chr1q22-q25	210768_x_at	NM_019026
6.33	6.37	0.04	8.18E-01	9.46E-01	CPT2	carnitine palmitoyltransferase II	chr1p32	204263_s_at	NM_000098
5.76	5.84	0.07	8.18E-01	9.46E-01	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	chr5q33.3	227413_at	NM_145049
5.10	5.17	0.07	8.18E-01	9.46E-01	RUNDC3A	RUN domain containing 3A	chr17q21.31	213439_x_at	NM_006695
4.87	4.92	0.05	8.18E-01	9.46E-01	LOC147646	hypothetical protein LOC147646	chr19q13.33	1560830_a_at	XM_001134195 /// XM_001134326 /// XM_001726058
3.36	3.41	0.05	8.18E-01	9.46E-01	SYS1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	chr20q13.12	238470_at	NM_033542
4.39	4.43	0.04	8.18E-01	9.46E-01	RAB40C	RAB40C, member RAS oncogene family	chr16p13.3	213466_at	NM_021168
6.21	6.25	0.04	8.18E-01	9.46E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	1555945_s_at	NM_014612
3.03	3.07	0.04	8.18E-01	9.46E-01	MSX1	Msh homeobox 1	chr4p16.3-p16.1	228473_at	NM_002448
2.65	2.68	0.04	8.18E-01	9.46E-01	C14orf126	chromosome 14 open reading frame 126	chr14q12	1553801_a_at	NM_080664
2.57	2.60	0.04	8.18E-01	9.46E-01	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	chr10q24	220017_x_at	NM_000771
3.07	3.11	0.03	8.18E-01	9.46E-01	WNT10A	Wingless-type MMTV integration site family, member 10A	chr2q35	229154_at	NM_025216
5.77	5.80	0.03	8.18E-01	9.46E-01	ADC	arginine decarboxylase	chr1p33-p34.3	228000_at	NM_052998
2.59	2.62	0.03	8.18E-01	9.46E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	211878_at	---
5.68	5.71	0.03	8.18E-01	9.46E-01	BBS1	Bardet-Biedl syndrome 1	chr11q13.1	229142_s_at	NM_024649
2.10	2.13	0.03	8.18E-01	9.46E-01	---	---	---	232385_x_at	---
2.41	2.44	0.03	8.18E-01	9.46E-01	---	---	---	244257_at	---
1.99	2.02	0.03	8.18E-01	9.46E-01	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	chr16p13.2	231384_at	NM_000833 /// NM_001134407 /// NM_001134408
2.53	2.56	0.03	8.18E-01	9.46E-01	---	---	---	1565909_at	---
2.36	2.39	0.03	8.18E-01	9.46E-01	TMEM131	transmembrane protein 131	chr2q11.2	235972_at	NM_015348
6.36	6.45	0.09	8.19E-01	9.46E-01	RNF141	ring finger protein 141	chr11p15.4	226106_at	NM_016422
5.53	5.58	0.05	8.19E-01	9.46E-01	---	---	---	1569409_x_at	---
3.38	3.43	0.05	8.19E-01	9.46E-01	---	---	---	1563453_at	---
2.45	2.49	0.04	8.19E-01	9.46E-01	---	---	---	1562961_at	---
2.41	2.44	0.04	8.19E-01	9.46E-01	---	---	---	1561528_at	---
2.29	2.32	0.03	8.19E-01	9.46E-01	FLJ40852	hypothetical LOC285962	chr7q34	1553634_a_at	NM_173677
2.11	2.14	0.03	8.19E-01	9.46E-01	MSH6	mutS homolog 6 (E. coli)	chr2p16	211449_at	NM_000179
2.31	2.34	0.03	8.19E-01	9.46E-01	LOC144742	hypothetical protein LOC144742	chr12q24.23	1564060_at	XM_001720552 /// XM_001723811 /// XM_001726538

2.17	2.19	0.03	8.19E-01	9.46E-01	SPRED2	Sprouty-related, EVH1 domain containing 2	chr2p14	214026_s_at	NM_001128210 /// NM_181784
1.90	1.92	0.02	8.19E-01	9.46E-01	PKD2L2	polycystic kidney disease 2-like 2	chr5q31	224226_at	NM_014386
2.11	2.13	0.02	8.19E-01	9.46E-01	---	---	---	237195_at	---
3.51	3.56	0.06	8.19E-01	9.46E-01	FAM64A	family with sequence similarity 64, member A	chr17p13.2	221591_s_at	NM_019013
2.77	2.82	0.05	8.19E-01	9.46E-01	---	---	---	1569321_at	---
2.11	2.14	0.04	8.19E-01	9.46E-01	SMC1A	structural maintenance of chromosomes 1A	chrXp11.22-p11.21	1555677_s_at	NM_006306
3.71	3.78	0.07	8.19E-01	9.46E-01	FLJ13137	hypothetical gene supported by AK125122	chr1q23.3	227019_at	NM_001085375
3.38	3.43	0.05	8.19E-01	9.46E-01	---	---	---	241941_at	---
4.42	4.46	0.04	8.19E-01	9.46E-01	ARVCF	armadillo repeat gene deletes in velocardiofacial syndrome	chr22q11.21	1556149_at	NM_001670
4.50	4.56	0.06	8.19E-01	9.46E-01	---	---	---	1566003_x_at	---
2.46	2.48	0.03	8.19E-01	9.46E-01	NDEL1	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	chr17p13.1	227553_at	NM_001025579 /// NM_030808
2.91	2.96	0.05	8.19E-01	9.46E-01	MYH10	myosin, heavy chain 10, non-muscle	chr17p13	213067_at	NM_005964
4.93	5.12	0.19	8.19E-01	9.46E-01	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	226211_at	NR_002766 /// NR_003530 /// NR_003531
2.15	2.18	0.03	8.19E-01	9.46E-01	DTNA	dystrobrevin, alpha	chr18q12	244142_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981
5.95	6.00	0.05	8.19E-01	9.46E-01	CEP68	centrosomal protein 68kDa	chr2p14	212675_s_at	NM_015147
2.26	2.31	0.05	8.19E-01	9.46E-01	FSD1L	fibronectin type III and SPRY domain containing 1-like	chr9q31	242586_at	NM_031919 /// NM_207647
2.38	2.42	0.04	8.19E-01	9.46E-01	---	---	---	1570503_at	---
2.49	2.52	0.03	8.19E-01	9.46E-01	DNAI2	dynein, axonemal, intermediate chain 2	chr17q25	221668_s_at	NM_023036
2.42	2.44	0.03	8.19E-01	9.46E-01	USH1C	Usher syndrome 1C (autosomal recessive, severe)	chr11p15.1-p14	221173_at	NM_005709 /// NM_153676
2.08	2.11	0.03	8.19E-01	9.46E-01	ETNK1	ethanolamine kinase 1	chr12p12.1	224454_at	NM_001039481 /// NM_018638
5.57	5.62	0.05	8.20E-01	9.46E-01	JMJD2C	jumonji domain containing 2C	chr9p24.1	209984_at	NM_015061
7.39	7.43	0.04	8.20E-01	9.46E-01	BLVRA	biliverdin reductase A	chr7p14-cen	211729_x_at	NM_000712
2.60	2.63	0.03	8.20E-01	9.46E-01	PAGE4	P antigen family, member 4 (prostate associated)	chrXp11.23	205564_at	NM_007003
1.88	1.90	0.03	8.20E-01	9.46E-01	TDH	L-threonine dehydrogenase	chr8p23.1	1553494_at	NR_001578
3.19	3.24	0.05	8.20E-01	9.46E-01	MAP3K9	mitogen-activated protein kinase kinase kinase 9	chr14q24.3-q31	214969_at	NM_033141
7.04	7.11	0.06	8.20E-01	9.46E-01	LOC158960	hypothetical protein BC009467	chrXq28	1558685_a_at	---
3.08	3.17	0.08	8.20E-01	9.46E-01	RPAP3	RNA polymerase II associated protein 3	chr12q13.11	218842_at	NM_024604
5.57	5.62	0.05	8.20E-01	9.46E-01	TMEM105	transmembrane protein 105	chr17q25.3	1561243_at	NM_178520
5.75	5.79	0.04	8.20E-01	9.46E-01	DMPK	dystrophia myotonica-protein kinase	chr19q13.3	217066_s_at	NM_001081560 /// NM_001081562 /// NM_001081563 /// NM_004409
2.19	2.22	0.04	8.20E-01	9.47E-01	TTC39B	Tetratricopeptide repeat domain 39B	chr9p22.3	232000_at	NM_152574
2.49	2.53	0.03	8.20E-01	9.47E-01	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	chr12p12.2-p11.2	223586_at	NM_020183
2.44	2.46	0.02	8.20E-01	9.47E-01	APAF1	apoptotic peptidase activating factor 1	chr12q23	211553_x_at	NM_001160 /// NM_013229 /// NM_181861 /// NM_181868 /// NM_181869
3.36	3.41	0.04	8.20E-01	9.47E-01	FAM131A	family with sequence similarity 131, member A	chr3q27.1	232806_s_at	NM_144635
6.44	6.49	0.06	8.20E-01	9.47E-01	MVK	mevalonate kinase	chr12q24	36907_at	NM_000431 /// NM_001114185
4.71	4.78	0.06	8.20E-01	9.47E-01	KIAA1881	KIAA1881	chr19p13.3	228409_at	NM_001080400
7.51	7.58	0.07	8.20E-01	9.47E-01	NFU1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	chr2p15-p13	218946_at	NM_001002755 /// NM_001002756 /// NM_001002757 /// NM_015700

5.97	6.06	0.09	8.20E-01	9.47E-01	TJP2	tight junction protein 2 (zona occludens 2)	chr9q13-q21	202085_at	NM_004817 /// NM_201629
1.92	1.95	0.03	8.20E-01	9.47E-01	CDC20B	Cell division cycle 20 homolog B (S. cerevisiae)	chr5q11.2	241120_s_at	NM_152623
4.64	4.74	0.10	8.21E-01	9.47E-01	---	---	---	227995_at	---
6.80	6.90	0.09	8.20E-01	9.47E-01	LRRC8B	leucine rich repeat containing 8 family, member B	chr1p22.2	212978_at	NM_001134476 /// NM_015350
4.14	4.22	0.08	8.21E-01	9.47E-01	---	---	---	215528_at	---
2.63	2.71	0.08	8.21E-01	9.47E-01	ADIPOQ	adiponectin, C1Q and collagen domain containing	chr3q27	207175_at	NM_004797
8.09	8.16	0.07	8.21E-01	9.47E-01	S100A11	S100 calcium binding protein A11	chr1q21	200660_at	NM_005620
5.19	5.26	0.07	8.21E-01	9.47E-01	TRIM62	tripartite motif-containing 62	chr1p35.1	219272_at	NM_018207
3.88	3.95	0.07	8.21E-01	9.47E-01	LOC100130776	similar to hCG2014417	chr12q14.1	1555907_at	XM_001717051 /// XM_001718716 /// XM_001723105
3.82	3.89	0.06	8.21E-01	9.47E-01	PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	chr1p13.3	230270_at	NM_018061
6.30	6.36	0.06	8.21E-01	9.47E-01	ACBD3	acyl-Coenzyme A binding domain containing 3	chr1q42.12	202324_s_at	NM_022735
3.55	3.60	0.05	8.21E-01	9.47E-01	C10orf88	chromosome 10 open reading frame 88	chr10q26.13	219240_s_at	NM_024942
3.64	3.69	0.05	8.21E-01	9.47E-01	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)	chr3q21	216678_at	NM_018262 /// NM_052985 /// NM_052989 /// NM_052990
3.77	3.82	0.05	8.21E-01	9.47E-01	KATNB1	Katanin p80 (WD repeat containing) subunit B 1	chr16q13	229077_at	NM_005886
7.63	7.67	0.05	8.21E-01	9.47E-01	DRAP1	DR1-associated protein 1 (negative cofactor 2 alpha)	chr11q13.3	203258_at	NM_006442
2.41	2.46	0.05	8.21E-01	9.47E-01	---	---	---	211614_at	---
2.56	2.61	0.04	8.21E-01	9.47E-01	GBA /// GBAP	glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid, pseudogene	chr1q21	216400_at	NM_000157 /// NM_001005741 /// NM_001005742 /// NM_001005749 /// NM_001005750 /// NR_002188 /// XR_042183
3.99	4.03	0.04	8.20E-01	9.47E-01	SLC30A2	solute carrier family 30 (zinc transporter), member 2	chr1p35.3	230084_at	NM_001004434 /// NM_032513
4.09	4.13	0.04	8.21E-01	9.47E-01	GGT1	gamma-glutamyltransferase 1	chr22q11.23	209919_x_at	NM_001032364 /// NM_001032365 /// NM_005265 /// NM_013430
2.06	2.10	0.04	8.21E-01	9.47E-01	NLGN1	neuroligin 1	chr3q26.31	205893_at	NM_014932
2.57	2.61	0.04	8.21E-01	9.47E-01	---	---	---	243939_at	---
4.63	4.67	0.04	8.21E-01	9.47E-01	LOC100128443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	chr5q12.3	1554652_s_at	NM_015183 /// NM_198828 /// XM_001720470 /// XM_001720479 /// XM_001722488
9.25	9.28	0.04	8.21E-01	9.47E-01	APLP2	amyloid beta (A4) precursor-like protein 2	chr11q23-q25|11q24	208704_x_at	NM_001642
3.13	3.17	0.04	8.21E-01	9.47E-01	---	---	---	215755_at	---
2.57	2.60	0.03	8.21E-01	9.47E-01	---	---	---	235813_at	---
2.26	2.29	0.03	8.21E-01	9.47E-01	---	---	---	234189_at	---
2.62	2.66	0.03	8.21E-01	9.47E-01	KIAA1975	KIAA1975 protein similar to MRIP2	chr10q23.2	1557380_at	NM_133447
2.27	2.31	0.03	8.21E-01	9.47E-01	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	chr9q33	241819_at	NM_001244
3.11	3.15	0.03	8.21E-01	9.47E-01	---	---	---	238170_at	---
2.18	2.21	0.03	8.21E-01	9.47E-01	ZNF7	zinc finger protein 7	chr8q24	1559980_at	NM_003416
2.03	2.06	0.03	8.21E-01	9.47E-01	BIVM	basic, immunoglobulin-like variable motif containing	chr13q32-q33.1	229478_x_at	NM_017693
2.09	2.12	0.03	8.21E-01	9.47E-01	FAM12A	family with sequence similarity 12, member A	chr14q11.2	217568_at	NM_006683
2.02	2.05	0.03	8.21E-01	9.47E-01	EPYC	epiphycan	chr12q21	206439_at	NM_004950
2.01	2.04	0.03	8.21E-01	9.47E-01	---	---	---	1563677_at	---
3.03	3.06	0.03	8.21E-01	9.47E-01	---	---	---	217036_at	---
1.90	1.93	0.03	8.21E-01	9.47E-01	FCRL5	Fc receptor-like 5	chr1q21	224405_at	NM_031281

1.73	1.76	0.03	8.21E-01	9.47E-01	AGBL3	ATP/GTP binding protein-like 3	chr7q33	1554820_at	XM_001723112 /// XM_001723784 /// XM_001726535 /// XM_001726650
2.18	2.20	0.02	8.21E-01	9.47E-01	LOC253805	hypothetical protein LOC253805	chr11q25	1556437_at	---
2.03	2.06	0.03	8.21E-01	9.47E-01	TTLL5	Tubulin tyrosine ligase-like family, member 5	chr14q24.3	1566101_at	NM_015072
2.13	2.17	0.04	8.22E-01	9.47E-01	---	---	---	237609_at	---
2.26	2.29	0.03	8.22E-01	9.47E-01	---	---	---	241536_at	---
4.14	4.19	0.04	8.22E-01	9.47E-01	CADM3	cell adhesion molecule 3	chr1q21.2-q22	221921_s_at	NM_001127173 /// NM_021189
8.49	8.59	0.09	8.22E-01	9.47E-01	CD163	CD163 molecule	chr12p13.3	203645_s_at	NM_004244 /// NM_203416
4.46	4.50	0.04	8.22E-01	9.47E-01	PDCD7	Programmed cell death 7	chr15q22.31	230182_at	NM_005707
3.70	3.74	0.04	8.22E-01	9.47E-01	MGC16275	hypothetical protein MGC16275	chr17q25.2	1558167_a_at	---
1.96	1.99	0.03	8.22E-01	9.47E-01	TOP1P2	topoisomerase (DNA) I pseudogene 2	chr22q11.2-q13.1|22q11.23	1566833_x_at	NR_001283
2.18	2.21	0.03	8.22E-01	9.47E-01	LMOD3	leiomodin 3 (fetal)	chr3p14.1	1555567_s_at	NM_198271
3.79	3.82	0.03	8.22E-01	9.47E-01	---	---	---	241686_x_at	---
2.24	2.27	0.03	8.22E-01	9.47E-01	EPAG	early lymphoid activation protein	chrXq21.33	217050_at	XM_926826 /// XM_938050
2.12	2.15	0.03	8.22E-01	9.47E-01	LOC100128079	hypothetical protein LOC100128079	chr16p11.2	1569620_s_at	XM_001720212 /// XM_001724906 /// XM_001725467
4.66	4.79	0.13	8.22E-01	9.47E-01	FAM5B	family with sequence similarity 5, member B	chr1q24.1-q25.3	214822_at	NM_021165
4.22	4.26	0.04	8.22E-01	9.47E-01	---	---	---	1557774_at	---
2.02	2.05	0.03	8.22E-01	9.47E-01	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	chr19q13.1	217075_x_at	NM_014727
2.33	2.37	0.04	8.22E-01	9.47E-01	---	---	---	242752_at	---
2.02	2.05	0.03	8.22E-01	9.47E-01	---	---	---	240800_x_at	---
3.20	3.25	0.05	8.22E-01	9.47E-01	SCN5A	sodium channel, voltage-gated, type V, alpha subunit	chr3p21	207413_s_at	NM_000335 /// NM_001099404 /// NM_001099405 /// NM_198056
3.39	3.43	0.04	8.23E-01	9.47E-01	TLR7	toll-like receptor 7	chrXp22.3	222952_s_at	NM_016562
5.73	5.76	0.04	8.22E-01	9.47E-01	CYHR1	cysteine/histidine-rich 1	chr8q24.3	213681_at	NM_001129888 /// NM_032687 /// NM_138496
3.21	3.25	0.04	8.23E-01	9.47E-01	---	---	---	1557375_at	---
2.23	2.26	0.03	8.23E-01	9.47E-01	LAX1	lymphocyte transmembrane adaptor 1	chr1q32.1	207734_at	NM_017773
2.85	2.90	0.05	8.23E-01	9.47E-01	---	---	---	1562797_at	---
3.48	3.53	0.05	8.23E-01	9.48E-01	---	---	---	243005_at	---
3.70	3.74	0.04	8.23E-01	9.48E-01	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	chr8p11.2	211027_s_at	NM_001556
2.15	2.18	0.03	8.23E-01	9.48E-01	GEN1	Gen homolog 1, endonuclease (Drosophila)	chr2p24.2	228286_at	NM_001130009 /// NM_182625
1.88	1.90	0.03	8.23E-01	9.48E-01	---	---	---	234426_x_at	---
2.19	2.22	0.02	8.23E-01	9.48E-01	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	chr15q22.2	220517_at	NM_001018088 /// NM_017684 /// NM_018080 /// NM_020821
4.63	4.68	0.06	8.23E-01	9.48E-01	NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	chr4q26	220183_s_at	NM_007083 /// NM_198041
3.07	3.11	0.03	8.23E-01	9.48E-01	EML4	echinoderm microtubule associated protein like 4	chr2p22-p21	232587_at	NM_019063
2.25	2.27	0.02	8.23E-01	9.48E-01	---	---	---	1569330_at	---
4.41	4.45	0.04	8.23E-01	9.48E-01	ADSSL1	Adenylosuccinate synthase like 1	chr14q32.33	238259_at	NM_152328 /// NM_199165
3.34	3.38	0.04	8.23E-01	9.48E-01	CTA-216E10.6	hypothetical FLJ23584	chr22q13.2	219309_at	XR_040813 /// XR_040814 /// XR_040815
5.56	5.63	0.07	8.23E-01	9.48E-01	---	---	---	229757_at	---
1.95	1.98	0.03	8.23E-01	9.48E-01	SLCO1A2	solute carrier organic anion transporter family, member 1A2	chr12p12	207308_at	NM_005075 /// NM_021094 /// NM_134431
2.14	2.17	0.03	8.23E-01	9.48E-01	---	---	---	1559066_at	---

2.98	3.02	0.04	8.23E-01	9.48E-01	LOC442715	similar to insulin receptor substrate like protein	---	217450_at	XM_499461
2.38	2.41	0.03	8.23E-01	9.48E-01	CPEB2	Cytoplasmic polyadenylation element binding protein 2	chr4p15.33	235462_at	NM_182485 /// NM_182646
2.79	2.82	0.03	8.24E-01	9.48E-01	D21S2090E	D21S2090E	---	1563362_at	---
2.16	2.19	0.03	8.23E-01	9.48E-01	---	---	---	240906_at	---
2.40	2.43	0.03	8.24E-01	9.48E-01	CHRM2	cholinergic receptor, muscarinic 2	chr7q31-q35	221330_at	NM_000739 /// NM_001006626 /// NM_001006627 /// NM_001006628 /// NM_001006629 /// NM_001006630 /// NM_001006631 /// NM_001006632
5.85	5.90	0.05	8.24E-01	9.48E-01	BAIAP2L1	BAI1-associated protein 2-like 1	chr7q21.3	222675_s_at	NM_018842
2.36	2.40	0.03	8.24E-01	9.48E-01	---	---	---	1558436_a_at	---
3.03	3.07	0.04	8.24E-01	9.48E-01	---	---	---	216577_at	---
1.97	2.00	0.03	8.24E-01	9.48E-01	DEFB127	defensin, beta 127	chr20p13	233343_at	NM_139074
2.12	2.14	0.02	8.24E-01	9.48E-01	---	---	---	237588_at	---
5.17	5.26	0.09	8.24E-01	9.48E-01	DZIP3	DAZ interacting protein 3, zinc finger	chr3q13.13	213186_at	NM_014648
2.72	2.77	0.06	8.24E-01	9.48E-01	DENND4A	DENN/MADD domain containing 4A	chr15q22.31	214787_at	NM_005848
8.59	8.66	0.07	8.24E-01	9.48E-01	LMAN1	Lectin, mannose-binding, 1	chr18q21.3-q22	224629_at	NM_005570
2.63	2.66	0.03	8.24E-01	9.48E-01	---	---	---	234047_at	---
2.21	2.24	0.03	8.24E-01	9.48E-01	---	---	---	244757_at	---
2.00	2.03	0.03	8.24E-01	9.48E-01	---	---	---	217578_at	---
1.97	1.99	0.03	8.24E-01	9.48E-01	---	---	---	239655_at	---
2.70	2.74	0.04	8.24E-01	9.48E-01	TAS2R5	taste receptor, type 2, member 5	chr7q31.3-q32	231757_at	NM_018980
6.14	6.23	0.08	8.24E-01	9.48E-01	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	chr3q25.31	217790_s_at	NM_007107
3.23	3.28	0.05	8.24E-01	9.48E-01	PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta	chr4p16.3	238085_at	NM_000283
2.25	2.30	0.05	8.25E-01	9.48E-01	NAV3	neuron navigator 3	chr12q14.3	216466_at	NM_014903
2.61	2.65	0.05	8.24E-01	9.48E-01	TCTE1	t-complex-associated-testis-expressed 1	chr6p21.1	237280_at	NM_182539
4.36	4.40	0.04	8.24E-01	9.48E-01	---	---	---	1564887_at	---
2.16	2.20	0.04	8.25E-01	9.48E-01	---	---	---	216731_s_at	---
3.53	3.56	0.03	8.25E-01	9.48E-01	---	---	---	1556982_at	---
3.25	3.29	0.03	8.24E-01	9.48E-01	USP32	Ubiquitin specific peptidase 32	chr17q23.2	237431_at	NM_032582
2.36	2.39	0.03	8.24E-01	9.48E-01	---	---	---	230752_at	---
1.98	2.00	0.03	8.25E-01	9.48E-01	---	---	---	1560424_at	---
2.19	2.22	0.02	8.24E-01	9.48E-01	OR10A3	olfactory receptor, family 10, subfamily A, member 3	chr11p15.4	1567250_at	NM_001003745
7.25	7.31	0.06	8.25E-01	9.48E-01	PICALM	phosphatidylinositol binding clathrin assembly protein	chr11q14	212506_at	NM_001008660 /// NM_007166
2.31	2.35	0.04	8.25E-01	9.48E-01	ZNF131	Zinc finger protein 131	chr5p12-p11	237844_at	NM_003432
3.67	3.72	0.05	8.25E-01	9.48E-01	---	---	---	236617_at	---
7.30	7.38	0.08	8.25E-01	9.48E-01	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	chr2q33-q35	202020_s_at	NM_006055
3.47	3.51	0.04	8.25E-01	9.48E-01	C10orf51	chromosome 10 open reading frame 51	chr10p12.1	231196_x_at	XR_040094 /// XR_040095 /// XR_040096
4.09	4.12	0.03	8.25E-01	9.48E-01	---	---	---	220490_at	---
3.14	3.17	0.03	8.25E-01	9.48E-01	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	chr10q25.3	236239_at	NM_020383
1.93	1.96	0.02	8.25E-01	9.48E-01	---	---	---	1563329_s_at	---
3.79	3.83	0.05	8.25E-01	9.48E-01	C1orf26	chromosome 1 open reading frame 26	chr1q25	223548_at	NM_001105518 /// NM_017673
2.07	2.11	0.04	8.25E-01	9.48E-01	---	---	---	234507_at	---
2.62	2.65	0.03	8.25E-01	9.48E-01	EPS8L2	EPS8-like 2	chr11p15.5	222546_s_at	NM_022772
2.74	2.78	0.04	8.25E-01	9.48E-01	UMPS	uridine monophosphate synthetase	chr3q13	202707_at	NM_000373
1.93	1.96	0.03	8.25E-01	9.48E-01	CACNA1E	calcium channel, voltage-dependent, R type, alpha 1E subunit	chr1q25-q31	242410_s_at	NM_000721
4.23	4.31	0.08	8.25E-01	9.48E-01	ZMYND11	zinc finger, MYND domain containing 11	chr10p14	202137_s_at	NM_006624 /// NM_212479
4.11	4.18	0.07	8.25E-01	9.48E-01	SLC22A23	solute carrier family 22, member 23	chr6p25.2	223194_s_at	NM_015482 /// NM_021945
5.77	5.83	0.06	8.25E-01	9.48E-01	ZFYVE26	zinc finger, FYVE domain containing 26	chr14q24.1	213073_at	NM_015346
4.14	4.18	0.04	8.25E-01	9.48E-01	SLC6A10P /// SLC6A8	Solute carrier family 6 (neurotransmitter transporter, creatine), member 10 (pseudogene) /// Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	chr16p11.2 /// chrXq28	226904_at	NM_005629 /// NR_003083 /// XR_042169
2.09	2.11	0.02	8.25E-01	9.48E-01	ERMN	ermin, ERM-like protein	chr2q24.1	231911_at	NM_001009959 /// NM_020711

4.31	4.38	0.07	8.25E-01	9.48E-01	UAP1L1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	chr9q34.3	214755_at	NM_207309
2.39	2.44	0.05	8.25E-01	9.48E-01	---	---	---	234744_x_at	---
7.34	7.38	0.04	8.25E-01	9.48E-01	MKL2	MKL/myocardin-like 2	chr16p13.12	218259_at	NM_014048
3.40	3.56	0.16	8.26E-01	9.48E-01	DMKN	dermokine	chr19q13.12	226926_at	NM_001035516 /// NM_001126056 /// NM_001126057 /// NM_001126058 /// NM_001126059 /// NM_001126061 /// NM_033317
3.90	4.01	0.11	8.26E-01	9.48E-01	SGPP1	sphingosine-1-phosphate phosphatase 1	chr14q23.2	221268_s_at	NM_030791
3.04	3.11	0.06	8.26E-01	9.48E-01	---	---	---	215608_at	---
1.90	1.92	0.02	8.26E-01	9.48E-01	C14orf105	chromosome 14 open reading frame 105	chr14q23.1	220084_at	NM_018168
4.14	4.27	0.13	8.26E-01	9.48E-01	COL5A1	collagen, type V, alpha 1	chr9q34.2-q34.3	212489_at	NM_000093
3.39	3.45	0.06	8.26E-01	9.48E-01	ZBTB44	zinc finger and BTB domain containing 44	chr11q24.3	220243_at	NM_014155
3.67	3.71	0.04	8.26E-01	9.48E-01	NUP214	nucleoporin 214kDa	chr9q34.1	228902_at	NM_005085
4.09	4.13	0.04	8.26E-01	9.48E-01	LOC389199	hypothetical gene supported by BC031673	chr4p16.1	1554809_at	XR_040590 /// XR_040591 /// XR_040592
4.31	4.39	0.08	8.26E-01	9.48E-01	ZMYND11	zinc finger, MYND domain containing 11	chr10p14	1554159_a_at	NM_006624 /// NM_212479
6.75	6.82	0.07	8.26E-01	9.48E-01	LITAF	lipopolysaccharide-induced TNF factor	chr16p13.13	200706_s_at	NM_004862
3.80	3.84	0.04	8.26E-01	9.48E-01	---	---	---	231443_at	---
2.23	2.26	0.03	8.26E-01	9.48E-01	---	---	---	232110_at	---
2.77	2.80	0.03	8.26E-01	9.48E-01	WNT16	wingless-type MMTV integration site family, member 16	chr7q31	221113_s_at	NM_016087 /// NM_057168
2.61	2.64	0.03	8.26E-01	9.48E-01	---	---	---	1570299_at	---
2.03	2.06	0.03	8.26E-01	9.48E-01	---	---	---	1560491_at	---
3.70	3.77	0.07	8.26E-01	9.49E-01	RIOK3	RIO kinase 3 (yeast)	chr18q11.2	202131_s_at	NM_003831
4.49	4.54	0.05	8.26E-01	9.49E-01	EFNA3	ephrin-A3	chr1q21-q22	210132_at	NM_004952
7.19	7.24	0.05	8.26E-01	9.49E-01	ZFAND3	zinc finger, AN1-type domain 3	chr6pter-p22.3	218020_s_at	NM_021943
3.33	3.37	0.04	8.26E-01	9.49E-01	IL20RA	interleukin 20 receptor, alpha	chr6q22.33-q23.1	222828_at	NM_014432
2.12	2.15	0.03	8.26E-01	9.49E-01	---	---	---	235144_at	---
2.16	2.19	0.03	8.26E-01	9.49E-01	---	---	---	216785_at	---
2.00	2.03	0.03	8.26E-01	9.49E-01	ADAMTSL1	ADAMTS-like 1	chr9p22.2-p22.1	1552808_at	NM_001040272 /// NM_052866
2.87	2.90	0.02	8.26E-01	9.49E-01	PUS10	Pseudouridylate synthase 10	chr2p16.1	229362_at	NM_144709
2.47	2.50	0.03	8.26E-01	9.49E-01	CACNG4	calcium channel, voltage-dependent, gamma subunit 4	chr17q24	221585_at	NM_014405
1.97	2.00	0.03	8.26E-01	9.49E-01	---	---	---	1562288_at	---
6.19	6.23	0.04	8.27E-01	9.49E-01	ASB8	ankyrin repeat and SOCS box-containing 8	chr12q13.11	226861_at	NM_024095
2.35	2.38	0.03	8.27E-01	9.49E-01	---	---	---	1563247_at	---
2.92	2.95	0.03	8.27E-01	9.49E-01	LUZP4	leucine zipper protein 4	chrXq23	220665_at	NM_016383
3.88	3.99	0.11	8.27E-01	9.49E-01	HSPA6	heat shock 70kDa protein 6 (HSP70B')	chr1q23	117_at	NM_002155
4.70	4.76	0.06	8.27E-01	9.49E-01	SEPP1	Selenoprotein P, plasma, 1	chr5q31	231669_at	NM_001085486 /// NM_001093726 /// NM_005410
2.28	2.31	0.03	8.27E-01	9.49E-01	---	---	---	1561445_at	---
2.00	2.02	0.02	8.27E-01	9.49E-01	---	---	---	1566087_at	---
4.25	4.32	0.07	8.27E-01	9.49E-01	TRAPPC10	trafficking protein particle complex 10	chr21q22.3	215269_at	NM_001001723 /// NM_003274
5.82	5.89	0.07	8.27E-01	9.49E-01	SLC15A3	solute carrier family 15, member 3	chr11q12.2	219593_at	NM_016582
3.12	3.18	0.06	8.27E-01	9.49E-01	CFDP1	craniofacial development protein 1	chr16q22.2-q22.3	210701_at	NM_006324
3.37	3.41	0.04	8.27E-01	9.49E-01	LOC283887	hypothetical protein LOC283887	chr16p12.1	1556709_a_at	XM_929898
3.05	3.08	0.03	8.27E-01	9.49E-01	GRM5	glutamate receptor, metabotropic 5	chr11q14.2-q14.3	1565389_s_at	NM_000842
2.63	2.68	0.05	8.27E-01	9.49E-01	---	---	---	1566482_at	---
4.14	4.19	0.05	8.27E-01	9.49E-01	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	chr6p21	209057_x_at	NM_001253
5.56	5.59	0.04	8.27E-01	9.49E-01	CDK10	cyclin-dependent kinase 10	chr16q24	203469_s_at	NM_001098533 /// NM_052987 /// NM_052988
3.98	4.02	0.03	8.27E-01	9.49E-01	BPIL1	bactericidal/permeability-increasing protein-like 1	chr20q11.21	232698_at	NM_025227
5.98	6.06	0.08	8.27E-01	9.49E-01	CIP29	cytokine induced protein 29 kDa	chr12q13.2	224914_s_at	NM_033082

6.98	7.06	0.07	8.28E-01	9.49E-01	CUL4B	cullin 4B	chrXq23	202214_s_at	NM_001079872 /// NM_003588
3.97	4.04	0.07	8.28E-01	9.49E-01	C9orf47	chromosome 9 open reading frame 47	chr9q22.1	1564274_at	NM_001001938
4.90	4.97	0.07	8.27E-01	9.49E-01	WWTR1	WW domain containing transcription regulator 1	chr3q23-q24	202132_at	NM_015472
6.07	6.12	0.05	8.28E-01	9.49E-01	NRM	nurim (nuclear envelope membrane protein)	chr6p21.33	225592_at	NM_007243
5.02	5.06	0.05	8.28E-01	9.49E-01	ZCCHC9	zinc finger, CCHC domain containing 9	chr5q14.1	225538_at	NM_001131035 /// NM_001131036 /// NM_032280
2.44	2.48	0.04	8.28E-01	9.49E-01	CADPS	Ca++-dependent secretion activator	chr3p14.2	1568604_a_at	NM_003716 /// NM_183393 /// NM_183394
2.60	2.64	0.04	8.28E-01	9.49E-01	---	---	---	237118_at	---
4.29	4.33	0.04	8.28E-01	9.49E-01	PBRM1	polybromo 1	chr3p21	224152_s_at	NM_018165 /// NM_018313 /// NM_181042
2.34	2.37	0.03	8.28E-01	9.49E-01	SIDT1	SID1 transmembrane family, member 1	chr3q13.2	219734_at	NM_017699
3.65	3.68	0.03	8.28E-01	9.49E-01	PHF7	PHD finger protein 7	chr3p21.1	221611_s_at	NM_016483 /// NM_173341
4.93	4.96	0.03	8.28E-01	9.49E-01	---	---	---	1567375_at	---
6.58	6.61	0.03	8.28E-01	9.49E-01	SART1	squamous cell carcinoma antigen recognized by T cells	chr11q13.1	200051_at	NM_005146
2.63	2.66	0.03	8.28E-01	9.49E-01	---	---	---	203539_s_at	---
2.08	2.11	0.03	8.27E-01	9.49E-01	---	---	---	1569753_at	---
2.12	2.14	0.03	8.28E-01	9.49E-01	---	---	---	1570298_at	---
2.06	2.08	0.03	8.28E-01	9.49E-01	IGHG1	Immunoglobulin heavy constant mu	chr14q32.33	1555710_at	---
2.37	2.39	0.02	8.28E-01	9.49E-01	---	---	---	232105_at	---
8.40	8.46	0.06	8.28E-01	9.49E-01	GTF2I /// GTF2IP1 /// LOC100093631	general transcription factor II, i /// general transcription factor II, i, pseudogene 1 /// general transcription factor II, i, pseudogene	chr7q11.23	201065_s_at	NM_001518 /// NM_032999 /// NM_033000 /// NM_033001 /// NR_002206 /// NR_003580
2.06	2.09	0.03	8.28E-01	9.49E-01	---	---	---	1556454_a_at	---
2.09	2.13	0.03	8.28E-01	9.49E-01	---	---	---	238382_x_at	---
2.38	2.41	0.04	8.28E-01	9.49E-01	---	---	---	240976_at	---
3.22	3.26	0.04	8.28E-01	9.49E-01	TRIM3	tripartite motif-containing 3	chr11p15.5	213884_s_at	NM_006458 /// NM_033278
2.19	2.23	0.04	8.28E-01	9.49E-01	SPRR1B	small proline-rich protein 1B (cornifin)	chr1q21-q22	205064_at	NM_003125
2.05	2.07	0.03	8.28E-01	9.49E-01	DUSP19	dual specificity phosphatase 19	chr2q32.1	1552705_at	NM_080876
6.30	6.37	0.07	8.28E-01	9.49E-01	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	chr17q24.2	202353_s_at	NM_002816
5.80	5.83	0.03	8.28E-01	9.49E-01	ETV6	ets variant gene 6 (TEL oncogene)	chr12p13	225764_at	NM_001987
2.86	2.92	0.06	8.28E-01	9.49E-01	---	---	---	1559149_at	---
2.05	2.07	0.02	8.28E-01	9.49E-01	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	chr11q12	228599_at	NM_021950 /// NM_152866
6.20	6.24	0.05	8.28E-01	9.49E-01	TMEM57	Transmembrane protein 57	chr1p36.11|1p36.11	241364_at	NM_018202
3.84	3.88	0.05	8.28E-01	9.49E-01	---	---	---	1560782_at	---
2.17	2.20	0.03	8.28E-01	9.49E-01	PBOV1	prostate and breast cancer overexpressed 1	chr6q23-q24	224257_s_at	NM_021635
1.71	1.74	0.03	8.28E-01	9.49E-01	KLHDC1	kelch domain containing 1	chr14q22.1	1564272_a_at	NM_172193
1.95	1.98	0.02	8.29E-01	9.49E-01	LOC643401	hypothetical protein LOC643401	chr5p14.1	1557765_at	XM_932012 /// XM_932015
4.73	4.78	0.04	8.29E-01	9.49E-01	CBR4	carbonyl reductase 4	chr4q32.3	1553693_s_at	NM_032783
2.35	2.39	0.04	8.29E-01	9.49E-01	---	---	---	1566900_at	---
2.18	2.21	0.03	8.29E-01	9.49E-01	CREB5	cAMP responsive element binding protein 5	chr7p15.1	229228_at	NM_001011666 /// NM_004904 /// NM_182898 /// NM_182899
2.84	2.89	0.05	8.29E-01	9.49E-01	---	---	---	1555977_at	---
3.62	3.68	0.06	8.29E-01	9.49E-01	RHOJ	ras homolog gene family, member J	chr14q23.2	238905_at	NM_020663
2.13	2.16	0.03	8.29E-01	9.49E-01	---	---	---	233035_at	---
2.10	2.14	0.03	8.29E-01	9.49E-01	MPZL2	myelin protein zero-like 2	chr11q24	203780_at	NM_005797 /// NM_144765
3.08	3.11	0.03	8.29E-01	9.49E-01	---	---	---	236116_at	---
3.26	3.30	0.04	8.29E-01	9.49E-01	DUSP7	dual specificity phosphatase 7	chr3p21	214793_at	NM_001947
4.42	4.46	0.04	8.29E-01	9.49E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	240294_at	NM_001113239 /// NM_022740
3.00	3.02	0.03	8.29E-01	9.49E-01	LCA5	Leber congenital amaurosis 5	chr6q14.1	244401_at	NM_001122769 /// NM_181714

4.66	4.71	0.05	8.29E-01	9.50E-01	RIMBP3 /// RIMBP3B /// RIMBP3C	RIMS binding protein 3 /// RIMS binding protein 3B /// RIMS binding protein 3C	chr22q11.21	230062_at	NM_001128633 /// NM_001128635 /// NM_015672 /// XM_036936 /// XM_036942																					
2.23	2.26	0.03	8.29E-01	9.50E-01	C15orf34	chromosome 15 open reading frame 34	chr15q24.1	220718_at	XR_040821 /// XR_040822 /// XR_040823																					
3.55	3.62	0.07	8.29E-01	9.50E-01	RNUXA	RNA U, small nuclear RNA export adaptor (phosphorylation regulated)	chr5q23.2	234405_s_at	NM_032177																					
3.55	3.60	0.05	8.29E-01	9.50E-01	GAS7	growth arrest-specific 7	chr17p13.1	210872_x_at	NM_001130831 /// NM_003644 /// NM_201432 /// NM_201433																					
3.95	3.99	0.04	8.29E-01	9.50E-01	CD79A	CD79a molecule, immunoglobulin-associated alpha	chr19q13.2	1555779_a_at	NM_001783 /// NM_021601																					
2.47	2.50	0.03	8.29E-01	9.50E-01	GBA3	glucosidase, beta, acid 3 (cytosolic)	chr4p15.31	219954_s_at	NM_001128432 /// NM_020973																					
5.03	5.20	0.18	8.30E-01	9.50E-01	ANP32E	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	chr1q21.2	229128_s_at	NM_030920																					
6.68	6.74	0.07	8.30E-01	9.50E-01	MACF1	microtubule-actin crosslinking factor 1	chr1p32-p31	208633_s_at	NM_012090 /// NM_033044																					
2.63	2.67	0.04	8.30E-01	9.50E-01	---	---	---	243533_x_at	---																					
2.21	2.24	0.03	8.30E-01	9.50E-01	HECTD2	HECT domain containing 2	chr10q23.32	1565699_at	NM_173497 /// NM_182765																					
5.27	5.33	0.06	8.30E-01	9.50E-01	ORAI1	ORAI calcium release-activated calcium modulator 1	chr12q24.31	226531_at	NM_032790																					
2.51	2.55	0.04	8.30E-01	9.50E-01	---	---	---	234046_at	---																					
1.72	1.74	0.02	8.30E-01	9.50E-01	---	---	---	242170_at	---																					
2.98	3.01	0.04	8.30E-01	9.50E-01	FUS	Fusion (involved in t(12;16) in malignant liposarcoma)	chr16p11.2	1565715_at	NM_004960																					
2.14	2.17	0.03	8.30E-01	9.50E-01	DCTN4	dynactin 4 (p62)	chr5q31-q32	233490_at	NM_016221																					
2.16	2.19	0.02	8.30E-01	9.50E-01	HIST1H2AG /// HIST1H2AH /// HIST1H2AI /// HIST1H2AJ /// HIST1H2AK /// HIST1H2AL /// HIST1H2AM	histone cluster 1, H2ag /// histone cluster 1, H2ah /// histone cluster 1, H2ai /// histone cluster 1, H2aj /// histone cluster 1, H2ak /// histone cluster 1, H2al /// histone cluster 1, H2am	chr6p21.33 /// chr6p22-p21.3 /// chr6p22.1	214554_at	NM_003509 /// NM_003510 /// NM_003511 /// NM_003514 /// NM_021064 /// NM_021066 /// NM_080596																					
5.84	5.88	0.04	8.30E-01	9.50E-01	HEYL	hairy/enhancer-of-split related with YRPW motif-like	chr1p34.3	220662_s_at	NM_014571																					
2.32	2.37	0.05	8.30E-01	9.50E-01	HYDIN2	hydrocephalus inducing homolog 2 (mouse)	chr1q21.1	1553468_at	XM_001717859																					
5.66	5.79	0.13	8.30E-01	9.50E-01	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	chr7q21	209576_at	NM_002069																					
6.32	6.36	0.05	8.30E-01	9.50E-01	NCOR1	nuclear receptor co-repressor 1	chr17p11.2	200854_at	NM_006311																					
1.87	1.90	0.02	8.30E-01	9.50E-01	---	---	---	241880_x_at	---																					
3.49	3.54	0.05	8.31E-01	9.50E-01	BRWD1	bromodomain and WD repeat domain containing 1	chr21q22.2	1553227_s_at	NM_001007246 /// NM_018963 /// NM_033656																					
5.60	5.69	0.09	8.31E-01	9.50E-01	NUP35	nucleoporin 35kDa	chr2q32.1	225470_at	NM_138285																					
7.11	7.17	0.06	8.31E-01	9.50E-01	---	---	---	226805_at	---																					
4.33	4.38	0.05	8.31E-01	9.50E-01	---	---	---	238573_at	---																					
4.40	4.45	0.04	8.31E-01	9.50E-01	ATHL1	ATH1, acid trehalase-like 1 (yeast)	chr11p15.5	219359_at	NM_025092																					
3.42	3.46	0.04	8.31E-01	9.50E-01	---	---	---	216934_at	---																					
3.71	3.74	0.04	8.31E-01	9.50E-01	KIAA0100	KIAA0100	chr17q11.2	201728_s_at	NM_014680																					
3.63	3.67	0.04	8.31E-01	9.50E-01	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	chr19p13.2	1557532_at	NM_005001																					
2.51	2.55	0.03	8.31E-01	9.50E-01	---	---	---	241516_at	---																					
2.17	2.20	0.03	8.31E-01	9.50E-01	TIMD4	T-cell immunoglobulin and mucin domain containing 4	chr5q33.3	1552280_at	NM_138379																					
1.81	1.83	0.02	8.31E-01	9.50E-01	PPP1R3A	protein phosphatase 1, regulatory (inhibitor) subunit 3A	chr7q31.1	211169_s_at	NM_002711																					
8.64	8.70	0.06	8.31E-01	9.50E-01	PRDX4	peroxiredoxin 4	chrXp22.11	201923_at	NM_006406																					
4.34	4.38	0.05	8.31E-01	9.50E-01	TPM2	tropomyosin 2 (beta)	chr9p13.2-p13.1	227397_at	NM_003289 /// NM_213674																					
6.48	6.52	0.05	8.31E-01	9.50E-01	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	chr7cen-q22	213333_at	NM_005918																					
3.44	3.48	0.05	8.31E-01	9.50E-01	FAM160A1	family with sequence similarity 160, member A1	chr4q31.3	1569465_at	NM_001109977 /// XM_001715912 /// XM_001715923 /// XM_001718535																					

3.05	3.09	0.05	8.31E-01	9.50E-01	PSPC1	Paraspeckle component 1	chr13q12.11	226724_s_at	NM_001042414 /// NR_003272																				
2.31	2.34	0.03	8.31E-01	9.50E-01	NSUN3	NOL1/NOP2/Sun domain family, member 3	chr3q11.2	1568913_at	NM_022072																				
2.18	2.21	0.03	8.31E-01	9.50E-01	---	---	---	1569910_at	---																				
2.04	2.06	0.03	8.31E-01	9.50E-01	---	---	---	240034_at	---																				
2.12	2.15	0.03	8.31E-01	9.50E-01	KLF12	Kruppel-like factor 12	chr13q22	206965_at	NM_007249																				
2.12	2.14	0.02	8.31E-01	9.50E-01	LOC285627	hypothetical protein LOC285627	chr5q33.3	1561401_at	---																				
2.01	2.04	0.02	8.31E-01	9.50E-01	MFSD4	major facilitator superfamily domain containing 4	chr1q32.1	238862_at	NM_181644																				
9.24	9.31	0.07	8.31E-01	9.50E-01	LMBRD1	LMBR1 domain containing 1	chr6q13	218191_s_at	NM_018368																				
3.67	3.72	0.05	8.31E-01	9.50E-01	CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	chr15q24	207608_x_at	NM_000761																				
9.26	9.30	0.04	8.31E-01	9.50E-01	TPP1	tripeptidyl peptidase I	chr11p15	200743_s_at	NM_000391																				
2.39	2.41	0.02	8.31E-01	9.50E-01	DAOA	D-amino acid oxidase activator	chr13q33.2|13q34	1555640_at	NM_172370																				
8.36	8.44	0.08	8.31E-01	9.50E-01	KCTD12	potassium channel tetramerisation domain containing 12	chr13q22.3	212188_at	NM_138444																				
4.16	4.21	0.05	8.31E-01	9.50E-01	KCMF1	potassium channel modulatory factor 1	chr2p11.2	222471_s_at	NM_020122																				
2.31	2.35	0.04	8.31E-01	9.50E-01	---	---	---	1566951_at	---																				
2.72	2.76	0.04	8.31E-01	9.50E-01	---	---	---	235695_at	---																				
5.42	5.45	0.03	8.32E-01	9.50E-01	WDR90	WD repeat domain 90	chr16p13.3	236049_at	NM_145294																				
2.07	2.10	0.02	8.32E-01	9.50E-01	RGPD5 /// RGPD6 /// RGPD7	RANBP2-like and GRIP domain containing 5 /// RANBP2-like and GRIP domain containing 6 /// RANBP2-like and GRIP domain containing 7	chr2q13	211324_s_at	NM_001037866 /// NM_001123363 /// NM_005054 /// NM_032260 /// XM_001133591																				
3.81	3.84	0.04	8.32E-01	9.50E-01	PFDN4	prefoldin subunit 4	chr20q13.2	205360_at	NM_002623																				
2.75	2.78	0.03	8.32E-01	9.50E-01	FAM71A	family with sequence similarity 71, member A	chr1q32.3	1552384_a_at	NM_153606																				
3.17	3.20	0.02	8.32E-01	9.50E-01	---	---	---	244525_at	---																				
3.05	3.09	0.04	8.32E-01	9.50E-01	LOC402779	hypothetical LOC402779	---	1569696_at	---																				
2.24	2.27	0.03	8.32E-01	9.50E-01	---	---	---	237127_at	---																				
2.86	2.89	0.03	8.32E-01	9.51E-01	AK2	adenylate kinase 2	chr1p34	212172_at	NM_001625 /// NM_013411																				
2.46	2.49	0.03	8.32E-01	9.51E-01	---	---	---	231165_at	---																				
7.52	7.63	0.10	8.32E-01	9.51E-01	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	chr12q24.11	225204_at	NM_139283																				
2.35	2.38	0.03	8.32E-01	9.51E-01	---	---	---	239684_at	---																				
7.97	8.02	0.05	8.32E-01	9.51E-01	YME1L1	YME1-like 1 (S. cerevisiae)	chr10p14	201352_at	NM_014263 /// NM_139312																				
2.40	2.43	0.03	8.32E-01	9.51E-01	JMJD2D	jumonji domain containing 2D	chr11q21	220278_at	NM_018039																				
2.29	2.33	0.04	8.32E-01	9.51E-01	---	---	---	232161_x_at	---																				
2.30	2.34	0.04	8.32E-01	9.51E-01	---	---	---	241503_at	---																				
3.65	3.69	0.04	8.32E-01	9.51E-01	---	---	---	241476_at	---																				
2.47	2.51	0.04	8.32E-01	9.51E-01	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	chr17p11.2	244461_at	NM_001033553 /// NM_001033554 /// NM_001033555 /// NM_152904																				
4.36	4.40	0.04	8.32E-01	9.51E-01	ZBTB41	zinc finger and BTB domain containing 41	chr1q31.3	226962_at	NM_194314																				
2.49	2.53	0.04	8.32E-01	9.51E-01	DOCK9	dedicator of cytokinesis 9	chr13q32.3	215041_s_at	NM_001130048 /// NM_001130049 /// NM_001130050 /// NM_015296																				
2.70	2.73	0.03	8.32E-01	9.51E-01	---	---	---	230667_at	---																				
2.04	2.07	0.03	8.32E-01	9.51E-01	WDR17	WD repeat domain 17	chr4q34	1552430_at	NM_170710 /// NM_181265																				
5.13	5.18	0.04	8.32E-01	9.51E-01	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	chr7p22.2	228762_at	NM_001040167 /// NM_001040168																				
2.61	2.65	0.04	8.33E-01	9.51E-01	---	---	---	217331_at	---																				
4.21	4.25	0.04	8.33E-01	9.51E-01	LOC100144603	hypothetical transcript	---	238557_at	NR_021492																				
3.75	3.78	0.03	8.33E-01	9.51E-01	KLF12	Kruppel-like factor 12	chr13q22	206966_s_at	NM_007249																				
5.35	5.40	0.06	8.33E-01	9.51E-01	ZNF207	Zinc finger protein 207	chr17q11.2	239937_at	NM_001032293 /// NM_001098507 /// NM_003457																				
2.22	2.25	0.04	8.33E-01	9.51E-01	MEGF11	multiple EGF-like-domains 11	chr15q22.31	1560334_at	NM_032445																				
7.80	7.88	0.09	8.33E-01	9.51E-01	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	chr18p11.22	225198_at	NM_003574 /// NM_194434																				
1.99	2.02	0.03	8.33E-01	9.51E-01	STL	Six-twelve leukemia gene	chr6q22.33	1563496_at	---																				

4.85	4.91	0.06	8.33E-01	9.51E-01	TGDS	TDP-glucose 4,6-dehydratase	chr13q32.1	208249_s_at	NM_014305
7.78	7.83	0.05	8.33E-01	9.51E-01	MRPS33	mitochondrial ribosomal protein S33	chr7q32-q34	218654_s_at	NM_016071 /// NM_053035
2.79	2.82	0.03	8.33E-01	9.51E-01	HCFC1	Host cell factor C1 (VP16-accessory protein)	chrXq28	231177_at	NM_005334
2.17	2.20	0.03	8.33E-01	9.51E-01	TTBK2	Tau tubulin kinase 2	chr15q15.2	240011_at	NM_173500
6.54	6.58	0.05	8.33E-01	9.51E-01	SKIP	skeletal muscle and kidney enriched inositol phosphatase	chr17p13.3	202781_s_at	NM_016532 /// NM_130766
2.56	2.59	0.03	8.33E-01	9.51E-01	LNX1	ligand of numb-protein X 1	chr4q12	223612_s_at	NM_001126328 /// NM_032622
2.08	2.10	0.03	8.33E-01	9.51E-01	ABCC12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	chr16q12.1	1552590_a_at	NM_033226
1.98	2.02	0.03	8.33E-01	9.51E-01	AMELX	amelogenin (amelogenesis imperfecta 1, X-linked)	chrXp22.31-p22.1	208410_x_at	NM_001142 /// NM_182680 /// NM_182681
5.19	5.26	0.07	8.33E-01	9.51E-01	ATP11C	ATPase, class VI, type 11C	chrXq27.1	226785_at	NM_001010986 /// NM_173694
3.99	4.04	0.06	8.33E-01	9.51E-01	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	chr19q13.11	204203_at	NM_001806
4.44	4.49	0.05	8.33E-01	9.51E-01	SLCO3A1	solute carrier organic anion transporter family, member 3A1	chr15q26	229776_at	NM_013272
4.18	4.22	0.03	8.33E-01	9.51E-01	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	chr1p36.3	239035_at	NM_005957
3.11	3.14	0.03	8.33E-01	9.51E-01	CCDC40	coiled-coil domain containing 40	chr17q25.3	220593_s_at	NM_017950
4.27	4.30	0.03	8.33E-01	9.51E-01	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	chr1p36	206729_at	NM_001243 /// NM_152942
5.38	5.46	0.08	8.33E-01	9.51E-01	SMAD5	SMAD family member 5	chr5q31	235451_at	NM_001001419 /// NM_001001420 /// NM_005903
5.57	5.64	0.07	8.33E-01	9.51E-01	C14orf139	chromosome 14 open reading frame 139	chr14q32.13	219563_at	XR_017975 /// XR_040801 /// XR_040802
3.49	3.54	0.05	8.33E-01	9.51E-01	---	---	---	238591_at	---
6.19	6.23	0.03	8.33E-01	9.51E-01	SAMD4B	sterile alpha motif domain containing 4B	chr19q13.2	226714_at	NM_018028
6.60	6.64	0.04	8.34E-01	9.51E-01	ZBED3	zinc finger, BED-type containing 3	chr5q14.1	228402_at	NM_032367
3.62	3.64	0.03	8.34E-01	9.51E-01	LRRC48	leucine rich repeat containing 48	chr17p11.2	208140_s_at	NM_001130090 /// NM_001130091 /// NM_001130092 /// NM_031294
4.30	4.37	0.07	8.34E-01	9.51E-01	ARMC8	armadillo repeat containing 8	chr3q22.3	203487_s_at	NM_014154 /// NM_015396 /// NM_213654
2.67	2.72	0.04	8.34E-01	9.51E-01	MPL	myeloproliferative leukemia virus oncogene	chr1p34	216825_s_at	NM_005373
2.00	2.02	0.02	8.34E-01	9.51E-01	CLDN18	claudin 18	chr3q22.3	232578_at	NM_001002026 /// NM_016369
2.16	2.20	0.04	8.34E-01	9.51E-01	ANKRD36B	ankyrin repeat domain 36B	chr2q11.2	214723_x_at	NM_025190
2.66	2.69	0.03	8.34E-01	9.51E-01	ARHGAP28	Rho GTPase activating protein 28	chr18p11.31	220382_s_at	NM_001010000 /// NM_030672
2.26	2.30	0.03	8.34E-01	9.51E-01	---	---	---	230091_at	---
3.83	3.88	0.05	8.34E-01	9.51E-01	C15orf59	chromosome 15 open reading frame 59	chr15q24.1	230475_at	NM_001039614
2.78	2.82	0.04	8.34E-01	9.51E-01	AKAP6	A kinase (PRKA) anchor protein 6	chr14q13.1	205359_at	NM_004274
4.71	4.74	0.03	8.34E-01	9.51E-01	---	---	---	242675_x_at	---
2.40	2.43	0.03	8.34E-01	9.51E-01	---	---	---	1556593_s_at	---
2.65	2.68	0.03	8.34E-01	9.51E-01	FLJ40243	hypothetical protein FLJ40243	chr5p13.1	240412_s_at	NM_173489
2.24	2.26	0.02	8.34E-01	9.51E-01	---	---	---	241085_at	---
5.90	5.94	0.04	8.35E-01	9.51E-01	PSEN2	presenilin 2 (Alzheimer disease 4)	chr1q31-q42	204262_s_at	NM_000447 /// NM_012486
2.37	2.40	0.03	8.35E-01	9.51E-01	---	---	---	239370_at	---
1.93	1.95	0.02	8.35E-01	9.51E-01	---	---	---	1562820_at	---
6.81	6.85	0.04	8.35E-01	9.51E-01	SH2B1	SH2B adaptor protein 1	chr16p11.2	209322_s_at	NM_015503
2.92	2.96	0.03	8.35E-01	9.52E-01	H2AFX	H2A histone family, member X	chr11q23.2-q23.3	212524_x_at	NM_002105
4.05	4.08	0.02	8.35E-01	9.52E-01	SFTPC	surfactant protein C	chr8p21	214387_x_at	NM_003018
2.38	2.41	0.03	8.35E-01	9.52E-01	---	---	---	231477_at	---
2.49	2.51	0.03	8.35E-01	9.52E-01	TRIM48	tripartite motif-containing 48	chr11q11	220534_at	NM_024114
1.83	1.86	0.02	8.35E-01	9.52E-01	---	---	---	233822_x_at	---
2.55	2.59	0.04	8.35E-01	9.52E-01	---	---	---	1565927_s_at	---
2.07	2.10	0.03	8.35E-01	9.52E-01	---	---	---	1570574_at	---
2.39	2.41	0.03	8.35E-01	9.52E-01	LOC285389	hypothetical protein LOC285389	chr3q29	1557004_at	---
3.71	3.77	0.06	8.35E-01	9.52E-01	---	---	---	213637_at	---
2.16	2.20	0.03	8.35E-01	9.52E-01	---	---	---	241168_at	---

2.31	2.34	0.03	8.35E-01	9.52E-01	---	---	---	1570635_at	---
3.64	3.68	0.04	8.35E-01	9.52E-01	SPRN	shadow of prion protein homolog (zebrafish)	chr10q26.3	238331_at	NM_001012508
4.30	4.35	0.05	8.35E-01	9.52E-01	---	---	---	1557315_a_at	---
2.51	2.55	0.04	8.35E-01	9.52E-01	KATNAL2	katanin p60 subunit A-like 2	chr18q21.1	1554234_at	NM_031303
2.07	2.10	0.03	8.35E-01	9.52E-01	ZNF90	zinc finger protein 90	chr19p13.1-p12	1562133_x_at	XM_001714809 /// XM_001718859 /// XM_001719752
5.28	5.31	0.04	8.35E-01	9.52E-01	C14orf133	chromosome 14 open reading frame 133	chr14q24.3-q31	233140_s_at	NM_022067
2.73	2.77	0.03	8.35E-01	9.52E-01	NT5C1B	5'-nucleotidase, cytosolic IB	chr2p24.2	243100_at	NM_001002006 /// NM_033253
2.42	2.45	0.03	8.35E-01	9.52E-01	---	---	---	224104_at	---
5.23	5.32	0.09	8.36E-01	9.52E-01	KIF3C	kinesin family member 3C	chr2p23	203390_s_at	NM_002254
8.03	8.12	0.10	8.36E-01	9.52E-01	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial	chr1q41	217900_at	NM_018060
4.20	4.25	0.05	8.36E-01	9.52E-01	LOC100129837	similar to ZNF124 protein	chr19p13.2	236485_at	XM_001718527 /// XM_001719630
2.27	2.30	0.03	8.36E-01	9.52E-01	FLJ30594	hypothetical locus FLJ30594	chr2p25.2	1553796_at	XR_041760 /// XR_041761 /// XR_041762
2.25	2.28	0.02	8.36E-01	9.52E-01	TET2	tet oncogene family member 2	chr4q24	235461_at	NM_001127208 /// NM_017628
5.86	5.96	0.10	8.36E-01	9.52E-01	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	chr5q11.2	212648_at	NM_019030
3.28	3.34	0.06	8.36E-01	9.52E-01	---	---	---	241775_at	---
7.40	7.45	0.05	8.36E-01	9.52E-01	RAB4B	RAB4B, member RAS oncogene family	chr19q13.2	233385_x_at	NM_016154
2.57	2.61	0.04	8.36E-01	9.52E-01	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	chr2q36.3	1552507_at	NM_080671
12.45	12.49	0.04	8.36E-01	9.52E-01	STAR	steroidogenic acute regulatory protein	chr8p11.2	204548_at	NM_000349 /// NM_001007243
3.06	3.10	0.04	8.36E-01	9.52E-01	---	---	---	240648_at	---
2.85	2.88	0.04	8.36E-01	9.52E-01	ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	chr19p13.3-p13.2	232133_at	NM_030957
2.03	2.06	0.03	8.36E-01	9.52E-01	---	---	---	1570046_at	---
2.07	2.10	0.03	8.36E-01	9.52E-01	---	---	---	239558_at	---
1.99	2.01	0.03	8.36E-01	9.52E-01	---	---	---	243232_at	---
2.01	2.03	0.03	8.36E-01	9.52E-01	---	---	---	244230_at	---
2.06	2.09	0.03	8.36E-01	9.52E-01	SAGE1	sarcoma antigen 1	chrXq26	220793_at	NM_018666
2.02	2.04	0.03	8.36E-01	9.52E-01	VIP	vasoactive intestinal peptide	chr6q25	206577_at	NM_003381 /// NM_194435
2.05	2.07	0.02	8.36E-01	9.52E-01	---	---	---	215448_at	---
2.30	2.33	0.02	8.36E-01	9.52E-01	CEP152	centrosomal protein 152kDa	chr15q21.1	215170_s_at	NM_014985
5.40	5.46	0.06	8.36E-01	9.52E-01	ANKDD1A	ankyrin repeat and death domain containing 1A	chr15q22.31	229497_at	NM_182703
5.09	5.14	0.05	8.37E-01	9.52E-01	NOC4L	nucleolar complex associated 4 homolog (S. cerevisiae)	chr12q24.33	218860_at	NM_024078
2.88	2.92	0.04	8.36E-01	9.52E-01	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	chr9q33.3	204199_at	NM_014636
2.28	2.32	0.04	8.37E-01	9.52E-01	LOC100129268	hypothetical protein LOC100129268	chr1q22	244489_at	XM_001723819 /// XM_001724965 /// XM_001724971
2.12	2.15	0.03	8.36E-01	9.52E-01	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	chr12q13	202454_s_at	NM_001005915 /// NM_001982
3.06	3.09	0.03	8.36E-01	9.52E-01	NCAM1	neural cell adhesion molecule 1	chr11q23.1	214952_at	NM_000615 /// NM_001076682 /// NM_181351
2.62	2.65	0.03	8.37E-01	9.52E-01	---	---	---	236878_at	---
2.60	2.63	0.03	8.37E-01	9.52E-01	FAM181B	family with sequence similarity 181, member B	chr11q14.1	231128_at	NM_175885
2.34	2.36	0.02	8.37E-01	9.52E-01	FAM9C	family with sequence similarity 9, member C	chrXp22.2	244644_at	NM_174901
2.17	2.19	0.02	8.37E-01	9.52E-01	KATNAL2	katanin p60 subunit A-like 2	chr18q21.1	233649_at	NM_031303
6.63	6.68	0.05	8.37E-01	9.52E-01	XPO7	exportin 7	chr8p21	212166_at	NM_001100161 /// NM_001100162 /// NM_015024
1.90	1.93	0.02	8.37E-01	9.52E-01	---	---	---	241547_at	---
2.86	2.91	0.05	8.37E-01	9.52E-01	---	---	---	1558714_at	---
5.69	5.74	0.05	8.37E-01	9.52E-01	ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	chr16q22.1	229336_at	NM_006927
4.28	4.33	0.05	8.37E-01	9.52E-01	DLL3	Delta-like 3 (Drosophila)	chr19q13	230568_x_at	NM_016941 /// NM_203486
7.96	8.00	0.04	8.37E-01	9.52E-01	MSN	moesin	chrXq11.2-q12	200600_at	NM_002444

3.72	3.76	0.04	8.37E-01	9.52E-01	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	chr4p16.3	213533_at	NM_001040101 /// NM_014392
2.38	2.41	0.03	8.37E-01	9.52E-01	---	---	---	233552_at	---
4.18	4.21	0.03	8.37E-01	9.52E-01	CNTROB	centrobin, centrosomal BRCA2 interacting protein	chr17p13.1	234688_x_at	NM_001037144 /// NM_053051
2.18	2.21	0.03	8.37E-01	9.52E-01	C6orf182	Chromosome 6 open reading frame 182	chr6q21	1560418_at	NM_001083535 /// NM_173830
2.43	2.46	0.02	8.37E-01	9.52E-01	---	---	---	1556402_at	---
2.00	2.03	0.03	8.37E-01	9.52E-01	---	---	---	1560025_at	---
1.89	1.91	0.02	8.37E-01	9.52E-01	---	---	---	233772_at	---
5.08	5.21	0.13	8.38E-01	9.52E-01	---	---	---	234074_at	---
5.98	6.08	0.11	8.37E-01	9.52E-01	CPM	carboxypeptidase M	chr12q14.3	206100_at	NM_001005502 /// NM_001874 /// NM_198320
8.35	8.40	0.05	8.38E-01	9.52E-01	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	chr16q22.1	224616_at	NM_006141
2.59	2.63	0.04	8.37E-01	9.52E-01	ADAMTSL4	ADAMTS-like 4	chr1q21.2	226071_at	NM_019032 /// NM_025008
1.90	1.93	0.03	8.37E-01	9.52E-01	---	---	---	1560998_x_at	---
5.04	5.17	0.13	8.38E-01	9.52E-01	RBMS3	RNA binding motif, single stranded interacting protein	chr3p24-p23	243041_s_at	NM_001003792 /// NM_001003793 /// NM_014483
5.20	5.27	0.07	8.38E-01	9.52E-01	EFNA4	ephrin-A4	chr1q21-q22	205107_s_at	NM_005227 /// NM_182689 /// NM_182690
6.30	6.36	0.06	8.38E-01	9.52E-01	TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	chr2q24.1-q24.2	225308_s_at	NM_033394
7.87	7.93	0.06	8.38E-01	9.52E-01	FLNA	filamin A, alpha (actin binding protein 280)	chrXq28	213746_s_at	NM_001110556 /// NM_001456
2.62	2.65	0.04	8.38E-01	9.52E-01	LOC339685	hypothetical protein LOC339685	chr22q13.31	1562264_at	---
3.88	3.91	0.03	8.38E-01	9.52E-01	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	chrXp22.32 and Yp11.3	211287_x_at	NM_006140 /// NM_172245 /// NM_172246 /// NM_172247 /// NM_172249
2.16	2.19	0.03	8.38E-01	9.52E-01	---	---	---	237212_at	---
1.93	1.96	0.03	8.38E-01	9.52E-01	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	chr7q31	209631_s_at	NM_005302
3.09	3.12	0.03	8.38E-01	9.52E-01	SLC25A41	solute carrier family 25, member 41	chr19p13.3	1555509_a_at	NM_173637
3.11	3.14	0.03	8.38E-01	9.52E-01	TMEM132E	transmembrane protein 132E	chr17q12	243708_at	NM_207313
3.84	3.89	0.05	8.38E-01	9.52E-01	KRTAP3-1 /// LOC100132802	keratin associated protein 3-1 /// hypothetical protein LOC100132802	chr17q12-q21	233537_at	NM_031958 /// XM_001722593
2.49	2.52	0.03	8.38E-01	9.52E-01	ZNF780B	zinc finger protein 780B	chr19q13.2	243294_at	NM_001005851
2.05	2.07	0.02	8.38E-01	9.52E-01	ZNF7	Zinc finger protein 7	chr8q24	234920_at	NM_003416
5.92	5.96	0.04	8.38E-01	9.52E-01	NTAN1	N-terminal asparagine amidase	chr16p13.11	213061_s_at	NM_173474
6.69	6.76	0.07	8.38E-01	9.52E-01	C1orf93	chromosome 1 open reading frame 93	chr1p36.32	231835_at	NM_152371
1.86	1.88	0.02	8.38E-01	9.52E-01	---	---	---	1558372_at	---
2.05	2.08	0.03	8.38E-01	9.52E-01	---	---	---	232963_at	---
1.83	1.85	0.02	8.38E-01	9.53E-01	PRIM2	primase, DNA, polypeptide 2 (58kDa)	chr6p12-p11.1	1554884_at	NM_000947
2.12	2.14	0.03	8.38E-01	9.53E-01	ZCCHC11	zinc finger, CCHC domain containing 11	chr1p32.3	217594_at	NM_001009881 /// NM_001009882 /// NM_015269
4.81	4.93	0.12	8.39E-01	9.53E-01	---	---	---	236236_at	---
2.56	2.62	0.06	8.39E-01	9.53E-01	FAM71B	family with sequence similarity 71, member B	chr5q33.3	1555585_a_at	NM_130899
11.28	11.33	0.06	8.38E-01	9.53E-01	IFITM3	interferon induced transmembrane protein 3 (1-8U)	chr11p15.5	212203_x_at	NM_021034
2.41	2.46	0.05	8.38E-01	9.53E-01	C6orf118	chromosome 6 open reading frame 118	chr6q27	230993_s_at	NM_144980
4.31	4.35	0.04	8.39E-01	9.53E-01	---	---	---	243203_at	---
1.98	2.01	0.03	8.39E-01	9.53E-01	---	---	---	236947_at	---
2.22	2.25	0.03	8.39E-01	9.53E-01	---	---	---	1556743_at	---
2.50	2.53	0.03	8.39E-01	9.53E-01	---	---	---	244618_at	---
2.31	2.34	0.03	8.39E-01	9.53E-01	---	---	---	240759_at	---
2.27	2.30	0.02	8.39E-01	9.53E-01	MIPOL1	mirror-image polydactyly 1	chr14q13.3-q21.1	1552573_s_at	NM_138731
7.52	7.55	0.04	8.39E-01	9.53E-01	KCTD10	potassium channel tetramerisation domain containing 10	chr12q24.11	226518_at	NM_031954

2.26	2.28	0.03	8.39E-01	9.53E-01	PMS2L4	postmeiotic segregation increased 2-like 4 pseudogene	chr7q11-q22	215192_at	NR_022007 /// XM_001714693 /// XM_001715426 /// XM_001715595 /// XM_001715786																					
2.29	2.33	0.05	8.39E-01	9.53E-01	WIF1	WNT inhibitory factor 1	chr12q14.3	204712_at	NM_007191																					
1.92	1.95	0.03	8.39E-01	9.53E-01	---	---	---	243273_at	---																					
5.78	5.81	0.04	8.39E-01	9.53E-01	DAPK3	death-associated protein kinase 3	chr19p13.3	203891_s_at	NM_001348																					
7.37	7.46	0.09	8.39E-01	9.53E-01	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF3 /// NBPF8 /// NBPF9 /// XXyac-YX155B6.1	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// CLIP-190-like	chr1p36.12 /// chr1p36.13 /// chr1q12-q21.2 /// chr1q21.1 /// chr1q21.2	230712_at	NM_001037675 /// NM_001039703 /// NM_001101663 /// NM_001102663 /// NM_015383 /// NM_017940 /// NM_032264 /// NM_173638 /// NM_183372 /// XM_001717398 /// XM_001717802 /// XM_001721345 /// XM_001721349 /// XM_001722184 /// XM_001723523 /// XM_001726946																					
5.87	5.94	0.07	8.39E-01	9.53E-01	STYXL1	serine/threonine/tyrosine interacting-like 1	chr7q11.23	233982_x_at	NM_016086																					
2.75	2.80	0.05	8.39E-01	9.53E-01	---	---	---	241289_at	---																					
9.41	9.46	0.05	8.39E-01	9.53E-01	MATR3	matrin 3	chr5q31.2	214363_s_at	NM_018834 /// NM_199189																					
3.82	3.86	0.04	8.39E-01	9.53E-01	ZNF644	Zinc finger protein 644	chr1p22.2	229684_s_at	NM_016620 /// NM_032186 /// NM_201269																					
8.70	8.75	0.04	8.39E-01	9.53E-01	TGOLN2	trans-golgi network protein 2	chr2p11.2	212043_at	NM_006464																					
5.30	5.34	0.04	8.39E-01	9.53E-01	KIFC1	kinesin family member C1	chr6p21.3	209680_s_at	NM_002263																					
3.05	3.09	0.04	8.39E-01	9.53E-01	CCNB2	cyclin B2	chr15q22.2	202705_at	NM_004701																					
2.43	2.47	0.04	8.39E-01	9.53E-01	HCG4P6	HLA complex group 4 pseudogene 6	chr6p21.3	215973_at	NR_001317																					
5.47	5.50	0.03	8.39E-01	9.53E-01	UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	chr11q13	219827_at	NM_003356 /// NM_022803																					
2.28	2.30	0.02	8.39E-01	9.53E-01	MGC15634	hypothetical protein MGC15634	chr1q42.13	230534_at	XM_927837 /// XM_938541																					
3.07	3.11	0.04	8.39E-01	9.53E-01	---	---	---	215515_at	---																					
2.10	2.14	0.04	8.39E-01	9.53E-01	PATE	expressed in prostate and testis	chr11q24.2	231279_at	NM_138294																					
2.05	2.08	0.03	8.39E-01	9.53E-01	DDX53	DEAD (Asp-Glu-Ala-Asp) box polypeptide 53	chrXp22.11	1555357_at	NM_182699																					
5.59	5.64	0.04	8.39E-01	9.53E-01	RBBP4	Retinoblastoma binding protein 4	chr1p35.1	239071_at	NM_005610																					
2.41	2.44	0.03	8.40E-01	9.53E-01	---	---	---	241315_at	---																					
2.07	2.10	0.03	8.40E-01	9.53E-01	LOC150568	hypothetical LOC150568	chr2q12.1	230495_at	---																					
4.78	4.82	0.05	8.40E-01	9.53E-01	MARK2	MAP/microtubule affinity-regulating kinase 2	chr11q12-q13	203942_s_at	NM_001039468 /// NM_001039469 /// NM_004954 /// NM_017490																					
2.66	2.68	0.02	8.40E-01	9.53E-01	CYLD	cylindromatosis (turban tumor syndrome)	chr16q12.1	60084_at	NM_001042355 /// NM_001042412 /// NM_015247																					
4.35	4.40	0.04	8.40E-01	9.53E-01	---	---	---	239555_at	---																					
2.29	2.33	0.04	8.40E-01	9.53E-01	---	---	---	215211_at	---																					

2.34	2.37	0.03	8.40E-01	9.53E-01	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	chr14q24-q31 /// chr19q13.2-q13.3 /// chr2p21	241619_at	NM_001743 /// NM_005184 /// NM_006888
2.74	2.76	0.03	8.40E-01	9.53E-01	---	---	---	1561045_a_at	---
1.96	1.98	0.02	8.40E-01	9.53E-01	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	chr8p21-p11.2	207987_s_at	NM_000825 /// NM_001083111
2.80	2.83	0.04	8.40E-01	9.53E-01	TLR4	toll-like receptor 4	chr9q32-q33	232068_s_at	NM_138554
6.64	6.72	0.08	8.40E-01	9.53E-01	---	---	---	235072_s_at	---
3.56	3.60	0.04	8.40E-01	9.53E-01	C14orf102	chromosome 14 open reading frame 102	chr14q32.11	235212_at	NM_017970 /// NM_199043
8.36	8.40	0.04	8.40E-01	9.53E-01	MRPL54	mitochondrial ribosomal protein L54	chr19p13.3	225797_at	NM_172251
1.96	2.00	0.03	8.41E-01	9.53E-01	HERC4	hect domain and RLD 4	chr10q21.3	208054_at	NM_015601 /// NM_022079
2.90	2.93	0.03	8.41E-01	9.53E-01	CARD10	Caspase recruitment domain family, member 10	chr22q13.1	214207_s_at	NM_014550
4.44	4.47	0.03	8.41E-01	9.53E-01	---	---	---	237764_at	---
2.85	2.88	0.03	8.41E-01	9.53E-01	UMOD	uromodulin	chr16p12.3	206716_at	NM_001008389 /// NM_003361
2.38	2.41	0.03	8.41E-01	9.53E-01	C9orf29	chromosome 9 open reading frame 29	chr9q31.3	1569839_s_at	XR_042069 /// XR_042070 /// XR_042071
3.52	3.57	0.04	8.41E-01	9.53E-01	MPPE1	Metallophosphoesterase 1	chr18p11.21	213924_at	NM_023075
2.87	2.89	0.02	8.41E-01	9.53E-01	CNTNAP5	contactin associated protein-like 5	chr2q14.3	1553013_at	NM_130773
2.12	2.15	0.03	8.41E-01	9.54E-01	TMEM171	transmembrane protein 171	chr5q13.2	240770_at	NM_173490
6.19	6.28	0.09	8.42E-01	9.54E-01	EHD4	EH-domain containing 4	chr15q11.1	209536_s_at	NM_139265
8.55	8.63	0.09	8.42E-01	9.54E-01	MOBKL3	MOB1, Mps One Binder kinase activator-like 3 (yeast)	chr2q33.1	202919_at	NM_001100819 /// NM_015387 /// NM_199482
5.85	5.94	0.08	8.42E-01	9.54E-01	TOR1AIP1	torsin A interacting protein 1	chr1q24.2	212409_s_at	NM_015602
4.74	4.81	0.07	8.42E-01	9.54E-01	XAF1	XIAP associated factor 1	chr17p13.2	228617_at	NM_017523 /// NM_199139
5.76	5.83	0.07	8.41E-01	9.54E-01	C12orf5	chromosome 12 open reading frame 5	chr12p13.3	219099_at	NM_020375
2.96	3.03	0.07	8.41E-01	9.54E-01	---	---	---	1563259_at	---
7.28	7.33	0.05	8.42E-01	9.54E-01	PDDC1	Parkinson disease 7 domain containing 1	chr11p15.5	227968_at	NM_182612
7.10	7.15	0.05	8.41E-01	9.54E-01	PAK4	p21 protein (Cdc42/Rac)-activated kinase 4	chr19q13.2	203154_s_at	NM_001014831 /// NM_001014832 /// NM_001014834 /// NM_001014835 /// NM_005884
7.01	7.05	0.04	8.42E-01	9.54E-01	BAT2	HLA-B associated transcript 2	chr6p21.3	208132_x_at	NM_080686
2.44	2.48	0.04	8.41E-01	9.54E-01	ACVR2B	activin A receptor, type IIB	chr3p22	1559548_at	NM_001106
2.99	3.03	0.04	8.41E-01	9.54E-01	C8B	complement component 8, beta polypeptide	chr1p32	206979_at	NM_000066
3.35	3.39	0.03	8.41E-01	9.54E-01	---	---	---	230671_at	---
2.33	2.36	0.03	8.42E-01	9.54E-01	ZNF92	zinc finger protein 92	chr7q11.21	1564963_x_at	NM_007139 /// NM_152626
7.05	7.09	0.03	8.41E-01	9.54E-01	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	chr19q13.2	203655_at	NM_006297
5.28	5.32	0.03	8.41E-01	9.54E-01	C14orf159	chromosome 14 open reading frame 159	chr14q32.12	1554039_at	NM_001102366 /// NM_001102367 /// NM_001102368 /// NM_001102369 /// NM_024952
3.11	3.15	0.03	8.42E-01	9.54E-01	---	---	---	1566841_at	---
3.42	3.45	0.03	8.42E-01	9.54E-01	FLJ42627	hypothetical LOC645644	chr16p13.3	232050_at	NM_001039907
2.48	2.51	0.03	8.41E-01	9.54E-01	OR2B6	olfactory receptor, family 2, subfamily B, member 6	chr6p21.3	216522_at	NM_012367
2.02	2.05	0.03	8.42E-01	9.54E-01	---	---	---	233062_at	---
2.85	2.88	0.03	8.42E-01	9.54E-01	STK38	Serine/threonine kinase 38	chr6p21	216451_at	NM_007271
2.21	2.24	0.03	8.41E-01	9.54E-01	TTL	tubulin tyrosine ligase	chr2q13	1559680_at	NM_153712
2.14	2.16	0.03	8.42E-01	9.54E-01	BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	chr11p14.2	205363_at	NM_003986
2.16	2.18	0.03	8.41E-01	9.54E-01	ATP11B	ATPase, class VI, type 11B	chr3q27	1554557_at	NM_014616
2.05	2.08	0.02	8.42E-01	9.54E-01	C17orf73	chromosome 17 open reading frame 73	chr17q21.33	207259_at	XR_017882 /// XR_041415 /// XR_041416
2.36	2.39	0.02	8.41E-01	9.54E-01	---	---	---	240131_at	---
2.37	2.39	0.02	8.41E-01	9.54E-01	---	---	---	1563188_at	---

3.15	3.19	0.03	8.42E-01	9.54E-01	RBPJ	recombination signal binding protein for immunoglobulin kappa J region	chr4p15.2	229540_at	NM_005349 /// NM_015874 /// NM_203283 /// NM_203284																					
5.28	5.36	0.08	8.42E-01	9.54E-01	NCF4	neutrophil cytosolic factor 4, 40kDa	chr22q13.1	205147_x_at	NM_000631 /// NM_013416																					
3.18	3.22	0.04	8.42E-01	9.54E-01	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D	chr7q22.1	233539_at	NM_001122838 /// NM_198990																					
2.95	2.98	0.03	8.42E-01	9.54E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	242079_at	NM_002926 /// NM_198227 /// NM_198229																					
2.56	2.59	0.03	8.42E-01	9.54E-01	---	---	---	238717_at	---																					
2.30	2.33	0.03	8.42E-01	9.54E-01	ANKRD18A	ankyrin repeat domain 18A	chr9p13.1	244297_at	XM_001713970 /// XM_001717620 /// XM_001726105																					
4.86	4.89	0.03	8.42E-01	9.54E-01	CHRNA2	cholinergic receptor, nicotinic, alpha 2 (neuronal)	chr8p21	207868_at	NM_000742																					
3.14	3.17	0.03	8.42E-01	9.54E-01	LOC388494	hypothetical gene supported by AL365406; BC034005	chr19p13.3	233064_at	XM_373788 /// XM_944421																					
2.28	2.31	0.03	8.42E-01	9.54E-01	IREB2	iron-responsive element binding protein 2	chr15q25.1	1555476_at	NM_004136																					
2.13	2.15	0.02	8.42E-01	9.54E-01	HMGA2	high mobility group AT-hook 2	chr12q15	1567224_at	NM_003483 /// NM_003484																					
7.82	7.89	0.07	8.42E-01	9.54E-01	RBM47	RNA binding motif protein 47	chr4p13-p12	222496_s_at	NM_001098634 /// NM_019027																					
3.64	3.68	0.04	8.42E-01	9.54E-01	TSSK6	testis-specific serine kinase 6	chr19p13.11	239524_at	NM_032037																					
2.57	2.61	0.04	8.42E-01	9.54E-01	HTR3C	5-hydroxytryptamine (serotonin) receptor 3, family member C	chr3q27.1	1553041_at	NM_130770																					
3.01	3.04	0.03	8.42E-01	9.54E-01	---	---	---	1567140_at	---																					
5.98	6.06	0.08	8.43E-01	9.54E-01	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	chr9p12	218393_s_at	NM_018225																					
4.46	4.49	0.03	8.43E-01	9.54E-01	SNORD116@	small nucleolar RNA, C/D box 116 cluster	chr15q11.2	232976_at	NR_003106																					
2.81	2.84	0.03	8.43E-01	9.54E-01	SIAE	sialic acid acetylesterase	chr11q24	223744_s_at	NM_170601																					
3.82	3.85	0.03	8.43E-01	9.54E-01	C8orf74	chromosome 8 open reading frame 74	chr8p23.1	1569246_a_at	NM_001040032																					
5.51	5.53	0.03	8.43E-01	9.54E-01	TAOK3	TAO kinase 3	chr12q	221508_at	NM_016281																					
2.41	2.43	0.03	8.43E-01	9.54E-01	---	---	---	242380_at	---																					
5.24	5.29	0.05	8.43E-01	9.54E-01	LRRC37A2	Leucine rich repeat containing 37, member A2	chr17q21.32	221740_x_at	NM_001006607																					
7.71	7.77	0.05	8.43E-01	9.54E-01	CNIH	cornichon homolog (Drosophila)	chr14q22.2	201653_at	NM_005776																					
7.47	7.52	0.05	8.43E-01	9.54E-01	NDFIP1	Nedd4 family interacting protein 1	chr5q31.3	222423_at	NM_030571																					
2.09	2.14	0.05	8.43E-01	9.54E-01	LOC100130829 /// ZFY	hypothetical protein LOC100130829 /// zinc finger protein, Y-linked	chrYp11.3	230760_at	NM_003411 /// XM_001713692																					
2.92	2.95	0.03	8.43E-01	9.54E-01	---	---	---	1560982_at	---																					
2.12	2.14	0.03	8.43E-01	9.54E-01	---	---	---	236577_at	---																					
1.89	1.92	0.03	8.43E-01	9.54E-01	---	---	---	1562686_at	---																					
3.47	3.51	0.04	8.43E-01	9.54E-01	---	---	---	239281_at	---																					
2.78	2.81	0.03	8.43E-01	9.54E-01	LOC286071	hypothetical protein LOC286071	chr8q11.22	231032_at	---																					
3.39	3.42	0.03	8.43E-01	9.54E-01	TOPORS	topoisomerase I binding, arginine/serine-rich	chr9p21	1564403_at	NM_005802																					
4.03	4.08	0.05	8.43E-01	9.54E-01	MBD5	methyl-CpG binding domain protein 5	chr2q23.1	227839_at	NM_018328																					
2.61	2.64	0.03	8.43E-01	9.54E-01	CCL1	chemokine (C-C motif) ligand 1	chr17q12	207533_at	NM_002981																					
2.53	2.56	0.03	8.43E-01	9.54E-01	---	---	---	1560615_a_at	---																					
2.54	2.57	0.03	8.43E-01	9.54E-01	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	chr4q21	210739_x_at	NM_001098484 /// NM_001134742 /// NM_003759																					
3.59	3.64	0.05	8.43E-01	9.54E-01	---	---	---	236321_at	---																					
3.78	3.81	0.03	8.44E-01	9.54E-01	ZER1	zer-1 homolog (C. elegans)	chr9q34.11	202448_s_at	NM_006336																					
2.87	2.90	0.03	8.44E-01	9.54E-01	TBK1	TANK-binding kinase 1	chr12q14.1	1554391_at	NM_013254																					
1.97	1.99	0.02	8.44E-01	9.54E-01	---	---	---	1560861_at	---																					
4.19	4.25	0.06	8.44E-01	9.54E-01	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	chr1p36.12	228302_x_at	NM_018584																					
5.75	5.81	0.05	8.44E-01	9.54E-01	NDRG3	NDRG family member 3	chr20q11.21-q11.23	224368_s_at	NM_022477 /// NM_032013																					
5.36	5.41	0.04	8.44E-01	9.54E-01	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	chrXq13.1	227205_at	NM_004606 /// NM_138923																					
4.23	4.27	0.04	8.44E-01	9.54E-01	MRPL30	mitochondrial ribosomal protein L30	chr2q11.2	224173_s_at	NM_145212 /// NM_145213																					
2.31	2.35	0.04	8.44E-01	9.54E-01	---	---	---	236606_at	---																					
3.33	3.36	0.04	8.44E-01	9.54E-01	---	---	---	243987_at	---																					

4.52	4.55	0.03	8.44E-01	9.54E-01	NCDN	neurochondrin	chr1p34.3	209557_s_at	NM_001014839 /// NM_001014841 /// NM_014284																				
4.76	4.79	0.03	8.44E-01	9.54E-01	---	---	---	240584_at	---																				
2.15	2.18	0.03	8.44E-01	9.54E-01	C9orf41	chromosome 9 open reading frame 41	chr9q21.13	241781_at	NM_152420																				
2.27	2.30	0.03	8.44E-01	9.54E-01	KIDINS220	Kinase D-interacting substrate of 220 kDa	chr2p24	242032_at	NM_020738																				
3.28	3.31	0.02	8.44E-01	9.54E-01	CWF19L1	CWF19-like 1, cell cycle control (S. pombe)	chr10q24.2-q24.31	229038_at	NM_018294																				
2.24	2.26	0.02	8.44E-01	9.54E-01	LOC729766	hypothetical LOC729766	chr1p31.1	241290_at	XM_001131228 /// XM_001133311 /// XM_001718390																				
3.22	3.25	0.03	8.44E-01	9.54E-01	NR6A1	nuclear receptor subfamily 6, group A, member 1	chr9q33-q34.1	210391_at	NM_001489 /// NM_033334																				
1.99	2.01	0.03	8.44E-01	9.54E-01	DLGAP2	discs, large (Drosophila) homolog-associated protein 2	chr8p23	210227_at	NM_004745																				
4.54	4.70	0.15	8.44E-01	9.54E-01	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	chr9q33.2	224940_s_at	NM_002581																				
3.25	3.28	0.03	8.44E-01	9.54E-01	DKFZp434H1419	hypothetical protein DKFZp434H1419	chr2q35	214717_at	---																				
6.00	6.09	0.09	8.45E-01	9.54E-01	NUCB2	nucleobindin 2	chr11p15.1-p14	203675_at	NM_005013																				
9.41	9.49	0.08	8.45E-01	9.54E-01	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	chr16p12-p11.2	211935_at	NM_015161																				
3.59	3.64	0.05	8.44E-01	9.54E-01	DKFZp434K191 /// DKFZP434P211 /// LOC100134009	hypothetical locus DKFZp434K191 /// POM121-like protein /// hypothetical protein LOC100134009	chr22q11.2 /// chr22q11.22	1553900_s_at	NR_003714 /// XM_001721522 /// XR_040035																				
2.07	2.10	0.03	8.44E-01	9.54E-01	GPNMB	glycoprotein (transmembrane) nmb	chr7p15	1554018_at	NM_001005340 /// NM_002510																				
2.72	2.75	0.03	8.44E-01	9.54E-01	hCG_1776047	hCG1776047	chr18q21.2	241064_at	XM_001127598 /// XM_001131423 /// XM_001719393																				
2.32	2.35	0.03	8.44E-01	9.54E-01	---	---	---	240578_at	---																				
2.17	2.19	0.03	8.44E-01	9.54E-01	RCHY1	ring finger and CHY zinc finger domain containing 1	chr4q21.1	235300_x_at	NM_001008925 /// NM_001009922 /// NM_015436																				
2.41	2.44	0.03	8.44E-01	9.54E-01	---	---	---	240173_at	---																				
1.92	1.94	0.02	8.45E-01	9.54E-01	---	---	---	217085_at	---																				
1.86	1.88	0.02	8.45E-01	9.54E-01	S100B	S100 calcium binding protein B	chr21q22.3	1561521_at	NM_006272																				
1.94	1.96	0.02	8.45E-01	9.54E-01	---	---	---	1556834_at	---																				
2.17	2.19	0.02	8.45E-01	9.54E-01	---	---	---	238705_at	---																				
5.96	6.03	0.07	8.45E-01	9.54E-01	TPRKB	TP53RK binding protein	chr2p24.3-p24.1	219030_at	NM_016058																				
3.15	3.19	0.04	8.45E-01	9.54E-01	---	---	---	238276_at	---																				
3.07	3.10	0.03	8.45E-01	9.54E-01	SLC39A9	Solute carrier family 39 (zinc transporter), member 9	chr14q24.1	216009_at	NM_018375																				
1.96	1.99	0.02	8.45E-01	9.54E-01	---	---	---	242117_at	---																				
2.39	2.42	0.03	8.45E-01	9.54E-01	---	---	---	237201_at	---																				
6.04	6.12	0.08	8.45E-01	9.55E-01	RFTN1	raftlin, lipid raft linker 1	chr3p24.3	212646_at	NM_015150																				
3.05	3.08	0.03	8.45E-01	9.55E-01	---	---	---	239124_at	---																				
3.40	3.43	0.03	8.45E-01	9.55E-01	PRM1	protamine 1	chr16p13.2	206358_at	NM_002761																				
2.80	2.84	0.04	8.45E-01	9.55E-01	---	---	---	236032_at	---																				
2.77	2.81	0.04	8.45E-01	9.55E-01	---	---	---	244490_at	---																				
3.92	3.96	0.04	8.45E-01	9.55E-01	LOC100133215	Hypothetical protein LOC100133215	chr9q22.32	1562733_at	XM_001715914 /// XM_001716485 /// XM_001717885																				
4.74	4.79	0.05	8.45E-01	9.55E-01	---	---	---	235399_at	---																				
2.17	2.20	0.03	8.45E-01	9.55E-01	SSTR1	somatostatin receptor 1	chr14q13	235591_at	NM_001049																				
5.76	5.84	0.08	8.46E-01	9.55E-01	TMEM173	transmembrane protein 173	chr5q31.2	224929_at	NM_198282																				
4.17	4.24	0.07	8.46E-01	9.55E-01	---	---	---	236889_at	---																				
3.64	3.70	0.06	8.46E-01	9.55E-01	CDADC1	cytidine and dCMP deaminase domain containing 1	chr13q14.2	233564_s_at	NM_030911																				
5.31	5.36	0.06	8.46E-01	9.55E-01	GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	chr9q34.13-q34.3	231780_at	NM_021996																				
5.28	5.32	0.04	8.46E-01	9.55E-01	HYLS1	hydrolethalus syndrome 1	chr11q24.2	227687_at	NM_145014																				
4.50	4.53	0.04	8.46E-01	9.55E-01	FOXO6	forkhead box protein O6	chr1p34.1	239657_x_at	---																				
2.75	2.78	0.03	8.46E-01	9.55E-01	PLUNC	palate, lung and nasal epithelium associated	chr20q11.2	220542_s_at	NM_016583 /// NM_130852																				
2.46	2.49	0.03	8.46E-01	9.55E-01	---	---	---	238724_at	---																				

5.83	5.86	0.03	8.46E-01	9.55E-01	LOC100128510	hypothetical protein LOC100128510	chr16p13.3	242633_x_at	XM_001715495 /// XM_001715759 /// XM_001717675																				
2.18	2.20	0.03	8.46E-01	9.55E-01	TTTY2	testis-specific transcript, Y-linked 2	chrYp11.2	216665_s_at	NR_001536																				
2.38	2.41	0.02	8.46E-01	9.55E-01	---	---	---	1566086_at	---																				
3.41	3.45	0.04	8.46E-01	9.55E-01	---	---	---	236402_at	---																				
2.39	2.41	0.02	8.46E-01	9.55E-01	LOC100129427	hypothetical protein LOC100129427	chr7p12.2	1564459_at	XM_001714883 /// XM_001715918 /// XM_001719355																				
5.31	5.39	0.07	8.46E-01	9.55E-01	JMJD1C	jumonji domain containing 1C	chr10q21.2-q21.3	221763_at	NM_004241 /// NM_032776																				
2.26	2.29	0.03	8.46E-01	9.55E-01	LOC100129064 /// LOC100131868 /// LOC100132773 /// PPP4R2	hypothetical LOC100129064 /// hypothetical LOC100131868 /// hypothetical LOC100132773 /// protein phosphatase 4, regulatory subunit 2	chr3p13 /// chr3q29 /// chr5p15.33	220764_at	NM_174907 /// XR_036874 /// XR_036945 /// XR_037699 /// XR_038143 /// XR_038303 /// XR_038399 /// XR_038940 /// XR_038994																				
5.05	5.08	0.03	8.46E-01	9.55E-01	VPS37C	vacuolar protein sorting 37 homolog C (S. cerevisiae)	chr11q12.2	1560059_at	NM_017966																				
4.07	4.19	0.12	8.46E-01	9.55E-01	NLRP1	NLR family, pyrin domain containing 1	chr17p13.2	218380_at	NM_001033053 /// NM_014922 /// NM_033004 /// NM_033006 /// NM_033007																				
6.55	6.64	0.09	8.46E-01	9.55E-01	PAWR	PRKC, apoptosis, WT1, regulator	chr12q21	204004_at	NM_002583																				
4.29	4.37	0.08	8.46E-01	9.55E-01	---	---	---	1562497_at	---																				
3.79	3.85	0.07	8.46E-01	9.55E-01	FRMD4A	FERM domain containing 4A	chr10p13	225167_at	NM_018027																				
7.09	7.15	0.06	8.46E-01	9.55E-01	FAM20B	family with sequence similarity 20, member B	chr1q25	202916_s_at	NM_014864																				
4.97	5.01	0.04	8.46E-01	9.55E-01	DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58	chr17q21.2	219364_at	NM_024119																				
2.85	2.88	0.04	8.46E-01	9.55E-01	TRO	trophinin	chrXp11.22-p11.21	211701_s_at	NM_001039705 /// NM_016157 /// NM_177556																				
2.24	2.27	0.03	8.46E-01	9.55E-01	MYRIP	myosin VIIA and Rab interacting protein	chr3p22.1	214156_at	NM_015460																				
2.87	2.90	0.03	8.46E-01	9.55E-01	---	---	---	1560943_s_at	---																				
2.61	2.63	0.02	8.46E-01	9.55E-01	---	---	---	237914_s_at	---																				
5.33	5.37	0.04	8.46E-01	9.55E-01	GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	chr8q24.3	206709_x_at	NM_005309																				
1.96	1.98	0.02	8.46E-01	9.55E-01	---	---	---	220899_at	---																				
2.64	2.67	0.03	8.47E-01	9.55E-01	GJA9 /// MYCBP	gap junction protein, alpha 9, 59kDa /// c-myc binding protein	chr1p33-p32.2 /// chr1p34	221415_s_at	NM_012333 /// NM_030772																				
4.67	4.70	0.04	8.47E-01	9.55E-01	AGER	advanced glycosylation end product-specific receptor	chr6p21.3	217046_s_at	NM_001136 /// NM_172197																				
3.33	3.36	0.03	8.47E-01	9.55E-01	DKFZp564N2472	hypothetical protein DKFZp564N2472	chr7p12.1	1556292_s_at	NM_182595																				
6.07	6.21	0.14	8.47E-01	9.55E-01	PRRX1	paired related homeobox 1	chr1q24	226695_at	NM_006902 /// NM_022716																				
7.37	7.42	0.05	8.47E-01	9.55E-01	S1PR3	sphingosine-1-phosphate receptor 3	chr9q22.1-q22.2	228176_at	NM_005226																				
8.34	8.38	0.04	8.47E-01	9.55E-01	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	chr17p13.3	210996_s_at	NM_006761 /// NR_024058																				
2.97	3.00	0.04	8.47E-01	9.55E-01	---	---	---	237441_at	---																				
7.83	7.87	0.04	8.47E-01	9.55E-01	RAB5C	RAB5C, member RAS oncogene family	chr17q21.2	201140_s_at	NM_004583 /// NM_201434																				
2.66	2.69	0.03	8.47E-01	9.55E-01	AURKB	aurora kinase B	chr17p13.1	209464_at	NM_004217																				
2.13	2.15	0.03	8.47E-01	9.55E-01	---	---	---	237514_at	---																				
2.57	2.60	0.03	8.47E-01	9.55E-01	---	---	---	1570601_at	---																				
2.38	2.41	0.03	8.47E-01	9.55E-01	---	---	---	237879_at	---																				
1.95	1.97	0.02	8.47E-01	9.55E-01	PIK3C2A	Phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11p15.5-p14	1569587_at	NM_002645																				
11.99	12.02	0.03	8.47E-01	9.55E-01	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	chr12p13	AFFX-HUMGAPDH/M33197_3_at	NM_002046																				
5.42	5.52	0.10	8.47E-01	9.55E-01	PAPD1	PAP associated domain containing 1	chr10p11.23	229676_at	NM_018109																				
1.88	1.91	0.03	8.47E-01	9.55E-01	---	---	---	224081_at	---																				
3.62	3.66	0.04	8.48E-01	9.55E-01	---	---	---	239179_at	---																				
2.99	3.02	0.03	8.48E-01	9.55E-01	EVC2	Ellis van Creveld syndrome 2	chr4p16.2-p16.1	1555256_at	NM_147127																				
12.28	12.30	0.02	8.48E-01	9.55E-01	ACTB	actin, beta	chr7p15-p12	213867_x_at	NM_001101																				
4.92	5.01	0.09	8.48E-01	9.55E-01	EXOC8	exocyst complex component 8	chr1q42.2	227577_at	NM_175876																				
3.11	3.15	0.05	8.48E-01	9.55E-01	CHIT1	chitinase 1 (chitotriosidase)	chr1q31-q32	208168_s_at	NM_003465																				

6.51	6.54	0.03	8.48E-01	9.55E-01	LOC151162	hypothetical LOC151162	chr2q21.3	212098_at	---
3.05	3.08	0.03	8.48E-01	9.55E-01	KLRC4 /// KLRK1	killer cell lectin-like receptor subfamily C, member 4 /// killer cell lectin-like receptor subfamily K, member 1	chr12p13.2-p12.3	1555691_a_at	NM_007360 /// NM_013431
2.16	2.19	0.03	8.48E-01	9.55E-01	---	---	---	233603_at	---
2.50	2.53	0.03	8.48E-01	9.55E-01	IRX4	iroquois homeobox 4	chr5p15.3	220225_at	NM_016358
9.50	9.53	0.03	8.48E-01	9.56E-01	MRPS15	mitochondrial ribosomal protein S15	chr1p35-p34.1	226296_s_at	NM_031280
4.13	4.16	0.03	8.48E-01	9.56E-01	C9orf24	chromosome 9 open reading frame 24	chr9p13.3	229012_at	NM_032596 /// NM_147168 /// NM_147169
2.00	2.02	0.02	8.48E-01	9.56E-01	---	---	---	AFFX-r2-Bs-dap-M_at	---
5.61	5.68	0.07	8.48E-01	9.56E-01	PAPOLA	poly(A) polymerase alpha	chr14q32.31	209388_at	NM_032632
4.96	5.02	0.07	8.48E-01	9.56E-01	XIAP	X-linked inhibitor of apoptosis	chrXq25	225859_at	NM_001167
6.10	6.15	0.05	8.48E-01	9.56E-01	TNFSF12	tumor necrosis factor (ligand) superfamily, member 12	chr17p13	205611_at	NM_003809
7.79	7.84	0.05	8.48E-01	9.56E-01	NUCB1	nucleobindin 1	chr19q13.2-q13.4	200649_at	NM_006184
2.57	2.61	0.05	8.48E-01	9.56E-01	ZCCHC7	zinc finger, CCHC domain containing 7	chr9p13.2	1555562_a_at	NM_032226
3.24	3.28	0.04	8.48E-01	9.56E-01	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	chr17q21-q22	206996_x_at	NM_000723 /// NM_199247 /// NM_199248
2.32	2.36	0.04	8.48E-01	9.56E-01	---	---	---	213802_at	---
2.48	2.51	0.03	8.48E-01	9.56E-01	ITGB8	integrin, beta 8	chr7p15.3	211488_s_at	NM_002214
3.24	3.27	0.03	8.48E-01	9.56E-01	KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4	chr1p21	228436_at	NM_001039574 /// NM_004978 /// NM_153763
2.38	2.41	0.03	8.48E-01	9.56E-01	EFCAB6	EF-hand calcium binding domain 6	chr22q13.1-q13.33	1562815_at	NM_022785 /// NM_198856
3.93	3.96	0.03	8.48E-01	9.56E-01	TCL6	T-cell leukemia/lymphoma 6	chr14q32.1	207894_s_at	NM_012468 /// NM_014418 /// NM_020550 /// NM_020552 /// NM_020553 /// NM_020554
2.02	2.05	0.03	8.48E-01	9.56E-01	---	---	---	234227_at	---
1.98	2.01	0.02	8.48E-01	9.56E-01	TPTEps1	TPTE pseudogene 1	chr13q14.3	1556876_s_at	---
2.28	2.31	0.03	8.48E-01	9.56E-01	LHX2	LIM homeobox 2	chr9q33-q34.1	211219_s_at	NM_004789
2.24	2.26	0.02	8.48E-01	9.56E-01	---	---	---	231310_at	---
4.90	4.92	0.03	8.49E-01	9.56E-01	---	---	---	232954_at	---
2.81	2.85	0.05	8.49E-01	9.56E-01	SYT17	Synaptotagmin XVII	chr16p12.3	229053_at	NM_016524
2.31	2.34	0.03	8.49E-01	9.56E-01	---	---	---	230767_at	---
5.68	5.72	0.04	8.49E-01	9.56E-01	NKRF	NFKB repressing factor	chrXq24	205004_at	NM_017544
2.10	2.13	0.02	8.49E-01	9.56E-01	---	---	---	217666_at	---
2.48	2.51	0.03	8.49E-01	9.56E-01	---	---	---	240468_at	---
3.63	3.67	0.04	8.49E-01	9.56E-01	ZFP161	zinc finger protein 161 homolog (mouse)	chr18pter-p11.2	208199_s_at	NM_003409
6.31	6.35	0.03	8.49E-01	9.56E-01	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	chr11q12.3	222264_at	NM_001079559
2.30	2.33	0.03	8.49E-01	9.56E-01	FAM55A	family with sequence similarity 55, member A	chr11q23.2	1553828_at	NM_152315
2.46	2.48	0.02	8.49E-01	9.56E-01	EREG	epiregulin	chr4q13.3	1569583_at	NM_001432
2.70	2.72	0.02	8.49E-01	9.56E-01	---	---	---	232827_at	---
3.71	3.76	0.05	8.49E-01	9.56E-01	---	---	---	241413_at	---
2.47	2.51	0.03	8.49E-01	9.56E-01	---	---	---	238744_at	---
2.12	2.15	0.03	8.49E-01	9.56E-01	---	---	---	236670_s_at	---
2.80	2.82	0.02	8.49E-01	9.56E-01	HMGA2	high mobility group AT-hook 2	chr12q15	1559891_at	NM_003483 /// NM_003484
2.48	2.52	0.04	8.49E-01	9.56E-01	---	---	---	1569750_at	---
2.66	2.70	0.03	8.49E-01	9.56E-01	C20orf56	chromosome 20 open reading frame 56	chr20p11.21	228004_at	XR_041830 /// XR_041831 /// XR_041832
2.47	2.50	0.03	8.49E-01	9.56E-01	OR12D3	olfactory receptor, family 12, subfamily D, member 3	chr6p22.1	221431_s_at	NM_030959
2.23	2.25	0.02	8.49E-01	9.56E-01	ZNF397OS	Zinc finger protein 397 opposite strand	chr18q12.2	1557104_at	NM_001112734 /// XM_001720071 /// XM_001722380 /// XM_001723235
3.60	3.63	0.03	8.49E-01	9.56E-01	TIGD1L	tigger transposable element derived 1-like	chr6p21.3	216679_at	---
6.59	6.66	0.07	8.50E-01	9.56E-01	BCCIP	BRCA2 and CDKN1A interacting protein	chr10q26.1	227322_s_at	NM_016567 /// NM_078468 /// NM_078469
6.67	6.70	0.04	8.49E-01	9.56E-01	LOC149832	hypothetical protein LOC149832	chr20p13	228456_s_at	---
2.86	2.89	0.03	8.49E-01	9.56E-01	MSX2	msh homeobox 2	chr5q34-q35	205555_s_at	NM_002449

2.30	2.33	0.03	8.49E-01	9.56E-01	SAMD5	sterile alpha motif domain containing 5	chr6q24.3	242626_at	NM_001030060																			
2.12	2.15	0.03	8.49E-01	9.56E-01	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	chr17q22	207869_s_at	NM_018896 /// NM_198376 /// NM_198377 /// NM_198378 /// NM_198379 /// NM_198380 /// NM_198382 /// NM_198383 /// NM_198384 /// NM_198385 /// NM_198386 /// NM_198387 /// NM_198388 /// NM_198396 /// NM_198397																		
2.73	2.77	0.03	8.50E-01	9.56E-01	FGF18	Fibroblast growth factor 18	chr5q34	214284_s_at	NM_003862																			
3.69	3.74	0.05	8.50E-01	9.56E-01	SNRPN	small nuclear ribonucleoprotein polypeptide N	chr15q11.2	216850_at	NM_003097 /// NM_022805 /// NM_022806 /// NM_022807 /// NM_022808 /// NR_001289 /// NR_001290 /// NR_001292 /// NR_001293 /// NR_001294 /// NR_001295 /// NR_003294 /// NR_003298 /// NR_003299 /// NR_003300 /// NR_003301 /// NR_003302 /// NR_003303 /// NR_003304 /// NR_003305 /// NR_003306 /// NR_003307 /// NR_003308 /// NR_003309 /// NR_003310 /// NR_003311 /// NR_003312 /// NR_003313 /// NR_003314 /// NR_003315 /// NR_003316 /// NR_003317 /// NR_003318 /// NR_003319 /// NR_003320 /// NR_003321 /// NR_003322 /// NR_003323 /// NR_003324 /// NR_003325 /// NR_003326 /// NR_003327 /// NR_003328 /// NR_003329 /// NR_003330 /// NR_003331 /// NR_003332 /// NR_003333 /// NR_003334 /// NR_003335 /// NR_003336 ///																		
3.23	3.26	0.04	8.50E-01	9.56E-01	LOC642852	hypothetical LOC642852	chr21q22.3	1569032_at	XM_001714922 /// XM_926249 /// XM_941790																			
2.28	2.31	0.03	8.50E-01	9.56E-01	---	---	---	243974_at	---																			
2.23	2.26	0.03	8.50E-01	9.56E-01	---	---	---	244135_at	---																			
1.99	2.01	0.02	8.50E-01	9.56E-01	LAMB4	laminin, beta 4	chr7q22-q31.2	215516_at	NM_007356																			
1.92	1.94	0.02	8.50E-01	9.56E-01	---	---	---	216089_at	---																			
4.85	4.89	0.04	8.50E-01	9.56E-01	RHOBTB2	Rho-related BTB domain containing 2	chr8p21.3	209441_at	NM_015178																			

2.69	2.73	0.04	8.50E-01	9.56E-01	FCF1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	chr14q24.3	215567_at	NM_015962
2.30	2.33	0.03	8.50E-01	9.56E-01	LOC440268	hypothetical LOC440268	chr15q13.3	243406_at	XR_041884 /// XR_041885 /// XR_041886
4.15	4.20	0.05	8.50E-01	9.56E-01	NFATC2	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	chr20q13.2-q13.3	226991_at	NM_012340 /// NM_173091
3.78	3.83	0.05	8.50E-01	9.56E-01	SDHALP2	Succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	chr3q29	1558220_at	NR_003265 /// XR_015171
1.98	2.01	0.02	8.50E-01	9.56E-01	CA6	carbonic anhydrase VI	chr1p36.2	1555572_at	NM_001215
3.13	3.19	0.07	8.51E-01	9.57E-01	---	---	---	239170_at	---
2.91	2.94	0.03	8.50E-01	9.57E-01	---	---	---	238658_at	---
2.31	2.33	0.02	8.51E-01	9.57E-01	SLC45A2	solute carrier family 45, member 2	chr5p13.3	221644_s_at	NM_001012509 /// NM_016180
3.71	3.75	0.04	8.51E-01	9.57E-01	---	---	---	244548_at	---
5.78	5.81	0.03	8.51E-01	9.57E-01	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	chr19p13.3	209415_at	NM_016263
4.30	4.37	0.07	8.51E-01	9.57E-01	ZNF302	zinc finger protein 302	chr19q13.11	228393_s_at	NM_001012320 /// NM_018443
2.00	2.02	0.02	8.51E-01	9.57E-01	SYNJ2BP	synaptojanin 2 binding protein	chr14q24.2	235722_at	NM_018373
7.52	7.58	0.06	8.51E-01	9.57E-01	CTSS	cathepsin S	chr1q21	232617_at	NM_004079
6.29	6.32	0.04	8.51E-01	9.57E-01	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand	chr1p35.1	228970_at	NM_178547
7.43	7.47	0.04	8.51E-01	9.57E-01	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	chr16p13.3	201499_s_at	NM_003470
6.33	6.37	0.05	8.51E-01	9.57E-01	CARHSP1	calcium regulated heat stable protein 1, 24kDa	chr16p13.2	224910_at	NM_001042476 /// NM_014316
2.67	2.70	0.03	8.51E-01	9.57E-01	TTC23L	tetratricopeptide repeat domain 23-like	chr5p13.2	239620_at	NM_144725
2.26	2.29	0.03	8.51E-01	9.57E-01	LOC415056	hypothetical gene LOC415056	chr9p13	1556771_a_at	---
1.97	1.99	0.02	8.51E-01	9.57E-01	---	---	---	1560209_at	---
7.55	7.63	0.08	8.51E-01	9.57E-01	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	chr11q13	208998_at	NM_003355
6.44	6.50	0.06	8.51E-01	9.57E-01	ABHD6 /// LOC643635	abhydrolase domain containing 6 /// similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11	chr1p36.33 /// chr3p14.3	45288_at	NM_020676 /// XM_926939
2.77	2.81	0.03	8.51E-01	9.57E-01	---	---	---	1559210_at	---
2.84	2.89	0.05	8.51E-01	9.57E-01	BCL2	B-cell CLL/lymphoma 2	chr18q21.33|18q21.3	203685_at	NM_000633 /// NM_000657
2.60	2.62	0.02	8.51E-01	9.57E-01	LOC286238	hypothetical protein LOC286238	chr9q22.1	1564709_at	NM_001100111
2.92	2.97	0.05	8.52E-01	9.57E-01	ZNF432 /// ZNF614	zinc finger protein 432 /// zinc finger protein 614	chr19q13.33	220721_at	NM_014650 /// NM_025040
3.49	3.54	0.05	8.52E-01	9.57E-01	DDAH1	dimethylarginine dimethylaminohydrolase 1	chr1p22	1553565_s_at	NM_001134445 /// NM_012137
2.43	2.47	0.04	8.52E-01	9.57E-01	GOPC	Golgi associated PDZ and coiled-coil motif containing	chr6q21	236862_at	NM_001017408 /// NM_020399
7.66	7.70	0.04	8.52E-01	9.57E-01	UBE2L6	ubiquitin-conjugating enzyme E2L 6	chr11q12	201649_at	NM_004223 /// NM_198183
2.16	2.19	0.03	8.52E-01	9.57E-01	UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1	chr5p13.2	236597_at	NM_152404
3.13	3.16	0.03	8.52E-01	9.57E-01	H1FOO	H1 histone family, member O, oocyte-specific	chr3q21.3	1553064_at	NM_153833
2.27	2.29	0.03	8.52E-01	9.57E-01	---	---	---	240872_at	---
2.07	2.09	0.03	8.52E-01	9.57E-01	LOC440117	hypothetical gene supported by BC037858	chr12q24.32	240268_at	---
3.29	3.32	0.02	8.52E-01	9.57E-01	HUWE1	HECT, UBA and WWE domain containing 1	chrXp11.22	214673_s_at	NM_031407
1.99	2.01	0.02	8.52E-01	9.57E-01	MEOX2	mesenchyme homeobox 2	chr7p22.1-p21.3	206202_at	NM_005924
2.51	2.54	0.03	8.52E-01	9.57E-01	ALPP	alkaline phosphatase, placental (Regan isozyme)	chr2q37	204664_at	NM_001632
3.26	3.29	0.03	8.52E-01	9.57E-01	ADAMTSL4	ADAMTS-like 4	chr1q21.2	220578_at	NM_019032 /// NM_025008
1.97	1.99	0.02	8.52E-01	9.57E-01	EIF3M	Eukaryotic translation initiation factor 3, subunit M	chr11p13	240513_at	NM_006360
2.05	2.07	0.02	8.52E-01	9.57E-01	---	---	---	242072_at	---
2.17	2.19	0.02	8.52E-01	9.57E-01	---	---	---	243192_at	---
2.22	2.25	0.03	8.52E-01	9.57E-01	---	---	---	1565921_a_at	---
3.11	3.13	0.03	8.52E-01	9.57E-01	---	---	---	244152_at	---
2.01	2.03	0.02	8.52E-01	9.57E-01	---	---	---	1570268_at	---
2.01	2.03	0.02	8.52E-01	9.57E-01	---	---	---	AFFX-r2-Bs-dap-3_at	---
2.92	2.95	0.03	8.52E-01	9.57E-01	NFIB	Nuclear factor I/B	chr9p24.1	233394_at	NM_005596
2.84	2.88	0.04	8.52E-01	9.57E-01	FGFBP1	fibroblast growth factor binding protein 1	chr4p16-p15	205014_at	NM_005130
5.77	5.80	0.04	8.53E-01	9.57E-01	MGC34774	ribosomal protein L13A pseudogene	chr7q21.11	1555083_at	NR_003680
2.45	2.48	0.03	8.53E-01	9.57E-01	ADFP	Adipose differentiation-related protein	chr9p22.1	215895_x_at	NM_001122
2.35	2.37	0.03	8.53E-01	9.57E-01	TTPA	tocopherol (alpha) transfer protein	chr8q13.1-q13.3	210614_at	NM_000370
3.94	3.97	0.02	8.53E-01	9.57E-01	LOC221122	hypothetical protein LOC221122	chr11p11.2	1560278_at	---
2.00	2.02	0.02	8.52E-01	9.57E-01	---	---	---	240657_at	---
4.90	4.99	0.09	8.53E-01	9.57E-01	RASA1	RAS p21 protein activator (GTPase activating protein) 1	chr5q13.3	210621_s_at	NM_002890 /// NM_022650
3.43	3.47	0.04	8.53E-01	9.57E-01	---	---	---	1569761_x_at	---
3.45	3.48	0.04	8.53E-01	9.57E-01	GP1BA	glycoprotein Ib (platelet), alpha polypeptide	chr17pter-p12	207389_at	NM_000173

2.67	2.71	0.03	8.53E-01	9.57E-01	EBF3	early B-cell factor 3	chr10q26.3	227243_s_at	NM_001005463
2.73	2.76	0.02	8.53E-01	9.57E-01	KIF14	kinesin family member 14	chr1q32.1	206364_at	NM_014875
6.04	6.14	0.10	8.53E-01	9.57E-01	PROX1	prospero homeobox 1	chr1q32.2-q32.3	228656_at	NM_002763
4.53	4.62	0.09	8.53E-01	9.57E-01	---	---	---	231644_at	---
3.94	4.02	0.08	8.53E-01	9.57E-01	PAPD4	PAP associated domain containing 4	chr5q14.1	225761_at	NM_001114393 /// NM_001114394 /// NM_173797
3.14	3.17	0.03	8.53E-01	9.57E-01	OR1J2	olfactory receptor, family 1, subfamily J, member 2	chr9q34.11	1567256_at	NM_054107
2.45	2.48	0.03	8.53E-01	9.57E-01	---	---	---	233310_at	---
2.16	2.18	0.02	8.53E-01	9.57E-01	---	---	---	238361_s_at	---
2.26	2.30	0.04	8.53E-01	9.57E-01	C1QL1	Complement component 1, q subcomponent-like 1	chr17q21	214346_at	NM_006688
7.20	7.27	0.07	8.53E-01	9.57E-01	GLT8D4	glycosyltransferase 8 domain containing 4	chr3p13	235371_at	NM_001080393
5.00	5.06	0.06	8.53E-01	9.57E-01	PIGB	phosphatidylinositol glycan anchor biosynthesis, class B	chr15q21-q22	205452_at	NM_004855
3.56	3.61	0.05	8.53E-01	9.57E-01	CLASP2	cytoplasmic linker associated protein 2	chr3p22.3	212308_at	NM_015097
5.63	5.67	0.05	8.53E-01	9.57E-01	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	chr12q13.11	204253_s_at	NM_000376 /// NM_001017535
3.15	3.19	0.04	8.53E-01	9.57E-01	COL25A1	collagen, type XXV, alpha 1	chr4q25	224388_s_at	NM_032518 /// NM_198721
3.64	3.68	0.04	8.53E-01	9.57E-01	KRTAP10-10 /// KRTAP10-11	keratin associated protein 10-10 /// keratin associated protein 10-11	chr21q22.3	1560897_a_at	NM_181688 /// NM_198692
3.12	3.16	0.03	8.53E-01	9.57E-01	DNAH2	dynein, axonemal, heavy chain 2	chr17p13.1	239499_at	NM_020877
3.82	3.86	0.03	8.53E-01	9.57E-01	LOC284100	hypothetical protein LOC284100	chr17q12	1563945_at	NM_001129906 /// XM_001716065 /// XM_001718301 /// XM_375443
7.65	7.68	0.03	8.53E-01	9.57E-01	DPH5	DPH5 homolog (S. cerevisiae)	chr1p21.2	219590_x_at	NM_001077394 /// NM_001077395 /// NM_015958
1.98	2.00	0.02	8.53E-01	9.57E-01	PRKD1	protein kinase D1	chr14q11	217705_at	NM_002742
2.26	2.28	0.02	8.53E-01	9.57E-01	---	---	---	216681_at	---
3.35	3.43	0.08	8.53E-01	9.57E-01	---	---	---	241837_at	---
3.17	3.19	0.03	8.53E-01	9.57E-01	KLHL14	kelch-like 14 (Drosophila)	chr18q12.1	1554942_a_at	NM_020805
3.76	3.80	0.03	8.54E-01	9.58E-01	ASB12	ankyrin repeat and SOCS box-containing 12	chrXq11.1	236033_at	NM_130388
3.77	3.81	0.04	8.54E-01	9.58E-01	ZCCHC6	Zinc finger, CCHC domain containing 6	chr9q21	238800_s_at	NM_024617
7.97	8.07	0.10	8.54E-01	9.58E-01	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	chr11p15	219059_s_at	NM_006691
2.48	2.51	0.03	8.54E-01	9.58E-01	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	chr18q21.3	204855_at	NM_002639
3.03	3.06	0.02	8.54E-01	9.58E-01	SLC34A3	solute carrier family 34 (sodium phosphate), member 3	chr9q34	1569926_s_at	NM_080877
2.05	2.07	0.02	8.54E-01	9.58E-01	LOC441245	hypothetical LOC441245	chr7q11.21	1561964_at	---
2.18	2.21	0.03	8.54E-01	9.58E-01	---	---	---	216826_at	---
2.09	2.12	0.04	8.54E-01	9.58E-01	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	chr4q21	1554027_a_at	NM_001098484 /// NM_001134742 /// NM_003759
2.25	2.27	0.02	8.54E-01	9.58E-01	---	---	---	240935_at	---
3.24	3.28	0.04	8.54E-01	9.58E-01	---	---	---	1557244_a_at	---
4.17	4.20	0.03	8.54E-01	9.58E-01	PKP3	plakophilin 3	chr11p15	209873_s_at	NM_007183
3.60	3.63	0.03	8.54E-01	9.58E-01	LOC728543	hypothetical protein LOC728543	chr12q24.13	234133_s_at	XR_041705 /// XR_041706 /// XR_041707
3.47	3.52	0.05	8.54E-01	9.58E-01	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	chr15q23	1567081_x_at	NM_017882
2.52	2.54	0.02	8.54E-01	9.58E-01	LAMA3	laminin, alpha 3	chr18q11.2	1560078_at	NM_000227 /// NM_001127717 /// NM_001127718 /// NM_198129
2.23	2.26	0.03	8.55E-01	9.58E-01	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	chr8q22.2	220400_at	NM_015243 /// NM_017890 /// NM_152564 /// NM_181661
4.22	4.26	0.04	8.55E-01	9.58E-01	FAM30A	family with sequence similarity 30, member A	chr14q32.33	220377_at	XM_001724472 /// XM_001725525
2.50	2.54	0.03	8.55E-01	9.58E-01	---	---	---	244625_at	---
2.18	2.21	0.02	8.55E-01	9.58E-01	TAF7L	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa	chrXq22.1	224380_s_at	NM_024885
2.04	2.06	0.02	8.55E-01	9.58E-01	---	---	---	242189_at	---

2.27	2.29	0.02	8.55E-01	9.58E-01	---	---	---	236582_at	---
2.06	2.08	0.02	8.55E-01	9.58E-01	---	---	---	AFFX-DapX-3_at	---
5.40	5.47	0.07	8.55E-01	9.58E-01	MEG3	maternally expressed 3 (non-protein coding)	chr14q32	212732_at	NR_002766 /// NR_003530 /// NR_003531
4.88	4.94	0.06	8.55E-01	9.58E-01	RECQL	RecQ protein-like (DNA helicase Q1-like)	chr12p12	212917_x_at	NM_002907 /// NM_032941
4.94	4.98	0.04	8.55E-01	9.58E-01	TSSK3	testis-specific serine kinase 3	chr1p35-p34	1552395_at	NM_052841
4.29	4.32	0.03	8.55E-01	9.58E-01	RIPK3	receptor-interacting serine-threonine kinase 3	chr14q11.2	228139_at	NM_006871
2.34	2.36	0.02	8.55E-01	9.58E-01	---	---	---	231095_at	---
3.59	3.62	0.03	8.55E-01	9.58E-01	---	---	---	239603_x_at	---
2.17	2.20	0.03	8.55E-01	9.58E-01	---	---	---	1561559_at	---
2.10	2.12	0.02	8.55E-01	9.58E-01	---	---	---	1561669_at	---
3.16	3.19	0.03	8.55E-01	9.58E-01	ITSN2	intersectin 2	chr2pter-p25.1	210545_at	NM_006277 /// NM_019595 /// NM_147152
4.60	4.64	0.03	8.55E-01	9.58E-01	MYT1	myelin transcription factor 1	chr20q13.33	215822_x_at	NM_004535
2.75	2.78	0.03	8.55E-01	9.58E-01	KY	kyphoscoliosis peptidase	chr3q22.2	1569991_at	NM_178554
2.07	2.09	0.03	8.55E-01	9.58E-01	---	---	---	241119_at	---
2.44	2.46	0.02	8.55E-01	9.58E-01	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	---	1553155_x_at	NM_152565
3.38	3.42	0.04	8.55E-01	9.58E-01	---	---	---	1565857_at	---
2.20	2.22	0.02	8.55E-01	9.58E-01	---	---	---	244671_at	---
6.14	6.19	0.05	8.56E-01	9.58E-01	SF3A3	splicing factor 3a, subunit 3, 60kDa	chr1p34.3	203818_s_at	NM_006802
5.43	5.52	0.09	8.56E-01	9.59E-01	ABI3BP	ABI gene family, member 3 (NESH) binding protein	chr3q12	223395_at	NM_015429
10.08	10.13	0.05	8.56E-01	9.59E-01	KIAA0391 /// PSMA6	KIAA0391 /// proteasome (prosome, macropain) subunit, alpha type, 6	chr14q13 /// chr14q13.2	208805_at	NM_002791 /// NM_014672
2.06	2.08	0.02	8.56E-01	9.59E-01	---	---	---	236575_at	---
4.17	4.21	0.04	8.56E-01	9.59E-01	KRTAP4-7 /// LOC729082	keratin associated protein 4-7 /// hypothetical protein LOC729082	chr15q15.1 /// chr17q12-q21	231808_at	NM_033061 /// XR_040992 /// XR_040993 /// XR_040994
2.81	2.84	0.03	8.56E-01	9.59E-01	PRRT1	proline-rich transmembrane protein 1	chr6p21.32	231739_at	NM_030651
2.08	2.10	0.02	8.56E-01	9.59E-01	---	---	---	1566607_at	---
4.96	5.00	0.04	8.56E-01	9.59E-01	---	---	---	236338_at	---
4.69	4.76	0.06	8.56E-01	9.59E-01	SAMD13	sterile alpha motif domain containing 13	chr1p31.1	229402_at	NM_001010971 /// NM_001134663 /// NM_001134664
2.53	2.56	0.03	8.56E-01	9.59E-01	C21orf116	chromosome 21 open reading frame 116	---	223951_at	---
4.42	4.44	0.02	8.56E-01	9.59E-01	---	---	---	238767_at	---
4.88	4.95	0.07	8.56E-01	9.59E-01	ZC3H14	zinc finger CCCH-type containing 14	chr14q31.3	213063_at	NM_024824 /// NM_207660 /// NM_207661 /// NM_207662
4.08	4.15	0.07	8.56E-01	9.59E-01	LRRC50	leucine rich repeat containing 50	chr16q24.1	222068_s_at	NM_178452
7.04	7.10	0.06	8.57E-01	9.59E-01	CACYBP	calcyclin binding protein	chr1q24-q25	211761_s_at	NM_001007214 /// NM_014412
7.78	7.83	0.05	8.57E-01	9.59E-01	BTF3L4	basic transcription factor 3-like 4	chr1p32.3	226963_at	NM_152265
6.57	6.61	0.04	8.56E-01	9.59E-01	SIPA1L1	signal-induced proliferation-associated 1 like 1	chr14q24.2	202255_s_at	NM_015556
3.41	3.44	0.04	8.57E-01	9.59E-01	VGLL2	vestigial like 2 (Drosophila)	chr6q22.2	236352_at	NM_153453 /// NM_182645
4.23	4.27	0.04	8.57E-01	9.59E-01	---	---	---	243135_x_at	---
3.48	3.51	0.03	8.57E-01	9.59E-01	C17orf60	chromosome 17 open reading frame 60	chr17q23.3	217513_at	NM_001085423
2.63	2.67	0.03	8.57E-01	9.59E-01	---	---	---	237964_at	---
2.78	2.81	0.03	8.56E-01	9.59E-01	---	---	---	233698_at	---
2.46	2.49	0.03	8.56E-01	9.59E-01	MKL2	MKL/myocardin-like 2	chr16p13.12	1558777_at	NM_014048
2.49	2.52	0.03	8.57E-01	9.59E-01	SDK1	sidekick homolog 1, cell adhesion molecule (chicken)	chr7p22.2	229912_at	NM_001079653 /// NM_152744
4.59	4.62	0.03	8.57E-01	9.59E-01	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	212078_s_at	NM_005933
2.30	2.32	0.03	8.56E-01	9.59E-01	MYL1	myosin, light chain 1, alkali; skeletal, fast	chr2q33-q34	209888_s_at	NM_079420 /// NM_079422
1.82	1.84	0.03	8.56E-01	9.59E-01	---	---	---	1562080_at	---
2.06	2.09	0.02	8.56E-01	9.59E-01	LOC1720	dihydrofolate reductase pseudogene	chr2p12	216659_at	---
1.94	1.97	0.02	8.56E-01	9.59E-01	---	---	---	240348_at	---
2.18	2.20	0.02	8.56E-01	9.59E-01	---	---	---	239291_at	---
2.23	2.25	0.02	8.56E-01	9.59E-01	---	---	---	216534_at	---
3.63	3.69	0.06	8.57E-01	9.59E-01	TIGD2	tigger transposable element derived 2	chr4q22.1	229983_at	NM_145715

6.89	6.94	0.05	8.57E-01	9.59E-01	C6orf106	chromosome 6 open reading frame 106	chr6p21.31	217925_s_at	NM_022758 /// NM_024294																					
4.04	4.07	0.04	8.57E-01	9.59E-01	MFSD2	major facilitator superfamily domain containing 2	chr1p34.2	225316_at	NM_032793																					
1.88	1.90	0.03	8.57E-01	9.59E-01	---	---	---	1559992_a_at	---																					
2.18	2.21	0.02	8.57E-01	9.59E-01	---	---	---	1561004_at	---																					
3.72	3.75	0.03	8.57E-01	9.59E-01	---	---	---	208301_at	---																					
8.54	8.58	0.04	8.57E-01	9.59E-01	HLA-F	major histocompatibility complex, class I, F	chr6p21.3	204806_x_at	NM_001098478 /// NM_001098479 /// NM_018950																					
2.97	3.00	0.03	8.57E-01	9.59E-01	FLJ14816	hypothetical protein FLJ14816	chr2q14.2	1553385_at	XR_017842 /// XR_017947 /// XR_040110																					
2.11	2.13	0.03	8.57E-01	9.59E-01	TPR	translocated promoter region (to activated MET oncogene)	chr1q25	215220_s_at	NM_003292																					
2.62	2.64	0.02	8.57E-01	9.59E-01	GPR161	G protein-coupled receptor 161	chr1q24.2	206971_at	NM_007369 /// NM_153832																					
2.16	2.18	0.02	8.57E-01	9.59E-01	---	---	---	1559589_a_at	---																					
3.50	3.54	0.03	8.57E-01	9.59E-01	PWP2	PWP2 periodic tryptophan protein homolog (yeast)	chr21q22.3	1565603_at	NM_005049																					
1.99	2.01	0.02	8.57E-01	9.59E-01	---	---	---	239480_at	---																					
4.61	4.65	0.03	8.57E-01	9.59E-01	LRRC45	leucine rich repeat containing 45	chr17q25.3	226253_at	NM_144999																					
2.96	2.99	0.03	8.57E-01	9.59E-01	---	---	---	236200_at	---																					
2.08	2.10	0.02	8.57E-01	9.59E-01	ADH4	Alcohol dehydrogenase 4 (class II), pi polypeptide	chr4q21-q24|4q22	231703_s_at	NM_000670																					
3.74	3.79	0.06	8.57E-01	9.59E-01	SFRS12	splicing factor, arginine/serine-rich 12	chr5q12.3	244287_at	NM_001077199 /// NM_139168																					
7.29	7.35	0.05	8.57E-01	9.59E-01	KLF2	Kruppel-like factor 2 (lung)	chr19p13.13-p13.11	219371_s_at	NM_016270																					
7.98	8.03	0.05	8.58E-01	9.59E-01	SERP1	stress-associated endoplasmic reticulum protein 1	chr3q25.1	200970_s_at	NM_014445																					
3.82	3.87	0.05	8.58E-01	9.59E-01	CASC4	cancer susceptibility candidate 4	chr15q15.3	1552719_at	NM_138423 /// NM_177974																					
4.51	4.55	0.04	8.58E-01	9.59E-01	LOC124220	similar to common salivary protein 1	chr16p13.3	228058_at	NM_145252																					
5.30	5.34	0.03	8.58E-01	9.59E-01	SNAPC4	small nuclear RNA activating complex, polypeptide 4, 190kDa	chr9q34.3	205658_s_at	NM_003086																					
2.15	2.18	0.03	8.58E-01	9.59E-01	ROBO2	Roundabout, axon guidance receptor, homolog 2 (Drosophila)	chr3p12.3	240425_x_at	NM_001128929 /// NM_002942																					
2.58	2.61	0.03	8.57E-01	9.59E-01	---	---	---	224085_at	---																					
2.22	2.24	0.03	8.57E-01	9.59E-01	---	---	---	240158_at	---																					
2.39	2.41	0.02	8.58E-01	9.59E-01	TCL6	T-cell leukemia/lymphoma 6	chr14q32.1	219840_s_at	NM_012468 /// NM_014418 /// NM_020550 /// NM_020552 /// NM_020553 /// NM_020554																					
2.66	2.68	0.02	8.57E-01	9.59E-01	CD22	CD22 molecule	chr19q13.1	220674_at	NM_001771																					
2.30	2.33	0.03	8.58E-01	9.59E-01	SGMS2	sphingomyelin synthase 2	chr4q25	242963_at	NM_152621																					
4.72	4.78	0.06	8.58E-01	9.59E-01	RBAK	RB-associated KRAB zinc finger	chr7p22.1	228571_at	NM_021163																					
2.72	2.74	0.02	8.58E-01	9.59E-01	FAM26F	Family with sequence similarity 26, member F	chr6q22.1	228362_s_at	NM_001010919																					
4.67	4.71	0.04	8.58E-01	9.59E-01	RREB1	ras responsive element binding protein 1	chr6p25	215032_at	NM_001003698 /// NM_001003699 /// NM_002955																					
2.82	2.84	0.03	8.58E-01	9.59E-01	MAP9	microtubule-associated protein 9	chr4q32.1	239415_at	NM_001039580																					
2.96	3.00	0.04	8.58E-01	9.59E-01	LOC474358	hypothetical BC042079 locus	chr10q23-q25	237425_at	---																					
3.24	3.27	0.03	8.58E-01	9.59E-01	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	chr10p12.2	205570_at	NM_005028																					
3.83	3.87	0.03	8.58E-01	9.59E-01	MIXL1	Mix1 homeobox-like 1 (Xenopus laevis)	chr1q42.12	231746_at	NM_031944																					
2.10	2.13	0.03	8.58E-01	9.59E-01	---	---	---	1557637_at	---																					
3.88	3.91	0.03	8.58E-01	9.59E-01	C11orf36	chromosome 11 open reading frame 36	chr11p15.4	1564439_a_at	XR_039843 /// XR_039844 /// XR_039845																					
12.28	12.31	0.02	8.58E-01	9.59E-01	ACTB	actin, beta	chr7p15-p12	224594_x_at	NM_001101																					
1.88	1.90	0.02	8.58E-01	9.59E-01	---	---	---	234907_x_at	---																					
4.67	4.74	0.07	8.58E-01	9.59E-01	ZFX	zinc finger protein, X-linked	chrXp21.3	229022_at	NM_003410																					

6.18	6.25	0.07	8.58E-01	9.59E-01	LOC92482	UPF0604 protein	chr10q25.2	228993_s_at	XM_001716109 /// XM_001725802 /// XM_001725803 /// XM_001725804 /// XM_001726022 /// XM_001726023 /// XM_001726024
3.12	3.17	0.05	8.58E-01	9.59E-01	MAPK8	mitogen-activated protein kinase 8	chr10q11.22	210671_x_at	NM_002750 /// NM_139046 /// NM_139047 /// NM_139049
2.33	2.35	0.02	8.58E-01	9.59E-01	---	---	---	242202_at	---
9.84	9.89	0.05	8.58E-01	9.59E-01	---	---	---	228479_at	---
5.32	5.35	0.03	8.58E-01	9.59E-01	MAP3K10	mitogen-activated protein kinase kinase kinase 10	chr19q13.2	206362_x_at	NM_002446
2.47	2.49	0.02	8.58E-01	9.59E-01	SOX6	SRY (sex determining region Y)-box 6	chr11p15.3	223865_at	NM_017508 /// NM_033326
3.05	3.09	0.04	8.59E-01	9.59E-01	LOC554202	hypothetical LOC554202	chr9p21.3	1554097_a_at	---
2.41	2.46	0.04	8.59E-01	9.59E-01	TUBB1	tubulin, beta 1	chr20q13.32	230690_at	NM_030773
4.75	4.80	0.05	8.59E-01	9.59E-01	BTRC	beta-transducin repeat containing	chr10q24.32	224471_s_at	NM_003939 /// NM_033637
2.26	2.29	0.03	8.59E-01	9.59E-01	DEPDC1	DEP domain containing 1	chr1p31.2	232278_s_at	NM_001114120 /// NM_017779
3.72	3.76	0.03	8.59E-01	9.59E-01	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	chr2p25	235878_at	NM_005680
3.54	3.57	0.03	8.59E-01	9.59E-01	SNHG7	small nucleolar RNA host gene 7 (non-protein coding)	chr9q34.3	1552729_at	NR_003672
2.36	2.38	0.02	8.59E-01	9.59E-01	DNAI2	dynein, axonemal, intermediate chain 2	chr17q25	220636_at	NM_023036
2.03	2.05	0.02	8.59E-01	9.59E-01	---	---	---	241578_x_at	---
2.12	2.15	0.02	8.59E-01	9.59E-01	C16orf73	chromosome 16 open reading frame 73	chr16p13.3	237265_at	NM_152764
6.28	6.33	0.05	8.59E-01	9.59E-01	---	---	---	1553979_at	---
2.39	2.43	0.03	8.59E-01	9.60E-01	LOC285370	hypothetical protein LOC285370	chr3p25.3	1556448_a_at	---
2.02	2.04	0.02	8.59E-01	9.60E-01	---	---	---	215713_at	---
4.61	4.67	0.06	8.60E-01	9.60E-01	SLC25A35	solute carrier family 25, member 35	chr17p13.1	228836_at	NM_201520
6.59	6.64	0.05	8.60E-01	9.60E-01	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	chr8q13	203449_s_at	NM_003218 /// NM_017489
7.24	7.29	0.04	8.59E-01	9.60E-01	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	chr19q13.32	208751_at	NM_003827
2.06	2.09	0.03	8.60E-01	9.60E-01	RBM15	RNA binding motif protein 15	chr1p13	232971_at	NM_022768
2.68	2.70	0.02	8.60E-01	9.60E-01	C11orf82	chromosome 11 open reading frame 82	chr11q14.1	228281_at	NM_145018
7.42	7.47	0.05	8.60E-01	9.60E-01	VBP1	von Hippel-Lindau binding protein 1	chrXq28	201472_at	NM_003372
3.18	3.23	0.05	8.60E-01	9.60E-01	C6orf115	chromosome 6 open reading frame 115	chr6q24.1	223361_at	NM_021243
2.79	2.82	0.03	8.60E-01	9.60E-01	IQGAP2	IQ motif containing GTPase activating protein 2	chr5q13.3	241723_at	NM_006633
2.82	2.85	0.03	8.60E-01	9.60E-01	NFX1	nuclear transcription factor, X-box binding 1	chr9p13.3	210268_at	NM_002504 /// NM_147133 /// NM_147134
2.11	2.14	0.03	8.60E-01	9.60E-01	---	---	---	241695_s_at	---
3.02	3.05	0.03	8.60E-01	9.60E-01	---	---	---	234091_at	---
2.57	2.59	0.02	8.60E-01	9.60E-01	CCDC146	coiled-coil domain containing 146	chr7q11.23	227091_at	NM_020879
1.96	1.98	0.02	8.60E-01	9.60E-01	---	---	---	1564128_at	---
2.83	2.86	0.03	8.60E-01	9.60E-01	PP2672	hypothetical LOC100130249	chr1q42.3	1555322_at	XM_001722682 /// XM_001722882 /// XM_001723081
2.93	2.96	0.03	8.60E-01	9.60E-01	SLC35F3	Solute carrier family 35, member F3	chr1q42.2	231520_at	NM_173508
4.42	4.45	0.03	8.60E-01	9.60E-01	APOA1	apolipoprotein A-I	chr11q23-q24	204450_x_at	NM_000039
6.57	6.62	0.06	8.60E-01	9.60E-01	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	chr3q23-q24	202620_s_at	NM_000935 /// NM_182943
1.87	1.89	0.02	8.60E-01	9.60E-01	TXNRD1	thioredoxin reductase 1	chr12q23-q24.1	1561080_at	NM_001093771 /// NM_003330 /// NM_182729 /// NM_182742 /// NM_182743
2.06	2.09	0.02	8.60E-01	9.60E-01	---	---	---	237850_at	---
2.45	2.50	0.04	8.60E-01	9.60E-01	---	---	---	233269_at	---
1.96	1.99	0.02	8.60E-01	9.60E-01	SCG3	secretogranin III	chr15q21	219196_at	NM_013243
2.38	2.41	0.03	8.60E-01	9.60E-01	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	chr14q23.1	229027_at	NM_021003 /// NM_177951 /// NM_177952

2.31	2.34	0.02	8.61E-01	9.60E-01	DEFB121	defensin, beta 121	chr20q11.1	234007_at	NM_001011878
2.19	2.22	0.02	8.61E-01	9.60E-01	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	chr4q21.23	224480_s_at	NM_032717
4.34	4.38	0.04	8.61E-01	9.60E-01	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	chr15q23	1567080_s_at	NM_017882
3.16	3.19	0.03	8.61E-01	9.60E-01	---	---	---	231419_at	---
5.38	5.41	0.03	8.61E-01	9.60E-01	HAB1	B1 for mucin	---	216875_x_at	---
2.41	2.44	0.03	8.61E-01	9.60E-01	---	---	---	236443_at	---
2.60	2.63	0.03	8.61E-01	9.60E-01	MUC8	mucin 8	chr12q24.3	217295_at	---
2.56	2.60	0.03	8.61E-01	9.60E-01	---	---	---	240435_at	---
3.88	3.91	0.03	8.61E-01	9.60E-01	RGS20	regulator of G-protein signaling 20	chr8q	1569303_s_at	NM_003702 /// NM_170587
2.37	2.39	0.02	8.61E-01	9.60E-01	LITAF	lipopolysaccharide-induced TNF factor	chr16p13.13	1555454_at	NM_004862
2.24	2.26	0.02	8.61E-01	9.60E-01	---	---	---	1569759_at	---
6.20	6.25	0.05	8.61E-01	9.60E-01	OSTF1	osteoclast stimulating factor 1	chr9q13-q21.2	204479_at	NM_012383
2.07	2.10	0.02	8.61E-01	9.60E-01	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	chr8q13-q21.1	1554686_at	NM_014393
3.58	3.63	0.05	8.61E-01	9.60E-01	KIAA1324	KIAA1324	chr1p13.3	226248_s_at	NM_020775
2.21	2.25	0.03	8.61E-01	9.60E-01	MUSK	muscle, skeletal, receptor tyrosine kinase	chr9q31.3-q32	207633_s_at	NM_005592
4.07	4.10	0.03	8.61E-01	9.60E-01	FLJ35848	Hypothetical protein FLJ35848	chr17q21.31	1566480_x_at	NM_001033659
2.61	2.65	0.04	8.61E-01	9.60E-01	---	---	---	240606_at	---
2.53	2.56	0.03	8.62E-01	9.60E-01	C9orf100	chromosome 9 open reading frame 100	chr9p13.3	230522_s_at	NM_032818
2.54	2.57	0.03	8.62E-01	9.60E-01	NXF3	nuclear RNA export factor 3	chrXq22-q23	222949_at	NM_022052
2.76	2.78	0.03	8.62E-01	9.60E-01	ZNF826	zinc finger protein 826	chr19p12	1560853_x_at	NM_001039884
2.76	2.79	0.02	8.61E-01	9.60E-01	ZNF585A	zinc finger protein 585A	chr19q13.12	229794_at	NM_152655 /// NM_199126
6.13	6.19	0.06	8.62E-01	9.60E-01	GFPT1	glutamine-fructose-6-phosphate transaminase 1	chr2p13	202721_s_at	NM_002056
2.40	2.44	0.03	8.62E-01	9.60E-01	---	---	---	236122_at	---
3.47	3.50	0.03	8.62E-01	9.60E-01	---	---	---	241878_at	---
4.43	4.46	0.03	8.62E-01	9.60E-01	---	---	---	237404_at	---
2.72	2.75	0.02	8.62E-01	9.60E-01	ASPHD2	aspartate beta-hydroxylase domain containing 2	chr22q12.1	227015_at	NM_020437
2.51	2.54	0.02	8.62E-01	9.60E-01	CYP19A1	Cytochrome P450, family 19, subfamily A, polypeptide 1	chr15q21.1	1560295_at	NM_000103 /// NM_031226
2.34	2.36	0.02	8.62E-01	9.60E-01	IGHD	immunoglobulin heavy constant delta	chr14q32.33	230877_at	---
6.58	6.67	0.09	8.62E-01	9.60E-01	SPTLC2	Serine palmitoyltransferase, long chain base subunit 2	chr14q24.3-q31	225095_at	NM_004863
4.06	4.13	0.07	8.62E-01	9.60E-01	---	---	---	242691_at	---
2.75	2.79	0.04	8.62E-01	9.60E-01	---	---	---	217170_at	---
2.76	2.79	0.02	8.62E-01	9.60E-01	---	---	---	215849_x_at	---
6.64	6.72	0.08	8.62E-01	9.60E-01	GALC	galactosylceramidase	chr14q31	204417_at	NM_000153 /// NM_001037525
2.60	2.63	0.03	8.62E-01	9.60E-01	ERAF	erythroid associated factor	chr16p11.2	219672_at	NM_016633
2.17	2.19	0.02	8.62E-01	9.60E-01	MPRIP	Myosin phosphatase Rho interacting protein	chr17p11.2	233414_at	NM_015134 /// NM_201274
1.91	1.93	0.02	8.62E-01	9.60E-01	---	---	---	216441_at	---
2.69	2.72	0.03	8.62E-01	9.60E-01	---	---	---	237589_at	---
6.17	6.20	0.03	8.62E-01	9.60E-01	SQSTM1	sequestosome 1	chr5q35	213112_s_at	NM_003900
1.85	1.87	0.02	8.62E-01	9.60E-01	HMGCLL1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	chr6p12.1	233576_at	NM_001042406 /// NM_019036
5.61	5.66	0.05	8.62E-01	9.60E-01	OPA1	optic atrophy 1 (autosomal dominant)	chr3q28-q29|3q28-q29	212213_x_at	NM_015560 /// NM_130831 /// NM_130832 /// NM_130833 /// NM_130834 /// NM_130835 /// NM_130836 /// NM_130837
4.48	4.53	0.05	8.62E-01	9.60E-01	LOC100130506	hypothetical protein LOC100130506	---	236656_s_at	XM_001720083 /// XM_001724500
2.83	2.87	0.04	8.62E-01	9.60E-01	HM13	Histocompatibility (minor) 13	chr20q11.21	1557148_at	NM_030789 /// NM_178580 /// NM_178581 /// NM_178582
4.97	5.01	0.04	8.63E-01	9.61E-01	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	chr1q32.1	201957_at	NM_002481 /// NM_032103 /// NM_032104 /// NM_032105
5.91	5.95	0.03	8.63E-01	9.61E-01	H2AFX	H2A histone family, member X	chr11q23.2-q23.3	212525_s_at	NM_002105
1.97	1.99	0.02	8.63E-01	9.61E-01	---	---	---	232656_at	---
2.03	2.05	0.02	8.63E-01	9.61E-01	---	---	---	1556331_a_at	---
1.92	1.94	0.02	8.63E-01	9.61E-01	KIAA1128	KIAA1128	chr10q23.1	1554131_at	NM_018999
3.87	3.90	0.03	8.63E-01	9.61E-01	KIF12	kinesin family member 12	chr9q32	229258_at	NM_138424

5.84	5.87	0.03	8.63E-01	9.61E-01	FAM63A	family with sequence similarity 63, member A	chr1q21.2	221856_s_at	NM_001040217 /// NM_018379
2.13	2.15	0.02	8.63E-01	9.61E-01	NEK1	NIMA (never in mitosis gene a)-related kinase 1	chr4q33	216213_at	NM_012224
3.65	3.69	0.03	8.63E-01	9.61E-01	ZNF184	zinc finger protein 184	chr6p21.3	213452_at	NM_007149
7.30	7.35	0.05	8.63E-01	9.61E-01	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily C, 5	chr5q31	209079_x_at	NM_002588 /// NM_003735 /// NM_003736 /// NM_014004 /// NM_018912 /// NM_018913 /// NM_018914 /// NM_018915 /// NM_018916 /// NM_018917 /// NM_018918 /// NM_018919 /// NM_018920 /// NM_018921 /// NM_018922 /// NM_018923 /// NM_018924 /// NM_018925 /// NM_018926 /// NM_018927 /// NM_018928 /// NM_018929 /// NM_031993 /// NM_032009 /// NM_032011 /// NM_032053 /// NM_032054 /// NM_032086 /// NM_032087 /// NM_032088 /// NM_032089 /// NM_032090 /// NM_032091 /// NM_032092 /// NM_032094 /// NM_032095 /// NM_032096 /// NM_032097 /// NM_032098 /// NM_032099 /// NM_032100 /// NM_032101 /// NM_032402 /// NM_032403 /// NM_032406 /// NM_032407
6.05	6.10	0.04	8.63E-01	9.61E-01	PARP14	poly (ADP-ribose) polymerase family, member 14	chr3q21.1	224701_at	NM_017554
2.43	2.45	0.02	8.63E-01	9.61E-01	DHODH	dihydroorotate dehydrogenase	chr16q22	213631_x_at	NM_001361
2.18	2.20	0.02	8.63E-01	9.61E-01	CST11	cystatin 11	chr20p11.21	233797_s_at	NM_080830 /// NM_130794
2.02	2.04	0.02	8.63E-01	9.61E-01	JMJD1A	jumonji domain containing 1A	chr2p11.2	242758_x_at	NM_018433
3.04	3.07	0.04	8.63E-01	9.61E-01	ACO2	aconitase 2, mitochondrial	chr22q11.2-q13.31|22q13.2|22q13.2-q13.31	217307_at	NM_001098
9.00	9.05	0.05	8.63E-01	9.61E-01	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	chr2p25.1	212426_s_at	NM_006826
3.12	3.15	0.04	8.63E-01	9.61E-01	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	chr19q13.2	225979_at	NM_022835
4.31	4.34	0.03	8.63E-01	9.61E-01	GDPD2	glycerophosphodiester phosphodiesterase domain containing 2	chrXq13.1	220291_at	NM_017711
6.36	6.39	0.03	8.63E-01	9.61E-01	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	chr18q11.1	230239_at	NM_005406 /// XM_001713904 /// XM_001722015 /// XM_001723570

3.27	3.30	0.03	8.64E-01	9.61E-01	---	---	---	239284_at	---
6.44	6.50	0.05	8.64E-01	9.61E-01	ANKRD46	Ankyrin repeat domain 46	chr8q22.3	238807_at	NM_198401
6.89	6.93	0.04	8.64E-01	9.61E-01	SPR	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	chr2p14-p12	203458_at	NM_003124
3.56	3.59	0.04	8.64E-01	9.61E-01	---	---	---	236830_at	---
3.23	3.26	0.03	8.64E-01	9.61E-01	CCKBR	cholecystokinin B receptor	chr11p15.4	210381_s_at	NM_176875
2.79	2.82	0.03	8.64E-01	9.61E-01	ZFP64	zinc finger protein 64 homolog (mouse)	chr20q13.2	222897_s_at	NM_018197 /// NM_022088 /// NM_199426 /// NM_199427
6.61	6.64	0.03	8.64E-01	9.61E-01	WDR68	WD repeat domain 68	chr17q23.3	221744_at	NM_005828
2.12	2.15	0.03	8.64E-01	9.61E-01	---	---	---	1564841_at	---
2.85	2.88	0.03	8.64E-01	9.61E-01	CSPG4LYP1 /// CSPG4LYP2	chondroitin sulfate proteoglycan 4-like, Y-linked pseudogene 1 /// chondroitin sulfate proteoglycan 4-like, Y-linked pseudogene 2	chrYq11.223 /// chrYq11.23	211461_at	NR_001554 /// NR_002194
2.61	2.64	0.03	8.64E-01	9.61E-01	---	---	---	1556250_at	---
2.65	2.67	0.03	8.64E-01	9.61E-01	CTRL	chymotrypsin-like	chr16q22.1	214377_s_at	NM_001907
2.06	2.08	0.02	8.64E-01	9.61E-01	---	---	---	234433_at	---
2.28	2.30	0.02	8.64E-01	9.61E-01	SPATA19	spermatogenesis associated 19	chr11q25	1559138_a_at	NM_174927
2.70	2.72	0.02	8.64E-01	9.61E-01	FLJ16124	FLJ16124 protein	chr2p14	1569900_at	NM_001004345
2.54	2.56	0.02	8.64E-01	9.61E-01	---	---	---	244309_at	---
2.52	2.54	0.02	8.64E-01	9.61E-01	CCNF	cyclin F	chr16p13.3	204827_s_at	NM_001761
3.71	3.74	0.03	8.64E-01	9.61E-01	SRF	serum response factor (c-fos serum response element-binding transcription factor)	chr6p21.1	202400_s_at	NM_003131
2.62	2.65	0.02	8.64E-01	9.61E-01	---	---	---	1566141_at	---
1.92	1.94	0.02	8.65E-01	9.61E-01	BRCA2	breast cancer 2, early onset	chr13q12.3	208368_s_at	NM_000059
2.43	2.45	0.02	8.65E-01	9.61E-01	OSBPL6	oxysterol binding protein-like 6	chr2q31-q32.1	236261_at	NM_032523 /// NM_145739
2.68	2.70	0.02	8.65E-01	9.61E-01	PRIM2	primase, DNA, polypeptide 2 (58kDa)	chr6p12-p11.1	205628_at	NM_000947
5.62	5.71	0.10	8.65E-01	9.61E-01	LGALS8	lectin, galactoside-binding, soluble, 8	chr1q42-q43	208936_x_at	NM_006499 /// NM_201543 /// NM_201544 /// NM_201545
3.84	3.90	0.06	8.65E-01	9.61E-01	MRAP2	melanocortin 2 receptor accessory protein 2	chr6q14.3	227226_at	NM_138409
5.34	5.40	0.06	8.65E-01	9.61E-01	ZFP62	zinc finger protein 62 homolog (mouse)	chr5p15.33	227796_at	NM_152283
3.24	3.27	0.03	8.65E-01	9.61E-01	---	---	---	1556962_at	---
4.12	4.15	0.03	8.65E-01	9.61E-01	CAPRIN2	caprin family member 2	chr12p11	1555608_at	NM_001002259 /// NM_023925 /// NM_032156
4.88	4.91	0.03	8.65E-01	9.61E-01	N-PAC	cytokine-like nuclear factor n-pac	chr16p13.3	222115_x_at	NM_032569
2.30	2.33	0.03	8.65E-01	9.61E-01	---	---	---	238822_at	---
2.71	2.74	0.03	8.65E-01	9.61E-01	KIF11	kinesin family member 11	chr10q24.1	204444_at	NM_004523
2.45	2.48	0.03	8.65E-01	9.61E-01	LOC285375	hypothetical protein LOC285375	chr3p25.1	1563043_at	---
2.24	2.27	0.03	8.65E-01	9.61E-01	---	---	---	231082_at	---
2.17	2.20	0.03	8.65E-01	9.61E-01	TTTY7	testis-specific transcript, Y-linked 7	chrYp11.2	234309_at	NR_001534
2.52	2.55	0.02	8.65E-01	9.61E-01	---	---	---	217038_at	---
2.16	2.18	0.02	8.65E-01	9.61E-01	TCP11L2	t-complex 11 (mouse)-like 2	chr12q23.3	1565525_a_at	NM_152772
3.36	3.38	0.02	8.65E-01	9.61E-01	---	---	---	231542_at	---
2.07	2.09	0.02	8.65E-01	9.61E-01	---	---	---	1563279_at	---
2.72	2.74	0.02	8.65E-01	9.61E-01	CSRP2BP	CSRP2 binding protein	chr20p11.23	227316_at	NM_020536 /// NM_177926
1.99	2.01	0.02	8.65E-01	9.61E-01	ALS2CR11	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	chr2q33.1	1563673_a_at	NM_152525
4.95	4.99	0.03	8.66E-01	9.61E-01	ANKRD39	ankyrin repeat domain 39	chr2q11.2	223532_at	NM_016466
3.53	3.56	0.03	8.66E-01	9.61E-01	CMAS	Cytidine monophosphate N-acetylneuraminic acid synthetase	chr12p12.1	241065_x_at	NM_018686
3.96	3.99	0.03	8.66E-01	9.61E-01	NAV1	neuron navigator 1	chr1q32.3	224774_s_at	NM_020443
7.70	7.77	0.07	8.66E-01	9.61E-01	C11orf58	chromosome 11 open reading frame 58	chr11p15.1	201784_s_at	NM_014267
6.13	6.18	0.05	8.66E-01	9.61E-01	CRIPT	cysteine-rich PDZ-binding protein	chr2p21	222702_x_at	NM_014171
4.76	4.81	0.05	8.66E-01	9.61E-01	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	chr9q21.31	235765_at	NM_007005
3.36	3.40	0.04	8.66E-01	9.61E-01	GIMAP1	GTPase, IMAP family member 1	chr7q36.1	1552318_at	NM_130759
3.48	3.51	0.03	8.66E-01	9.61E-01	C20orf7	chromosome 20 open reading frame 7	chr20p12.1	219524_s_at	NM_001039375 /// NM_024120
2.31	2.34	0.03	8.66E-01	9.61E-01	---	---	---	243942_at	---
3.60	3.62	0.03	8.66E-01	9.61E-01	FRMD1	FERM domain containing 1	chr6q27	220819_at	NM_001122841 /// NM_024919
2.09	2.11	0.03	8.66E-01	9.61E-01	---	---	---	234202_at	---
2.82	2.84	0.03	8.66E-01	9.61E-01	TBX5	T-box 5	chr12q24.1	240715_at	NM_000192 /// NM_080717 /// NM_080718 /// NM_181486
2.59	2.61	0.03	8.66E-01	9.61E-01	CCDC75	coiled-coil domain containing 75	chr2p22.2	1559893_at	NM_174931

2.56	2.59	0.03	8.66E-01	9.61E-01	ZDHHC13	Zinc finger, DHHC-type containing 13	chr11p15.1	232440_at	NM_001001483 /// NM_019028
5.56	5.59	0.03	8.66E-01	9.61E-01	---	---	---	240595_at	---
2.34	2.37	0.02	8.66E-01	9.61E-01	---	---	---	1561026_a_at	---
2.14	2.16	0.02	8.66E-01	9.61E-01	---	---	---	1561333_at	---
2.01	2.03	0.02	8.66E-01	9.61E-01	---	---	---	236827_at	---
6.43	6.47	0.04	8.66E-01	9.61E-01	CHD3	chromodomain helicase DNA binding protein 3	chr17p13.1	208807_s_at	NM_001005271 /// NM_001005273 /// NM_005852
2.73	2.76	0.03	8.66E-01	9.61E-01	---	---	---	1560433_at	---
2.93	2.96	0.03	8.66E-01	9.61E-01	---	---	---	239127_at	---
3.38	3.41	0.03	8.66E-01	9.61E-01	---	---	---	240085_at	---
3.20	3.22	0.03	8.66E-01	9.61E-01	MAP1A	microtubule-associated protein 1A	chr15q13-qter	215384_s_at	NM_002373
2.64	2.66	0.02	8.66E-01	9.61E-01	TMEM170A	Transmembrane protein 170A	chr16q23.1	230414_s_at	NM_145254
6.41	6.48	0.07	8.66E-01	9.62E-01	EXOC6	exocyst complex component 6	chr10q23.33	226259_at	NM_001013848 /// NM_019053
3.13	3.16	0.04	8.66E-01	9.62E-01	FER1L4	fer-1-like 4 (C. elegans)	chr20q11.22	222245_s_at	XM_001732892 /// XM_001732893 /// XM_001732894
5.43	5.46	0.03	8.66E-01	9.62E-01	ZNF830	zinc finger protein 830	chr17q12	226315_at	NM_052857
4.93	4.96	0.03	8.67E-01	9.62E-01	APOBEC3F /// APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F /// apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	chr22q13.1 /// chr22q13.1-q13.2	243912_x_at	NM_001006666 /// NM_021822 /// NM_145298
4.44	4.47	0.03	8.67E-01	9.62E-01	NDOR1	NADPH dependent diflavin oxidoreductase 1	chr9q34.3	219899_x_at	NM_014434 /// XM_001716570
2.28	2.30	0.02	8.67E-01	9.62E-01	CYSLTR1	cysteinyl leukotriene receptor 1	chrXq13.2-q21.1	216288_at	NM_006639
2.16	2.18	0.02	8.67E-01	9.62E-01	DNASE2B	deoxyribonuclease II beta	chr1p22.3	220380_at	NM_021233 /// NM_058248
6.86	6.93	0.06	8.67E-01	9.62E-01	MRPL39	mitochondrial ribosomal protein L39	chr21q21.3	218558_s_at	NM_017446 /// NM_080794
4.35	4.42	0.08	8.67E-01	9.62E-01	PGM3	phosphoglucomutase 3	chr6q14.1-q15	210041_s_at	NM_015599
2.25	2.30	0.05	8.67E-01	9.62E-01	STXBP5	syntaxin binding protein 5 (tomosyn)	chr6q24.3	226794_at	NM_001127715 /// NM_139244
3.32	3.37	0.05	8.67E-01	9.62E-01	PIGB	phosphatidylinositol glycan anchor biosynthesis, class B	chr15q21-q22	242760_x_at	NM_004855
5.32	5.37	0.05	8.67E-01	9.62E-01	FAM167B	family with sequence similarity 167, member B	chr1p35.1	223657_at	NM_032648
3.92	3.96	0.05	8.67E-01	9.62E-01	LINS1	lines homolog 1 (Drosophila)	chr15q26.3	1554456_a_at	NM_001040614 /// NM_001040615 /// NM_001040616 /// NM_018148
2.86	2.91	0.04	8.67E-01	9.62E-01	FAM46C	family with sequence similarity 46, member C	chr1p12	220306_at	NM_017709
4.15	4.19	0.04	8.67E-01	9.62E-01	LRMP	lymphoid-restricted membrane protein	chr12p12.1	204674_at	NM_006152
2.97	3.01	0.04	8.67E-01	9.62E-01	RTDR1	Rhabdoid tumor deletion region gene 1	chr22q11.2	229977_at	NM_014433
4.34	4.38	0.04	8.67E-01	9.62E-01	GLB1L2	galactosidase, beta 1-like 2	chr11q25	213713_s_at	NM_138342
8.10	8.14	0.04	8.67E-01	9.62E-01	RAB6A /// RAB6C	RAB6A, member RAS oncogene family /// RAB6C, member RAS oncogene family	chr11q13.3 /// chr2q21.1	210406_s_at	NM_002869 /// NM_032144 /// NM_198896
5.52	5.55	0.04	8.67E-01	9.62E-01	BMP1	bone morphogenetic protein 1	chr8p21.3	206725_x_at	NM_001199 /// NM_006128 /// NM_006129
6.98	7.01	0.03	8.67E-01	9.62E-01	KLHL24	kelch-like 24 (Drosophila)	chr3q27.1	206551_x_at	NM_017644
4.56	4.60	0.03	8.67E-01	9.62E-01	TRAPPC9	trafficking protein particle complex 9	chr8q24.3	221672_s_at	NM_031466
2.63	2.66	0.03	8.67E-01	9.62E-01	PVRL3	poliovirus receptor-related 3	chr3q13	213325_at	NM_015480
2.12	2.15	0.03	8.67E-01	9.62E-01	ZEB1	zinc finger E-box binding homeobox 1	chr10p11.2	210875_s_at	NM_001128128 /// NM_030751
2.26	2.28	0.03	8.67E-01	9.62E-01	---	---	---	243839_s_at	---
3.42	3.44	0.03	8.67E-01	9.62E-01	LOC100128198	hypothetical protein LOC100128198	chr21q22.11	239564_at	XM_001720415 /// XM_001724862 /// XM_001725495
6.33	6.35	0.03	8.67E-01	9.62E-01	ACTR8	ARP8 actin-related protein 8 homolog (yeast)	---	222707_s_at	NM_022899
2.04	2.06	0.02	8.67E-01	9.62E-01	---	---	---	243197_at	---
2.16	2.18	0.02	8.67E-01	9.62E-01	LIG3	ligase III, DNA, ATP-dependent	chr17q11.2-q12	1555169_at	NM_002311 /// NM_013975
2.06	2.07	0.02	8.67E-01	9.62E-01	---	---	---	233853_at	---

1.92	1.94	0.02	8.67E-01	9.62E-01	SNRPB2	Small nuclear ribonucleoprotein polypeptide B"	chr20p12.2-p11.22	1561965_at	NM_003092 /// NM_198220
2.13	2.15	0.02	8.67E-01	9.62E-01	---	---	---	1559663_at	---
2.00	2.01	0.02	8.67E-01	9.62E-01	TRPC4	transient receptor potential cation channel, subfamily C, member 4	chr13q13.1-q13.2	224219_s_at	NM_016179
4.02	4.08	0.06	8.68E-01	9.62E-01	DENND2A	DENN/MADD domain containing 2A	chr7q34	221885_at	NM_015689
2.38	2.42	0.04	8.68E-01	9.62E-01	PCDHB14	protocadherin beta 14	chr5q31	231726_at	NM_018934
2.68	2.70	0.03	8.68E-01	9.62E-01	---	---	---	237112_at	---
2.06	2.10	0.03	8.68E-01	9.62E-01	FLJ33297	hypothetical gene supported by AK090616	chr12p13.33	1558308_at	---
2.53	2.56	0.03	8.68E-01	9.62E-01	UCHL1	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	chr4p14	1555834_at	NM_004181
2.08	2.11	0.02	8.68E-01	9.62E-01	C5orf47	chromosome 5 open reading frame 47	chr5q35.2	1557057_a_at	XM_001715744 /// XM_376444 /// XM_941190
2.04	2.06	0.02	8.68E-01	9.62E-01	---	---	---	237074_at	---
2.03	2.05	0.02	8.68E-01	9.62E-01	BHLHB9	Basic helix-loop-helix domain containing, class B, 9	chrXq23	1559510_at	NM_030639
1.91	1.92	0.02	8.68E-01	9.62E-01	---	---	---	1555932_at	---
6.00	6.07	0.07	8.68E-01	9.62E-01	HNRNPA3 /// HNRNPA3P1	heterogeneous nuclear ribonucleoprotein A3 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	chr10q11.21 /// chr2q31.2	206809_s_at	NM_194247 /// NR_002726
3.41	3.44	0.03	8.68E-01	9.62E-01	---	---	---	1566137_s_at	---
2.19	2.21	0.02	8.68E-01	9.62E-01	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	chr5q33.1-qter	244578_at	NM_005565
3.54	3.57	0.03	8.68E-01	9.62E-01	IKIP	IKK interacting protein	chr12q23.1	236249_at	NM_153687 /// NM_201612 /// NM_201613
2.36	2.38	0.02	8.68E-01	9.62E-01	ARHGAP6	Rho GTPase activating protein 6	chrXp22.3	208085_s_at	NM_001174 /// NM_006125 /// NM_013422 /// NM_013423 /// NM_013427
2.94	2.97	0.04	8.69E-01	9.62E-01	---	---	---	240100_at	---
10.02	10.04	0.03	8.68E-01	9.62E-01	TMBIM4	transmembrane BAX inhibitor motif containing 4	chr12q14.1|12q14.1-q15	223892_s_at	NM_016056
1.92	1.94	0.02	8.68E-01	9.62E-01	---	---	---	234582_at	---
2.17	2.19	0.02	8.69E-01	9.62E-01	LOC157503	hypothetical protein LOC157503	chr8q11.23	230692_at	---
2.07	2.09	0.02	8.69E-01	9.62E-01	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	chr22q13.31-q13.33	237750_at	NM_022098
3.45	3.48	0.03	8.69E-01	9.62E-01	IGL@	immunoglobulin lambda locus	chr22q11.1-q11.2	234366_x_at	---
1.92	1.94	0.02	8.69E-01	9.62E-01	FUT9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	chr6q16	207696_at	NM_006581
2.58	2.60	0.02	8.69E-01	9.62E-01	ODF3L1	outer dense fiber of sperm tails 3-like 1	chr15q24.2	236245_at	NM_175881
2.97	3.00	0.03	8.69E-01	9.62E-01	RIF1	RAP1 interacting factor homolog (yeast)	chr2q23.3	241820_at	NM_018151
3.63	3.66	0.03	8.69E-01	9.62E-01	CCDC27	coiled-coil domain containing 27	chr1p36.32	1552948_at	NM_152492
2.21	2.23	0.02	8.69E-01	9.62E-01	WDR66	WD repeat domain 66	chr12q24.31	230193_at	NM_144668
3.28	3.30	0.02	8.69E-01	9.62E-01	---	---	---	229698_at	---
4.46	4.51	0.05	8.69E-01	9.62E-01	---	---	---	227089_at	---
2.87	2.91	0.04	8.69E-01	9.62E-01	LOXL2	Lysyl oxidase-like 2	chr8p21.3-p21.2	228808_s_at	NM_002318
2.08	2.10	0.02	8.69E-01	9.62E-01	---	---	---	230319_at	---
4.89	4.94	0.05	8.69E-01	9.63E-01	---	---	---	228180_at	---
3.16	3.19	0.03	8.69E-01	9.63E-01	C2orf39	chromosome 2 open reading frame 39	chr2p23.3	231133_at	NM_145038
2.33	2.35	0.02	8.69E-01	9.63E-01	---	---	---	1560422_at	---
6.45	6.49	0.04	8.69E-01	9.63E-01	JRK	jerky homolog (mouse)	chr8q24.3	216309_x_at	NM_001077527 /// NM_003724
4.92	5.01	0.09	8.69E-01	9.63E-01	SNAP23	synaptosomal-associated protein, 23kDa	chr15q15.1	214544_s_at	NM_003825 /// NM_130798
2.63	2.66	0.03	8.69E-01	9.63E-01	---	---	---	229156_s_at	---
3.88	3.90	0.03	8.69E-01	9.63E-01	PDLIM4	PDZ and LIM domain 4	chr5q31.1	218690_at	NM_001131027 /// NM_003687
2.37	2.39	0.02	8.69E-01	9.63E-01	CUGBP2	CUG triplet repeat, RNA binding protein 2	chr10p13	1556323_at	NM_001025076 /// NM_001025077 /// NM_001083591 /// NM_006561
2.73	2.75	0.02	8.69E-01	9.63E-01	MPZL2	myelin protein zero-like 2	chr11q24	230518_at	NM_005797 /// NM_144765
2.05	2.07	0.02	8.69E-01	9.63E-01	EVI1	ecotropic viral integration site 1	chr3q24-q28	215851_at	NM_001105077 /// NM_001105078 /// NM_005241
4.49	4.51	0.02	8.69E-01	9.63E-01	PRO0461	hypothetical LOC652276	chr16p13.3	1553130_at	XR_017077 /// XR_040461
2.04	2.06	0.02	8.70E-01	9.63E-01	CRB1	crumbs homolog 1 (Drosophila)	chr1q31-q32.1	244403_at	NM_201253

2.90	2.93	0.03	8.70E-01	9.63E-01	SH3BP2	SH3-domain binding protein 2	chr4p16.3	209371_s_at	NM_001122681 /// NM_003023
3.14	3.16	0.03	8.70E-01	9.63E-01	IGL@ /// IGLC2 /// IGLV2-14 /// IGLV7-43 /// IGLV7-46	immunoglobulin lambda locus /// immunoglobulin lambda constant 2 (Kern-Oz- marker) /// immunoglobulin lambda variable 2-14 /// immunoglobulin lambda variable 7-43 /// immunoglobulin lambda variable 7-46	chr22q11.1-q11.2 /// chr22q11.2	1558176_at	---
2.72	2.76	0.04	8.70E-01	9.63E-01	SOBP	sine oculis binding protein homolog (Drosophila)	chr6q21	1569351_at	NM_018013
2.38	2.41	0.02	8.70E-01	9.63E-01	---	---	---	236775_s_at	---
9.18	9.24	0.06	8.70E-01	9.63E-01	C12orf57	chromosome 12 open reading frame 57	chr12p13.31	224719_s_at	NM_138425
2.26	2.28	0.02	8.70E-01	9.63E-01	---	---	---	243988_at	---
2.13	2.15	0.02	8.70E-01	9.63E-01	LOC286272	hypothetical protein LOC286272	chr9q12	232182_at	---
7.37	7.44	0.07	8.70E-01	9.63E-01	PNPLA8	patatin-like phospholipase domain containing 8	chr7q31	223982_s_at	NM_015723
5.68	5.73	0.05	8.70E-01	9.63E-01	CACYBP	calcyclin binding protein	chr1q24-q25	210691_s_at	NM_001007214 /// NM_014412
5.13	5.17	0.04	8.70E-01	9.63E-01	C6orf97	chromosome 6 open reading frame 97	chr6q25.1	220581_at	NM_025059
6.68	6.71	0.03	8.70E-01	9.63E-01	PARN	poly(A)-specific ribonuclease (deadenylation nuclease)	chr16p13	203905_at	NM_001134477 /// NM_002582
2.47	2.50	0.03	8.70E-01	9.63E-01	---	---	---	221105_at	---
2.27	2.30	0.02	8.70E-01	9.63E-01	IL21R	interleukin 21 receptor	chr16p11	221658_s_at	NM_021798 /// NM_181078 /// NM_181079
2.99	3.01	0.02	8.70E-01	9.63E-01	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	chr8p23.1	232007_at	NM_018361
2.24	2.26	0.02	8.70E-01	9.63E-01	COL4A6	collagen, type IV, alpha 6	chrXq22	211473_s_at	NM_001847 /// NM_033641
1.90	1.92	0.02	8.70E-01	9.63E-01	C20orf69 /// DKFZP434B2016 /// LOC643670 /// LOC728105 /// LOC728323 /// PCMTD2 /// tcag7.907	chromosome 20 open reading frame 69 /// similar to hypothetical protein LOC284701 /// similar to hCG1739109 /// similar to hCG1739109 /// hypothetical LOC728323 /// protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 /// hypothetical LOC402483	chr16q24.3 /// chr1p36.33 /// chr20q13.33 /// chr2q37.3 /// chr3q29 /// chr7q32.1	232953_at	NM_001104925 /// NM_018257 /// XM_001720425 /// XM_932064 /// XM_932068 /// XM_932075 /// XR_015328 /// XR_039242 /// XR_040932 /// XR_040933 /// XR_040934 /// XR_040935
5.80	5.89	0.09	8.70E-01	9.63E-01	---	---	---	235652_at	---
3.91	3.95	0.04	8.71E-01	9.63E-01	C18orf8	Chromosome 18 open reading frame 8	chr18q11.2	232345_at	NM_013326
3.44	3.48	0.03	8.70E-01	9.63E-01	---	---	---	216739_at	---
1.86	1.88	0.02	8.70E-01	9.63E-01	---	---	---	234022_at	---
2.58	2.60	0.02	8.71E-01	9.63E-01	ANGEL1	Angel homolog 1 (Drosophila)	chr14q24.3	244685_at	NM_015305
3.98	4.01	0.03	8.71E-01	9.63E-01	ZNF219	zinc finger protein 219	chr14q11	222864_s_at	NM_001101672 /// NM_001102454 /// NM_016423
2.55	2.58	0.03	8.71E-01	9.63E-01	---	---	---	230235_at	---
2.77	2.80	0.02	8.71E-01	9.63E-01	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	chr12q21.2	235038_at	NM_007043
1.94	1.96	0.02	8.71E-01	9.63E-01	---	---	---	1560528_at	---
2.65	2.67	0.02	8.71E-01	9.63E-01	OR8D1	olfactory receptor, family 8, subfamily D, member 1	chr11q24.2	1555661_at	NM_001002917
4.93	4.99	0.06	8.71E-01	9.63E-01	FAM179B	family with sequence similarity 179, member B	chr14q21.3	213304_at	NM_015091
2.21	2.24	0.03	8.71E-01	9.63E-01	C12orf48	chromosome 12 open reading frame 48	chr12q23.2	224147_at	NM_017915
7.28	7.39	0.11	8.71E-01	9.63E-01	CYB5A	cytochrome b5 type A (microsomal)	chr18q23	207843_x_at	NM_001914 /// NM_148923
3.20	3.22	0.03	8.71E-01	9.63E-01	GMIP	GEM interacting protein	chr19p12-p11	222782_s_at	NM_016573
2.28	2.30	0.02	8.71E-01	9.63E-01	LOC728853	similar to RIKEN cDNA 4930432E11	chr19q13.13	1568689_at	XR_015396 /// XR_015633 /// XR_037738
2.01	2.04	0.03	8.71E-01	9.63E-01	MMP12	matrix metallopeptidase 12 (macrophage elastase)	chr11q22.3	204580_at	NM_002426
7.74	7.78	0.04	8.71E-01	9.63E-01	ZMAT2	zinc finger, matrin type 2	chr5q31.3	224782_at	NM_144723
6.24	6.29	0.05	8.72E-01	9.63E-01	PEX19	peroxisomal biogenesis factor 19	chr1q23.2	201707_at	NM_001131039 /// NM_002857
3.13	3.18	0.05	8.72E-01	9.63E-01	PCDH17	protocadherin 17	chr13q21.1	228863_at	NM_001040429
6.04	6.09	0.05	8.72E-01	9.63E-01	GLT8D1	glycosyltransferase 8 domain containing 1	chr3p21.1	218147_s_at	NM_001010983 /// NM_018446 /// NM_152932

6.31	6.35	0.04	8.72E-01	9.63E-01	C2orf7	chromosome 2 open reading frame 7	chr2p13.2	223312_at	NM_032319
4.00	4.04	0.04	8.72E-01	9.63E-01	ZNF510	zinc finger protein 510	chr9q22.33	206053_at	NM_014930
6.05	6.09	0.03	8.72E-01	9.63E-01	HHLA3	HERV-H LTR-associating 3	chr1p31.1	234665_x_at	NM_001031693 /// NM_001036645 /// NM_001036646 /// NM_007071
4.69	4.72	0.03	8.71E-01	9.63E-01	---	---	---	226497_s_at	---
2.69	2.72	0.03	8.72E-01	9.63E-01	---	---	---	1560509_at	---
6.05	6.08	0.03	8.71E-01	9.63E-01	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	chr20q13.33	219653_at	NM_144703
2.71	2.74	0.03	8.72E-01	9.63E-01	SPRR3	small proline-rich protein 3	chr1q21-q22	218990_s_at	NM_001097589 /// NM_005416
5.79	5.82	0.03	8.72E-01	9.63E-01	ZBTB45	zinc finger and BTB domain containing 45	chr19q13.43	229862_x_at	NM_032792
2.10	2.13	0.03	8.71E-01	9.63E-01	TMPRSS11B	transmembrane protease, serine 11B	chr4q13.2	1560712_at	NM_182502
2.42	2.44	0.02	8.72E-01	9.63E-01	CASC2	cancer susceptibility candidate 2	chr10q26.11	1556630_at	XR_041332 /// XR_041333 /// XR_041334
3.12	3.14	0.02	8.72E-01	9.63E-01	---	---	---	240962_at	---
2.23	2.25	0.02	8.71E-01	9.63E-01	REPS1	RALBP1 associated Eps domain containing 1	---	215922_at	NM_001128617 /// NM_031922
1.97	1.99	0.02	8.71E-01	9.63E-01	---	---	---	207477_at	---
2.53	2.57	0.04	8.72E-01	9.63E-01	LOC100130648 /// SSX2 /// SSX2B	similar to Protein SSX2 (Synovial sarcoma, X breakpoint 2) (Cancer/testis antigen 5.2) (CT5.2) (SSX) (HOM-MEL-40) /// synovial sarcoma, X breakpoint 2 /// synovial sarcoma, X breakpoint 2B	chrXp11.22	216471_x_at	NM_003147 /// NM_175698 /// XM_001719568 /// XM_001720499
3.03	3.06	0.03	8.72E-01	9.63E-01	KLHL28	kelch-like 28 (Drosophila)	chr14q21.3	220374_at	NM_017658
2.98	3.01	0.03	8.72E-01	9.63E-01	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	chr21q22.3	232755_at	NM_003343 /// NM_182688
4.52	4.54	0.02	8.72E-01	9.63E-01	LOC100132357 /// LOC100132784 /// LOC100134805	similar to hCG1656091 /// similar to hCG1795400 /// hypothetical protein LOC100134805	chr9p11.2 /// chr9q12	237085_x_at	XM_001714380 /// XM_001719203 /// XM_001720461
7.78	7.81	0.03	8.72E-01	9.63E-01	SYNGR2	synaptogyrin 2	chr17q25.3	201079_at	NM_004710
2.88	2.91	0.03	8.72E-01	9.63E-01	FAM81A /// LOC100130999	family with sequence similarity 81, member A /// hypothetical protein LOC100130999	chr15q22.2	227756_at	NM_152450 /// XM_001723321 /// XM_001726025 /// XM_001726451
1.88	1.90	0.02	8.72E-01	9.63E-01	EPHA5	EPH receptor A5	chr4q13.1	237939_at	NM_004439 /// NM_182472
3.92	3.97	0.04	8.72E-01	9.63E-01	---	---	---	1559820_at	---
4.73	4.77	0.04	8.72E-01	9.63E-01	WIZ	widely interspaced zinc finger motifs	chr19p13.1	221784_at	NM_021241
4.23	4.25	0.02	8.72E-01	9.63E-01	DTWD2	DTW domain containing 2	chr5q23.1	231277_x_at	NM_173666
2.55	2.57	0.02	8.72E-01	9.63E-01	---	---	---	244005_at	---
3.01	3.04	0.03	8.72E-01	9.64E-01	LOC283551	Hypothetical protein LOC283551	chr14q22.1	1569274_at	NM_001012706
2.19	2.21	0.02	8.73E-01	9.64E-01	---	---	---	229814_at	---
3.65	3.71	0.05	8.73E-01	9.64E-01	MLF1	myeloid leukemia factor 1	chr3q25.1	204783_at	NM_001130156 /// NM_001130157 /// NM_022443
2.32	2.34	0.02	8.73E-01	9.64E-01	---	---	---	237676_at	---
3.36	3.39	0.03	8.73E-01	9.64E-01	KLK15	kallikrein-related peptidase 15	chr19q13.41	221462_x_at	NM_017509 /// NM_138563 /// NM_138564
3.42	3.43	0.02	8.73E-01	9.64E-01	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	chr10p15-p14	217626_at	NM_001353 /// XM_001724839
3.27	3.31	0.03	8.73E-01	9.64E-01	C8orf60	chromosome 8 open reading frame 60	chr8q24.3	220712_at	---
7.62	7.67	0.04	8.73E-01	9.64E-01	CD276	CD276 molecule	chr15q23-q24	224859_at	NM_001024736 /// NM_025240
6.68	6.79	0.11	8.73E-01	9.64E-01	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	chrXp11.3-p11.23	212515_s_at	NM_001356
6.18	6.24	0.07	8.73E-01	9.64E-01	PFKP	phosphofructokinase, platelet	chr10p15.3-p15.2	201037_at	NM_002627
2.46	2.49	0.03	8.73E-01	9.64E-01	SLC15A2	solute carrier family 15 (H+/peptide transporter), member 2	chr3q13.33	240159_at	NM_021082
6.44	6.47	0.03	8.73E-01	9.64E-01	LMF2	lipase maturation factor 2	chr22q13.33	212682_s_at	NM_033200

4.65	4.68	0.03	8.73E-01	9.64E-01	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	chr21q22.3	224282_s_at	NM_001037553 /// NM_020132
5.77	5.79	0.02	8.73E-01	9.64E-01	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	chr17q11.2	35846_at	NM_003250 /// NM_199334
2.15	2.17	0.02	8.73E-01	9.64E-01	---	---	---	1562341_at	---
5.20	5.22	0.02	8.73E-01	9.64E-01	FGFR1	fibroblast growth factor receptor 1	chr8p11.2-p11.1	215404_x_at	NM_015850 /// NM_023105 /// NM_023106 /// NM_023107 /// NM_023108 /// NM_023110 /// NM_023111
2.64	2.66	0.02	8.73E-01	9.64E-01	UHRF1BP1L	UHRF1 binding protein 1-like	chr12q23.1	1554291_at	NM_001006947 /// NM_015054
2.06	2.08	0.02	8.73E-01	9.64E-01	---	---	---	233957_at	---
2.06	2.08	0.02	8.73E-01	9.64E-01	---	---	---	1561272_at	---
6.65	6.70	0.05	8.74E-01	9.64E-01	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	chr14q32	201877_s_at	NM_002719 /// NM_178586 /// NM_178587 /// NM_178588
3.84	3.89	0.05	8.73E-01	9.64E-01	---	---	---	229383_at	---
2.76	2.79	0.03	8.74E-01	9.64E-01	LYZL6	lysozyme-like 6	chr17q11.2	207343_at	NM_020426
3.38	3.41	0.03	8.74E-01	9.64E-01	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	chr10q24.31	217511_at	NM_030929
2.11	2.13	0.02	8.74E-01	9.64E-01	GYPA	Glycophorin A (MNS blood group)	chr4q28.2-q31.1	1559520_at	NM_002099
4.30	4.33	0.03	8.74E-01	9.64E-01	C14orf80	chromosome 14 open reading frame 80	chr14q32.33	228558_at	NM_173608
4.70	4.74	0.04	8.74E-01	9.64E-01	---	---	---	238806_at	---
3.56	3.60	0.03	8.74E-01	9.64E-01	---	---	---	239064_at	---
2.90	2.93	0.03	8.74E-01	9.64E-01	DTNA	dystrobrevin, alpha	chr18q12	208430_s_at	NM_001128175 /// NM_001390 /// NM_001391 /// NM_001392 /// NM_032975 /// NM_032978 /// NM_032979 /// NM_032980 /// NM_032981
2.80	2.83	0.03	8.74E-01	9.64E-01	---	---	---	1560332_at	---
2.78	2.81	0.02	8.74E-01	9.64E-01	GJB5	gap junction protein, beta 5, 31.1kDa	chr1p35.1	206156_at	NM_005268
1.97	1.99	0.02	8.74E-01	9.64E-01	---	---	---	234242_at	---
2.01	2.03	0.03	8.74E-01	9.64E-01	---	---	---	1566481_at	---
5.40	5.44	0.04	8.74E-01	9.64E-01	C10orf57	chromosome 10 open reading frame 57	chr10q22.3	222545_s_at	NM_025125
4.38	4.52	0.14	8.74E-01	9.64E-01	---	---	---	233286_at	---
3.90	3.97	0.07	8.74E-01	9.64E-01	---	---	---	232356_at	---
5.91	5.97	0.06	8.74E-01	9.64E-01	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	chr12q15-q21	201603_at	NM_002480
2.02	2.04	0.02	8.74E-01	9.64E-01	---	---	---	231486_x_at	---
2.06	2.08	0.02	8.74E-01	9.64E-01	---	---	---	234823_at	---
2.99	3.04	0.04	8.74E-01	9.64E-01	TARP /// TRGC2	TCR gamma alternate reading frame protein /// T cell receptor gamma constant 2	chr7p14 /// chr7p15-p14	216920_s_at	NM_001003799 /// NM_001003806
5.50	5.54	0.04	8.75E-01	9.64E-01	FAM100A	family with sequence similarity 100, member A	chr16p13.3	225874_at	NM_145253
4.32	4.36	0.04	8.74E-01	9.64E-01	RGS12	regulator of G-protein signaling 12	chr4p16.3	205823_at	NM_002926 /// NM_198227 /// NM_198229
2.64	2.67	0.04	8.74E-01	9.64E-01	ABHD13	abhydrolase domain containing 13	chr13q33.3	234993_at	NM_032859
4.22	4.25	0.03	8.75E-01	9.64E-01	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	chr12q14.2	1569269_s_at	NM_020762
2.89	2.92	0.03	8.74E-01	9.64E-01	TBX5	T-box 5	chr12q24.1	211886_s_at	NM_000192 /// NM_080717 /// NM_080718 /// NM_181486
3.11	3.14	0.03	8.75E-01	9.64E-01	DAPK2	death-associated protein kinase 2	chr15q22.31	215184_at	NM_014326
3.17	3.20	0.03	8.75E-01	9.64E-01	CCDC88C	coiled-coil domain containing 88C	chr14q32.12	231288_at	NM_001080414
3.30	3.33	0.03	8.74E-01	9.64E-01	UBXN1	UBX domain protein 1	chr11q12.3	210623_at	NM_015853
8.12	8.14	0.02	8.74E-01	9.64E-01	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	chr8p11.23	225136_at	NM_021623
2.44	2.46	0.02	8.74E-01	9.64E-01	LOC728342	Hypothetical protein LOC728342	chr5q23.1	239319_at	XR_041032 /// XR_041033 /// XR_041034
2.18	2.20	0.02	8.75E-01	9.64E-01	---	---	---	242228_at	---
2.18	2.21	0.02	8.75E-01	9.64E-01	LOC283737	hypothetical protein LOC283737	chr15q25.3	237687_at	---

2.14	2.16	0.02	8.74E-01	9.64E-01	ZNF781	zinc finger protein 781	chr19q13.12	1552785_at	NM_152605
2.10	2.11	0.02	8.74E-01	9.64E-01	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	chr7p11	203820_s_at	NM_006547
3.12	3.14	0.02	8.74E-01	9.64E-01	---	---	---	1560576_at	---
2.09	2.11	0.02	8.75E-01	9.64E-01	TTBK2	tau tubulin kinase 2	chr15q15.2	1554293_at	NM_173500
2.01	2.03	0.02	8.75E-01	9.64E-01	---	---	---	1558869_at	---
2.35	2.37	0.02	8.75E-01	9.64E-01	---	---	---	237193_s_at	---
7.44	7.50	0.06	8.75E-01	9.64E-01	---	---	---	224811_at	---
6.44	6.49	0.05	8.75E-01	9.64E-01	S100A11P	S100 calcium binding protein A11 pseudogene	chr7q22.1	208540_x_at	XM_001126350 /// XM_001131859 /// XM_001727033
2.90	2.94	0.04	8.75E-01	9.64E-01	---	---	---	233994_at	---
5.31	5.35	0.04	8.75E-01	9.64E-01	C19orf42	chromosome 19 open reading frame 42	chr19p13.11	224712_x_at	NM_024104
3.58	3.60	0.03	8.75E-01	9.64E-01	---	---	---	231533_at	---
2.48	2.50	0.02	8.75E-01	9.64E-01	---	---	---	1562057_at	---
2.15	2.17	0.02	8.75E-01	9.64E-01	LOC653739	hypothetical protein LOC653739	chr7q33	1561894_at	XM_930550
2.04	2.07	0.02	8.75E-01	9.64E-01	---	---	---	229695_at	---
2.68	2.70	0.02	8.75E-01	9.64E-01	---	---	---	241608_at	---
2.08	2.10	0.02	8.75E-01	9.64E-01	BCAN	brevican	chr1q31	221623_at	NM_021948 /// NM_198427
2.84	2.87	0.03	8.75E-01	9.64E-01	LOC404266	hypothetical LOC404266	chr17q21.32	230743_at	XR_042278 /// XR_042279 /// XR_042280
2.25	2.28	0.03	8.75E-01	9.64E-01	CLIC5	chloride intracellular channel 5	chr6p21.1-p12.1	213317_at	NM_001114086 /// NM_016929
2.78	2.80	0.02	8.75E-01	9.64E-01	KIR3DL2 /// LOC727787	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 /// similar to killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I NK cell receptor) (Natural killer-associated transcript 4) (NKAT-4) (p70 natural killer cell receptor clone CL-5) (CD158k antigen)	chr19q13.4	211688_x_at	NM_006737 /// XM_001718625
4.55	4.67	0.12	8.75E-01	9.64E-01	---	---	---	231576_at	---
5.64	5.70	0.07	8.75E-01	9.64E-01	ANKRD50	ankyrin repeat domain 50	chr4q28.1	225731_at	NM_020337
5.52	5.58	0.05	8.76E-01	9.64E-01	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	---	223140_s_at	NM_001114397 /// NM_020865
3.03	3.07	0.04	8.75E-01	9.64E-01	LOC100131904	hypothetical protein LOC100131904	chr6q12	240329_at	XM_001715122 /// XM_001724596 /// XM_001724759
6.88	6.91	0.04	8.75E-01	9.64E-01	ABL1	c-abl oncogene 1, receptor tyrosine kinase	chr9q34.1	202123_s_at	NM_005157 /// NM_007313
8.22	8.26	0.04	8.75E-01	9.64E-01	FCGRT	Fc fragment of IgG, receptor, transporter, alpha	chr19q13.3	218831_s_at	NM_004107
2.09	2.12	0.03	8.75E-01	9.64E-01	CYB5A	cytochrome b5 type A (microsomal)	chr18q23	217021_at	NM_001914 /// NM_148923
4.47	4.51	0.03	8.75E-01	9.64E-01	GLT8D3	glycosyltransferase 8 domain containing 3	chr12q12	226868_at	NM_001099650 /// NM_173601
3.96	3.99	0.03	8.75E-01	9.64E-01	INE1	inactivation escape 1 (non-protein coding)	chrXp11.4-p11.3	207252_at	XR_040628 /// XR_040629 /// XR_040630
2.92	2.95	0.03	8.75E-01	9.64E-01	NOTCH2	Notch homolog 2 (Drosophila)	chr1p13-p11	202445_s_at	NM_024408
2.92	2.95	0.03	8.75E-01	9.64E-01	WBSCR16	Williams-Beuren syndrome chromosome region 16	chr7q11.23	238132_at	NM_030798
2.27	2.29	0.02	8.76E-01	9.64E-01	EFCAB6	EF-hand calcium binding domain 6	chr22q13.1-q13.33	234853_s_at	NM_022785 /// NM_198856
3.41	3.43	0.02	8.76E-01	9.64E-01	---	---	---	1561689_at	---
2.23	2.25	0.02	8.76E-01	9.64E-01	INTS6	integrator complex subunit 6	chr13q14.12-q14.2	1568695_s_at	NM_001039937 /// NM_001039938 /// NM_012141
1.88	1.90	0.02	8.76E-01	9.64E-01	---	---	---	236503_at	---
2.79	2.82	0.03	8.76E-01	9.64E-01	C14orf102	chromosome 14 open reading frame 102	chr14q32.11	221231_s_at	NM_017970 /// NM_199043
3.08	3.10	0.02	8.76E-01	9.64E-01	C7orf28A	chromosome 7 open reading frame 28A	chr7p22.1	201974_s_at	NM_015622
3.31	3.34	0.03	8.76E-01	9.64E-01	KCTD15	potassium channel tetramerisation domain containing 15	chr19q13.11	218553_s_at	NM_001129994 /// NM_001129995 /// NM_024076
4.25	4.28	0.03	8.76E-01	9.64E-01	---	---	---	232867_at	---
2.13	2.15	0.02	8.76E-01	9.64E-01	OLFM3	olfactomedin 3	chr1p22	1554524_a_at	NM_058170
3.60	3.63	0.03	8.76E-01	9.65E-01	---	---	---	213821_s_at	---

1.81	1.83	0.02	8.76E-01	9.65E-01	LOC153364	similar to metallo-beta-lactamase superfamily protein	chr5q14.3	1554619_at	NM_203406																					
5.75	5.80	0.05	8.76E-01	9.65E-01	KCTD21	potassium channel tetramerisation domain containing 21	chr11q14.1	229873_at	NM_001029859																					
4.78	4.82	0.04	8.76E-01	9.65E-01	POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	chr1q21.1	210573_s_at	NM_006468																					
2.09	2.10	0.02	8.77E-01	9.65E-01	LOC728052	similar to hCG2031213	chr6q12	1558795_at	XM_001126435 /// XM_001128968 /// XM_001717850																					
2.35	2.36	0.02	8.77E-01	9.65E-01	HNRNPAB	Heterogeneous nuclear ribonucleoprotein A/B	chr5q35.3	231060_at	NM_004499 /// NM_031266																					
3.55	3.58	0.04	8.77E-01	9.65E-01	---	---	---	226974_at	---																					
2.87	2.89	0.02	8.77E-01	9.65E-01	---	---	---	231546_at	---																					
2.50	2.52	0.03	8.77E-01	9.65E-01	C10orf31	chromosome 10 open reading frame 31	chr10p14	1560255_at	XR_041926 /// XR_041927																					
2.70	2.72	0.02	8.77E-01	9.65E-01	TBX1	T-box 1	chr22q11.21	207662_at	NM_005992 /// NM_080646 /// NM_080647																					
5.96	6.03	0.07	8.77E-01	9.65E-01	NBL1	neuroblastoma, suppression of tumorigenicity 1	chr1p36.13|1p36.13-p36.11	37005_at	NM_005380 /// NM_182744																					
2.77	2.83	0.05	8.77E-01	9.65E-01	GOPC	golgi associated PDZ and coiled-coil motif containing	chr6q21	227214_at	NM_001017408 /// NM_020399																					
2.75	2.79	0.04	8.77E-01	9.65E-01	---	---	---	233180_at	---																					
5.59	5.63	0.04	8.77E-01	9.65E-01	RECQL5	RecQ protein-like 5	chr17q25.2-q25.3	221686_s_at	NM_001003715 /// NM_001003716 /// NM_004259																					
2.65	2.67	0.03	8.77E-01	9.65E-01	LAMB4	laminin, beta 4	chr7q22-q31.2	234334_s_at	NM_007356																					
3.27	3.30	0.03	8.77E-01	9.65E-01	C14orf178	chromosome 14 open reading frame 178	chr14q24.3	1564816_at	NM_174943																					
3.53	3.55	0.02	8.77E-01	9.65E-01	C2orf55	Chromosome 2 open reading frame 55	chr2q11.2	214134_at	NM_207362																					
1.84	1.85	0.02	8.77E-01	9.65E-01	RPL22	Ribosomal protein L22	chr1p36.3-p36.2	238370_x_at	NM_000983																					
2.15	2.17	0.02	8.78E-01	9.65E-01	PKN2	protein kinase N2	chr1p22.2	210969_at	NM_006256																					
7.42	7.47	0.05	8.78E-01	9.65E-01	CLTB	clathrin, light chain (Lcb)	chr4q2-q3|5q35	206284_x_at	NM_001834 /// NM_007097																					
5.10	5.13	0.03	8.78E-01	9.65E-01	MAST2	microtubule associated serine/threonine kinase 2	chr1p34.1	211593_s_at	NM_015112																					
4.47	4.50	0.03	8.78E-01	9.65E-01	FKBP3	FK506 binding protein 3, 25kDa	chr14q21.3	222485_at	NM_002013																					
2.12	2.14	0.02	8.78E-01	9.65E-01	LOC100131980 /// ZNF705G	similar to zinc finger protein 705A /// Putative zinc finger protein 705G	chr8p23.1	237711_at	XM_001720517 /// XM_001720524 /// XM_938635																					
3.74	3.77	0.02	8.78E-01	9.65E-01	LOC100130078	hypothetical protein LOC100130078	chr17q25.3	1562627_at	XM_001716792 /// XM_001721732 /// XM_001726783																					
3.08	3.11	0.03	8.78E-01	9.65E-01	IGHD	immunoglobulin heavy constant delta	chr14q32.33	215621_s_at	---																					
6.05	6.08	0.02	8.78E-01	9.65E-01	MECP2	methyl CpG binding protein 2 (Rett syndrome)	chrXq28	202618_s_at	NM_001110792 /// NM_004992																					
2.44	2.47	0.02	8.78E-01	9.65E-01	---	---	---	1561058_at	---																					
2.19	2.21	0.02	8.78E-01	9.65E-01	---	---	---	234517_at	---																					
5.88	5.93	0.06	8.78E-01	9.65E-01	PGGT1B	protein geranylgeranyltransferase type I, beta subunit	chr5q22.3	235615_at	NM_005023																					
2.51	2.54	0.03	8.78E-01	9.65E-01	RGS8	regulator of G-protein signaling 8	chr1q25	244675_at	NM_001102450 /// NM_033345																					
2.85	2.87	0.02	8.78E-01	9.65E-01	---	---	---	1564338_at	---																					
2.13	2.15	0.02	8.78E-01	9.65E-01	KCNK15	potassium channel, subfamily K, member 15	chr20q12-q13	220540_at	NM_022358																					
4.91	4.95	0.05	8.78E-01	9.65E-01	---	---	---	239166_at	---																					
2.80	2.84	0.04	8.78E-01	9.65E-01	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	chr4p14-p12	210192_at	NM_001105529 /// NM_006095																					
2.96	2.99	0.03	8.78E-01	9.65E-01	KLHDC4	kelch domain containing 4	chr16q24.3	234738_s_at	NM_017566																					
3.88	3.91	0.02	8.78E-01	9.65E-01	HRH3	histamine receptor H3	chr20q13.33	1555215_a_at	NM_007232																					
2.29	2.31	0.02	8.78E-01	9.65E-01	---	---	---	230928_at	---																					
1.88	1.90	0.02	8.78E-01	9.65E-01	LOC440704	hypothetical gene supported by BC042042	chr1q31.1-q31.2	1562558_at	XM_498826 /// XM_944716																					
4.65	4.73	0.08	8.78E-01	9.65E-01	DOCK5	Dedicator of cytokinesis 5	chr8p21.2	230206_at	NM_024940																					
4.00	4.05	0.04	8.78E-01	9.65E-01	SLC39A9	solute carrier family 39 (zinc transporter), member 9	chr14q24.1	217859_s_at	NM_018375																					

4.84	4.87	0.03	8.78E-01	9.65E-01	PRDX2	peroxiredoxin 2	chr19p13.2	201006_at	NM_005809 /// NM_181738
2.32	2.35	0.03	8.78E-01	9.65E-01	HES6	hairy and enhancer of split 6 (Drosophila)	chr2q37.3	228169_s_at	NM_018645
4.26	4.28	0.02	8.78E-01	9.65E-01	MAGOHB	mago-nashi homolog B (Drosophila)	chr12p13.2	218894_s_at	NM_018048
3.27	3.29	0.02	8.78E-01	9.65E-01	HNRNPH2	Heterogeneous nuclear ribonucleoprotein H2 (H')	chrXq22	243201_at	NM_001032393 /// NM_019597
3.09	3.11	0.02	8.78E-01	9.65E-01	KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	chr17p11.2	232289_at	NM_021012
6.87	6.91	0.05	8.79E-01	9.65E-01	DCTN1	dynactin 1 (p150, glued homolog, Drosophila)	chr2p13	201082_s_at	NM_004082 /// NM_023019
5.92	5.96	0.04	8.79E-01	9.65E-01	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	chr19p13.2	212520_s_at	NM_001128844 /// NM_001128845 /// NM_001128846 /// NM_001128847 /// NM_001128848 /// NM_001128849 /// NM_003072
4.79	4.82	0.02	8.79E-01	9.65E-01	---	---	---	1568691_at	---
2.64	2.66	0.02	8.79E-01	9.65E-01	C15orf2	chromosome 15 open reading frame 2	chr15q11-q13	221300_at	NM_018958
2.32	2.34	0.02	8.79E-01	9.65E-01	PSG1	pregnancy specific beta-1-glycoprotein 1	chr19q13.2	210195_s_at	NM_006905
2.63	2.66	0.02	8.79E-01	9.65E-01	HESX1	HESX homeobox 1	chr3p14.3	211267_at	NM_003865
2.16	2.18	0.02	8.79E-01	9.65E-01	---	---	---	1570578_at	---
6.27	6.32	0.05	8.79E-01	9.65E-01	LEMD3	LEM domain containing 3	chr12q14	218604_at	NM_014319
2.38	2.40	0.02	8.79E-01	9.65E-01	---	---	---	215642_at	---
4.21	4.24	0.03	8.79E-01	9.66E-01	ZNF765	zinc finger protein 765	chr19q13.41	1558942_at	NM_001040185
3.63	3.65	0.02	8.79E-01	9.66E-01	---	---	---	1561419_at	---
2.33	2.35	0.02	8.79E-01	9.66E-01	---	---	---	237102_at	---
2.63	2.65	0.02	8.79E-01	9.66E-01	PHRF1	PHD and ring finger domains 1	chr11p15.5	237379_at	NM_020901
7.45	7.47	0.02	8.79E-01	9.66E-01	MAP2K3	mitogen-activated protein kinase kinase 3	chr17q11.2	215499_at	NM_002756 /// NM_145109
2.30	2.31	0.02	8.79E-01	9.66E-01	---	---	---	241228_at	---
4.25	4.27	0.02	8.79E-01	9.66E-01	LOC642346	hypothetical LOC642346	chr15q25.2	232402_at	XM_001129399 /// XM_001732819
2.61	2.63	0.02	8.79E-01	9.66E-01	SMAD9	SMAD family member 9	chr13q12-q14	206320_s_at	NM_001127217 /// NM_005905
7.33	7.38	0.05	8.80E-01	9.66E-01	RNF128	ring finger protein 128	chrXq22.3	219263_at	NM_024539 /// NM_194463
4.93	4.96	0.03	8.80E-01	9.66E-01	ZNF92	zinc finger protein 92	chr7q11.21	235170_at	NM_007139 /// NM_152626
2.43	2.46	0.03	8.80E-01	9.66E-01	---	---	---	244170_at	---
2.63	2.66	0.03	8.80E-01	9.66E-01	TTTY6	testis-specific transcript, Y-linked 6	chrYq11.223	224041_at	NR_001527
2.76	2.79	0.03	8.80E-01	9.66E-01	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	chr11q13.3	210236_at	NM_003626 /// NM_177423
2.55	2.58	0.02	8.80E-01	9.66E-01	---	---	---	240569_at	---
3.37	3.39	0.02	8.80E-01	9.66E-01	KIAA1530	KIAA1530	chr4p16.3	1555107_a_at	NM_020894 /// XM_001720077
2.28	2.31	0.02	8.80E-01	9.66E-01	---	---	---	239963_at	---
2.19	2.21	0.02	8.80E-01	9.66E-01	---	---	---	234277_at	---
5.36	5.42	0.07	8.80E-01	9.66E-01	NID1	nidogen 1	chr1q43	202007_at	NM_002508
2.63	2.66	0.03	8.80E-01	9.66E-01	---	---	---	1565777_at	---
1.89	1.91	0.02	8.80E-01	9.66E-01	---	---	---	1569545_at	---
2.82	2.85	0.03	8.80E-01	9.66E-01	SPRR3	small proline-rich protein 3	chr1q21-q22	232082_x_at	NM_001097589 /// NM_005416
3.01	3.02	0.02	8.80E-01	9.66E-01	FLJ13773	FLJ13773	---	1559011_at	---
3.36	3.39	0.03	8.80E-01	9.66E-01	NAP1L4	nucleosome assembly protein 1-like 4	chr11p15.5	1556567_at	NM_005969
3.58	3.60	0.02	8.80E-01	9.66E-01	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	chr3p25-p24	228756_at	NM_001134367 /// NM_001134368 /// NM_003043
2.17	2.19	0.02	8.80E-01	9.66E-01	C8orf79	chromosome 8 open reading frame 79	chr8p22	214796_at	NM_001099677 /// NM_020844
2.10	2.12	0.02	8.80E-01	9.66E-01	---	---	---	1561584_at	---

2.16	2.18	0.02	8.80E-01	9.66E-01	---	---	---	216891_at	---
2.31	2.33	0.02	8.80E-01	9.66E-01	ARL17	ADP-ribosylation factor-like 17	chr17q21.31	1555144_at	NM_001039083 /// NM_001103154
6.50	6.57	0.07	8.81E-01	9.66E-01	CSNK1A1	casein kinase 1, alpha 1	chr5q32	208867_s_at	NM_001025105 /// NM_001892
4.45	4.52	0.07	8.81E-01	9.66E-01	METAP2	methionyl aminopeptidase 2	chr12q22	213899_at	NM_006838
6.46	6.52	0.06	8.81E-01	9.66E-01	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	chr4q28.1	212558_at	NM_005841 /// NM_199327
3.03	3.08	0.06	8.80E-01	9.66E-01	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	chr1p31.3	1555105_a_at	NM_001077700 /// NM_001077701 /// NM_001077702 /// NM_001077703 /// NM_001077704 /// NM_020948
3.94	4.00	0.06	8.81E-01	9.66E-01	EDN1	endothelin 1	chr6p24.1	218995_s_at	NM_001955
7.82	7.87	0.05	8.80E-01	9.66E-01	ARL1	ADP-ribosylation factor-like 1	chr12q23.2	201658_at	NM_001177
6.81	6.85	0.04	8.81E-01	9.66E-01	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	chr12q13.13	212126_at	NM_001127321 /// NM_001127322 /// NM_012117
8.64	8.67	0.03	8.81E-01	9.66E-01	GRN	granulin	chr17q21.32	200678_x_at	NM_002087
5.63	5.66	0.03	8.81E-01	9.66E-01	THG1L	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	chr5q33.3	219122_s_at	NM_017872
3.29	3.32	0.03	8.81E-01	9.66E-01	KCTD15	potassium channel tetramerisation domain containing 15	chr19q13.11	222664_at	NM_001129994 /// NM_001129995 /// NM_024076
4.39	4.42	0.03	8.81E-01	9.66E-01	SMAD1	SMAD family member 1	chr4q31	227798_at	NM_001003688 /// NM_005900
2.65	2.68	0.03	8.80E-01	9.66E-01	---	---	---	240696_at	---
2.80	2.83	0.03	8.81E-01	9.66E-01	SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6	chr14q32.1	206325_at	NM_001756
5.82	5.85	0.03	8.81E-01	9.66E-01	SSNA1	Sjogren syndrome nuclear autoantigen 1	chr9q34.3	244192_x_at	NM_003731
9.05	9.08	0.02	8.81E-01	9.66E-01	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	chr3p21	201533_at	NM_001098209 /// NM_001098210 /// NM_001904
5.62	5.65	0.02	8.81E-01	9.66E-01	---	---	---	228612_at	---
2.54	2.56	0.02	8.81E-01	9.66E-01	FAM161A	family with sequence similarity 161, member A	chr2p15	242584_at	NM_032180
2.55	2.58	0.02	8.81E-01	9.66E-01	TMTC2	Transmembrane and tetratricopeptide repeat containing 2	chr12q21.31	228574_at	NM_152588
2.60	2.62	0.02	8.81E-01	9.66E-01	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	chr22q13.3	204539_s_at	NM_014246
1.97	1.99	0.02	8.81E-01	9.66E-01	LOC284661	hypothetical protein LOC284661	chr1p36.32	1561383_at	---
1.98	2.00	0.02	8.81E-01	9.66E-01	DOCK5	dedicator of cytokinesis 5	chr8p21.2	1561276_at	NM_024940
2.76	2.78	0.02	8.80E-01	9.66E-01	FLJ30375	Hypothetical gene supported by AK054937	chr3q24	1557154_at	XM_001724993 /// XM_001725199 /// XM_001725628
2.33	2.36	0.02	8.81E-01	9.66E-01	ANKH	Ankylosis, progressive homolog (mouse)	chr5p15.1	1560370_x_at	NM_054027
3.67	3.69	0.02	8.81E-01	9.66E-01	---	---	---	237747_at	---
3.01	3.03	0.02	8.81E-01	9.66E-01	DKFZp451M2119 /// LOC100130691	hypothetical protein DKFZp451M2119 /// hypothetical protein LOC100130691	chr2q31.2	231540_at	NM_182585 /// XM_001716191 /// XM_001716660 /// XM_001718897
2.48	2.50	0.02	8.81E-01	9.66E-01	GTSF1L	gametocyte specific factor 1-like	chr20q13.12	232821_at	NM_001008901 /// NM_176791
2.26	2.28	0.02	8.81E-01	9.66E-01	NFIB	Nuclear factor I/B	chr9p24.1	233304_at	NM_005596
2.01	2.02	0.02	8.81E-01	9.66E-01	KIAA0746	KIAA0746 protein	chr4p15.2	235353_at	NM_015187
2.78	2.81	0.03	8.81E-01	9.66E-01	EGLN1	egl nine homolog 1 (C. elegans)	chr1q42.1	223045_at	NM_022051
4.10	4.13	0.03	8.81E-01	9.66E-01	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	chr19q13.4	211101_x_at	NM_001130917 /// NM_006866
2.30	2.33	0.03	8.81E-01	9.66E-01	---	---	---	1568817_at	---

3.00	3.04	0.04	8.82E-01	9.66E-01	---	---	---	1560536_at	---
2.33	2.36	0.03	8.82E-01	9.66E-01	KSR2	kinase suppressor of ras 2	chr12q24.22-q24.23	230551_at	NM_173598
6.09	6.13	0.04	8.82E-01	9.66E-01	DUSP16	dual specificity phosphatase 16	chr12p13	1555399_a_at	NM_030640
3.35	3.39	0.04	8.82E-01	9.66E-01	TRAK1	trafficking protein, kinesin binding 1	chr3p25.3-p24.1	202079_s_at	NM_001042646 /// NM_014965
3.66	3.69	0.03	8.82E-01	9.66E-01	CDK3	cyclin-dependent kinase 3	chr17q22-qter	207188_at	NM_001258
7.62	7.65	0.03	8.82E-01	9.66E-01	DPH5	DPH5 homolog (S. cerevisiae)	chr1p21.2	224196_x_at	NM_001077394 /// NM_001077395 /// NM_015958
4.03	4.06	0.03	8.82E-01	9.66E-01	TTC9B	tetratricopeptide repeat domain 9B	chr19q13.2	235375_x_at	NM_152479
2.54	2.57	0.02	8.82E-01	9.66E-01	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	chr9q22.1	207152_at	NM_001007097 /// NM_001018064 /// NM_001018065 /// NM_001018066 /// NM_006180
4.61	4.64	0.03	8.82E-01	9.66E-01	FGD2	FYVE, RhoGEF and PH domain containing 2	chr6p21.2	1559091_s_at	NM_173558
10.08	10.10	0.03	8.82E-01	9.66E-01	PABPC3	poly(A) binding protein, cytoplasmic 3	chr13q12-q13	208113_x_at	NM_030979
2.23	2.25	0.03	8.82E-01	9.66E-01	---	---	---	242777_at	---
4.97	5.03	0.06	8.82E-01	9.66E-01	HERC5	hect domain and RLD 5	chr4q22.1	219863_at	NM_016323
4.30	4.34	0.05	8.82E-01	9.66E-01	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	chr2q33	231075_x_at	NM_203365 /// NM_213589
6.04	6.08	0.05	8.82E-01	9.66E-01	C8orf32	chromosome 8 open reading frame 32	chr8q24.13	219060_at	NM_018024
5.85	5.89	0.04	8.82E-01	9.66E-01	TROVE2	TROVE domain family, member 2	chr1q31	213027_at	NM_001042369 /// NM_001042370 /// NM_004600
3.03	3.07	0.03	8.82E-01	9.66E-01	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	chr3p22.1	224470_at	NM_004206 /// NM_032970
4.16	4.19	0.03	8.82E-01	9.66E-01	AIM1L	absent in melanoma 1-like	chr1p36.11	220290_at	NM_001039775 /// NM_017977
2.24	2.27	0.02	8.82E-01	9.66E-01	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	chr5q12.3	232084_at	NM_019072
4.66	4.68	0.02	8.82E-01	9.66E-01	PRSS1 /// TRY6	protease, serine, 1 (trypsin 1) /// trypsinogen C	chr7q32-qter|7q34 /// chr7q34	215395_x_at	NM_002769 /// NR_001296 /// XR_042156
1.95	1.97	0.02	8.82E-01	9.66E-01	ST7OT4	ST7 overlapping transcript 4 (non-protein coding)	chr7q31.1-q31.2	1559208_at	NR_002329
3.18	3.21	0.04	8.83E-01	9.67E-01	CASQ2	calsequestrin 2 (cardiac muscle)	chr1p13.3-p11	207317_s_at	NM_001232
4.21	4.24	0.03	8.83E-01	9.67E-01	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	chr12q12	221025_x_at	NM_001098614 /// NM_001098615 /// NM_031292
2.09	2.11	0.02	8.83E-01	9.67E-01	DOCK4	dedicator of cytokinesis 4	chr7q31.1	1558691_a_at	NM_014705
2.03	2.05	0.02	8.83E-01	9.67E-01	CHM	choroideremia (Rab escort protein 1)	chrXq21.2	1569183_a_at	NM_000390
1.78	1.79	0.01	8.83E-01	9.67E-01	ADAM30	ADAM metallopeptidase domain 30	chr1p13-p11	243520_x_at	NM_021794
1.94	1.96	0.02	8.83E-01	9.67E-01	---	---	---	1557424_at	---
2.12	2.14	0.02	8.83E-01	9.67E-01	PTPRJ	protein tyrosine phosphatase, receptor type, J	chr11p11.2	210173_at	NM_001098503 /// NM_002843
2.00	2.01	0.01	8.83E-01	9.67E-01	LYPD6	LY6/PLAUR domain containing 6	chr2q23.2	227763_at	NM_194317
2.16	2.18	0.02	8.83E-01	9.67E-01	CASC5	cancer susceptibility candidate 5	chr15q14	1552682_a_at	NM_144508 /// NM_170589
4.86	4.90	0.04	8.83E-01	9.67E-01	MAPK8	mitogen-activated protein kinase 8	chr10q11.22	226048_at	NM_002750 /// NM_139046 /// NM_139047 /// NM_139049
2.44	2.46	0.02	8.83E-01	9.67E-01	FOXP1	forkhead box P1	chr3p14.1	1558996_at	NM_001012505 /// NM_032682
11.00	11.03	0.02	8.83E-01	9.67E-01	ALDOA	aldolase A, fructose-bisphosphate	chr16p11.2	214687_x_at	NM_000034 /// NM_001127617 /// NM_184041 /// NM_184043
2.33	2.36	0.02	8.83E-01	9.67E-01	---	---	---	243221_at	---
6.00	6.07	0.07	8.83E-01	9.67E-01	EMCN	endomucin	chr4q23	222885_at	NM_016242

5.76	5.80	0.04	8.83E-01	9.67E-01	YY1	YY1 transcription factor	chr14q	224718_at	NM_003403
3.71	3.79	0.08	8.84E-01	9.67E-01	---	---	---	239798_at	---
2.55	2.58	0.03	8.84E-01	9.67E-01	---	---	---	243879_at	---
2.81	2.84	0.02	8.84E-01	9.67E-01	---	---	---	244520_at	---
5.52	5.54	0.02	8.84E-01	9.67E-01	---	---	---	240198_at	---
10.73	10.78	0.05	8.84E-01	9.67E-01	HSPB1	heat shock 27kDa protein 1	chr7q11.23	201841_s_at	NM_001540
3.44	3.46	0.02	8.84E-01	9.67E-01	C6orf221	chromosome 6 open reading frame 221	chr6q13	231474_at	NM_001017361
2.88	2.91	0.03	8.84E-01	9.67E-01	---	---	---	1565152_at	---
2.04	2.06	0.02	8.84E-01	9.67E-01	---	---	---	234961_at	---
2.09	2.11	0.02	8.84E-01	9.67E-01	D21S2088E	D21S2088E	---	1559470_at	---
12.65	12.67	0.02	8.84E-01	9.67E-01	TPT1	tumor protein, translationally-controlled 1	chr13q12-q14	211943_x_at	NM_003295
7.23	7.27	0.04	8.84E-01	9.67E-01	RERG	RAS-like, estrogen-regulated, growth inhibitor	chr12p12.3	227758_at	NM_032918
2.63	2.65	0.03	8.84E-01	9.67E-01	---	---	---	236353_at	---
1.96	1.98	0.02	8.84E-01	9.67E-01	---	---	---	240050_s_at	---
4.46	4.49	0.03	8.84E-01	9.67E-01	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	chr15q24.2	228911_at	NM_014272
3.58	3.64	0.06	8.85E-01	9.67E-01	C1orf71	chromosome 1 open reading frame 71	chr1q44	1554661_s_at	NM_152609
7.99	8.04	0.06	8.85E-01	9.67E-01	MTUS1	mitochondrial tumor suppressor 1	chr8p22	212096_s_at	NM_001001924 /// NM_001001925 /// NM_001001931 /// NM_020749
6.89	6.94	0.05	8.85E-01	9.67E-01	LOC401152	HCV F-transactivated protein 1	chr4q26	224605_at	NM_001001701
5.82	5.86	0.04	8.84E-01	9.67E-01	NCK1	NCK adaptor protein 1	chr3q21	211063_s_at	NM_006153
5.02	5.05	0.03	8.85E-01	9.67E-01	UBAP2L	ubiquitin associated protein 2-like	chr1q21.3	209947_at	NM_001127320 /// NM_014847
2.64	2.67	0.03	8.84E-01	9.67E-01	ZMYM6	zinc finger, MYM-type 6	chr1p34.2	227595_at	NM_007167
3.84	3.87	0.03	8.84E-01	9.67E-01	TCEA3	Transcription elongation factor A (SII), 3	chr1p36.12	241976_at	NM_003196
2.54	2.57	0.03	8.85E-01	9.67E-01	---	---	---	229569_at	---
3.28	3.31	0.03	8.85E-01	9.67E-01	ARHGAP27	Rho GTPase activating protein 27	chr17q21.31	225618_at	NM_199282
3.06	3.09	0.02	8.84E-01	9.67E-01	---	---	---	1565852_at	---
6.56	6.59	0.02	8.85E-01	9.67E-01	ATAD3B /// LOC732419	ATPase family, AAA domain containing 3B /// similar to AAA-ATPase TOB3	chr1p36.33	227237_x_at	NM_031921 /// XM_001718658
5.17	5.20	0.02	8.84E-01	9.67E-01	RAD1	RAD1 homolog (S. pombe)	chr5p13.2	228535_at	NM_002853 /// NM_133377
2.36	2.39	0.02	8.85E-01	9.67E-01	RHOT1	ras homolog gene family, member T1	chr17q11.2	224044_at	NM_001033566 /// NM_001033568 /// NM_018307
6.40	6.42	0.02	8.84E-01	9.67E-01	ISY1	ISY1 splicing factor homolog (S. cerevisiae)	chr3q21.3	223831_x_at	NM_020701
1.88	1.89	0.02	8.85E-01	9.67E-01	IQWD1	IQ motif and WD repeats 1	chr1q24.2	241209_at	NM_001017977 /// NM_018442
1.91	1.93	0.02	8.85E-01	9.67E-01	---	---	---	240768_x_at	---
2.32	2.33	0.02	8.84E-01	9.67E-01	C20orf62	chromosome 20 open reading frame 62	chr20q13.12	1570327_at	NM_178476
4.93	4.99	0.06	8.85E-01	9.67E-01	SMTN	smoothelin	chr22q12.2	207390_s_at	NM_006932 /// NM_134269 /// NM_134270
4.55	4.57	0.02	8.85E-01	9.67E-01	MAPRE3	Microtubule-associated protein, RP/EB family, member 3	chr2p23.3-p23.1	229682_at	NM_012326
8.27	8.30	0.03	8.85E-01	9.67E-01	MXI1	MAX interactor 1	chr10q24-q25	202364_at	NM_001008541 /// NM_005962 /// NM_130439
2.44	2.47	0.03	8.85E-01	9.67E-01	C10orf113	chromosome 10 open reading frame 113	chr10p12.31	244077_at	NM_001010896
2.81	2.83	0.02	8.85E-01	9.67E-01	MASP2	mannan-binding lectin serine peptidase 2	chr1p36.3-p36.2	207041_at	NM_006610 /// NM_139208
5.88	5.95	0.07	8.85E-01	9.67E-01	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	chr8q11	210543_s_at	NM_001081640 /// NM_006904
5.21	5.23	0.02	8.85E-01	9.67E-01	LPAR1	lysophosphatidic acid receptor 1	chr9q31.3	204038_s_at	NM_001401 /// NM_057159
2.11	2.13	0.02	8.85E-01	9.67E-01	---	---	---	231417_at	---
2.08	2.10	0.02	8.85E-01	9.67E-01	EPAS1	Endothelial PAS domain protein 1	chr2p21-p16	241055_at	NM_001430
1.99	2.00	0.02	8.85E-01	9.67E-01	ZNF713	zinc finger protein 713	chr7p11.2	1560201_at	NM_182633
2.91	2.94	0.03	8.86E-01	9.67E-01	---	---	---	1568558_x_at	---
2.15	2.17	0.02	8.85E-01	9.67E-01	USP45	ubiquitin specific peptidase 45	chr6q16.3	224441_s_at	NM_001080481
2.02	2.04	0.02	8.86E-01	9.67E-01	ZNF100	zinc finger protein 100	chr19p12	1569637_at	NM_173531
1.95	1.97	0.02	8.85E-01	9.67E-01	---	---	---	231680_at	---
7.24	7.28	0.04	8.86E-01	9.67E-01	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	chr3p14.1	212459_x_at	NM_003848
1.94	1.96	0.02	8.86E-01	9.67E-01	RHOB	ras homolog gene family, member B	chr2p24	1553963_at	NM_004040

8.44	8.47	0.02	8.86E-01	9.67E-01	GNPTG	N-acetylglucosamine-1-phosphate transferase, gamma subunit	chr16p13.3	224887_at	NM_032520
2.33	2.34	0.02	8.86E-01	9.67E-01	---	---	---	1560656_at	---
2.84	2.86	0.02	8.86E-01	9.67E-01	---	---	---	238507_at	---
2.33	2.35	0.02	8.86E-01	9.67E-01	TPD52	tumor protein D52	chr8q21	236655_at	NM_001025252 /// NM_001025253 /// NM_005079
3.36	3.39	0.03	8.86E-01	9.67E-01	SH2D1A	SH2 domain protein 1A	chrXq25-q26	211209_x_at	NM_001114937 /// NM_002351
2.15	2.17	0.02	8.86E-01	9.68E-01	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	chr21q22.3	206947_at	NM_006057 /// NM_033170 /// NM_033171 /// NM_033172 /// NM_033173
1.99	2.01	0.02	8.86E-01	9.68E-01	POSTN	periostin, osteoblast specific factor	chr13q13.3	214981_at	NM_006475
1.98	1.99	0.02	8.86E-01	9.68E-01	WDR72	WD repeat domain 72	chr15q21.3	227174_at	NM_182758
1.95	1.97	0.02	8.86E-01	9.68E-01	SYCP1	synaptonemal complex protein 1	chr1p13-p12	216917_s_at	NM_003176
2.32	2.34	0.02	8.86E-01	9.68E-01	RAB3C	RAB3C, member RAS oncogene family	chr5q13	241977_s_at	NM_138453
2.27	2.29	0.02	8.86E-01	9.68E-01	LOC284294	hypothetical protein LOC284294	chr18q22.1	1561455_at	---
2.23	2.25	0.02	8.86E-01	9.68E-01	LOC439951	hypothetical LOC439951	chr10p14	1555209_at	XR_017773 /// XR_017778
2.21	2.22	0.01	8.86E-01	9.68E-01	FLJ33996	hypothetical protein FLJ33996	chr12q13.13	235969_at	XR_000901 /// XR_001317
6.00	6.05	0.05	8.86E-01	9.68E-01	---	---	---	213500_at	---
6.01	6.06	0.05	8.87E-01	9.68E-01	LARP5	La ribonucleoprotein domain family, member 5	chr10p15.3	208953_at	NM_015155
6.13	6.17	0.04	8.86E-01	9.68E-01	FAM13B1	family with sequence similarity 13, member B1	chr5q31	218518_at	NM_001101800 /// NM_001101801 /// NM_016603
2.98	3.01	0.03	8.86E-01	9.68E-01	---	---	---	238617_at	---
2.66	2.69	0.03	8.87E-01	9.68E-01	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)	chrXq22.3	1563272_at	NM_017752 /// NM_198881
2.76	2.78	0.03	8.87E-01	9.68E-01	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	chr13q14.3	216870_x_at	NR_002612
4.73	4.76	0.03	8.87E-01	9.68E-01	ZNF254	zinc finger protein 254	chr19p12	242602_x_at	NM_203282
3.32	3.35	0.03	8.87E-01	9.68E-01	---	---	---	226819_at	---
4.36	4.39	0.03	8.86E-01	9.68E-01	CDRT15	CMT1A duplicated region transcript 15	chr17p12	240760_at	NM_001007530
5.18	5.20	0.02	8.86E-01	9.68E-01	ATP9B	ATPase, class II, type 9B	chr18q23	214010_s_at	NM_198531
2.49	2.51	0.02	8.86E-01	9.68E-01	C6orf146	chromosome 6 open reading frame 146	chr6p25.2	237619_at	NM_173563
2.40	2.42	0.02	8.87E-01	9.68E-01	CENPE	centromere protein E, 312kDa	chr4q24-q25	205046_at	NM_001813
2.18	2.20	0.02	8.87E-01	9.68E-01	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	chr2q14	216277_at	NM_004336
1.99	2.01	0.02	8.87E-01	9.68E-01	---	---	---	217709_at	---
1.96	1.98	0.02	8.87E-01	9.68E-01	---	---	---	241583_x_at	---
1.97	1.99	0.02	8.86E-01	9.68E-01	FAM152A	family with sequence similarity 152, member A	chr1q44	219875_s_at	NM_016076
1.89	1.90	0.02	8.87E-01	9.68E-01	---	---	---	220726_at	---
2.53	2.54	0.02	8.87E-01	9.68E-01	CARS	cysteinyl-tRNA synthetase	chr11p15.5	240982_at	NM_001014437 /// NM_001014438 /// NM_001751 /// NM_139273
3.99	4.02	0.03	8.87E-01	9.68E-01	---	---	---	1563707_at	---
4.32	4.35	0.03	8.87E-01	9.68E-01	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10q25.3	212759_s_at	NM_030756
2.39	2.42	0.02	8.87E-01	9.68E-01	TRPC6	transient receptor potential cation channel, subfamily C, member 6	chr11q21-q22	206528_at	NM_004621
3.77	3.82	0.05	8.87E-01	9.68E-01	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	chr1q25	212105_s_at	NM_001357
3.43	3.48	0.05	8.87E-01	9.68E-01	---	---	---	230967_s_at	---
2.56	2.59	0.02	8.87E-01	9.68E-01	ADAL	adenosine deaminase-like	chr15q15.3	239711_at	NM_001012969
1.98	2.00	0.02	8.87E-01	9.68E-01	---	---	---	1562747_at	---
2.34	2.36	0.02	8.87E-01	9.68E-01	---	---	---	1561266_at	---
6.46	6.49	0.02	8.87E-01	9.68E-01	LNX2	ligand of numb-protein X 2	chr13q12.2	227569_at	NM_153371
8.15	8.20	0.05	8.87E-01	9.68E-01	MBNL2	muscleblind-like 2 (Drosophila)	chr13q32.1	203640_at	NM_144778 /// NM_207304
3.09	3.13	0.04	8.88E-01	9.68E-01	PLAC2	placenta-specific 2 (non-protein coding)	chr19p13.3	229385_s_at	XR_040439 /// XR_040440 /// XR_040441
6.33	6.36	0.03	8.88E-01	9.68E-01	MTRF1L	mitochondrial translational release factor 1-like	chr6q25-q26	225206_s_at	NM_001114184 /// NM_019041
4.15	4.22	0.07	8.88E-01	9.68E-01	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	chr13q22.1	222607_s_at	NM_001128226 /// NM_014953
3.63	3.65	0.02	8.88E-01	9.68E-01	---	---	---	215576_at	---
2.76	2.79	0.03	8.88E-01	9.68E-01	---	---	---	1559620_at	---

2.49	2.51	0.02	8.88E-01	9.68E-01	LOC100128570	hypothetical protein LOC100128570	chr15q25.1	239746_at	XM_001720242 /// XM_001720250 /// XM_001726884
2.50	2.52	0.02	8.88E-01	9.68E-01	MAGEC2	melanoma antigen family C, 2	chrXq27	215932_at	NM_016249
3.66	3.71	0.06	8.88E-01	9.68E-01	RRM2	ribonucleotide reductase M2 polypeptide	chr2p25-p24	209773_s_at	NM_001034
5.25	5.31	0.05	8.88E-01	9.68E-01	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	chr2q21.3	212932_at	NM_012233
5.17	5.22	0.05	8.88E-01	9.68E-01	C1orf71	chromosome 1 open reading frame 71	chr1q44	225551_at	NM_152609
2.52	2.54	0.02	8.88E-01	9.68E-01	ZNF254	Zinc finger protein 254	chr19p12	1559449_a_at	NM_203282
2.27	2.29	0.02	8.88E-01	9.68E-01	DGKH	diacylglycerol kinase, eta	chr13q14.11	1553300_a_at	NM_152910 /// NM_178009
2.49	2.51	0.02	8.88E-01	9.68E-01	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	chr10p11.23	1568601_at	NM_000818 /// NM_001134366
7.36	7.39	0.03	8.88E-01	9.68E-01	RPL27A	Ribosomal protein L27a	chr11p15	212044_s_at	NM_000990
2.39	2.41	0.02	8.88E-01	9.68E-01	FAM26F	family with sequence similarity 26, member F	chr6q22.1	229915_at	NM_001010919
3.62	3.68	0.06	8.88E-01	9.68E-01	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	chr1p31.1	220979_s_at	NM_030965
5.70	5.79	0.09	8.88E-01	9.68E-01	PDE2A	phosphodiesterase 2A, cGMP-stimulated	chr11q13.4	204134_at	NM_002599
2.59	2.61	0.03	8.88E-01	9.68E-01	DGKZ	diacylglycerol kinase, zeta 104kDa	chr11p11.2	239342_at	NM_001105540 /// NM_003646 /// NM_201532 /// NM_201533
4.18	4.20	0.02	8.88E-01	9.68E-01	F2R	coagulation factor II (thrombin) receptor	chr5q13	203989_x_at	NM_001992
3.06	3.08	0.02	8.88E-01	9.68E-01	ZNF789	zinc finger protein 789	chr7q22.1	242307_at	NM_001013258 /// NM_213603
2.24	2.26	0.02	8.88E-01	9.68E-01	MAGEB2	melanoma antigen family B, 2	chrXp21.3	206218_at	NM_002364
3.65	3.67	0.02	8.88E-01	9.68E-01	PLD4	phospholipase D family, member 4	chr14q32.33	1566433_at	NM_138790
5.69	5.80	0.12	8.88E-01	9.68E-01	ECHDC3	enoyl Coenzyme A hydratase domain containing 3	chr10p14	219298_at	NM_024693
2.07	2.09	0.01	8.88E-01	9.68E-01	TRPM1	Transient receptor potential cation channel, subfamily M, member 1	chr15q13-q14	240386_at	NM_002420
2.71	2.74	0.03	8.88E-01	9.68E-01	FOXN1	forkhead box N1	chr17q11-q12	207683_at	NM_003593
6.27	6.31	0.04	8.89E-01	9.68E-01	STK11	serine/threonine kinase 11	chr19p13.3	231017_at	NM_000455
4.09	4.11	0.02	8.89E-01	9.68E-01	EPHA10	EPH receptor A10	chr1p34.3	236073_at	NM_001099439 /// NM_173641
6.72	6.76	0.04	8.89E-01	9.68E-01	TMEM192 /// ZNF320	transmembrane protein 192 /// zinc finger protein 320	chr19q13.41 /// chr4q32.3	1555790_a_at	NM_001100389 /// NM_207333
8.21	8.24	0.03	8.89E-01	9.68E-01	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	chr19p13.3	213041_s_at	NM_001001975 /// NM_001687
6.16	6.22	0.06	8.89E-01	9.68E-01	NUP107	nucleoporin 107kDa	chr12q15	218768_at	NM_020401
9.54	9.59	0.05	8.89E-01	9.68E-01	TAGLN	transgelin	chr11q23.2	205547_s_at	NM_001001522 /// NM_003186
6.08	6.12	0.04	8.89E-01	9.68E-01	41523	septin 6	chrXq24	212415_at	NM_015129 /// NM_145799 /// NM_145800 /// NM_145802
4.06	4.08	0.03	8.89E-01	9.68E-01	VASH1	vasohibin 1	chr14q24.3	239810_at	NM_014909
2.64	2.66	0.03	8.89E-01	9.68E-01	C19orf44	chromosome 19 open reading frame 44	chr19p13.11	228154_at	NM_032207
2.76	2.79	0.03	8.89E-01	9.68E-01	VAC14	Vac14 homolog (S. cerevisiae)	chr16q22.1	216501_at	NM_018052 /// XM_001724197 /// XM_001724956 /// XM_001726731
3.62	3.64	0.02	8.89E-01	9.68E-01	ELA2	elastase 2, neutrophil	chr19p13.3	206871_at	NM_001972
2.47	2.49	0.02	8.89E-01	9.68E-01	LOC440366	hect domain and RLD 2 pseudogene	chr16p11.2	216196_at	NR_002828 /// XR_042154
2.02	2.04	0.02	8.89E-01	9.68E-01	---	---	---	1565851_at	---
2.19	2.20	0.01	8.89E-01	9.68E-01	---	---	---	216777_at	---
4.77	4.79	0.02	8.89E-01	9.68E-01	IVD	Isovaleryl Coenzyme A dehydrogenase	chr15q14-q15	216495_x_at	NM_002225
4.89	4.94	0.04	8.89E-01	9.68E-01	IDI2	isopentenyl-diphosphate delta isomerase 2	chr10p15.3	228002_at	NM_033261
2.76	2.79	0.02	8.89E-01	9.68E-01	C14orf179	chromosome 14 open reading frame 179	chr14q24.3	1568699_at	NM_001102564 /// NM_052873
3.33	3.36	0.02	8.89E-01	9.68E-01	ANKMY1	ankyrin repeat and MYND domain containing 1	chr2q37.3	1554610_at	NM_016552 /// NM_017844
5.18	5.26	0.08	8.89E-01	9.68E-01	AGGF1	angiogenic factor with G patch and FHA domains 1	chr5q13.3	218534_s_at	NM_018046
5.50	5.54	0.04	8.89E-01	9.68E-01	KLHDC5	kelch domain containing 5	chr12p11.22	225732_at	NM_020782
2.19	2.21	0.02	8.89E-01	9.68E-01	MAGEA6	melanoma antigen family A, 6	chrXq28	214612_x_at	NM_005363 /// NM_175868

2.23	2.24	0.01	8.89E-01	9.68E-01	CCDC88A	coiled-coil domain containing 88A	chr2p16.1	219387_at	NM_018084
2.89	2.93	0.03	8.89E-01	9.68E-01	ZNF23	zinc finger protein 23 (KOX 16)	chr16q22	213934_s_at	NM_145911
3.53	3.55	0.02	8.89E-01	9.68E-01	POU5F1P4	POU class 5 homeobox 1 pseudogene 4	chr1q22	210905_x_at	---
2.05	2.07	0.02	8.89E-01	9.69E-01	---	---	---	1562932_at	---
3.50	3.53	0.03	8.89E-01	9.69E-01	---	---	---	1561989_at	---
1.83	1.84	0.01	8.90E-01	9.69E-01	---	---	---	1555717_at	---
3.96	4.00	0.04	8.90E-01	9.69E-01	ARRB1	arrestin, beta 1	chr11q13	222912_at	NM_004041 /// NM_020251
4.53	4.56	0.03	8.90E-01	9.69E-01	---	---	---	240929_at	---
3.68	3.70	0.02	8.90E-01	9.69E-01	DAPK2	death-associated protein kinase 2	chr15q22.31	206324_s_at	NM_014326
2.12	2.14	0.01	8.90E-01	9.69E-01	---	---	---	1561567_at	---
2.16	2.17	0.02	8.90E-01	9.69E-01	MTM1	myotubularin 1	chrXq28	204101_at	NM_000252
4.22	4.26	0.03	8.90E-01	9.69E-01	C19orf40	chromosome 19 open reading frame 40	chr19q13.11	214816_x_at	NM_152266
2.04	2.06	0.02	8.90E-01	9.69E-01	AMBRA1	autophagy/beclin-1 regulator 1	chr11p11.2	234236_at	NM_017749
2.86	2.89	0.02	8.90E-01	9.69E-01	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	chr6p22-p21.3	207051_at	NM_005495
2.71	2.73	0.02	8.90E-01	9.69E-01	---	---	---	236540_at	---
2.71	2.74	0.03	8.90E-01	9.69E-01	LOC100128108 /// LOC400464	hypothetical protein LOC100128108 /// similar to FLJ43276 protein	chr15q26.3	243957_at	XM_001721901 /// XR_041114 /// XR_041115
2.59	2.61	0.02	8.90E-01	9.69E-01	CSHL1	chorionic somatomammotropin hormone-like 1	chr17q24.2	205958_x_at	NM_001318 /// NM_022579 /// NM_022580 /// NM_022581
1.96	1.97	0.01	8.90E-01	9.69E-01	PDLIM5	PDZ and LIM domain 5	chr4q22	211680_at	NM_001011513 /// NM_001011515 /// NM_001011516 /// NM_006457 /// NR_003257
2.47	2.50	0.03	8.90E-01	9.69E-01	CHD2	chromodomain helicase DNA binding protein 2	chr15q26	203461_at	NM_001042572 /// NM_001271
2.83	2.85	0.02	8.90E-01	9.69E-01	---	---	---	1565587_at	---
2.37	2.39	0.02	8.90E-01	9.69E-01	MS4A12	membrane-spanning 4-domains, subfamily A, member 12	chr11q12	220834_at	NM_017716
1.95	1.97	0.02	8.91E-01	9.69E-01	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	chr2q24.1	236129_at	NM_014568
2.56	2.58	0.02	8.91E-01	9.69E-01	---	---	---	1570014_at	---
1.93	1.95	0.02	8.91E-01	9.69E-01	---	---	---	1565638_at	---
3.73	3.76	0.03	8.91E-01	9.69E-01	SMC1A	structural maintenance of chromosomes 1A	chrXp11.22-p11.21	217555_at	NM_006306
2.78	2.81	0.02	8.91E-01	9.69E-01	LPAL2	lipoprotein, Lp(a)-like 2	chr6q26-q27	207762_at	NM_024492 /// NM_145727
1.98	2.00	0.02	8.91E-01	9.69E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	1561614_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
3.22	3.24	0.02	8.91E-01	9.69E-01	THBS1	Thrombospondin 1	chr15q15	235086_at	NM_003246
6.36	6.38	0.02	8.91E-01	9.69E-01	APTX	aprataxin	chr9p13.3	218527_at	NM_017692 /// NM_175069 /// NM_175071 /// NM_175072 /// NM_175073
12.23	12.28	0.05	8.91E-01	9.69E-01	RPL4	ribosomal protein L4	chr15q22	211710_x_at	NM_000968
5.52	5.56	0.04	8.91E-01	9.69E-01	---	---	---	228650_at	---
2.64	2.67	0.03	8.91E-01	9.69E-01	LOC286058	hypothetical protein LOC286058	chr8p21.2	1562247_at	---
2.43	2.45	0.02	8.91E-01	9.69E-01	---	---	---	216065_at	---
2.44	2.46	0.02	8.91E-01	9.69E-01	TUBD1	tubulin, delta 1	chr17q23.1	231853_at	NM_016261
4.94	5.01	0.07	8.91E-01	9.70E-01	---	---	---	235856_at	---
2.99	3.01	0.02	8.91E-01	9.70E-01	---	---	---	237039_at	---
3.45	3.47	0.02	8.91E-01	9.70E-01	---	---	---	1556480_a_at	---
2.61	2.64	0.02	8.92E-01	9.70E-01	---	---	---	1565880_at	---
5.24	5.38	0.14	8.92E-01	9.70E-01	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	chr22q13.1	208719_s_at	NM_001098504 /// NM_001098505 /// NM_006386 /// NM_030881
6.92	6.96	0.03	8.92E-01	9.70E-01	ZSWIM1	zinc finger, SWIM-type containing 1	chr20q13.12	223607_x_at	NM_080603
2.48	2.49	0.02	8.92E-01	9.70E-01	ANKRD26	ankyrin repeat domain 26	chr10pter-q22.1	205705_at	NM_014915
2.47	2.50	0.03	8.92E-01	9.70E-01	CDH4	cadherin 4, type 1, R-cadherin (retinal)	chr20q13.3	1563587_at	NM_001794
5.96	5.99	0.04	8.92E-01	9.70E-01	RAD51C	RAD51 homolog C (S. cerevisiae)	chr17q22-q23	209849_s_at	NM_002876 /// NM_058216

2.14	2.16	0.02	8.92E-01	9.70E-01	LOC100128176	hypothetical protein LOC100128176	chr6q25.1	1557742_a_at	XM_001718081 /// XM_001719798																					
2.99	3.04	0.05	8.92E-01	9.70E-01	PCDHB5	protocadherin beta 5	chr5q31	223629_at	NM_015669																					
2.28	2.30	0.02	8.92E-01	9.70E-01	---	---	---	1560995_s_at	---																					
6.31	6.36	0.04	8.92E-01	9.70E-01	HDAC2	histone deacetylase 2	chr6q21	201833_at	NM_001527																					
2.58	2.60	0.02	8.92E-01	9.70E-01	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	chr9p13	216627_s_at	NM_001497																					
1.89	1.91	0.02	8.92E-01	9.70E-01	---	---	---	237608_at	---																					
3.01	3.06	0.05	8.93E-01	9.70E-01	NRN1	neuritin 1	chr6p25.1	218625_at	NM_016588																					
3.00	3.03	0.03	8.93E-01	9.70E-01	CHRM4	cholinergic receptor, muscarinic 4	chr11p12-p11.2	221357_at	NM_000741																					
2.15	2.17	0.02	8.93E-01	9.70E-01	---	---	---	240708_at	---																					
4.18	4.20	0.02	8.93E-01	9.70E-01	CUL7	cullin 7	chr6p21.1	241747_s_at	NM_014780																					
3.59	3.61	0.02	8.92E-01	9.70E-01	CXorf36	chromosome X open reading frame 36	chrXp11.3	219652_s_at	NM_024689 /// NM_176819																					
2.36	2.38	0.02	8.93E-01	9.70E-01	FLJ31945	hypothetical gene supported by AK056507	chr13q14.3	1556578_a_at	XM_001714983 /// XM_001716811 /// XM_001718431																					
2.72	2.74	0.02	8.93E-01	9.70E-01	---	---	---	1565714_at	---																					
2.57	2.59	0.02	8.92E-01	9.70E-01	---	---	---	233685_at	---																					
2.00	2.02	0.02	8.93E-01	9.70E-01	---	---	---	240749_at	---																					
2.44	2.46	0.02	8.93E-01	9.70E-01	AHSG /// LOC100131613	alpha-2-HS-glycoprotein /// PRO1454	chr12q15 /// chr3q27	210929_s_at	NM_001622 /// XM_001723128 /// XM_001724337 /// XM_001726579																					
1.83	1.84	0.01	8.93E-01	9.70E-01	CCDC11	coiled-coil domain containing 11	chr18q21.1	1552325_at	NM_145020																					
2.88	2.90	0.02	8.93E-01	9.70E-01	ADORA1	adenosine A1 receptor	chr1q32.1	205481_at	NM_000674 /// NM_001048230																					
5.95	6.03	0.08	8.93E-01	9.70E-01	IL7R	interleukin 7 receptor	chr5p13	205798_at	NM_002185																					
2.83	2.87	0.03	8.93E-01	9.70E-01	NFIB	nuclear factor I/B	chr9p24.1	211466_at	NM_005596																					
2.81	2.83	0.02	8.93E-01	9.70E-01	TSHB	thyroid stimulating hormone, beta	chr1p13	214529_at	NM_000549																					
2.02	2.03	0.01	8.93E-01	9.70E-01	---	---	---	208045_at	---																					
6.74	6.79	0.05	8.93E-01	9.70E-01	NGDN	neuroguidin, EIF4E binding protein	chr14q11.2	213794_s_at	NM_001042635 /// NM_015514																					
6.26	6.29	0.03	8.93E-01	9.70E-01	OGFR	opioid growth factor receptor	chr20q13.3	210443_x_at	NM_007346																					
1.97	1.99	0.02	8.93E-01	9.70E-01	---	---	---	1569407_at	---																					
4.78	4.82	0.04	8.93E-01	9.70E-01	ATN1	atrophin 1	chr12p13.31	208871_at	NM_001007026 /// NM_001940																					
3.54	3.57	0.03	8.93E-01	9.70E-01	---	---	---	231602_at	---																					
4.18	4.20	0.02	8.93E-01	9.70E-01	---	---	---	1559245_at	---																					
4.20	4.26	0.06	8.93E-01	9.70E-01	REPS2	RALBP1 associated Eps domain containing 2	chrXp22.2	242571_at	NM_001080975 /// NM_004726																					
2.00	2.02	0.02	8.94E-01	9.70E-01	---	---	---	1560538_at	---																					
1.89	1.91	0.02	8.94E-01	9.70E-01	---	---	---	1562290_at	---																					
2.58	2.60	0.02	8.94E-01	9.70E-01	WDR93	WD repeat domain 93	chr15q26.1	232620_at	NM_020212																					
5.40	5.44	0.04	8.94E-01	9.70E-01	TLR3	toll-like receptor 3	chr4q35	206271_at	NM_003265																					
2.10	2.11	0.02	8.94E-01	9.70E-01	---	---	---	242057_at	---																					
3.89	3.95	0.06	8.94E-01	9.70E-01	ADAM10	ADAM metallopeptidase domain 10	chr15q2|15q22	202604_x_at	NM_001110																					
3.70	3.73	0.03	8.94E-01	9.70E-01	PLXNA2	plexin A2	chr1q32.2	227032_at	NM_025179																					
3.87	3.89	0.02	8.94E-01	9.70E-01	---	---	---	240129_at	---																					
1.86	1.88	0.02	8.94E-01	9.70E-01	LIX1	Lix1 homolog (chicken)	chr5q15	230865_at	NM_153234																					

3.04	3.06	0.02	8.94E-01	9.70E-01	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	chr14q32.1	230318_at	NM_000295 /// NM_001002235 /// NM_001002236 /// NM_001127700 /// NM_001127701 /// NM_001127702 /// NM_001127703 /// NM_001127704 /// NM_001127705 /// NM_001127706 /// NM_001127707
2.00	2.02	0.02	8.94E-01	9.71E-01	---	---	---	220880_at	---
2.90	2.91	0.02	8.94E-01	9.71E-01	MFSD2	major facilitator superfamily domain containing 2	chr1p34.2	1553386_at	NM_032793
1.94	1.96	0.02	8.94E-01	9.71E-01	---	---	---	238343_x_at	---
5.03	5.10	0.07	8.94E-01	9.71E-01	MBD4	methyl-CpG binding domain protein 4	chr3q21-q22	209580_s_at	NM_003925
8.09	8.15	0.06	8.94E-01	9.71E-01	MSI2	musashi homolog 2 (Drosophila)	chr17q22	225240_s_at	NM_138962 /// NM_170721
2.23	2.24	0.02	8.94E-01	9.71E-01	---	---	---	1566680_at	---
6.15	6.20	0.05	8.95E-01	9.71E-01	TMEM64	transmembrane protein 64	chr8q21.3	225974_at	NM_001008495
6.68	6.73	0.05	8.95E-01	9.71E-01	ENOPH1	enolase-phosphatase 1	chr4q21.22	217956_s_at	NM_021204
4.31	4.35	0.04	8.95E-01	9.71E-01	VAV1	vav 1 guanine nucleotide exchange factor	chr19p13.2	206219_s_at	NM_005428
4.28	4.31	0.03	8.95E-01	9.71E-01	KRTAP5-9	keratin associated protein 5-9	chr11q13.5	214517_at	NM_005553
4.25	4.27	0.02	8.95E-01	9.71E-01	TTLL9	tubulin tyrosine ligase-like family, member 9	chr20q11.21	234337_at	NM_001008409
2.01	2.03	0.02	8.95E-01	9.71E-01	---	---	---	1560929_at	---
5.51	5.54	0.03	8.95E-01	9.71E-01	AOAH	acyloxyacyl hydrolase (neutrophil)	chr7p14-p12	205639_at	NM_001637
3.14	3.21	0.07	8.95E-01	9.71E-01	HECTD1	HECT domain containing 1	chr14q12	1557100_s_at	NM_015382
3.64	3.68	0.03	8.95E-01	9.71E-01	---	---	---	242878_at	---
2.35	2.37	0.02	8.95E-01	9.71E-01	---	---	---	235877_at	---
3.57	3.64	0.07	8.95E-01	9.71E-01	LOC729222 /// PPFIBP1	similar to mKIAA1230 protein /// PTPRF interacting protein, binding protein 1 (liprin beta 1)	chr12p11.23 /// chr12p11.23-p11.22	214375_at	NM_003622 /// NM_177444 /// XR_015484 /// XR_037707 /// XR_037871
2.55	2.58	0.03	8.95E-01	9.71E-01	BRD3	bromodomain containing 3	chr9q34	1555028_at	NM_007371
2.95	2.98	0.02	8.95E-01	9.71E-01	MGC23284	hypothetical LOC197187	chr16q24.3	1568683_at	---
2.25	2.27	0.02	8.95E-01	9.71E-01	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	chr12p12	215129_at	NM_004570
2.06	2.07	0.01	8.95E-01	9.71E-01	NFIA	Nuclear factor I/A	chr1p31.3-p31.2	1557639_at	NM_001134673 /// NM_005595
3.88	3.90	0.02	8.95E-01	9.71E-01	MTERF	mitochondrial transcription termination factor	chr7q21-q22	204871_at	NM_006980
3.27	3.29	0.02	8.95E-01	9.71E-01	---	---	---	241818_at	---
2.31	2.33	0.02	8.95E-01	9.71E-01	---	---	---	1569850_at	---
7.78	7.81	0.03	8.95E-01	9.71E-01	METTL5	methyltransferase like 5	chr2q31.1	221570_s_at	NM_014168
2.35	2.37	0.02	8.95E-01	9.71E-01	---	---	---	237832_at	---
2.23	2.25	0.02	8.96E-01	9.71E-01	LOC440896	hypothetical gene LOC440896	chr9q12	1556378_a_at	NM_001039940 /// NR_015361
5.62	5.66	0.04	8.96E-01	9.71E-01	NUPL1	Nucleoporin like 1	chr13q12.13	241425_at	NM_001008564 /// NM_001008565 /// NM_014089
2.46	2.49	0.02	8.96E-01	9.71E-01	GK2	glycerol kinase 2	chr4q13	215430_at	NM_033214
2.49	2.51	0.02	8.96E-01	9.71E-01	LOC646522	hypothetical LOC646522	chr11q25	1563013_at	XR_040072 /// XR_040073 /// XR_040074
2.37	2.38	0.02	8.96E-01	9.71E-01	---	---	---	1556809_a_at	---
2.38	2.40	0.02	8.96E-01	9.71E-01	---	---	---	1568730_at	---
2.38	2.40	0.02	8.96E-01	9.71E-01	CECR9	cat eye syndrome chromosome region, candidate 9	---	1567686_at	---
2.74	2.76	0.01	8.96E-01	9.71E-01	---	---	---	1557022_at	---
2.50	2.53	0.03	8.96E-01	9.71E-01	LMLN	leishmanolysin-like (metallopeptidase M8 family)	chr3q29	1553284_s_at	NM_033029
4.56	4.62	0.06	8.96E-01	9.71E-01	---	---	---	233832_at	---
6.95	6.99	0.04	8.96E-01	9.71E-01	TFE3	transcription factor binding to IGHM enhancer 3	chrXp11.22	206649_s_at	NM_006521
3.19	3.22	0.03	8.96E-01	9.71E-01	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	chr1p36.13	1570511_at	NM_001011722 /// NM_018125

4.25	4.28	0.03	8.96E-01	9.71E-01	TMOD3	tropomodulin 3 (ubiquitous)	chr15q21.1-q21.2	223077_at	NM_014547
3.12	3.15	0.03	8.96E-01	9.71E-01	GPRIN2	G protein regulated inducer of neurite outgrowth 2	chr10q11.22	1554541_a_at	NM_014696
3.87	3.89	0.02	8.96E-01	9.71E-01	RICS	Rho GTPase-activating protein	chr11q24-q25	210791_s_at	NM_014715
3.06	3.08	0.02	8.96E-01	9.71E-01	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	chr1p21	244606_at	NM_000701 /// NM_001001586
2.54	2.56	0.02	8.96E-01	9.71E-01	LOC646982	TTL/TEL fusion protein TTL-T	chr13q14.11	1555264_a_at	XM_929953 /// XM_941294
2.39	2.41	0.02	8.96E-01	9.71E-01	SPOCD1	SPOC domain containing 1	chr1p35.2	1562415_a_at	NM_144569
2.13	2.14	0.02	8.96E-01	9.71E-01	ALB	albumin	chr4q11-q13	211298_s_at	NM_000477
2.38	2.40	0.01	8.96E-01	9.71E-01	OR5E1P	olfactory receptor, family 5, subfamily E, member 1 pseudogene	chr11p15.4	1566277_at	---
2.20	2.22	0.01	8.96E-01	9.71E-01	---	---	---	1570152_at	---
2.05	2.07	0.02	8.96E-01	9.71E-01	MSH3	mutS homolog 3 (E. coli)	chr5q11-q12	229662_at	NM_002439
3.36	3.52	0.16	8.96E-01	9.71E-01	JARID1D	jumonji, AT rich interactive domain 1D	chrYq11|Yq11	206700_s_at	NM_004653
4.29	4.34	0.05	8.96E-01	9.71E-01	SP140L	SP140 nuclear body protein-like	chr2q37.1	214791_at	NM_138402
5.96	6.00	0.04	8.96E-01	9.71E-01	DNAJC25	DnaJ (Hsp40) homolog, subfamily C , member 25	chr9q31.3	226859_at	NM_001015882
3.87	3.90	0.03	8.97E-01	9.71E-01	C9orf130	chromosome 9 open reading frame 130	chr9q22.32	227893_at	NR_023389 /// NR_023390 /// XM_001722853 /// XM_001724349 /// XM_001732875
2.70	2.71	0.01	8.96E-01	9.71E-01	---	---	---	1569962_at	---
4.48	4.54	0.06	8.97E-01	9.71E-01	CDC42SE2	CDC42 small effector 2	chr5q31.1	1552612_at	NM_001038702 /// NM_020240
2.36	2.38	0.02	8.97E-01	9.71E-01	---	---	---	1556518_at	---
2.08	2.09	0.01	8.97E-01	9.71E-01	UGT8	UDP glycosyltransferase 8	chr4q26	228956_at	NM_001128174 /// NM_003360
2.37	2.39	0.02	8.97E-01	9.71E-01	---	---	---	241884_at	---
6.15	6.17	0.02	8.97E-01	9.71E-01	UBE2G1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	chr1q42|17p13.2	226005_at	NM_003342
7.48	7.52	0.05	8.97E-01	9.71E-01	NCOA1	nuclear receptor coactivator 1	chr2p23	210249_s_at	NM_003743 /// NM_147223 /// NM_147233
7.06	7.10	0.04	8.97E-01	9.71E-01	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	chr1q32.1	201821_s_at	NM_006335
4.26	4.30	0.04	8.97E-01	9.71E-01	ZNF575	zinc finger protein 575	chr19q13.31	1557119_a_at	NM_174945
3.21	3.24	0.03	8.97E-01	9.71E-01	FAIM3	Fas apoptotic inhibitory molecule 3	chr1q32.1	221602_s_at	NM_005449
2.89	2.92	0.03	8.97E-01	9.71E-01	KCNG3	potassium voltage-gated channel, subfamily G, member 3	chr2p21	1552897_a_at	NM_133329 /// NM_172344
2.85	2.88	0.03	8.97E-01	9.71E-01	KLK7	kallikrein-related peptidase 7	chr19q13.33	205778_at	NM_005046 /// NM_139277
3.77	3.80	0.03	8.97E-01	9.71E-01	ACACA	acetyl-Coenzyme A carboxylase alpha	chr17q21	214358_at	NM_198834 /// NM_198836 /// NM_198837 /// NM_198838 /// NM_198839
3.58	3.60	0.02	8.97E-01	9.71E-01	---	---	---	240491_at	---
2.19	2.21	0.02	8.97E-01	9.71E-01	OR5J2	olfactory receptor, family 5, subfamily J, member 2	chr11q12.3	1567245_at	NM_001005492
5.94	5.96	0.02	8.97E-01	9.71E-01	---	---	---	234675_x_at	---
3.15	3.17	0.02	8.97E-01	9.71E-01	FGFR4	fibroblast growth factor receptor 4	chr5q35.1-qter	1554961_at	NM_002011 /// NM_022963 /// NM_213647
2.46	2.48	0.02	8.97E-01	9.71E-01	FETUB	fetuin B	chr3q27	210520_at	NM_014375
2.67	2.69	0.02	8.97E-01	9.71E-01	ACRV1	acrosomal vesicle protein 1	chr11q23-q24	207969_x_at	NM_001612 /// NM_020069 /// NM_020107 /// NM_020108 /// NM_020109 /// NM_020110 /// NM_020111 /// NM_020113 /// NM_020115
2.58	2.60	0.02	8.97E-01	9.71E-01	YPEL1	yippee-like 1 (Drosophila)	chr22q11.2	228296_at	NM_013313
2.96	2.99	0.03	8.98E-01	9.71E-01	FAM172A	family with sequence similarity 172, member A	chr5q15	223882_at	NM_032042
3.13	3.15	0.02	8.97E-01	9.71E-01	CTLA4	cytotoxic T-lymphocyte-associated protein 4	chr2q33	234895_at	NM_001037631 /// NM_005214
3.18	3.20	0.02	8.97E-01	9.71E-01	---	---	---	236092_at	---

4.30	4.33	0.03	8.98E-01	9.72E-01	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	chrXp22.2	228415_at	NM_003916
2.17	2.19	0.02	8.98E-01	9.72E-01	---	---	---	1570594_at	---
5.62	5.65	0.03	8.98E-01	9.72E-01	PARVA	parvin, alpha	chr11p15.3	222454_s_at	NM_018222
6.61	6.63	0.03	8.98E-01	9.72E-01	UBL7	ubiquitin-like 7 (bone marrow stromal cell-derived)	chr15q24.1	225063_at	NM_032907 /// NM_201265
2.65	2.68	0.03	8.98E-01	9.72E-01	---	---	---	235898_at	---
6.73	6.76	0.03	8.98E-01	9.72E-01	FAM160B1	family with sequence similarity 160, member B1	chr10q25.3	226155_at	NM_020940
6.62	6.65	0.03	8.98E-01	9.72E-01	LOC100132767	hypothetical protein LOC100132767	chr16p11.2	1569522_at	XM_001720251 /// XM_001725561
2.27	2.30	0.03	8.98E-01	9.72E-01	C7orf38	chromosome 7 open reading frame 38	chr7q22.1	238609_at	NM_145111
2.54	2.56	0.02	8.98E-01	9.72E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	216851_at	---
2.64	2.66	0.01	8.98E-01	9.72E-01	---	---	---	234274_at	---
3.80	3.83	0.02	8.98E-01	9.72E-01	---	---	---	239632_at	---
1.95	1.96	0.01	8.98E-01	9.72E-01	---	---	---	1565656_x_at	---
2.79	2.82	0.02	8.98E-01	9.72E-01	CDH23	cadherin-like 23	chr10q21-q22	232846_s_at	NM_022124 /// NM_052836
2.53	2.55	0.03	8.98E-01	9.72E-01	RARS2	arginyl-tRNA synthetase 2, mitochondrial	chr6q16.1	232901_at	NM_020320
7.69	7.71	0.02	8.98E-01	9.72E-01	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	chr10p12.31	222620_s_at	NM_022365
2.60	2.62	0.02	8.98E-01	9.72E-01	---	---	---	1564886_at	---
2.86	2.89	0.03	8.98E-01	9.72E-01	CHIA	chitinase, acidic	chr1p13.1-p21.3	220630_s_at	NM_021797 /// NM_201653
2.87	2.90	0.02	8.99E-01	9.72E-01	LOC100129447	hypothetical protein LOC100129447	chr12q24.13	1559618_at	XM_001719594 /// XM_001723232 /// XM_001726389
5.77	5.81	0.04	8.99E-01	9.72E-01	CARM1	coactivator-associated arginine methyltransferase 1	chr19p13.2	212512_s_at	NM_199141
11.13	11.16	0.04	8.99E-01	9.72E-01	GJA1	gap junction protein, alpha 1, 43kDa	chr6q21-q23.2	201667_at	NM_000165
4.62	4.65	0.02	8.99E-01	9.72E-01	LOC388630	hypothetical LOC388630	chr1p33	241707_at	XM_001132797 /// XM_001717552 /// XM_371250
2.07	2.09	0.02	8.99E-01	9.72E-01	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	chr4p15.2	1553167_a_at	NM_016955 /// NM_153825
6.36	6.41	0.05	8.99E-01	9.72E-01	WTAP	Wilms tumor 1 associated protein	chr6q25-q27	210285_x_at	NM_004906 /// NM_152857 /// NM_152858
7.76	7.81	0.05	8.99E-01	9.72E-01	LRRC8D	leucine rich repeat containing 8 family, member D	chr1p22.2	218684_at	NM_001134479 /// NM_018103
3.28	3.32	0.04	8.99E-01	9.72E-01	FOSL1	FOS-like antigen 1	chr11q13	204420_at	NM_005438
4.90	4.94	0.04	9.00E-01	9.72E-01	LRFN3	leucine rich repeat and fibronectin type III domain containing 3	chr19q13.12	219346_at	NM_024509
3.85	3.88	0.03	8.99E-01	9.72E-01	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	chr9q33.3	1555452_at	NM_014636
2.62	2.64	0.03	8.99E-01	9.72E-01	---	---	---	244542_at	---
4.89	4.91	0.02	9.00E-01	9.72E-01	LOC441108	Hypothetical gene supported by AK128882	chr5q31.1	232253_at	NM_001013717
2.48	2.50	0.02	9.00E-01	9.72E-01	LOC388946	Hypothetical LOC388946	chr2p21	1556490_a_at	XM_001718876 /// XM_371491 /// XM_941345
2.68	2.70	0.02	8.99E-01	9.72E-01	PCCB	Propionyl Coenzyme A carboxylase, beta polypeptide	chr3q21-q22	1557502_at	NM_000532
2.83	2.85	0.02	9.00E-01	9.72E-01	CSH1	chorionic somatomammotropin hormone 1 (placental lactogen)	chr17q24.2	206475_x_at	NM_001317 /// NM_022640 /// NM_022641
3.08	3.10	0.02	8.99E-01	9.72E-01	ZNF740	zinc finger protein 740	chr12q13.13	1558277_at	NM_001004304
10.46	10.48	0.02	8.99E-01	9.72E-01	HLA-C	major histocompatibility complex, class I, C	chr6p21.3	214459_x_at	NM_002117 /// XM_001715881 /// XM_001717045 /// XM_001719879
2.05	2.06	0.02	8.99E-01	9.72E-01	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	chr7q22	1568884_at	NM_001129887 /// NM_014377
5.00	5.02	0.02	8.99E-01	9.72E-01	LOC100131998	hypothetical protein LOC100131998	chr16p12.1	232540_x_at	XM_001725049
2.52	2.53	0.02	9.00E-01	9.72E-01	---	---	---	231597_x_at	---
1.94	1.95	0.02	8.99E-01	9.72E-01	HSD17B4	Hydroxysteroid (17-beta) dehydrogenase 4	chr5q21	1563696_at	NM_000414
1.91	1.93	0.02	8.99E-01	9.72E-01	MEX3C	mex-3 homolog C (C. elegans)	chr18q21.2	1556873_at	NM_016626
2.24	2.25	0.02	8.99E-01	9.72E-01	---	---	---	1563296_at	---
2.09	2.10	0.01	9.00E-01	9.72E-01	---	---	---	216070_at	---
2.02	2.04	0.01	8.99E-01	9.72E-01	---	---	---	237490_at	---
2.26	2.27	0.01	9.00E-01	9.72E-01	LOC440731	Similar to hCG1817424	chr1q42.2	237564_at	XM_933693
1.83	1.85	0.01	8.99E-01	9.72E-01	---	---	---	216625_at	---
2.00	2.02	0.01	8.99E-01	9.72E-01	---	---	---	1565915_at	---

2.13	2.14	0.01	8.99E-01	9.72E-01	RPAIN	RPA interacting protein	chr17p13.2	1564301_a_at	NM_001033002																					
6.97	7.03	0.06	9.00E-01	9.72E-01	C14orf147	chromosome 14 open reading frame 147	chr14q13.1	212460_at	NM_138288																					
3.36	3.38	0.03	9.00E-01	9.72E-01	CCDC82	coiled-coil domain containing 82	chr11q21	223301_s_at	NM_024725																					
3.28	3.30	0.02	9.00E-01	9.72E-01	---	---	---	1563181_a_at	---																					
1.96	1.97	0.01	9.00E-01	9.72E-01	---	---	---	231438_x_at	---																					
2.84	2.86	0.02	9.00E-01	9.72E-01	ARID4A	AT rich interactive domain 4A (RBP1-like)	chr14q23.1	230141_at	NM_002892 /// NM_023000 /// NM_023001																					
7.42	7.45	0.03	9.00E-01	9.72E-01	AMZ2	archaelysin family metallopeptidase 2	chr17q24.2	218167_at	NM_001033569 /// NM_001033570 /// NM_001033571 /// NM_001033572 /// NM_001033574 /// NM_016627																					
6.96	6.98	0.03	9.00E-01	9.72E-01	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	chr14q23.1	203966_s_at	NM_021003 /// NM_177951 /// NM_177952																					
3.11	3.14	0.03	9.00E-01	9.72E-01	LRRC52	leucine rich repeat containing 52	chr1q23.3	1556484_at	NM_001005214																					
2.32	2.34	0.02	9.00E-01	9.72E-01	PSEN1	Presenilin 1	chr14q24.3	1567440_at	NM_000021 /// NM_007318																					
5.33	5.38	0.04	9.00E-01	9.72E-01	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	chr2q33	225188_at	NM_203365 /// NM_213589																					
2.26	2.28	0.02	9.00E-01	9.72E-01	CCR9	chemokine (C-C motif) receptor 9	chr3p21.3	207445_s_at	NM_006641 /// NM_031200																					
2.02	2.04	0.02	9.00E-01	9.72E-01	ZNF441	zinc finger protein 441	chr19p13.2	1553192_at	NM_152355																					
2.48	2.49	0.02	9.00E-01	9.72E-01	HEXA	hexosaminidase A (alpha polypeptide)	chr15q23-q24	1556426_at	NM_000520																					
2.73	2.74	0.01	9.00E-01	9.72E-01	ZNF343	zinc finger protein 343	chr20p13	207296_at	NM_024325																					
2.71	2.74	0.02	9.01E-01	9.72E-01	DHRS9	dehydrogenase/reductase (SDR family) member 9	chr2q31.1	224009_x_at	NM_005771 /// NM_199204																					
2.56	2.58	0.02	9.01E-01	9.72E-01	STAG3L4	stromal antigen 3-like 4	chr7p11.2-q11.2	218994_s_at	NM_022906																					
3.02	3.04	0.02	9.01E-01	9.72E-01	CTSS	cathepsin S	chr1q21	202901_x_at	NM_004079																					
2.97	2.99	0.02	9.01E-01	9.72E-01	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	chr14q22.1	1554177_a_at	NM_001003803 /// NM_001003805 /// NM_015684																					
2.64	2.66	0.03	9.01E-01	9.72E-01	DLL3	delta-like 3 (Drosophila)	chr19q13	219537_x_at	NM_016941 /// NM_203486																					
2.17	2.19	0.02	9.01E-01	9.72E-01	GPR98	G protein-coupled receptor 98	chr5q13	215396_at	NM_032119 /// NR_003149																					
2.41	2.43	0.01	9.01E-01	9.73E-01	C17orf45	chromosome 17 open reading frame 45	chr17p11.2	244807_at	NM_152350																					
7.06	7.09	0.03	9.01E-01	9.73E-01	LRRC32	leucine rich repeat containing 32	chr11q13.5-q14	203835_at	NM_001128922 /// NM_005512																					
2.57	2.58	0.02	9.01E-01	9.73E-01	C17orf78	chromosome 17 open reading frame 78	chr17q12	1553486_a_at	NM_173625																					
2.45	2.47	0.02	9.01E-01	9.73E-01	PPIH	Peptidylprolyl isomerase H (cyclophilin H)	chr1p34.1	236142_at	NM_006347																					
2.51	2.52	0.02	9.01E-01	9.73E-01	---	---	---	239986_at	---																					
1.97	1.99	0.01	9.01E-01	9.73E-01	---	---	---	240490_at	---																					
4.87	4.91	0.05	9.01E-01	9.73E-01	FGD3	FYVE, RhoGEF and PH domain containing 3	---	227811_at	NM_001083536 /// NM_033086																					
2.68	2.70	0.02	9.01E-01	9.73E-01	FLJ20433	hypothetical protein FLJ20433	chr9q34.3	1555914_a_at	NM_017820																					
2.05	2.07	0.02	9.01E-01	9.73E-01	---	---	---	1557438_at	---																					
2.22	2.24	0.02	9.01E-01	9.73E-01	C2CD3	C2 calcium-dependent domain containing 3	chr11q13.4	1558756_at	NM_015531																					
3.98	4.00	0.03	9.01E-01	9.73E-01	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	chr11q12.3	230049_at	NM_006473																					
2.44	2.47	0.03	9.01E-01	9.73E-01	PIGA	phosphatidylinositol glycan anchor biosynthesis, class A	chrXp22.1	205281_s_at	NM_002641 /// NM_020473																					
3.59	3.61	0.02	9.01E-01	9.73E-01	POLH	polymerase (DNA directed), eta	chr6p21.1	233852_at	NM_006502																					
3.01	3.02	0.01	9.02E-01	9.73E-01	N6AMT1	N-6 adenine-specific DNA methyltransferase 1 (putative)	chr21q21.3	234698_at	NM_013240 /// NM_182749																					
6.99	7.04	0.05	9.02E-01	9.73E-01	41523	septin 6	chrXq24	1555526_a_at	NM_015129 /// NM_145799 /// NM_145800 /// NM_145802																					
4.46	4.49	0.03	9.02E-01	9.73E-01	CYGB	cytoglobin	chr17q25.3	1553572_a_at	NM_134268																					
4.67	4.73	0.06	9.02E-01	9.73E-01	FNDC3A	fibronectin type III domain containing 3A	chr13q14.2	215910_s_at	NM_001079673 /// NM_014923																					

3.44	3.50	0.05	9.02E-01	9.73E-01	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	chr17q24.3	241705_at	NM_018672 /// NM_172232
2.69	2.73	0.04	9.02E-01	9.73E-01	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	chr7q21-q31	203788_s_at	NM_006379
5.62	5.66	0.04	9.03E-01	9.73E-01	FLJ20628	hypothetical protein FLJ20628	chr2p23.2	221229_s_at	NM_017910
6.70	6.74	0.04	9.02E-01	9.73E-01	GGNBP2	gametogenetin binding protein 2	chr17q12	218079_s_at	NM_024835
6.57	6.60	0.03	9.02E-01	9.73E-01	CLDN12	claudin 12	chr7q21	223249_at	NM_012129
6.03	6.06	0.03	9.03E-01	9.73E-01	PLD2	phospholipase D2	chr17p13.1	209643_s_at	NM_002663
3.61	3.63	0.03	9.02E-01	9.73E-01	C12orf53	chromosome 12 open reading frame 53	chr12p13.31	1553566_at	NM_153685
2.94	2.97	0.02	9.03E-01	9.73E-01	CCDC57	coiled-coil domain containing 57	chr17q25.3	234661_at	NM_198082
2.40	2.42	0.02	9.03E-01	9.73E-01	FAM65A	family with sequence similarity 65, member A	chr16q22.1	230806_s_at	NM_024519
3.81	3.84	0.02	9.02E-01	9.73E-01	---	---	---	228626_at	---
2.49	2.52	0.02	9.02E-01	9.73E-01	SSTR2	somatostatin receptor 2	chr17q24	217455_s_at	NM_001050
3.05	3.07	0.02	9.02E-01	9.73E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	211805_s_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
4.00	4.02	0.02	9.02E-01	9.73E-01	---	---	---	1570330_at	---
6.26	6.28	0.02	9.03E-01	9.73E-01	GCSH /// LOC730107	glycine cleavage system protein H (aminomethyl carrier) /// similar to Glycine cleavage system H protein, mitochondrial	chr16q23.2 /// chr1q24.2	213133_s_at	NM_004483 /// XM_001134369 /// XM_001721064
2.42	2.44	0.02	9.02E-01	9.73E-01	LOC100128191	hypothetical protein LOC100128191	chr12q23.1	227578_at	XM_001715166 /// XM_001717944 /// XM_001718586
2.64	2.66	0.02	9.03E-01	9.73E-01	ELL	elongation factor RNA polymerase II	chr19p13.1	1565254_s_at	NM_006532
2.65	2.67	0.02	9.02E-01	9.73E-01	C12orf31	Chromosome 12 open reading frame 31	chr12q14.3	209779_at	NM_032338
1.94	1.96	0.02	9.03E-01	9.73E-01	---	---	---	243644_at	---
2.25	2.27	0.02	9.02E-01	9.73E-01	LOC100129656	hypothetical protein LOC100129656	chr1q44	237436_at	XM_001717015 /// XM_001717020
2.92	2.94	0.02	9.02E-01	9.73E-01	---	---	---	235438_at	---
2.75	2.77	0.02	9.02E-01	9.73E-01	ERICH1	glutamate-rich 1	chr8p23.3	1556766_at	NM_207332
2.15	2.16	0.02	9.02E-01	9.73E-01	NNT	Nicotinamide nucleotide transhydrogenase	chr5p13.1-cen	244531_at	NM_012343 /// NM_182977
1.98	1.99	0.02	9.02E-01	9.73E-01	---	---	---	238399_x_at	---
2.35	2.36	0.01	9.02E-01	9.73E-01	ZNF846	zinc finger protein 846	chr19p13.2	1569157_s_at	NM_001077624
2.35	2.37	0.01	9.03E-01	9.73E-01	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	chr1q32.2	229842_at	NM_001114309 /// NM_004433
2.02	2.03	0.01	9.02E-01	9.73E-01	KIDINS220	kinase D-interacting substrate of 220 kDa	chr2p24	214932_at	NM_020738
1.93	1.94	0.01	9.02E-01	9.73E-01	---	---	---	243936_x_at	---
1.92	1.94	0.01	9.03E-01	9.73E-01	AQP4	aquaporin 4	chr18q11.2-q12.1	226228_at	NM_001650 /// NM_004028
1.98	1.99	0.01	9.03E-01	9.73E-01	C10orf79	chromosome 10 open reading frame 79	chr10q25.1	220919_s_at	NM_025145
2.74	2.76	0.02	9.03E-01	9.73E-01	---	---	---	216154_at	---
1.90	1.92	0.02	9.03E-01	9.73E-01	LOC100130155	Hypothetical protein LOC100130155	chr8q12.3	242193_at	XM_001720201 /// XM_001720202 /// XM_001720219
2.28	2.30	0.02	9.03E-01	9.73E-01	---	---	---	1561075_at	---
4.93	4.97	0.04	9.03E-01	9.73E-01	SOCS4	suppressor of cytokine signaling 4	chr14q22.3	226178_at	NM_080867 /// NM_199421
2.82	2.84	0.02	9.03E-01	9.73E-01	AKAP1	A kinase (PRKA) anchor protein 1	chr17q21-q23	210626_at	NM_003488
3.26	3.28	0.02	9.03E-01	9.73E-01	LOC389641	Hypothetical gene supported by AK124295	chr8p21.3	244886_at	XM_374260 /// XM_944097
2.32	2.34	0.02	9.04E-01	9.73E-01	---	---	---	1561861_a_at	---
2.43	2.45	0.02	9.04E-01	9.73E-01	LOC644620	Similar to hCG2041997	chr9q31.2	1561398_at	XM_001716736 /// XM_001717475 /// XM_001718226
1.91	1.92	0.02	9.04E-01	9.73E-01	CCDC67	coiled-coil domain containing 67	chr11q21	1554072_s_at	NM_181645
2.00	2.01	0.01	9.04E-01	9.73E-01	---	---	---	240980_at	---

4.21	4.23	0.03	9.04E-01	9.73E-01	CPT1A	carnitine palmitoyltransferase 1A (liver)	chr11q13.1-q13.2	210688_s_at	NM_001031847 /// NM_001876
2.01	2.03	0.01	9.04E-01	9.73E-01	---	---	---	1558522_at	---
5.40	5.45	0.05	9.04E-01	9.73E-01	LOC144871	hypothetical protein LOC144871	chr13q32.1	1558080_s_at	---
5.05	5.12	0.06	9.04E-01	9.73E-01	USPL1	ubiquitin specific peptidase like 1	chr3q12-q14	204190_at	NM_005800
2.88	2.89	0.02	9.04E-01	9.74E-01	CLEC1B	C-type lectin domain family 1, member B	chr12p13.2	220496_at	NM_001099431 /// NM_016509
8.99	9.04	0.05	9.04E-01	9.74E-01	CCT2	chaperonin containing TCP1, subunit 2 (beta)	chr12q15	201947_s_at	NM_006431
3.23	3.25	0.03	9.04E-01	9.74E-01	KIR3DL1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	chr19q13.4	211687_x_at	NM_013289
5.46	5.50	0.04	9.04E-01	9.74E-01	RMND1	required for meiotic nuclear division 1 homolog (S. cerevisiae)	chr6q25.1	220329_s_at	NM_017909
3.25	3.28	0.03	9.04E-01	9.74E-01	LOC283194	hypothetical protein LOC283194	chr11q12.2	1563867_at	---
2.42	2.44	0.02	9.04E-01	9.74E-01	---	---	---	1561194_at	---
2.98	3.00	0.02	9.04E-01	9.74E-01	GMEB1	glucocorticoid modulatory element binding protein 1	chr1p35.3	230613_at	NM_006582 /// NM_024482
7.50	7.51	0.02	9.04E-01	9.74E-01	DNASE2	deoxyribonuclease II, lysosomal	chr19p13.2	209831_x_at	NM_001375
2.53	2.55	0.02	9.04E-01	9.74E-01	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	chr2q37.1	1568943_at	NM_001017915 /// NM_005541
4.74	4.77	0.03	9.04E-01	9.74E-01	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	chr20q13.33	224613_s_at	NM_025219
3.66	3.68	0.02	9.04E-01	9.74E-01	ING5	Inhibitor of growth family, member 5	chr2q37.3	241447_at	NM_032329
1.83	1.85	0.01	9.04E-01	9.74E-01	LOC283587	hypothetical protein LOC283587	chr14q31.3	1559363_at	---
2.05	2.06	0.01	9.04E-01	9.74E-01	NOX1	NADPH oxidase 1	chrXq22	206418_at	NM_007052 /// NM_013955
3.51	3.56	0.05	9.05E-01	9.74E-01	---	---	---	217584_at	---
3.81	3.83	0.02	9.04E-01	9.74E-01	---	---	---	234214_at	---
3.76	3.78	0.02	9.05E-01	9.74E-01	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	chr9q34.3	210781_x_at	NM_000832 /// NM_007327 /// NM_021569
3.28	3.33	0.05	9.05E-01	9.74E-01	---	---	---	244008_at	---
6.44	6.48	0.04	9.05E-01	9.74E-01	SIGLEC11	sialic acid binding Ig-like lectin 11	chr19q13.33	1552910_at	NM_052884
9.85	9.94	0.09	9.05E-01	9.74E-01	SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	chr10q21.1	227506_at	NM_194298
2.09	2.11	0.01	9.05E-01	9.74E-01	LOC285766	hypothetical protein LOC285766	chr6p25.3	1564253_at	---
6.63	6.66	0.03	9.05E-01	9.74E-01	RRAS	related RAS viral (r-ras) oncogene homolog	chr19q13.3-qter	212647_at	NM_006270
2.57	2.59	0.02	9.05E-01	9.74E-01	DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	chr7q22-q31	205762_s_at	NM_181581
2.17	2.18	0.02	9.05E-01	9.74E-01	---	---	---	1566209_at	---
2.20	2.21	0.01	9.05E-01	9.74E-01	---	---	---	1559697_a_at	---
3.44	3.47	0.03	9.05E-01	9.74E-01	STAT1	signal transducer and activator of transcription 1, 91kDa	chr2q32.2	AFFX-HUMISGF3A/M97935_5_at	NM_007315 /// NM_139266
2.34	2.36	0.02	9.05E-01	9.74E-01	BAGE2 /// BAGE3 /// BAGE5 /// MLL3	B melanoma antigen family, member 2 /// B melanoma antigen family, member 3 /// B melanoma antigen family, member 5 /// myeloid/lymphoid or mixed-lineage leukemia 3	chr13cen /// chr21p /// chr21p11.2 /// chr7q36.1	1555409_a_at	NM_170606 /// NM_182481 /// NM_182482 /// NM_182484
1.92	1.93	0.02	9.05E-01	9.74E-01	---	---	---	1561553_at	---
2.05	2.06	0.01	9.05E-01	9.74E-01	---	---	---	1562418_at	---
7.96	7.99	0.03	9.05E-01	9.74E-01	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	chr2p21	215000_s_at	NM_001042548 /// NM_005102
3.53	3.56	0.03	9.05E-01	9.74E-01	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	1558211_s_at	NM_005417 /// NM_198291
2.66	2.68	0.02	9.05E-01	9.74E-01	---	---	---	1559537_at	---
3.08	3.10	0.02	9.05E-01	9.74E-01	CUL7	cullin 7	chr6p21.1	241746_at	NM_014780
2.53	2.54	0.02	9.05E-01	9.74E-01	---	---	---	244136_at	---
1.98	1.99	0.02	9.05E-01	9.74E-01	---	---	---	1563941_at	---
2.30	2.32	0.02	9.05E-01	9.74E-01	DSC2	desmocollin 2	chr18q12.1	204750_s_at	NM_004949 /// NM_024422
2.29	2.30	0.01	9.05E-01	9.74E-01	---	---	---	1569978_x_at	---
5.98	6.00	0.02	9.06E-01	9.74E-01	EIF1	eukaryotic translation initiation factor 1	chr17q21.2	217672_x_at	NM_005801
2.28	2.30	0.02	9.06E-01	9.74E-01	C9orf107	chromosome 9 open reading frame 107	chr9q31.1	1563260_at	---
2.55	2.57	0.02	9.06E-01	9.74E-01	LOC100130837	Hypothetical protein LOC100130837	chr10p15.3	230198_at	XM_001717688 /// XM_001720700 /// XM_001724535
2.38	2.40	0.02	9.06E-01	9.74E-01	CCDC18	coiled-coil domain containing 18	chr1p22.1	232362_at	NM_206886
3.49	3.52	0.03	9.06E-01	9.74E-01	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	chr1q23.3	211396_at	NM_001005410 /// NM_001005411 /// NM_201563

5.29	5.34	0.05	9.06E-01	9.74E-01	LGALS8	lectin, galactoside-binding, soluble, 8	chr1q42-q43	208933_s_at	NM_006499 /// NM_201543 /// NM_201544 /// NM_201545																					
4.90	4.95	0.05	9.06E-01	9.74E-01	---	---	---	226237_at	---																					
2.71	2.73	0.02	9.06E-01	9.74E-01	---	---	---	241112_at	---																					
1.92	1.94	0.01	9.06E-01	9.74E-01	MGC16075	hypothetical protein MGC16075	chr7p12.3	1553708_at	XR_000600 /// XR_000617 /// XR_001277																					
2.62	2.63	0.02	9.06E-01	9.74E-01	LOC340037	hypothetical protein LOC340037	chr5q35.3	1560448_at	---																					
4.56	4.63	0.07	9.06E-01	9.74E-01	---	---	---	231040_at	---																					
5.35	5.55	0.19	9.06E-01	9.74E-01	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	chr6p21.3	209728_at	NM_021983 /// XM_001723414 /// XM_001723417 /// XM_001723419																					
3.09	3.11	0.02	9.06E-01	9.74E-01	---	---	---	239063_at	---																					
2.82	2.84	0.03	9.06E-01	9.74E-01	AVPR2	arginine vasopressin receptor 2	chrXq28	208108_s_at	NM_000054																					
5.07	5.12	0.05	9.06E-01	9.74E-01	S1PR1	sphingosine-1-phosphate receptor 1	chr1p21	204642_at	NM_001400																					
4.26	4.29	0.03	9.06E-01	9.74E-01	NR2F2	nuclear receptor subfamily 2, group F, member 2	chr15q26	209119_x_at	NM_021005																					
3.07	3.10	0.02	9.06E-01	9.74E-01	SLC23A3	solute carrier family 23 (nucleobase transporters), member 3	chr2q35	230949_at	NM_144712																					
5.26	5.28	0.02	9.06E-01	9.74E-01	QSOX2	quiescin Q6 sulfhydryl oxidase 2	chr9q34.3	227146_at	NM_181701																					
2.74	2.76	0.02	9.06E-01	9.74E-01	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	chr11p15.3	206275_s_at	NM_014632																					
5.62	5.64	0.02	9.06E-01	9.74E-01	DGCR2	DiGeorge syndrome critical region gene 2	chr22q11.21	202099_s_at	NM_005137																					
3.47	3.49	0.01	9.06E-01	9.74E-01	FH	fumarate hydratase	chr1q42.1	216349_at	NM_000143																					
2.67	2.69	0.02	9.06E-01	9.74E-01	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	chr1p22.3	210871_x_at	NM_014021																					
3.52	3.57	0.05	9.07E-01	9.74E-01	---	---	---	238455_at	---																					
5.51	5.55	0.05	9.07E-01	9.74E-01	---	---	---	242688_at	---																					
5.46	5.50	0.03	9.07E-01	9.74E-01	---	---	---	244587_at	---																					
7.42	7.45	0.03	9.07E-01	9.74E-01	TTC3	tetratricopeptide repeat domain 3	chr21q22.2	210645_s_at	NM_001001894 /// NM_003316																					
2.29	2.32	0.03	9.07E-01	9.74E-01	TAT	tyrosine aminotransferase	chr16q22.1	1555189_a_at	NM_000353																					
3.65	3.68	0.03	9.07E-01	9.74E-01	SEZ6L	seizure related 6 homolog (mouse)-like	chr22q12.1	211894_x_at	NM_021115																					
6.96	6.99	0.02	9.07E-01	9.74E-01	FAM3A	family with sequence similarity 3, member A	chrXq28	209405_s_at	NM_021806																					
4.66	4.68	0.02	9.07E-01	9.74E-01	FGFR1	fibroblast growth factor receptor 1	chr8p11.2-p11.1	207937_x_at	NM_015850 /// NM_023105 /// NM_023106 /// NM_023107 /// NM_023108 /// NM_023110 /// NM_023111																					
4.14	4.16	0.02	9.07E-01	9.74E-01	---	---	---	220824_at	---																					
3.53	3.55	0.02	9.07E-01	9.74E-01	GRID1	glutamate receptor, ionotropic, delta 1	chr10q22	1555268_a_at	NM_017551																					
3.69	3.71	0.02	9.06E-01	9.74E-01	ARID3A	AT rich interactive domain 3A (BRIGHT-like)	chr19p13.3	205865_at	NM_005224																					
2.44	2.46	0.02	9.07E-01	9.74E-01	TMC7	transmembrane channel-like 7	chr16p12.3	220021_at	NM_024847																					
2.58	2.59	0.02	9.07E-01	9.74E-01	ZBTB37	zinc finger and BTB domain containing 37	chr1q25.1	223953_s_at	NM_001122770 /// NM_032522																					
2.75	2.77	0.02	9.07E-01	9.74E-01	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	chr8p11.23	217677_at	NM_021623																					
2.83	2.85	0.02	9.07E-01	9.74E-01	---	---	---	237708_at	---																					
2.08	2.10	0.02	9.07E-01	9.74E-01	---	---	---	233434_at	---																					
2.03	2.05	0.01	9.07E-01	9.74E-01	---	---	---	230260_s_at	---																					
2.18	2.19	0.01	9.07E-01	9.74E-01	---	---	---	1556800_a_at	---																					
1.88	1.89	0.01	9.07E-01	9.74E-01	---	---	---	243373_at	---																					
1.96	1.97	0.01	9.07E-01	9.74E-01	EFHC2	EF-hand domain (C-terminal) containing 2	chrXp11.3	220523_at	NM_025184																					
6.81	6.85	0.04	9.07E-01	9.74E-01	ZNF703	zinc finger protein 703	chr8p12	222760_at	NM_025069																					
3.77	3.79	0.02	9.07E-01	9.74E-01	ZDHHC22	Zinc finger, DHHC-type containing 22	chr14q24.3	229805_at	NM_174976																					
2.01	2.02	0.01	9.07E-01	9.74E-01	AADACL2	arylacetamide deacetylase-like 2	chr3q25.1	240420_at	NM_207365																					
2.87	2.89	0.02	9.07E-01	9.75E-01	AGTRAP	Angiotensin II receptor-associated protein	chr1p36.22	238135_at	NM_001040194 /// NM_001040195 /// NM_001040196 /// NM_001040197 /// NM_020350																					

3.28	3.30	0.02	9.08E-01	9.75E-01	LOC728613 /// PDCD6	programmed cell death 6 pseudogene /// programmed cell death 6	chr5p15.33	1568764_x_at	NM_013232 /// NR_003713 /// XM_001714855 /// XM_001720072 /// XM_001723249
2.38	2.40	0.01	9.08E-01	9.75E-01	---	---	---	244336_at	---
6.61	6.63	0.02	9.08E-01	9.75E-01	CCDC101	coiled-coil domain containing 101	chr16p11.2	48117_at	NM_138414
2.58	2.60	0.01	9.08E-01	9.75E-01	N4BP3	Nedd4 binding protein 3	chr5q35.3	214775_at	NM_015111
6.67	6.70	0.03	9.08E-01	9.75E-01	SMYD3	SET and MYND domain containing 3	chr1q44	218788_s_at	NM_022743
1.99	2.01	0.02	9.08E-01	9.75E-01	SYCP3	Synaptonemal complex protein 3	chr12q	241861_at	NM_153694
3.21	3.24	0.03	9.08E-01	9.75E-01	ZNF354A	zinc finger protein 354A	chr5q35.3	205427_at	NM_005649
7.00	7.04	0.04	9.08E-01	9.75E-01	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	chr8p11	202423_at	NM_001099412 /// NM_001099413 /// NM_006766
3.04	3.06	0.02	9.08E-01	9.75E-01	---	---	---	243673_at	---
2.05	2.07	0.01	9.08E-01	9.75E-01	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	chr13q14	1557763_at	NM_005767
2.28	2.30	0.02	9.08E-01	9.75E-01	---	---	---	1563190_at	---
2.27	2.29	0.01	9.08E-01	9.75E-01	IL1F5	interleukin 1 family, member 5 (delta)	chr2q14	222223_s_at	NM_012275 /// NM_173170
4.40	4.42	0.02	9.08E-01	9.75E-01	DNM3	dynamin 3	chr1q24.3	1558502_s_at	NM_015569
4.66	4.72	0.06	9.08E-01	9.75E-01	ANKRD13C	ankyrin repeat domain 13C	chr1p32.3-p31.3	1554471_a_at	NM_030816
3.12	3.14	0.02	9.08E-01	9.75E-01	C14orf21	chromosome 14 open reading frame 21	chr14q12	1555390_at	NM_174913
2.63	2.66	0.03	9.09E-01	9.75E-01	CLDN3	claudin 3	chr7q11.23	203953_s_at	NM_001306
2.10	2.11	0.01	9.09E-01	9.75E-01	DEFB107A /// DEFB107B	defensin, beta 107A /// defensin, beta 107B	chr8p23.1	1563450_at	NM_001037668 /// NM_001040705
2.55	2.57	0.02	9.09E-01	9.75E-01	IRF6	interferon regulatory factor 6	chr1q32.3-q41	1552478_a_at	NM_006147
2.63	2.64	0.02	9.09E-01	9.75E-01	LRMP	lymphoid-restricted membrane protein	chr12p12.1	35974_at	NM_006152
5.03	5.05	0.02	9.09E-01	9.75E-01	TCOF1	Treacher Collins-Franceschetti syndrome 1	chr5q32-q33.1	202384_s_at	NM_000356 /// NM_001008656 /// NM_001008657
4.38	4.41	0.03	9.09E-01	9.75E-01	SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	chr9p22.3	204001_at	NM_001039697
2.94	2.97	0.03	9.09E-01	9.75E-01	---	---	---	231619_at	---
4.10	4.15	0.05	9.09E-01	9.75E-01	C9orf58	chromosome 9 open reading frame 58	chr9q34.13-q34.3	223075_s_at	NM_031426
6.49	6.54	0.05	9.09E-01	9.75E-01	RBP7	retinol binding protein 7, cellular	chr1p36.22	238066_at	NM_052960
4.12	4.14	0.02	9.09E-01	9.75E-01	---	---	---	222331_at	---
3.41	3.43	0.02	9.09E-01	9.75E-01	HYDIN /// HYDIN2	hydrocephalus inducing homolog (mouse) /// hydrocephalus inducing homolog 2 (mouse)	chr16q22.1-q22.3 /// chr1q21.1	220098_at	NM_017558 /// NM_032821 /// XM_001717859
3.20	3.22	0.02	9.09E-01	9.75E-01	TUB	tubby homolog (mouse)	chr11p15.5	208431_s_at	NM_003320 /// NM_177972
2.69	2.71	0.02	9.09E-01	9.75E-01	PPIA	peptidylprolyl isomerase A (cyclophilin A)	chr7p13	217602_at	NM_021130
8.32	8.35	0.02	9.09E-01	9.75E-01	NOL7	nucleolar protein 7, 27kDa	chr6p23	202882_x_at	NM_016167
2.28	2.30	0.02	9.10E-01	9.75E-01	LOC728868	hypothetical protein LOC728868	chr8p23.1	1559586_at	XM_001129694
3.34	3.36	0.02	9.10E-01	9.75E-01	---	---	---	1569339_s_at	---
2.57	2.59	0.02	9.10E-01	9.75E-01	---	---	---	1559195_at	---
2.83	2.85	0.02	9.09E-01	9.75E-01	SCML4	sex comb on midleg-like 4 (Drosophila)	chr6q21	1563542_a_at	NM_198081
8.40	8.42	0.02	9.10E-01	9.75E-01	PNPLA2	patatin-like phospholipase domain containing 2	chr11p15.5	39854_r_at	NM_020376
2.34	2.36	0.02	9.09E-01	9.75E-01	FGFR1OP	FGFR1 oncogene partner	chr6q27	205587_at	NM_007045 /// NM_194429
2.16	2.17	0.02	9.10E-01	9.75E-01	LOC100129917	Hypothetical protein LOC100129917	chr4p16.3	1559528_at	XM_001716393 /// XM_001719767 /// XM_001721215
2.36	2.37	0.01	9.10E-01	9.75E-01	ZNF470	zinc finger protein 470	chr19q13.43	234921_at	NM_001001668
1.92	1.94	0.01	9.10E-01	9.75E-01	SLC5A12	solute carrier family 5 (sodium/glucose cotransporter), member 12	chr11p14.2	231424_at	NM_178498
2.07	2.08	0.01	9.10E-01	9.75E-01	---	---	---	1564872_at	---
5.23	5.24	0.01	9.09E-01	9.75E-01	KIAA0090	KIAA0090	chr1p36.13	212395_s_at	NM_015047
3.36	3.38	0.02	9.10E-01	9.75E-01	---	---	---	229531_at	---

4.76	4.79	0.03	9.10E-01	9.75E-01	BBS9	Bardet-Biedl syndrome 9	chr7p14	37549_g_at	NM_001033604 /// NM_001033605 /// NM_014451 /// NM_198428																				
2.30	2.32	0.02	9.10E-01	9.75E-01	C19orf61	chromosome 19 open reading frame 61	chr19q13.31	233990_at	NM_019108																				
4.61	4.66	0.05	9.10E-01	9.75E-01	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	chr4q31.1	218313_s_at	NM_017423																				
5.55	5.59	0.04	9.10E-01	9.75E-01	MAOA	monoamine oxidase A	chrXp11.3	204388_s_at	NM_000240																				
5.97	6.01	0.03	9.10E-01	9.75E-01	PCNX	pecanex homolog (Drosophila)	chr14q24.2	213159_at	NM_014982																				
6.03	6.06	0.03	9.10E-01	9.75E-01	CAPN1	calpain 1, (mu/I) large subunit	chr11q13	200752_s_at	NM_005186																				
7.40	7.43	0.03	9.10E-01	9.75E-01	PTK2	PTK2 protein tyrosine kinase 2	chr8q24-qter	208820_at	NM_005607 /// NM_153831																				
3.24	3.26	0.02	9.10E-01	9.75E-01	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	chr16q24	208056_s_at	NM_005187 /// NM_175931																				
3.87	3.90	0.02	9.10E-01	9.75E-01	SPAG4L	sperm associated antigen 4-like	chr20q11.21	237188_x_at	NM_080675																				
2.65	2.67	0.02	9.10E-01	9.75E-01	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19p13.3	217271_at	NM_002067																				
2.40	2.42	0.02	9.10E-01	9.75E-01	---	---	---	231611_at	---																				
4.74	4.76	0.02	9.10E-01	9.75E-01	CCDC33	coiled-coil domain containing 33	chr15q24.1	1563090_at	NM_025055 /// NM_182791																				
2.57	2.59	0.02	9.10E-01	9.75E-01	---	---	---	243598_at	---																				
2.66	2.68	0.02	9.10E-01	9.75E-01	LOC200609	Hypothetical protein LOC200609	chr2q37.3	233209_at	---																				
2.36	2.38	0.02	9.10E-01	9.75E-01	PM20D1	peptidase M20 domain containing 1	chr1q32.1	239929_at	NM_152491																				
2.87	2.88	0.02	9.10E-01	9.75E-01	OPRK1	opioid receptor, kappa 1	chr8q11.2	207553_at	NM_000912																				
2.28	2.30	0.02	9.10E-01	9.75E-01	MDM2	Mdm2 p53 binding protein homolog (mouse)	chr12q14.3-q15	237891_at	NM_002392 /// NM_006878 /// NM_006879 /// NM_006881 /// NM_006882																				
2.36	2.38	0.02	9.10E-01	9.75E-01	LOC642103 /// MGAM	similar to Maltase-glucoamylase, intestinal /// maltase-glucoamylase (alpha-glucosidase)	chr7q34	206522_at	NM_004668 /// XM_936233																				
2.46	2.48	0.02	9.10E-01	9.75E-01	---	---	---	236343_at	---																				
2.36	2.38	0.02	9.10E-01	9.75E-01	---	---	---	217654_at	---																				
7.25	7.33	0.08	9.11E-01	9.75E-01	CYB5A	cytochrome b5 type A (microsomal)	chr18q23	209366_x_at	NM_001914 /// NM_148923																				
2.22	2.23	0.01	9.11E-01	9.75E-01	---	---	---	239679_at	---																				
4.09	4.18	0.09	9.11E-01	9.75E-01	---	---	---	243240_at	---																				
3.35	3.37	0.02	9.11E-01	9.75E-01	LOC401320	hypothetical LOC401320	chr7p15.1	238540_at	XM_379482 /// XM_380098 /// XM_938539																				
2.38	2.39	0.01	9.11E-01	9.75E-01	DICER1	dicer 1, ribonuclease type III	chr14q32.13	216260_at	NM_030621 /// NM_177438																				
2.39	2.41	0.02	9.11E-01	9.75E-01	COMMD7	COMM domain containing 7	chr20q11.21	244178_at	NM_001099339 /// NM_053041																				
2.97	3.00	0.03	9.11E-01	9.76E-01	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	chr11p15.1	235440_at	NM_194285																				
2.28	2.29	0.02	9.11E-01	9.76E-01	EGR4	early growth response 4	chr2p13	207768_at	NM_001965																				
2.70	2.72	0.02	9.11E-01	9.76E-01	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	chr11q23.1-q23.2	233613_x_at	NM_015523																				
1.94	1.96	0.02	9.11E-01	9.76E-01	---	---	---	237149_at	---																				
2.40	2.41	0.01	9.11E-01	9.76E-01	FGF14	fibroblast growth factor 14	chr13q34	221310_at	NM_004115 /// NM_175929																				
6.60	6.65	0.04	9.11E-01	9.76E-01	PAM	peptidylglycine alpha-amidating monooxygenase	chr5q14-q21	214620_x_at	NM_000919 /// NM_138766 /// NM_138821 /// NM_138822																				
4.39	4.43	0.04	9.11E-01	9.76E-01	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	chr2q23.3	215044_s_at	NM_005843																				
4.16	4.18	0.02	9.11E-01	9.76E-01	LOC100131144	hypothetical protein LOC100131144	chr8q24.3	226708_at	XM_001714981 /// XM_001715886 /// XM_001720722																				
2.59	2.61	0.02	9.11E-01	9.76E-01	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	chr8q21.13	225622_at	NM_018440																				
4.15	4.21	0.06	9.11E-01	9.76E-01	---	---	---	238712_at	---																				
4.66	4.67	0.02	9.11E-01	9.76E-01	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	chr3q23	229709_at	NM_001679																				

2.69	2.71	0.01	9.11E-01	9.76E-01	TMEM148	transmembrane protein 148	chr16q24.1	1552856_at	XR_017879 /// XR_017979 /// XR_040060
2.19	2.21	0.02	9.11E-01	9.76E-01	---	---	---	210500_at	---
2.25	2.27	0.01	9.11E-01	9.76E-01	GPR110	G protein-coupled receptor 110	chr6p12.3	235988_at	NM_025048 /// NM_153840
2.50	2.52	0.02	9.12E-01	9.76E-01	FAM111B	family with sequence similarity 111, member B	chr11q12.1	1557128_at	NM_198947
4.31	4.34	0.03	9.12E-01	9.76E-01	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	chr11q23.3	201333_s_at	NM_015313
2.26	2.28	0.01	9.12E-01	9.76E-01	LOC285144	hypothetical protein LOC285144	chr2p25.3	1565684_at	---
3.88	3.92	0.04	9.12E-01	9.76E-01	hCG_2024410 /// RPE	rcRPE /// ribulose-5-phosphate-3-epimerase	chr10q24.33 /// chr2q32-q33.3	216574_s_at	NM_006916 /// NM_199229 /// XM_001133007 /// XM_001723111 /// XM_001725597
5.59	5.65	0.06	9.12E-01	9.76E-01	KLF9	Kruppel-like factor 9	chr9q13	203543_s_at	NM_001206
3.99	4.01	0.02	9.12E-01	9.76E-01	RORC	RAR-related orphan receptor C	chr1q21	206419_at	NM_001001523 /// NM_005060
5.17	5.18	0.01	9.12E-01	9.76E-01	C1orf149	chromosome 1 open reading frame 149	chr1p35.3-p33	228517_at	NM_022756
2.10	2.11	0.01	9.12E-01	9.76E-01	---	---	---	233275_at	---
2.45	2.46	0.01	9.12E-01	9.76E-01	EBF2	early B-cell factor 2	chr8p21.2	1562477_at	NM_022659
2.37	2.39	0.02	9.12E-01	9.76E-01	TFEC	transcription factor EC	chr7q31.2	206715_at	NM_001018058 /// NM_012252
2.51	2.53	0.02	9.12E-01	9.76E-01	PPARD	peroxisome proliferator-activated receptor delta	chr6p21.2-p21.1	210636_at	NM_006238
2.28	2.29	0.01	9.12E-01	9.76E-01	---	---	---	1559021_at	---
2.01	2.02	0.01	9.12E-01	9.76E-01	XYLB	xylulokinase homolog (H. influenzae)	chr3p22-p21.3	214776_x_at	NM_005108
2.57	2.59	0.02	9.12E-01	9.76E-01	---	---	---	1557493_x_at	---
2.94	2.95	0.02	9.12E-01	9.76E-01	FGD2	FYVE, RhoGEF and PH domain containing 2	chr6p21.2	1565751_at	NM_173558
4.98	4.99	0.01	9.12E-01	9.76E-01	N-PAC	cytokine-like nuclear factor n-pac	chr16p13.3	222652_s_at	NM_032569
9.45	9.49	0.03	9.13E-01	9.76E-01	FSTL1	follistatin-like 1	chr3q13.33	208782_at	NM_007085
2.88	2.90	0.02	9.13E-01	9.76E-01	MAP2	microtubule-associated protein 2	chr2q34-q35	210015_s_at	NM_001039538 /// NM_002374 /// NM_031845 /// NM_031847
3.74	3.76	0.02	9.13E-01	9.76E-01	FOXD1	Forkhead box D1	chr5q12-q13	213972_at	NM_004472
2.51	2.53	0.02	9.13E-01	9.76E-01	C18orf62	chromosome 18 open reading frame 62	chr18q22.3	1564400_at	NM_001037331
2.18	2.19	0.02	9.13E-01	9.76E-01	EVI5	ecotropic viral integration site 5	chr1p22.1	208298_at	NM_005665
2.19	2.21	0.01	9.13E-01	9.76E-01	ADAM5P	ADAM metallopeptidase domain 5 pseudogene	chr8p11.23	217003_s_at	NR_001448
2.43	2.45	0.02	9.13E-01	9.76E-01	hCG_1741344 /// LOC100130477 /// SCGB1C1	secretoglobin, family 1C, member 1-like /// hypothetical protein LOC100130477 /// secretoglobin, family 1C, member 1	chr11p15.5	1552449_a_at	NM_001097610 /// NM_145651 /// XM_001713759 /// XM_001723174
1.95	1.96	0.01	9.13E-01	9.76E-01	---	---	---	213663_s_at	---
2.46	2.47	0.01	9.13E-01	9.76E-01	GRP	gastrin-releasing peptide	chr18q21.1-q21.32	206326_at	NM_001012512 /// NM_001012513 /// NM_002091
6.28	6.30	0.02	9.13E-01	9.76E-01	LPPR2	lipid phosphate phosphatase-related protein type 2	chr19p13.2	218509_at	NM_022737
5.75	5.77	0.02	9.13E-01	9.76E-01	SUPT3H	suppressor of Ty 3 homolog (S. cerevisiae)	chr6p21.1-p21.3	206506_s_at	NM_003599 /// NM_181356
3.14	3.16	0.02	9.13E-01	9.76E-01	ZNF460	zinc finger protein 460	chr19q13.4	216273_at	NM_006635
2.51	2.52	0.02	9.13E-01	9.76E-01	CRB1	crumbs homolog 1 (Drosophila)	chr1q31-q32.1	220522_at	NM_201253
2.19	2.21	0.02	9.13E-01	9.76E-01	KIAA0802	KIAA0802	chr18p11.22	240448_at	NM_015210
2.36	2.38	0.02	9.13E-01	9.76E-01	LOC157740	hypothetical protein C8orf9	chr8p23.1	239877_at	XR_042029 /// XR_042030 /// XR_042031
2.58	2.59	0.01	9.13E-01	9.76E-01	CDK9	Cyclin-dependent kinase 9	chr9q34.1	228901_at	NM_001261
2.53	2.54	0.02	9.13E-01	9.77E-01	CCL16	chemokine (C-C motif) ligand 16	chr17q11.2	207354_at	NM_004590
2.48	2.49	0.02	9.13E-01	9.77E-01	SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	chr12p13	206058_at	NM_001122847 /// NM_001122848 /// NM_003044
4.66	4.68	0.02	9.13E-01	9.77E-01	PRAM1	PML-RARA regulated adaptor molecule 1	chr19p13.2	241742_at	NM_032152
3.02	3.04	0.02	9.13E-01	9.77E-01	C15orf49	chromosome 15 open reading frame 49	chr15q11.2	234386_s_at	XR_040061 /// XR_040062
2.30	2.32	0.01	9.13E-01	9.77E-01	---	---	---	217701_x_at	---
2.03	2.05	0.01	9.13E-01	9.77E-01	SPATA22	spermatogenesis associated 22	chr17p13.3	231114_at	NM_032598

3.21	3.23	0.02	9.13E-01	9.77E-01	PDE7A	phosphodiesterase 7A	chr8q13	223359_s_at	NM_002603 /// NM_002604
2.02	2.03	0.02	9.13E-01	9.77E-01	TC2N	tandem C2 domains, nuclear	chr14q32.12	244272_s_at	NM_001128595 /// NM_001128596 /// NM_152332
2.13	2.14	0.01	9.13E-01	9.77E-01	KIAA1383	KIAA1383	chr1q42.2	232039_at	NM_019090
3.10	3.12	0.02	9.13E-01	9.77E-01	---	---	---	216644_at	---
2.39	2.41	0.02	9.13E-01	9.77E-01	---	---	---	1561627_at	---
2.75	2.78	0.03	9.14E-01	9.77E-01	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	chr2q32.1	221782_at	NM_018981
2.44	2.46	0.02	9.14E-01	9.77E-01	RPH3AL	rabphilin 3A-like (without C2 domains)	chr17p13.3	233134_at	NM_006987
1.78	1.79	0.01	9.14E-01	9.77E-01	---	---	---	1555364_at	---
3.88	3.90	0.02	9.14E-01	9.77E-01	WASF1	WAS protein family, member 1	chr6q21-q22	204165_at	NM_001024934 /// NM_001024935 /// NM_001024936 /// NM_003931
2.40	2.42	0.02	9.14E-01	9.77E-01	MKL2	MKL/myocardin-like 2	chr16p13.12	1570202_a_at	NM_014048
3.08	3.10	0.02	9.14E-01	9.77E-01	---	---	---	236199_at	---
2.57	2.58	0.01	9.14E-01	9.77E-01	C4orf30	chromosome 4 open reading frame 30	chr4p15.32	239187_at	NM_017741
1.91	1.92	0.01	9.14E-01	9.77E-01	---	---	---	237225_at	---
6.04	6.08	0.03	9.14E-01	9.77E-01	CLINT1	clathrin interactor 1	chr5q33.3	201768_s_at	NM_014666 /// XM_001715730 /// XM_001723151 /// XM_001725023
3.71	3.73	0.02	9.14E-01	9.77E-01	KBTBD7	kelch repeat and BTB (POZ) domain containing 7	chr13q14.11	229298_at	NM_032138
2.52	2.53	0.02	9.14E-01	9.77E-01	---	---	---	242509_at	---
4.43	4.46	0.03	9.14E-01	9.77E-01	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	chr17q21.2	229511_at	NM_003079
3.80	3.82	0.02	9.14E-01	9.77E-01	TRIM15	tripartite motif-containing 15	chr6p21.3	210885_s_at	NM_033229
2.57	2.59	0.02	9.14E-01	9.77E-01	MDM4	Mdm4 p53 binding protein homolog (mouse)	chr1q32	205655_at	NM_002393
2.79	2.81	0.02	9.14E-01	9.77E-01	FAM76A	family with sequence similarity 76, member A	chr1p35.3	216897_s_at	NM_152660
9.46	9.47	0.01	9.14E-01	9.77E-01	TEGT	testis enhanced gene transcript	chr12q12-q13	200803_s_at	NM_001098576 /// NM_003217
3.47	3.50	0.03	9.14E-01	9.77E-01	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	chr5p15	211056_s_at	NM_001047
2.50	2.52	0.02	9.14E-01	9.77E-01	LOC729070	Similar to hCG2030186	chr6q24.1	1555869_a_at	XM_001132470 /// XM_001133421 /// XM_001723282
1.98	1.99	0.01	9.14E-01	9.77E-01	LRRC31	leucine rich repeat containing 31	chr3q26.2	220622_at	NM_024727
2.43	2.45	0.02	9.14E-01	9.77E-01	---	---	---	1562793_at	---
2.08	2.10	0.01	9.14E-01	9.77E-01	C6orf142	Chromosome 6 open reading frame 142	chr6p12.1	1568554_x_at	NM_138569
2.78	2.80	0.02	9.14E-01	9.77E-01	PPYR1	pancreatic polypeptide receptor 1	chr10q11.2	210956_at	NM_005972
4.36	4.39	0.03	9.15E-01	9.77E-01	UFSP1	UFM1-specific peptidase 1 (non-functional)	chr7q22.1	240280_at	NM_001015072
3.27	3.29	0.02	9.15E-01	9.77E-01	---	---	---	1557757_at	---
3.73	3.75	0.02	9.15E-01	9.77E-01	HS3ST3B1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	chr17p12-p11.2	1561908_a_at	NM_006041
1.99	2.01	0.01	9.15E-01	9.77E-01	---	---	---	1556500_a_at	---
11.02	11.06	0.03	9.15E-01	9.77E-01	RPL4	ribosomal protein L4	chr15q22	200089_s_at	NM_000968
3.04	3.06	0.02	9.15E-01	9.77E-01	EFNA5	Ephrin-A5	chr5q21	233814_at	NM_001962
1.86	1.87	0.01	9.15E-01	9.77E-01	---	---	---	231709_x_at	---
4.36	4.39	0.04	9.15E-01	9.77E-01	RNGTT	RNA guanylyltransferase and 5'-phosphatase	chr6q16	204208_at	NM_003800
3.05	3.09	0.04	9.15E-01	9.77E-01	---	---	---	238443_at	---
6.07	6.10	0.03	9.15E-01	9.77E-01	LRBA	LPS-responsive vesicle trafficking, beach and anchor containing	chr4q31.3	212692_s_at	NM_006726
3.32	3.35	0.02	9.15E-01	9.77E-01	NEU3	sialidase 3 (membrane sialidase)	chr11q13.5	216083_s_at	NM_006656
2.80	2.82	0.02	9.15E-01	9.77E-01	ADAM20	ADAM metallopeptidase domain 20	chr14q24.1	207423_s_at	NM_003814
11.33	11.37	0.04	9.15E-01	9.77E-01	LOC644315 /// RPS7	similar to ribosomal protein S7 /// ribosomal protein S7	chr17q21.32 /// chr2p25	200082_s_at	NM_001011 /// XR_015900 /// XR_017529 /// XR_038829
3.87	3.93	0.06	9.15E-01	9.77E-01	---	---	---	233364_s_at	---
4.62	4.65	0.03	9.15E-01	9.77E-01	SPN	sialophorin	chr16p11.2	1568964_x_at	NM_001030288 /// NM_003123
8.15	8.17	0.02	9.15E-01	9.77E-01	CFL2	cofilin 2 (muscle)	chr14q12	224663_s_at	NM_021914 /// NM_138638

2.33	2.35	0.02	9.15E-01	9.77E-01	FCRL2	Fc receptor-like 2	chr1q21	221239_s_at	NM_030764 /// NM_138738
2.04	2.05	0.01	9.15E-01	9.77E-01	PCDHB2	protocadherin beta 2	chr5q31	231725_at	NM_018936
2.20	2.21	0.01	9.15E-01	9.77E-01	---	---	---	217037_at	---
2.90	2.91	0.02	9.16E-01	9.77E-01	TSPAN5	tetraspanin 5	chr4q23	225388_at	NM_005723
4.11	4.13	0.02	9.16E-01	9.77E-01	SEC14L4	SEC14-like 4 (S. cerevisiae)	chr22q12.2	216402_at	NM_174977
2.13	2.15	0.02	9.16E-01	9.77E-01	---	---	---	1566881_at	---
2.34	2.35	0.01	9.16E-01	9.77E-01	---	---	---	1570237_at	---
3.51	3.56	0.05	9.16E-01	9.77E-01	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	chr2q37.3	223492_s_at	NM_004735
3.34	3.36	0.02	9.16E-01	9.77E-01	---	---	---	223929_s_at	---
2.55	2.56	0.01	9.16E-01	9.77E-01	LOC203274	Hypothetical protein LOC203274	chr9q21.11	232034_at	---
2.39	2.40	0.01	9.16E-01	9.77E-01	FOXA2	forkhead box A2	chr20p11	40284_at	NM_021784 /// NM_153675
2.83	2.84	0.01	9.16E-01	9.77E-01	---	---	---	215753_at	---
2.57	2.59	0.02	9.16E-01	9.77E-01	ZNF204	zinc finger protein 204 pseudogene	chr6p21.3	214823_at	NR_002722
6.74	6.79	0.04	9.16E-01	9.77E-01	LOC100133166 /// NBR1	similar to neighbor of BRCA1 gene 1 /// neighbor of BRCA1 gene 1	chr17q21.31	201383_s_at	NM_005899 /// NM_031858 /// NM_031862 /// XM_001719040
4.01	4.02	0.02	9.16E-01	9.78E-01	---	---	---	235750_at	---
4.93	4.95	0.02	9.17E-01	9.78E-01	GPR155	G protein-coupled receptor 155	chr2q31.1	244509_at	NM_001033045 /// NM_152529
4.49	4.53	0.04	9.17E-01	9.78E-01	MAP2K4	mitogen-activated protein kinase kinase 4	chr17p11.2	203265_s_at	NM_003010
3.06	3.09	0.02	9.17E-01	9.78E-01	ATOH8	Atonal homolog 8 (Drosophila)	chr2p11.2	1558706_a_at	NM_032827
2.40	2.42	0.02	9.17E-01	9.78E-01	PHLPPL	PH domain and leucine rich repeat protein phosphatase-like	chr16q22.3	214944_at	NM_015020
3.22	3.23	0.02	9.17E-01	9.78E-01	TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	chr10q25.3	241605_at	NM_139169
5.00	5.04	0.04	9.17E-01	9.78E-01	AHCTF1	AT hook containing transcription factor 1	chr1q44	226115_at	NM_015446
5.25	5.27	0.02	9.17E-01	9.78E-01	TRAF6	TNF receptor-associated factor 6	chr11p12	205558_at	NM_004620 /// NM_145803
3.08	3.09	0.01	9.17E-01	9.78E-01	CSNK1G1	casein kinase 1, gamma 1	chr15q22.1-q22.31	221673_s_at	NM_022048
3.40	3.45	0.04	9.18E-01	9.78E-01	GIMAP2	GTPase, IMAP family member 2	chr7q36.1	232024_at	NM_015660
4.37	4.41	0.03	9.17E-01	9.78E-01	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	chr2q37.1	225696_at	NM_022730
6.06	6.09	0.03	9.18E-01	9.78E-01	PREX1	phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1	chr20q13.13	224925_at	NM_020820
3.21	3.24	0.02	9.18E-01	9.78E-01	---	---	---	214912_at	---
5.19	5.21	0.02	9.17E-01	9.78E-01	C7orf60	chromosome 7 open reading frame 60	chr7q31.1	228149_at	NM_152556
5.92	5.94	0.02	9.17E-01	9.78E-01	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	chr9q21.33	221425_s_at	NM_030940
2.71	2.73	0.02	9.17E-01	9.78E-01	---	---	---	240010_at	---
4.27	4.29	0.02	9.18E-01	9.78E-01	CUGBP2	CUG triplet repeat, RNA binding protein 2	chr10p13	202156_s_at	NM_001025076 /// NM_001025077 /// NM_001083591 /// NM_006561
3.55	3.57	0.02	9.17E-01	9.78E-01	---	---	---	207748_at	---
3.58	3.60	0.02	9.18E-01	9.78E-01	ARL17 /// ARL17P1	ADP-ribosylation factor-like 17 /// ADP-ribosylation factor-like 17 pseudogene 1	chr17q21.31 /// chr17q21.32	1555964_at	NM_001039083 /// NM_001103154 /// NM_001113738 /// NM_016632
3.17	3.19	0.02	9.18E-01	9.78E-01	USP34	ubiquitin specific peptidase 34	chr2p15	215013_s_at	NM_014709
2.43	2.45	0.02	9.17E-01	9.78E-01	OXR1	oxidation resistance 1	chr8q23	238409_x_at	NM_018002 /// NM_181354
3.65	3.66	0.02	9.18E-01	9.78E-01	PEX11A	peroxisomal biogenesis factor 11 alpha	chr15q26.1	205161_s_at	NM_003847
2.25	2.27	0.02	9.18E-01	9.78E-01	---	---	---	243424_at	---
2.62	2.63	0.01	9.17E-01	9.78E-01	---	---	---	237890_at	---
2.24	2.26	0.01	9.17E-01	9.78E-01	RIMS2	regulating synaptic membrane exocytosis 2	chr8q22.3	215478_at	NM_001100117 /// NM_014677
2.14	2.16	0.01	9.18E-01	9.78E-01	---	---	---	234652_at	---
2.57	2.58	0.01	9.17E-01	9.78E-01	---	---	---	217233_at	---
2.00	2.01	0.01	9.17E-01	9.78E-01	FLJ43080	hypothetical protein LOC642987	chr5q22.1	239776_at	NM_001039763 /// XM_001718501 /// XM_001719018 /// XM_001724089
1.95	1.96	0.01	9.17E-01	9.78E-01	NEUROD1	neurogenic differentiation 1	chr2q32	206282_at	NM_002500
2.30	2.31	0.01	9.18E-01	9.78E-01	---	---	---	1568448_at	---

8.44	8.47	0.03	9.18E-01	9.78E-01	MRPL41	mitochondrial ribosomal protein L41	chr9q34.3	225425_s_at	NM_032477
2.16	2.17	0.01	9.18E-01	9.78E-01	KIF18A	kinesin family member 18A	chr11p14.1	221258_s_at	NM_031217
3.65	3.67	0.02	9.18E-01	9.78E-01	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	chr9q32	1566721_at	NM_153366
3.58	3.59	0.01	9.18E-01	9.78E-01	ZBTB46	zinc finger and BTB domain containing 46	chr20q13.33	227358_at	NM_025224
2.52	2.54	0.01	9.18E-01	9.78E-01	---	---	---	1557386_at	---
2.02	2.03	0.01	9.18E-01	9.78E-01	---	---	---	216353_s_at	---
2.03	2.05	0.01	9.18E-01	9.78E-01	---	---	---	1560906_at	---
6.85	6.87	0.02	9.18E-01	9.78E-01	GAMT	guanidinoacetate N-methyltransferase	chr19p13.3	1552474_a_at	NM_000156 /// NM_138924
5.97	6.01	0.03	9.18E-01	9.78E-01	ZNF791	zinc finger protein 791	chr19p13.2-p13.13	1553704_x_at	NM_153358
2.51	2.53	0.02	9.18E-01	9.78E-01	---	---	---	1566503_at	---
2.62	2.64	0.02	9.18E-01	9.78E-01	TULP4	tubby like protein 4	chr6q25-q26	224170_s_at	NM_001007466 /// NM_020245
5.13	5.17	0.04	9.18E-01	9.78E-01	---	---	---	225950_at	---
4.55	4.59	0.04	9.19E-01	9.78E-01	RPS27A /// UBB /// UBC	ribosomal protein S27a /// ubiquitin B /// ubiquitin C	chr12q24.3 /// chr17p12-p11.2 /// chr2p16	242214_at	NM_002954 /// NM_018955 /// NM_021009
4.80	4.83	0.04	9.19E-01	9.78E-01	LOC150166	Hypothetical protein LOC150166	chr22q11.21	229101_at	---
6.22	6.25	0.03	9.18E-01	9.78E-01	SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)	chr10q22.1	212894_at	NM_003171
2.53	2.56	0.02	9.19E-01	9.78E-01	BTBD9	BTB (POZ) domain containing 9	chr6p21	234682_at	NM_001099272 /// NM_052893 /// NM_152733
5.02	5.04	0.02	9.19E-01	9.78E-01	CCNL2	cyclin L2	chr1p36.33	232274_at	NM_001039577 /// NM_030937
2.94	2.96	0.02	9.19E-01	9.78E-01	DOCK10	dedicator of cytokinesis 10	chr2q36.2	215151_at	NM_014689
3.61	3.62	0.02	9.19E-01	9.78E-01	---	---	---	238099_at	---
3.69	3.71	0.02	9.18E-01	9.78E-01	RBBP6	retinoblastoma binding protein 6	chr16p12.2	228814_at	NM_006910 /// NM_018703 /// NM_032626
2.59	2.61	0.02	9.18E-01	9.78E-01	RIBC2	RIB43A domain with coiled-coils 2	chr22q13.31	206526_at	NM_015653
1.97	1.98	0.01	9.18E-01	9.78E-01	---	---	---	1561244_at	---
1.85	1.86	0.01	9.19E-01	9.78E-01	---	---	---	1564580_at	---
1.95	1.97	0.01	9.19E-01	9.78E-01	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1	chr7q31-q32	220503_at	NM_022444
3.36	3.37	0.01	9.19E-01	9.78E-01	TPM4	Tropomyosin 4	chr19p13.1	1559989_at	NM_003290
3.36	3.37	0.01	9.19E-01	9.78E-01	MEX3A	mex-3 homolog A (C. elegans)	chr1q22	226346_at	NM_001093725
1.87	1.88	0.01	9.19E-01	9.78E-01	TRIM58	tripartite motif-containing 58	chr1q44	215047_at	NM_015431
2.28	2.29	0.01	9.18E-01	9.78E-01	---	---	---	237275_at	---
2.21	2.23	0.01	9.19E-01	9.78E-01	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	chr7p15.1-p14.3	1554378_a_at	NM_005020
3.32	3.33	0.01	9.19E-01	9.78E-01	THEG	Theg homolog (mouse)	chr19pter-p13	220808_at	NM_016585 /// NM_199202
4.08	4.12	0.04	9.19E-01	9.78E-01	EXOC2	exocyst complex component 2	chr6p25.3	219349_s_at	NM_018303
6.32	6.36	0.04	9.19E-01	9.78E-01	ADORA3	adenosine A3 receptor	chr1p13.2	206171_at	NM_000677 /// NM_001081976 /// NM_020683
3.24	3.26	0.03	9.19E-01	9.78E-01	LOC100129701	Hypothetical protein LOC100129701	chr3q21.3	237943_at	XM_001723786 /// XM_001724509 /// XM_001725856
2.49	2.51	0.01	9.19E-01	9.78E-01	TEKT5	tektin 5	chr16p13.13	1553489_a_at	NM_144674
1.90	1.91	0.01	9.19E-01	9.78E-01	FLJ39632	Hypothetical LOC642477	chr14q11.1	239010_at	XR_015133 /// XR_041395
6.26	6.29	0.02	9.19E-01	9.78E-01	TRAF7	TNF receptor-associated factor 7	chr16p13.3	223029_s_at	NM_032271
6.38	6.40	0.02	9.19E-01	9.78E-01	KIAA1143	KIAA1143	chr3p21.31	226816_s_at	NM_020696
6.33	6.34	0.02	9.19E-01	9.78E-01	RPL37	Ribosomal protein L37	chr5p13	224767_at	NM_000997
2.20	2.22	0.01	9.19E-01	9.78E-01	---	---	---	1561699_a_at	---
2.97	2.98	0.01	9.19E-01	9.78E-01	PHEX	phosphate regulating endopeptidase homolog, X-linked	chrXp22.2-p22.1	210617_at	NM_000444
2.71	2.73	0.02	9.19E-01	9.78E-01	ZNF775	Zinc finger protein 775	chr7q36.1	229931_at	NM_173680
6.39	6.44	0.05	9.20E-01	9.78E-01	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	chrXp22.12	201017_at	NM_001412
3.92	3.97	0.04	9.19E-01	9.78E-01	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	chr6p25-p24	202150_s_at	NM_006403 /// NM_182966
6.72	6.76	0.04	9.20E-01	9.78E-01	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	chr4q24	202542_s_at	NM_004757
6.52	6.56	0.04	9.20E-01	9.78E-01	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	chr7p14.3	212447_at	NM_015483
4.29	4.31	0.03	9.20E-01	9.78E-01	NUP50	nucleoporin 50kDa	chr22q13.31	222583_s_at	NM_007172 /// NM_153645

2.97	2.99	0.02	9.20E-01	9.78E-01	DHX35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	chr20q11.22-q12	234728_s_at	NM_021931
3.18	3.20	0.02	9.20E-01	9.78E-01	---	---	---	1562770_at	---
3.65	3.67	0.02	9.20E-01	9.78E-01	WNK2	WNK lysine deficient protein kinase 2	chr9q22.3	1560866_at	NM_006648
7.12	7.14	0.02	9.20E-01	9.78E-01	EFHD2	EF-hand domain family, member D2	chr1p36.21	222483_at	NM_024329
2.26	2.27	0.02	9.20E-01	9.78E-01	---	---	---	243283_at	---
2.57	2.59	0.01	9.20E-01	9.78E-01	---	---	---	1569275_at	---
2.50	2.51	0.01	9.20E-01	9.78E-01	DLGAP1	discs, large (Drosophila) homolog-associated protein 1	chr18p11.3	206489_s_at	NM_001003809 /// NM_004746
2.37	2.38	0.01	9.20E-01	9.78E-01	BMP1	Bone morphogenetic protein 1	chr8p21	1570383_at	NM_001199 /// NM_006128 /// NM_006129
2.13	2.15	0.01	9.20E-01	9.78E-01	---	---	---	243082_at	---
1.90	1.91	0.01	9.20E-01	9.78E-01	TUBE1	Tubulin, epsilon 1	chr6q21	230891_at	NM_016262
3.50	3.51	0.02	9.20E-01	9.79E-01	OCA2	oculocutaneous albinism II	chr15q11.2-q12	206498_at	NM_000275
9.67	9.69	0.02	9.20E-01	9.79E-01	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	chr18p11.22	208780_x_at	NM_003574 /// NM_194434
6.24	6.28	0.04	9.21E-01	9.79E-01	C3orf63	chromosome 3 open reading frame 63	chr3p14.3	209284_s_at	NM_001112736 /// NM_015224
2.73	2.74	0.02	9.21E-01	9.79E-01	ATP9B	ATPase, class II, type 9B	chr18q23	236762_at	NM_198531
2.50	2.52	0.01	9.21E-01	9.79E-01	ANAPC5	anaphase promoting complex subunit 5	chr12q24.31	239651_at	NM_016237
2.18	2.19	0.01	9.21E-01	9.79E-01	---	---	---	233798_at	---
2.18	2.20	0.01	9.21E-01	9.79E-01	XYLT2	xylosyltransferase II	chr17q21.3-q22	1570528_at	NM_022167
2.10	2.11	0.01	9.21E-01	9.79E-01	ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13	chr21q11.2	1552583_s_at	NR_003087 /// NR_003088
5.88	5.90	0.01	9.21E-01	9.79E-01	TOX4	TOX high mobility group box family member 4	chr14q11.2	201683_x_at	NM_014828
2.12	2.13	0.01	9.21E-01	9.79E-01	---	---	---	242046_at	---
2.10	2.11	0.01	9.21E-01	9.79E-01	---	---	---	1570300_at	---
3.56	3.58	0.03	9.21E-01	9.79E-01	ORAI2	ORAI calcium release-activated calcium modulator 2	chr7q22.1	217529_at	NM_001126340 /// NM_032831
4.51	4.55	0.05	9.21E-01	9.79E-01	FBXW11	F-box and WD repeat domain containing 11	chr5q35.1	209456_s_at	NM_012300 /// NM_033644 /// NM_033645
4.38	4.43	0.05	9.21E-01	9.79E-01	ZC3H11A	zinc finger CCCH-type containing 11A	chr1q32.1	205787_x_at	NM_014827
3.73	3.78	0.04	9.21E-01	9.79E-01	SFRS3	Splicing factor, arginine/serine-rich 3	chr6p21	235324_at	NM_003017
9.72	9.76	0.04	9.21E-01	9.79E-01	EPAS1	endothelial PAS domain protein 1	chr2p21-p16	200878_at	NM_001430
5.82	5.86	0.04	9.21E-01	9.79E-01	LOC100131851 /// LOC100134497 /// LOC401002 /// LOC646674 /// SSBP3	hypothetical protein LOC100131851 /// hypothetical protein LOC100134497 /// similar to single stranded DNA binding protein 3 /// hypothetical LOC646674 /// single stranded DNA binding protein 3	chr1p32.3 /// chr2q21.1 /// chr7p14.1	222482_at	NM_001009955 /// NM_018070 /// NM_145716 /// XM_001716920 /// XM_001717865 /// XM_001718694 /// XR_018284 /// XR_039216 /// XR_039309 /// XR_042303 /// XR_042397 /// XR_042399
5.59	5.62	0.03	9.21E-01	9.79E-01	FAM176B	family with sequence similarity 176, member B	chr1p34.3	220134_x_at	NM_018166
3.05	3.08	0.03	9.22E-01	9.79E-01	---	---	---	1565975_at	---
7.06	7.09	0.03	9.21E-01	9.79E-01	CLTB	clathrin, light chain (Lcb)	chr4q2-q3|5q35	205172_x_at	NM_001834 /// NM_007097
3.22	3.24	0.02	9.21E-01	9.79E-01	---	---	---	244855_at	---
2.25	2.27	0.02	9.21E-01	9.79E-01	TRPC1	transient receptor potential cation channel, subfamily C, member 1	chr3q22-q24	205803_s_at	NM_003304
2.35	2.37	0.02	9.21E-01	9.79E-01	IL8RB	interleukin 8 receptor, beta	chr2q35	207008_at	NM_001557
2.30	2.31	0.01	9.21E-01	9.79E-01	LOC283214	hypothetical protein LOC283214	chr11q13.5	1561491_at	---
7.62	7.63	0.01	9.21E-01	9.79E-01	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	chr2q37.3	225787_at	NM_080678
3.22	3.23	0.01	9.22E-01	9.79E-01	FLJ25404	hypothetical protein FLJ25404	chr16p11.2	1557162_at	NM_001109659 /// NM_001109660
2.49	2.50	0.01	9.21E-01	9.79E-01	CD207	CD207 molecule, langerin	chr2p13	220428_at	NM_015717
1.81	1.82	0.01	9.22E-01	9.79E-01	---	---	---	1563040_s_at	---
2.65	2.66	0.01	9.22E-01	9.79E-01	---	---	---	234188_at	---
2.42	2.44	0.02	9.22E-01	9.79E-01	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	chr2q35	232633_at	NM_021141
2.07	2.09	0.02	9.22E-01	9.79E-01	FAM46D	family with sequence similarity 46, member D	chrXq21.1	1552461_at	NM_152630
3.11	3.13	0.02	9.22E-01	9.79E-01	---	---	---	1560189_at	---
2.36	2.38	0.01	9.22E-01	9.79E-01	---	---	---	233735_at	---

1.96	1.97	0.01	9.22E-01	9.79E-01	---	---	---	1568366_at	---
2.34	2.35	0.01	9.22E-01	9.79E-01	USP36	ubiquitin specific peptidase 36	chr17q25.3	1554836_at	NM_025090
6.53	6.57	0.03	9.22E-01	9.79E-01	C20orf29	chromosome 20 open reading frame 29	chr20p13	219706_at	NM_018347
4.69	4.71	0.02	9.22E-01	9.79E-01	PSIP1	PC4 and SFRS1 interacting protein 1	chr9p22.3	210758_at	NM_001128217 /// NM_021144 /// NM_033222
5.44	5.46	0.02	9.22E-01	9.79E-01	TEAD2	TEA domain family member 2	chr19q13.3	238322_s_at	NM_003598
2.77	2.79	0.02	9.22E-01	9.79E-01	ACRV1	acrosomal vesicle protein 1	chr11q23-q24	207990_x_at	NM_001612 /// NM_020069 /// NM_020107 /// NM_020108 /// NM_020109 /// NM_020110 /// NM_020111 /// NM_020113 /// NM_020115
2.68	2.70	0.02	9.22E-01	9.79E-01	PEX13	peroxisomal biogenesis factor 13	chr2p14-p16	1556009_at	NM_002618
3.60	3.61	0.02	9.22E-01	9.79E-01	TOX3	TOX high mobility group box family member 3	chr16q12.1	230745_s_at	NM_001080430
2.34	2.35	0.01	9.22E-01	9.79E-01	---	---	---	231676_s_at	---
1.95	1.96	0.01	9.22E-01	9.79E-01	ZNF99	zinc finger protein 99	chr19p12	1553885_x_at	NM_001080409
4.86	4.91	0.05	9.23E-01	9.79E-01	---	---	---	232726_at	---
4.04	4.09	0.04	9.22E-01	9.79E-01	TRA@ /// TRAC /// TRAJ17 /// TRAV20	T cell receptor alpha locus /// T cell receptor alpha constant /// T cell receptor alpha joining 17 /// T cell receptor alpha variable 20	chr14q11 /// chr14q11.2	210972_x_at	---
7.17	7.21	0.04	9.23E-01	9.79E-01	AGA	aspartylglucosaminidase	chr4q32-q33	204332_s_at	NM_000027
6.25	6.28	0.03	9.23E-01	9.79E-01	RBM8A	RNA binding motif protein 8A	chr1q12	214113_s_at	NM_005105
4.92	4.94	0.02	9.22E-01	9.79E-01	ATP8B2	ATPase, class I, type 8B, member 2	chr1q21.3	216873_s_at	NM_001005855 /// NM_020452
3.35	3.37	0.02	9.22E-01	9.79E-01	MEX3D	mex-3 homolog D (C. elegans)	chr19p13.3	244712_at	NM_001085363 /// NM_203304
3.84	3.86	0.02	9.23E-01	9.79E-01	IGHA1 /// IGHD /// IGHG1 /// IGHG3 /// IGHM	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 3 (G3m marker) /// immunoglobulin heavy constant mu	chr14q32.33	216706_x_at	---
3.75	3.77	0.02	9.23E-01	9.79E-01	COL9A2	Collagen, type IX, alpha 2	chr1p33-p32	232542_at	NM_001852
7.18	7.19	0.02	9.22E-01	9.79E-01	BAG5	BCL2-associated athanogene 5	chr14q32.33	202985_s_at	NM_001015048 /// NM_001015049 /// NM_004873
2.97	2.98	0.02	9.23E-01	9.79E-01	---	---	---	1557147_a_at	---
3.44	3.45	0.02	9.23E-01	9.79E-01	CDK6	cyclin-dependent kinase 6	chr7q21-q22	231198_at	NM_001259
2.35	2.36	0.01	9.22E-01	9.79E-01	---	---	---	1563287_at	---
2.47	2.49	0.01	9.23E-01	9.79E-01	---	---	---	1560212_a_at	---
2.24	2.25	0.01	9.23E-01	9.79E-01	---	---	---	235454_at	---
2.14	2.16	0.01	9.23E-01	9.79E-01	COPG2	coatomer protein complex, subunit gamma 2	chr7q32	233569_at	NM_012133
2.54	2.55	0.01	9.23E-01	9.79E-01	PCDHAC1	protocadherin alpha subfamily C, 1	chr5q31	1553235_at	NM_018898 /// NM_031882
1.86	1.87	0.01	9.23E-01	9.79E-01	IFNA5	interferon, alpha 5	chr9p22	214569_at	NM_002169
3.16	3.17	0.02	9.23E-01	9.79E-01	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	chr12p13.3	207184_at	NM_016615
2.98	2.99	0.01	9.23E-01	9.79E-01	C20orf112	chromosome 20 open reading frame 112	chr20q11.1-q11.23	234031_at	NM_080616
3.70	3.75	0.04	9.24E-01	9.79E-01	AFF4	AF4/FMR2 family, member 4	chr5q31	219199_at	NM_014423
5.19	5.23	0.03	9.23E-01	9.79E-01	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	chr1p21.1-p13.2	223331_s_at	NM_007204
3.46	3.49	0.03	9.23E-01	9.79E-01	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	chr8q22	205528_s_at	NM_004349 /// NM_175634 /// NM_175635 /// NM_175636
7.32	7.34	0.03	9.23E-01	9.79E-01	MYCBP2	MYC binding protein 2	chr13q22	201960_s_at	NM_015057
2.77	2.80	0.02	9.23E-01	9.79E-01	FRS2	fibroblast growth factor receptor substrate 2	chr12q15	238486_at	NM_001042555 /// NM_006654
4.93	4.95	0.02	9.24E-01	9.79E-01	ACVR2A	activin A receptor, type IIA	chr2q22.3	205327_s_at	NM_001616
2.58	2.59	0.02	9.23E-01	9.79E-01	CCDC123	coiled-coil domain containing 123	chr19q13.11	1560599_a_at	NM_032816
2.35	2.37	0.01	9.23E-01	9.79E-01	---	---	---	1570155_at	---
2.24	2.25	0.01	9.23E-01	9.79E-01	KRT78	keratin 78	chr12q13.13	1553213_a_at	NM_173352
3.41	3.43	0.01	9.24E-01	9.79E-01	C14orf64	chromosome 14 open reading frame 64	chr14q32.2	1560499_at	NR_015430

2.50	2.52	0.02	9.24E-01	9.79E-01	LOC92973	hypothetical LOC92973	chr9p13.3	214344_at	NR_024006 /// XM_001721062 /// XM_001724284 /// XM_001725920
2.29	2.31	0.02	9.24E-01	9.79E-01	MMP28	matrix metallopeptidase 28	chr17q11-q21.1	239272_at	NM_001032278 /// NM_024302
3.82	3.85	0.03	9.24E-01	9.79E-01	KIAA1109	KIAA1109	chr4q27	216294_s_at	NM_015312
7.92	7.94	0.02	9.24E-01	9.79E-01	HYPK	Huntingtin interacting protein K	chr15q15.3	218680_x_at	NM_016400
5.21	5.24	0.03	9.24E-01	9.79E-01	KIAA1432	KIAA1432	chr9p24.1	226221_at	NM_020829
5.25	5.26	0.01	9.24E-01	9.79E-01	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	chr1p36.1	202818_s_at	NM_003198
2.01	2.02	0.01	9.24E-01	9.79E-01	CADM2	cell adhesion molecule 2	chr3p12.1	1552754_a_at	NM_153184
3.27	3.29	0.02	9.24E-01	9.79E-01	TRIM61	Tripartite motif-containing 61	chr4q32.3	238990_x_at	NM_001012414
3.01	3.03	0.02	9.24E-01	9.79E-01	MAGED4 /// MAGED4B	melanoma antigen family D, 4 /// melanoma antigen family D, 4B	chrXp11.22	221261_x_at	NM_001098800 /// NM_030801 /// NM_177535 /// NM_177537
3.08	3.12	0.04	9.24E-01	9.79E-01	DKFZP761C1711	Hypothetical protein DKFZp761C1711	---	234480_at	---
3.70	3.74	0.04	9.24E-01	9.79E-01	SCML1	sex comb on midleg-like 1 (Drosophila)	chrXp22.2-p22.1	222747_s_at	NM_001037535 /// NM_001037536 /// NM_001037540 /// NM_006746
5.86	5.90	0.03	9.24E-01	9.79E-01	UMPS	uridine monophosphate synthetase	chr3q13	202706_s_at	NM_000373
4.14	4.17	0.03	9.24E-01	9.79E-01	DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	chr12q24.33	1554085_at	NM_175066
5.52	5.54	0.02	9.24E-01	9.79E-01	UBE3A	ubiquitin protein ligase E3A	chr15q11-q13	213128_s_at	NM_000462 /// NM_130838 /// NM_130839
2.56	2.58	0.02	9.24E-01	9.79E-01	NLRP4	NLR family, pyrin domain containing 4	chr19q13.42	242334_at	NM_134444
2.02	2.03	0.01	9.24E-01	9.79E-01	---	---	---	1565801_at	---
2.07	2.08	0.01	9.24E-01	9.79E-01	MCF2L2	MCF.2 cell line derived transforming sequence-like 2	chr3q27.1	215112_x_at	NM_015078
2.27	2.28	0.01	9.24E-01	9.79E-01	HOXD10	homeobox D10	chr2q31.1	207373_at	NM_002148
3.74	3.78	0.04	9.24E-01	9.79E-01	SOS2	son of sevenless homolog 2 (Drosophila)	chr14q21	211665_s_at	NM_006939
7.09	7.11	0.02	9.24E-01	9.79E-01	ZNF574	zinc finger protein 574	chr19q13.2	218762_at	NM_022752
7.09	7.11	0.02	9.25E-01	9.79E-01	LPCAT3	lysophosphatidylcholine acyltransferase 3	chr12p13	202793_at	NM_005768
2.63	2.64	0.02	9.25E-01	9.79E-01	ARL6	ADP-ribosylation factor-like 6	chr3q11.2	235320_at	NM_032146 /// NM_177976
2.32	2.33	0.02	9.25E-01	9.79E-01	---	---	---	230399_at	---
2.33	2.35	0.02	9.25E-01	9.79E-01	LOC728192	Hypothetical protein LOC728192	chr13q33.3	1563062_at	XM_001128662
2.00	2.01	0.01	9.25E-01	9.79E-01	---	---	---	230248_x_at	---
2.73	2.75	0.01	9.25E-01	9.79E-01	SLC26A9	solute carrier family 26, member 9	chr1q31-q32	242271_at	NM_052934 /// NM_134325
6.69	6.75	0.06	9.25E-01	9.79E-01	---	---	---	238521_at	---
3.66	3.68	0.03	9.25E-01	9.79E-01	MX2	myxovirus (influenza virus) resistance 2 (mouse)	chr21q22.3	204994_at	NM_002463
2.97	3.00	0.02	9.25E-01	9.79E-01	---	---	---	232800_at	---
2.90	2.92	0.02	9.25E-01	9.79E-01	C13orf34	chromosome 13 open reading frame 34	chr13q22.1	219544_at	NM_024808
3.62	3.64	0.02	9.25E-01	9.79E-01	---	---	---	239601_at	---
3.57	3.59	0.01	9.25E-01	9.79E-01	TMCC1	Transmembrane and coiled-coil domain family 1	chr3q21.3	239029_at	NM_001017395 /// NM_001128224 /// NM_015008
3.57	3.60	0.02	9.25E-01	9.79E-01	ACTC1	actin, alpha, cardiac muscle 1	chr15q11-q14	205132_at	NM_005159
3.01	3.03	0.02	9.25E-01	9.79E-01	PAX3	paired box 3	chr2q35-q37|2q35	207680_x_at	NM_000438 /// NM_001127366 /// NM_013942 /// NM_181457 /// NM_181458 /// NM_181459 /// NM_181460 /// NM_181461
5.70	5.73	0.03	9.25E-01	9.79E-01	MRPL50	mitochondrial ribosomal protein L50	chr9q31.1	225581_s_at	NM_019051
4.21	4.25	0.04	9.25E-01	9.79E-01	ZNF561	zinc finger protein 561	chr19p13.2	230205_at	NM_152289
5.34	5.37	0.03	9.25E-01	9.79E-01	HIPK2	homeodomain interacting protein kinase 2	chr7q32-q34	225115_at	NM_001113239 /// NM_022740
9.76	9.79	0.03	9.25E-01	9.79E-01	C1QA	complement component 1, q subcomponent, A chain	chr1p36.12	218232_at	NM_015991

3.65	3.68	0.02	9.26E-01	9.79E-01	TRSPAP1	tRNA selenocysteine associated protein 1	chr1p35.3	222800_at	NM_017846 /// NR_003109																				
2.62	2.63	0.02	9.26E-01	9.79E-01	OR1D2	olfactory receptor, family 1, subfamily D, member 2	chr17p13-p12|17p13.3	221464_at	NM_002548																				
2.31	2.33	0.02	9.25E-01	9.79E-01	NHSL1	NHS-like 1	chr6q23.3	234324_at	XM_001723403 /// XM_496826 /// XM_941807																				
5.81	5.82	0.02	9.25E-01	9.79E-01	EDA	ectodysplasin A	chrXq12-q13.1|Xq12	206217_at	NM_001005609 /// NM_001005610 /// NM_001005611 /// NM_001005612 /// NM_001005615 /// NM_001399																				
3.39	3.40	0.02	9.25E-01	9.79E-01	KLF13	Kruppel-like factor 13	chr15q12	219878_s_at	NM_015995																				
3.06	3.07	0.01	9.26E-01	9.79E-01	PAGE1	P antigen family, member 1 (prostate associated)	chrXp11.23	206897_at	NM_003785																				
2.51	2.53	0.01	9.25E-01	9.79E-01	---	---	---	216820_at	---																				
2.47	2.48	0.01	9.25E-01	9.79E-01	---	---	---	1569912_at	---																				
2.07	2.09	0.01	9.26E-01	9.79E-01	---	---	---	1566953_x_at	---																				
2.04	2.06	0.01	9.26E-01	9.79E-01	hCG_1994895	hCG1994895	chr1q23.1	1564235_at	XM_001133436 /// XM_001134272 /// XM_001722874																				
2.21	2.22	0.01	9.25E-01	9.79E-01	---	---	---	241096_at	---																				
2.36	2.37	0.01	9.25E-01	9.79E-01	TAS2R41	taste receptor, type 2, member 41	chr7q35	1553558_at	NM_176883																				
2.43	2.44	0.01	9.25E-01	9.79E-01	---	---	---	238954_at	---																				
2.32	2.33	0.01	9.25E-01	9.79E-01	CADM1	cell adhesion molecule 1	chr11q23.2	244345_at	NM_001098517 /// NM_014333																				
2.02	2.03	0.01	9.26E-01	9.79E-01	LOC100128260 /// LOC100132169	similar to hCG1742852 /// similar to hCG1742852	chr16p13.3 /// chrXq28	1568838_at	XM_001714753 /// XM_001714847 /// XM_001715193 /// XM_001717013																				
2.24	2.25	0.01	9.26E-01	9.79E-01	PDE10A	phosphodiesterase 10A	chr6q26	211170_s_at	NM_001130690 /// NM_006661																				
2.14	2.15	0.01	9.26E-01	9.79E-01	LOC646736	similar to Alu subfamily SX sequence contamination warning entry	chr2q36.3	1570289_at	XM_933872																				
3.54	3.56	0.02	9.26E-01	9.79E-01	LOC148189	Hypothetical protein LOC148189	chr19q12	236653_at	---																				
3.62	3.63	0.02	9.26E-01	9.79E-01	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	chr3p21.3	203070_at	NM_001005914 /// NM_004636																				
5.55	5.58	0.03	9.26E-01	9.80E-01	RHOT1	ras homolog gene family, member T1	chr17q11.2	218323_at	NM_001033566 /// NM_001033568 /// NM_018307																				
5.44	5.47	0.02	9.26E-01	9.80E-01	RSC1A1	regulatory solute carrier protein, family 1, member 1	chr1p36.1	225780_at	NM_006511																				
7.96	7.98	0.02	9.26E-01	9.80E-01	RAB7A	RAB7A, member RAS oncogene family	chr3q21.3	211961_s_at	NM_004637																				
3.95	3.96	0.01	9.26E-01	9.80E-01	---	---	---	236078_at	---																				
4.51	4.54	0.03	9.26E-01	9.80E-01	---	---	---	1557400_at	---																				
2.13	2.14	0.01	9.26E-01	9.80E-01	CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)	chr3p21.3	39966_at	NM_006574																				
3.29	3.31	0.01	9.26E-01	9.80E-01	SUZ12P	Suppressor of zeste 12 homolog pseudogene	chr17q11.2	217704_x_at	---																				
8.16	8.19	0.02	9.26E-01	9.80E-01	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3	chr1p35-p34.3	221269_s_at	NM_031286																				
6.67	6.68	0.01	9.26E-01	9.80E-01	LARP1	La ribonucleoprotein domain family, member 1	chr5q33.2	210966_x_at	NM_015315 /// NM_033551																				
2.84	2.85	0.01	9.26E-01	9.80E-01	CTA-221G9.4	KIAA1671 protein	chr22q11.23	1565618_at	XR_040421 /// XR_040422 /// XR_040423																				
3.23	3.25	0.02	9.26E-01	9.80E-01	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2	chr8q13.2	208172_s_at	NM_004770																				
2.63	2.64	0.01	9.26E-01	9.80E-01	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	chr16p12.1	233459_at	NM_018119																				
2.01	2.02	0.01	9.27E-01	9.80E-01	DSCAM	Down syndrome cell adhesion molecule	chr21q22.2	240218_at	NM_001389																				
2.73	2.74	0.01	9.27E-01	9.80E-01	NKTR	natural killer-tumor recognition sequence	chr3p23-p21	1557736_at	NM_005385																				
2.07	2.08	0.01	9.27E-01	9.80E-01	OR2B2	olfactory receptor, family 2, subfamily B, member 2	chr6p22.3-p21.3	216408_at	NM_033057																				

2.05	2.06	0.01	9.27E-01	9.80E-01	FLJ42875	hypothetical LOC440556	chr1p36.32	236360_at	XM_928346 /// XM_932794 /// XM_942662 /// XM_946195
2.54	2.55	0.01	9.27E-01	9.80E-01	---	---	---	1570331_at	---
2.07	2.08	0.01	9.27E-01	9.80E-01	PADI2	peptidyl arginine deiminase, type II	chr1p36.13	1554384_at	NM_007365
5.12	5.14	0.03	9.27E-01	9.80E-01	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	chr5p15.3-p15.2	203199_s_at	NM_002454 /// NM_024010
2.29	2.31	0.01	9.27E-01	9.80E-01	BPY2	basic charge, Y-linked, 2	chrYq11	208331_at	NM_004678
6.05	6.07	0.02	9.27E-01	9.80E-01	FNIP2	folliculin interacting protein 2	chr4q32.1	225922_at	NM_020840
2.73	2.75	0.02	9.27E-01	9.80E-01	DNAH17	dynein, axonemal, heavy chain 17	chr17q25.3	214229_at	NM_173628
7.10	7.14	0.04	9.27E-01	9.80E-01	---	---	---	229498_at	---
2.64	2.66	0.02	9.28E-01	9.80E-01	---	---	---	223850_at	---
2.63	2.64	0.01	9.28E-01	9.80E-01	---	---	---	234171_at	---
3.24	3.25	0.02	9.28E-01	9.80E-01	MGC52282	hypothetical locus MGC52282	chr16p13.3	231638_at	XR_039869 /// XR_039870 /// XR_039871
7.06	7.16	0.10	9.28E-01	9.80E-01	VWF	von Willebrand factor	chr12p13.3	202112_at	NM_000552
9.08	9.11	0.02	9.28E-01	9.80E-01	TST	thiosulfate sulfurtransferase (rhodanese)	chr22q13.1	209605_at	NM_003312
3.20	3.21	0.02	9.28E-01	9.80E-01	CA5A	carbonic anhydrase VA, mitochondrial	chr16q24.3	207421_at	NM_001739
3.60	3.62	0.03	9.28E-01	9.80E-01	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	chr12q13-q14	203183_s_at	NM_003076 /// NM_139071
11.03	11.05	0.02	9.28E-01	9.80E-01	LGALS1	lectin, galactoside-binding, soluble, 1	chr22q13.1	201105_at	NM_002305
2.04	2.05	0.01	9.28E-01	9.80E-01	DGKB	diacylglycerol kinase, beta 90kDa	chr7p21.2	216307_at	NM_004080 /// NM_145695
2.33	2.35	0.01	9.28E-01	9.80E-01	CUZD1	CUB and zona pellucida-like domains 1	chr10q26.13	220275_at	NM_022034
5.70	5.72	0.03	9.28E-01	9.81E-01	---	---	---	229710_at	---
2.64	2.66	0.02	9.28E-01	9.81E-01	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	chr4p15.2	235516_at	NM_016955 /// NM_153825
3.05	3.06	0.01	9.28E-01	9.81E-01	OR1F1	olfactory receptor, family 1, subfamily F, member 1	chr16p13.3	221402_at	NM_012360
2.27	2.28	0.01	9.28E-01	9.81E-01	---	---	---	1568682_a_at	---
2.05	2.06	0.01	9.28E-01	9.81E-01	C10orf137	chromosome 10 open reading frame 137	chr10q26.13-q26.2	215072_x_at	NM_015608
2.09	2.10	0.01	9.28E-01	9.81E-01	ZPLD1	zona pellucida-like domain containing 1	chr3q12.3	1561969_at	NM_175056
2.05	2.06	0.01	9.29E-01	9.81E-01	BMP5	bone morphogenetic protein 5	chr6p12.1	205430_at	NM_021073
3.25	3.26	0.01	9.29E-01	9.81E-01	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	chr16q22.1	231732_at	NM_018667
2.90	2.91	0.01	9.29E-01	9.81E-01	---	---	---	1562447_a_at	---
2.07	2.08	0.01	9.29E-01	9.81E-01	P53AIP1	p53-regulated apoptosis-inducing protein 1	chr11q24	220402_at	NM_022112
2.56	2.57	0.01	9.29E-01	9.81E-01	POU3F2	POU class 3 homeobox 2	chr6q16	207084_at	NM_005604
5.44	5.45	0.01	9.29E-01	9.81E-01	MYBPC3	myosin binding protein C, cardiac	chr11p11.2	208040_s_at	NM_000256
2.14	2.15	0.01	9.29E-01	9.81E-01	---	---	---	1561215_at	---
5.16	5.17	0.01	9.29E-01	9.81E-01	---	---	---	241181_x_at	---
2.24	2.25	0.01	9.29E-01	9.81E-01	DTWD1	DTW domain containing 1	chr15q21.2	1555210_at	NM_020234
2.14	2.15	0.01	9.29E-01	9.81E-01	CAPZA1	Capping protein (actin filament) muscle Z-line, alpha 1	chr1p13.2	241275_at	NM_006135
3.81	3.83	0.02	9.29E-01	9.81E-01	CTTNBP2NL	CTTNBP2 N-terminal like	chr1p13.2	214731_at	NM_018704
2.70	2.72	0.02	9.29E-01	9.81E-01	---	---	---	236428_at	---
4.03	4.04	0.01	9.29E-01	9.81E-01	C10orf67	chromosome 10 open reading frame 67	chr10p12.2	1553843_at	NM_153714
2.54	2.56	0.02	9.29E-01	9.81E-01	AGTR2	angiotensin II receptor, type 2	chrXq22-q23	222321_at	NM_000686
6.46	6.48	0.02	9.30E-01	9.81E-01	BMS1	BMS1 homolog, ribosome assembly protein (yeast)	chr10q11.21	203082_at	NM_014753
2.75	2.77	0.02	9.30E-01	9.81E-01	---	---	---	1558275_at	---
3.08	3.10	0.02	9.30E-01	9.81E-01	KIAA1919	KIAA1919	chr6q22	238828_at	NM_153369
2.34	2.36	0.01	9.30E-01	9.81E-01	---	---	---	231364_at	---
2.18	2.19	0.01	9.30E-01	9.81E-01	---	---	---	217029_at	---
2.40	2.41	0.01	9.30E-01	9.81E-01	---	---	---	1555876_at	---
2.00	2.01	0.01	9.30E-01	9.81E-01	LOC400796	hypothetical LOC400796	chr1q25.2	242977_at	XM_001132413 /// XM_001718751 /// XM_378917
2.64	2.66	0.02	9.30E-01	9.81E-01	---	---	---	1552955_at	---
2.29	2.31	0.02	9.30E-01	9.81E-01	---	---	---	239788_at	---
6.18	6.23	0.04	9.30E-01	9.81E-01	PRRC1	proline-rich coiled-coil 1	chr5q23.2	224643_at	NM_130809
11.60	11.63	0.03	9.30E-01	9.81E-01	RPL4	ribosomal protein L4	chr15q22	201154_x_at	NM_000968
8.27	8.30	0.03	9.30E-01	9.81E-01	TGFBR3	transforming growth factor, beta receptor III	chr1p33-p32	226625_at	NM_003243
4.46	4.48	0.02	9.30E-01	9.81E-01	ANKRD13D	ankyrin repeat domain 13 family, member D	chr11q13.1	226205_at	NM_207354
5.93	5.95	0.02	9.30E-01	9.81E-01	---	---	---	230921_s_at	---
2.80	2.82	0.01	9.30E-01	9.81E-01	PKP3	plakophilin 3	chr11p15	209872_s_at	NM_007183
2.17	2.19	0.01	9.30E-01	9.81E-01	---	---	---	1559278_at	---
2.14	2.15	0.01	9.30E-01	9.81E-01	---	---	---	216719_s_at	---
1.99	2.00	0.01	9.30E-01	9.81E-01	MGC4859	hypothetical LOC79150	chr7p	207775_at	---
2.41	2.42	0.01	9.30E-01	9.81E-01	---	---	---	216140_at	---
2.21	2.22	0.01	9.30E-01	9.81E-01	---	---	---	239287_at	---
3.62	3.64	0.01	9.31E-01	9.81E-01	MYH7	myosin, heavy chain 7, cardiac muscle, beta	chr14q12	216265_x_at	NM_000257

6.50	6.54	0.04	9.31E-01	9.81E-01	C14orf100	chromosome 14 open reading frame 100	chr14q23.1	223215_s_at	NM_001098625 /// NM_016475
7.12	7.15	0.04	9.31E-01	9.81E-01	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	chr5p13	202800_at	NM_004172
3.12	3.14	0.02	9.31E-01	9.81E-01	C1orf175 /// TTC4	chromosome 1 open reading frame 175 /// tetratricopeptide repeat domain 4	chr1p32.3	214147_at	NM_001039464 /// NM_004623 /// XM_001726392 /// XM_001726400 /// XM_001726506
7.87	7.89	0.02	9.31E-01	9.81E-01	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	chr19p13.3	211752_s_at	NM_024407
2.77	2.78	0.02	9.31E-01	9.81E-01	EXO1	exonuclease 1	chr1q42-q43	204603_at	NM_003686 /// NM_006027 /// NM_130398
7.06	7.08	0.02	9.31E-01	9.81E-01	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	chr1q23	220081_x_at	NM_016371
2.42	2.43	0.01	9.31E-01	9.81E-01	HIST1H2BM	histone cluster 1, H2bm	chr6p22-p21.3	208515_at	NM_003521
2.47	2.49	0.01	9.31E-01	9.81E-01	SPACA1	sperm acrosome associated 1	chr6q15	220982_s_at	NM_030960
5.07	5.08	0.02	9.31E-01	9.81E-01	CLTA	Clathrin, light chain (Lca)	chr9p13	216293_at	NM_001076677 /// NM_001833 /// NM_007096
2.70	2.71	0.01	9.31E-01	9.81E-01	SNHG10	Small nucleolar RNA host gene 10 (non-protein coding)	chr14q32.13	229209_at	NR_001459 /// NR_003138
2.02	2.03	0.01	9.31E-01	9.81E-01	LOC286297	hypothetical protein LOC286297	chr9q12	1556704_s_at	XM_372109 /// XM_933054 /// XM_933058
7.17	7.21	0.05	9.31E-01	9.82E-01	OLFML3	olfactomedin-like 3	chr1p13.2	218162_at	NM_020190
7.20	7.23	0.03	9.31E-01	9.82E-01	SNX7	sorting nexin 7	chr1p21.3	205573_s_at	NM_015976 /// NM_152238
6.84	6.87	0.03	9.31E-01	9.82E-01	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	chr20q13.33	212406_s_at	NM_001104925 /// NM_018257
5.48	5.51	0.03	9.31E-01	9.82E-01	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	chr4q11-q12	203934_at	NM_002253
3.47	3.49	0.02	9.32E-01	9.82E-01	CA12	carbonic anhydrase XII	chr15q22	215867_x_at	NM_001218 /// NM_206925
2.53	2.54	0.01	9.32E-01	9.82E-01	LOC100133233 /// TRAF3IP3	hypothetical protein LOC100133233 /// TRAF3 interacting protein 3	chr1q32.2 /// chr1q32.3-q41	213888_s_at	NM_025228 /// XM_001718033 /// XM_001718553 /// XM_001720826
3.39	3.41	0.01	9.32E-01	9.82E-01	---	---	---	239811_at	---
2.42	2.43	0.01	9.31E-01	9.82E-01	HIST1H2AD /// HIST1H2BN /// HIST1H3A /// HIST1H3B /// HIST1H3C /// HIST1H3D /// HIST1H3E /// HIST1H3F /// HIST1H3G /// HIST1H3H /// HIST1H3I /// HIST1H3J	histone cluster 1, H2ad /// histone cluster 1, H2bn /// histone cluster 1, H3a /// histone cluster 1, H3b /// histone cluster 1, H3c /// histone cluster 1, H3d /// histone cluster 1, H3e /// histone cluster 1, H3f /// histone cluster 1, H3g /// histone cluster 1, H3h /// histone cluster 1, H3i /// histone cluster 1, H3j	chr6p21.3 /// chr6p22-p21.3 /// chr6p22.1	208577_at	NM_003520 /// NM_003529 /// NM_003530 /// NM_003531 /// NM_003532 /// NM_003533 /// NM_003534 /// NM_003535 /// NM_003536 /// NM_003537 /// NM_021018 /// NM_021065
2.09	2.10	0.01	9.32E-01	9.82E-01	---	---	---	1557431_at	---
1.78	1.79	0.01	9.31E-01	9.82E-01	LCA5	Leber congenital amaurosis 5	chr6q14.1	229953_x_at	NM_001122769 /// NM_181714

2.67	2.69	0.01	9.32E-01	9.82E-01	LOC100129858	hypothetical protein LOC100129858	chr4q31.1	1556736_at	XM_001720192 /// XM_001720230 /// XM_001725468
3.27	3.29	0.02	9.32E-01	9.82E-01	NCKAP1	NCK-associated protein 1	chr2q32	217465_at	NM_013436 /// NM_205842
2.80	2.81	0.01	9.32E-01	9.82E-01	---	---	---	242053_at	---
2.09	2.10	0.01	9.32E-01	9.82E-01	SCEL	sciellin	chr13q22	206884_s_at	NM_003843 /// NM_144777
1.94	1.95	0.01	9.32E-01	9.82E-01	---	---	---	239351_at	---
6.70	6.74	0.03	9.32E-01	9.82E-01	CCDC47	coiled-coil domain containing 47	chr17q23.3	217814_at	NM_020198
4.44	4.47	0.03	9.32E-01	9.82E-01	LPAR5	lysophosphatidic acid receptor 5	chr12p13.31	230252_at	NM_020400
3.52	3.53	0.01	9.32E-01	9.82E-01	C15orf29	chromosome 15 open reading frame 29	chr15q14	218791_s_at	NM_024713
2.12	2.13	0.01	9.32E-01	9.82E-01	PLGLB1 /// PLGLB2	plasminogen-like B1 /// plasminogen-like B2	chr2p11-q11 /// chr2p11.2	1558603_at	NM_001032392 /// NM_002665
2.64	2.66	0.02	9.32E-01	9.82E-01	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	chr2q33-q34	238516_at	NM_001204
2.92	2.94	0.02	9.32E-01	9.82E-01	CDH3	cadherin 3, type 1, P-cadherin (placental)	chr16q22.1	203256_at	NM_001793
2.86	2.88	0.02	9.32E-01	9.82E-01	FIP1L1	FIP1 like 1 (S. cerevisiae)	chr4q12	1554424_at	NM_030917
5.46	5.48	0.02	9.32E-01	9.82E-01	HTR4	5-hydroxytryptamine (serotonin) receptor 4	chr5q31-q33	207578_s_at	NM_000870 /// NM_001040169 /// NM_001040171 /// NM_001040172 /// NM_001040173 /// NM_001040174 /// NM_199453
3.14	3.16	0.02	9.32E-01	9.82E-01	---	---	---	237494_at	---
3.39	3.41	0.02	9.33E-01	9.82E-01	TCHP	trichoplein, keratin filament binding	chr12q24.11	223456_s_at	NM_032300
1.92	1.93	0.01	9.33E-01	9.82E-01	---	---	---	240972_at	---
4.38	4.40	0.02	9.33E-01	9.82E-01	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	chr7p12	211607_x_at	NM_005228 /// NM_201282 /// NM_201283 /// NM_201284
3.46	3.48	0.02	9.33E-01	9.82E-01	---	---	---	232072_at	---
2.82	2.84	0.02	9.33E-01	9.82E-01	---	---	---	228115_at	---
4.52	4.53	0.01	9.33E-01	9.82E-01	ASRGL1	asparaginase like 1	chr11q12.3	218857_s_at	NM_001083926 /// NM_025080
2.82	2.83	0.01	9.33E-01	9.82E-01	PLCE1	Phospholipase C, epsilon 1	chr10q23	1566739_at	NM_016341
2.81	2.83	0.01	9.33E-01	9.82E-01	TRIM4	Tripartite motif-containing 4	chr7q22-q31.1	230173_at	NM_033017 /// NM_033091
2.35	2.36	0.01	9.33E-01	9.82E-01	---	---	---	1562957_at	---
2.17	2.19	0.01	9.33E-01	9.82E-01	---	---	---	216516_at	---
2.08	2.09	0.01	9.33E-01	9.82E-01	CCDC123	coiled-coil domain containing 123	chr19q13.11	1554513_s_at	NM_032816
2.31	2.32	0.01	9.33E-01	9.82E-01	---	---	---	237133_at	---
3.60	3.61	0.01	9.33E-01	9.82E-01	PCDHA5	protocadherin alpha 5	chr5q31	211838_x_at	NM_018908 /// NM_031501
7.89	7.92	0.03	9.33E-01	9.82E-01	PALLD	palladin, cytoskeletal associated protein	chr4q32.3	200907_s_at	NM_016081
2.92	2.93	0.01	9.33E-01	9.82E-01	ZNF710	Zinc finger protein 710	chr15q26.1	235090_at	NM_198526
2.59	2.60	0.01	9.33E-01	9.82E-01	MYH11	myosin, heavy chain 11, smooth muscle	chr16p13.11	1568760_at	NM_001040113 /// NM_001040114 /// NM_002474 /// NM_022844
2.20	2.21	0.01	9.33E-01	9.82E-01	---	---	---	243854_at	---
1.90	1.91	0.01	9.33E-01	9.82E-01	SMEK3P	SMEK homolog 3, suppressor of mek1 (Dictyostelium) pseudogene	chrXp21.3	1562054_at	NR_002784
5.79	5.81	0.02	9.34E-01	9.82E-01	ZNF385A	zinc finger protein 385A	chr12q13.13	226111_s_at	NM_001130967 /// NM_001130968 /// NM_015481
2.41	2.42	0.02	9.34E-01	9.82E-01	IGL@	Immunoglobulin lambda joining 3	chr22q11.1-q11.2	230128_at	---
2.49	2.51	0.01	9.34E-01	9.82E-01	KRTAP4-6	keratin associated protein 4-6	chr17q12-q21	234683_at	XM_001714702 /// XM_926610 /// XM_937152

1.98	1.99	0.01	9.34E-01	9.82E-01	FLJ21369	hypothetical protein FLJ21369	chr19q13.11	220401_at	XR_040672 /// XR_040673
10.90	10.92	0.01	9.34E-01	9.82E-01	LAMP1	lysosomal-associated membrane protein 1	chr13q34	201553_s_at	NM_005561
2.95	2.96	0.01	9.34E-01	9.82E-01	ACTRT2	actin-related protein T2	chr1p36.32	237360_at	NM_080431
1.98	1.99	0.01	9.34E-01	9.82E-01	---	---	---	1562276_at	---
2.21	2.23	0.01	9.34E-01	9.82E-01	---	---	---	1569673_at	---
4.78	4.80	0.02	9.34E-01	9.82E-01	---	---	---	227585_at	---
2.88	2.90	0.02	9.34E-01	9.82E-01	DTYMK	deoxythymidylate kinase (thymidylate kinase)	chr2q37.3	1553983_at	NM_012145
2.48	2.50	0.02	9.34E-01	9.82E-01	PLEKHA6	pleckstrin homology domain containing, family A member 6	chr1q32.1	229245_at	NM_014935
2.25	2.26	0.01	9.34E-01	9.82E-01	---	---	---	1566106_at	---
6.39	6.42	0.03	9.34E-01	9.82E-01	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	chr6p24.3-p25.1	204905_s_at	NM_004280
2.16	2.17	0.01	9.34E-01	9.82E-01	SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	chr6p23	1569938_at	NM_012241 /// NM_031244
4.12	4.16	0.04	9.34E-01	9.82E-01	TLCD1	TLC domain containing 1	chr17q11.2	227804_at	NM_138463
3.99	4.03	0.03	9.34E-01	9.82E-01	PDZD8	PDZ domain containing 8	chr10q25.3-q26.11	225830_at	NM_173791
3.32	3.33	0.01	9.34E-01	9.82E-01	---	---	---	240933_at	---
6.22	6.24	0.01	9.34E-01	9.82E-01	USP9X	ubiquitin specific peptidase 9, X-linked	chrXp11.4	229573_at	NM_001039590 /// NM_001039591
3.16	3.17	0.01	9.34E-01	9.82E-01	DYM	dymeclin	chr18q12-q21.1	220774_at	NM_017653
4.07	4.10	0.03	9.34E-01	9.82E-01	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	chr19p13.1	227677_at	NM_000215
7.28	7.31	0.03	9.34E-01	9.82E-01	TMEM87A	transmembrane protein 87A	chr15q15.1	212204_at	NM_001110503 /// NM_015497
8.37	8.39	0.02	9.35E-01	9.82E-01	DYNLT3	dynein, light chain, Tctex-type 3	chrXp21	203303_at	NM_006520
2.95	2.97	0.02	9.35E-01	9.82E-01	OSBPL10	oxysterol binding protein-like 10	chr3p22.3	217017_at	NM_017784
4.28	4.30	0.02	9.35E-01	9.82E-01	TSGA14	testis specific, 14	chr7q32	225484_at	NM_018718
2.86	2.88	0.02	9.35E-01	9.82E-01	---	---	---	240507_at	---
2.99	3.00	0.01	9.35E-01	9.82E-01	---	---	---	244864_at	---
2.89	2.90	0.01	9.35E-01	9.82E-01	---	---	---	232134_at	---
5.48	5.52	0.03	9.35E-01	9.82E-01	RBM15	RNA binding motif protein 15	chr1p13	1555760_a_at	NM_022768
3.43	3.44	0.02	9.35E-01	9.82E-01	MLX	MAX-like protein X	chr17q21.1	1570347_at	NM_170607 /// NM_198204 /// NM_198205
7.76	7.79	0.03	9.35E-01	9.82E-01	LOC728866 /// MAGT1	hypothetical LOC728866 /// magnesium transporter 1	chrXq21.1	224899_s_at	NM_032121 /// XM_001717240
3.19	3.21	0.02	9.35E-01	9.82E-01	ZNF280D	zinc finger protein 280D	chr15q21.3	221213_s_at	NM_001002843 /// NM_001002844 /// NM_017661
2.83	2.85	0.02	9.35E-01	9.82E-01	LOC727815	hypothetical LOC727815	chr12p13.31	243631_at	XM_001722487 /// XM_001722665 /// XR_015164
2.57	2.58	0.01	9.35E-01	9.82E-01	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	chr12q24.13	223736_at	NM_014055 /// NM_031473
2.63	2.64	0.02	9.35E-01	9.82E-01	PLEKHH3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	chr17q21.31	220259_at	NM_024927
6.14	6.17	0.03	9.35E-01	9.82E-01	RALYL	RALY RNA binding protein-like	chr8q21.2	213967_at	NM_001100391 /// NM_001100392 /// NM_001100393 /// NM_173848
2.35	2.37	0.02	9.35E-01	9.82E-01	---	---	---	237971_at	---
2.96	2.97	0.01	9.35E-01	9.82E-01	---	---	---	1565706_at	---
3.37	3.39	0.02	9.35E-01	9.82E-01	LOC284933	hypothetical protein LOC284933	chr22q13.32	240754_at	---
4.17	4.20	0.03	9.35E-01	9.83E-01	ZNF514	zinc finger protein 514	chr2q11.1	235729_at	NM_032788
2.05	2.06	0.01	9.35E-01	9.83E-01	---	---	---	1558857_at	---
7.00	7.03	0.03	9.35E-01	9.83E-01	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	chr21q22.3	218019_s_at	NM_003681
2.63	2.64	0.01	9.36E-01	9.83E-01	DSCAM	Down syndrome cell adhesion molecule	chr21q22.2	237268_at	NM_001389
6.63	6.67	0.04	9.36E-01	9.83E-01	CNRIP1	cannabinoid receptor interacting protein 1	chr2p14	226751_at	NM_001111101 /// NM_015463
1.93	1.95	0.01	9.36E-01	9.83E-01	---	---	---	1561613_at	---
2.74	2.75	0.01	9.36E-01	9.83E-01	CD200	CD200 molecule	chr3q12-q13	209583_s_at	NM_001004196 /// NM_005944
2.29	2.30	0.01	9.36E-01	9.83E-01	---	---	---	228440_at	---
2.99	3.00	0.01	9.36E-01	9.83E-01	---	---	---	1556346_at	---
7.56	7.62	0.06	9.36E-01	9.83E-01	NNMT	nicotinamide N-methyltransferase	chr11q23.1	202237_at	NM_006169

9.32	9.35	0.03	9.36E-01	9.83E-01	TAGLN	transgelin	chr11q23.2	1555724_s_at	NM_001001522 /// NM_003186																				
4.42	4.45	0.03	9.36E-01	9.83E-01	LZTFL1	leucine zipper transcription factor-like 1	chr3p21.3	222632_s_at	NM_020347																				
5.98	6.01	0.03	9.36E-01	9.83E-01	HDGFRP3	hepatoma-derived growth factor, related protein 3	chr15q25.2	209526_s_at	NM_016073																				
4.60	4.62	0.02	9.36E-01	9.83E-01	MOSPD2	motile sperm domain containing 2	chrXp22.2	221895_at	NM_152581																				
6.03	6.05	0.02	9.36E-01	9.83E-01	FLJ22536	hypothetical locus LOC401237	chr6p22.3	229280_s_at	XM_379398																				
5.63	5.65	0.02	9.36E-01	9.83E-01	RPUSD1	RNA pseudouridylate synthase domain containing 1	chr16p13.3	226078_at	NM_058192																				
2.71	2.73	0.01	9.36E-01	9.83E-01	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	chr6q21	211706_s_at	NM_015076																				
8.04	8.05	0.01	9.36E-01	9.83E-01	RNF130	ring finger protein 130	chr5q35.3	217865_at	NM_018434																				
2.38	2.39	0.01	9.36E-01	9.83E-01	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	chr15q22-q24	238868_at	NM_001008224 /// NM_018003																				
2.44	2.45	0.01	9.36E-01	9.83E-01	---	---	---	234346_x_at	---																				
1.93	1.94	0.01	9.36E-01	9.83E-01	---	---	---	1561234_at	---																				
1.92	1.92	0.01	9.36E-01	9.83E-01	RP11-165H20.1	CHIA-like pseudogene	chr1p13.2	1570015_at	NR_003928																				
1.98	1.99	0.01	9.36E-01	9.83E-01	ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif, 20	chr12q12	220717_at	NM_025003																				
6.45	6.48	0.04	9.36E-01	9.83E-01	PTGIS	prostaglandin I2 (prostacyclin) synthase	chr20q13.13	208131_s_at	NM_000961																				
7.03	7.05	0.02	9.36E-01	9.83E-01	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19p13.3	214679_x_at	NM_002067																				
4.33	4.34	0.01	9.36E-01	9.83E-01	HOXC5	homeobox C5	chr12q13.3	206739_at	NM_018953 /// NR_003084																				
2.36	2.37	0.01	9.36E-01	9.83E-01	---	---	---	243540_at	---																				
2.86	2.87	0.02	9.36E-01	9.83E-01	---	---	---	241835_at	---																				
1.81	1.82	0.01	9.36E-01	9.83E-01	---	---	---	1560760_s_at	---																				
5.97	6.04	0.07	9.37E-01	9.83E-01	CCDC80	coiled-coil domain containing 80	chr3q13.2	225242_s_at	NM_199511 /// NM_199512																				
6.94	6.98	0.04	9.37E-01	9.83E-01	PSD3	pleckstrin and Sec7 domain containing 3	chr8pter-p23.3	218613_at	NM_015310 /// NM_206909																				
4.91	4.94	0.03	9.36E-01	9.83E-01	RIT1	Ras-like without CAAX 1	chr1q22	236224_at	NM_006912																				
7.24	7.25	0.02	9.37E-01	9.83E-01	BLVRA	biliverdin reductase A	chr7p14-cen	203773_x_at	NM_000712																				
11.44	11.46	0.01	9.37E-01	9.83E-01	RPL22	ribosomal protein L22	chr1p36.3-p36.2	221775_x_at	NM_000983																				
2.38	2.40	0.01	9.36E-01	9.83E-01	TIGD4	tigger transposable element derived 4	chr4q31.3	1552523_a_at	NM_145720																				
9.85	9.86	0.01	9.37E-01	9.83E-01	TMBIM4	transmembrane BAX inhibitor motif containing 4	chr12q14.1|12q14.1-q15	222845_x_at	NM_016056																				
2.25	2.26	0.01	9.37E-01	9.83E-01	BRD8	bromodomain containing 8	chr5q31	210352_at	NM_006696 /// NM_139199 /// NM_183359																				
2.25	2.26	0.01	9.37E-01	9.83E-01	---	---	---	1570630_at	---																				
5.97	6.01	0.03	9.37E-01	9.83E-01	RANBP9	RAN binding protein 9	chr6p23	202583_s_at	NM_005493																				
6.78	6.80	0.02	9.37E-01	9.83E-01	MOSPD3	motile sperm domain containing 3	chr7q22	219070_s_at	NM_001040097 /// NM_001040098 /// NM_001040099 /// NM_023948																				
3.50	3.52	0.02	9.37E-01	9.83E-01	GPR62	G protein-coupled receptor 62	chr3p21.1	1554559_at	NM_080865																				
2.38	2.39	0.01	9.37E-01	9.83E-01	---	---	---	1569147_at	---																				
1.91	1.93	0.01	9.37E-01	9.83E-01	---	---	---	1556849_at	---																				
2.16	2.17	0.01	9.37E-01	9.83E-01	CYLC2	cylicin, basic protein of sperm head cytoskeleton 2	chr9q31.1	207780_at	NM_001340																				
6.41	6.42	0.01	9.37E-01	9.83E-01	CD2BP2	CD2 (cytoplasmic tail) binding protein 2	chr16p11.2	202256_at	NM_006110																				
2.26	2.27	0.01	9.37E-01	9.83E-01	---	---	---	238139_at	---																				
5.91	5.93	0.02	9.37E-01	9.83E-01	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	chr10p15.3	212503_s_at	NM_014974																				
3.21	3.22	0.01	9.37E-01	9.83E-01	PANX2	pannexin 2	chr22q13.33	239067_s_at	NM_052839																				
3.81	3.83	0.02	9.37E-01	9.83E-01	TRIM7	tripartite motif-containing 7	chr5q35.3	1554735_a_at	NM_033342 /// NM_203293 /// NM_203294 /// NM_203295 /// NM_203296 /// NM_203297																				
2.63	2.65	0.02	9.37E-01	9.83E-01	GML	glycosylphosphatidylinositol anchored molecule like protein	chr8q24.3	208000_at	NM_002066																				
3.71	3.73	0.02	9.37E-01	9.83E-01	SNCG	synuclein, gamma (breast cancer-specific protein 1)	chr10q23.2-q23.3	208584_at	NM_003087																				
2.09	2.10	0.01	9.37E-01	9.83E-01	---	---	---	1570488_at	---																				
5.06	5.08	0.01	9.38E-01	9.83E-01	---	---	---	233701_at	---																				
12.10	12.11	0.01	9.38E-01	9.83E-01	ACTB	actin, beta	chr7p15-p12	AFFX-HSAC07/X00351_3_at	NM_001101																				

2.04	2.05	0.01	9.38E-01	9.83E-01	C18orf54	chromosome 18 open reading frame 54	chr18q21.2	1553652_a_at	NM_173529
7.95	7.99	0.04	9.38E-01	9.83E-01	CYR61	cysteine-rich, angiogenic inducer, 61	chr1p31-p22	210764_s_at	NM_001554
3.09	3.10	0.01	9.38E-01	9.83E-01	---	---	---	243489_at	---
3.05	3.06	0.01	9.38E-01	9.83E-01	LOC389328	hypothetical LOC389328	chr5q31.1	1569561_at	XM_374137 /// XM_943867
4.85	4.87	0.01	9.38E-01	9.83E-01	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	chr15q11.2	208797_s_at	NM_181077 /// XM_001714558
2.03	2.04	0.01	9.38E-01	9.83E-01	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4 /// LOC732447	deleted in azoospermia 1 /// deleted in azoospermia 2 /// deleted in azoospermia 3 /// deleted in azoospermia 4 /// similar to deleted in azoospermia-like	chrYq11.223	208282_x_at	NM_001005375 /// NM_001005785 /// NM_001005786 /// NM_004081 /// NM_020363 /// NM_020364 /// NM_020420 /// XM_001718583 /// XM_001720105 /// XM_001722775
2.14	2.15	0.01	9.38E-01	9.83E-01	RIMS1	regulating synaptic membrane exocytosis 1	chr6q12-q13	1552922_at	NM_014989
2.33	2.35	0.01	9.38E-01	9.83E-01	---	---	---	1566194_at	---
2.23	2.24	0.01	9.38E-01	9.83E-01	---	---	---	234547_at	---
3.10	3.11	0.01	9.38E-01	9.83E-01	KIAA0040	KIAA0040	chr1q24-q25	203144_s_at	NR_015350 /// XR_041163 /// XR_041164 /// XR_041165
3.88	3.91	0.03	9.38E-01	9.83E-01	---	---	---	220711_at	---
3.62	3.64	0.02	9.38E-01	9.83E-01	NSBP1	nucleosomal binding protein 1	chrXq13.3	221606_s_at	NM_030763
5.05	5.06	0.01	9.38E-01	9.83E-01	RNF31	Ring finger protein 31	chr14q11.2	231635_x_at	NM_017999
2.43	2.45	0.01	9.38E-01	9.83E-01	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	chr11p11.2	217483_at	NM_001014986 /// NM_004476
2.68	2.69	0.01	9.38E-01	9.83E-01	MED23	mediator complex subunit 23	chr6q22.33-q24.1	223946_at	NM_004830 /// NM_015979
5.13	5.14	0.01	9.38E-01	9.83E-01	EXOSC3	exosome component 3	chr9p11	223489_x_at	NM_001002269 /// NM_016042
11.40	11.41	0.01	9.38E-01	9.83E-01	RPL22	ribosomal protein L22	chr1p36.3-p36.2	220960_x_at	NM_000983
2.41	2.42	0.01	9.38E-01	9.83E-01	SNX1	sorting nexin 1	chr15q22.31	216357_at	NM_003099 /// NM_148955 /// NM_152826
6.42	6.44	0.02	9.38E-01	9.83E-01	ARL8A	ADP-ribosylation factor-like 8A	chr1q32.1	225347_at	NM_138795
7.35	7.37	0.02	9.38E-01	9.83E-01	CENTD2	centaurin, delta 2	chr11q13.4	34206_at	NM_001040118 /// NM_015242 /// NM_139181
4.41	4.43	0.02	9.38E-01	9.83E-01	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	chr15q14-q21	205874_at	NM_002220
5.05	5.06	0.01	9.38E-01	9.83E-01	NELF	Nasal embryonic LHRH factor	chr9q34.3	230189_x_at	NM_001130969 /// NM_001130970 /// NM_001130971 /// NM_015537
2.77	2.78	0.01	9.38E-01	9.83E-01	---	---	---	236285_at	---
3.32	3.34	0.02	9.39E-01	9.83E-01	---	---	---	230543_at	---
6.52	6.54	0.02	9.39E-01	9.83E-01	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	chr3q23	203588_s_at	NM_006286
2.86	2.87	0.02	9.39E-01	9.83E-01	STX11	syntaxin 11	chr6q24.2	235670_at	NM_003764
3.21	3.22	0.01	9.39E-01	9.83E-01	RASAL2	RAS protein activator like 2	chr1q24	234910_at	NM_004841 /// NM_170692
2.72	2.73	0.01	9.39E-01	9.83E-01	OR1J2	olfactory receptor, family 1, subfamily J, member 2	chr9q34.11	1567257_at	NM_054107
2.99	3.00	0.01	9.39E-01	9.83E-01	PSG1	pregnancy specific beta-1-glycoprotein 1	chr19q13.2	208257_x_at	NM_006905
4.14	4.16	0.02	9.39E-01	9.83E-01	CHRNE	cholinergic receptor, nicotinic, epsilon	chr17p13-p12	207274_at	NM_000080
3.86	3.87	0.01	9.39E-01	9.83E-01	LAD1	ladinin 1	chr1q25.1-q32.3	203287_at	NM_005558
5.60	5.63	0.03	9.39E-01	9.83E-01	CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	chr10q11	212905_at	NM_015235
3.36	3.39	0.02	9.39E-01	9.83E-01	ANK2	Ankyrin 2, neuronal	chr4q25-q27	216195_at	NM_001127493 /// NM_001148 /// NM_020977
2.80	2.82	0.01	9.39E-01	9.83E-01	RNF115	Ring finger protein 115	chr1q21.1	239383_at	NM_014455
4.32	4.34	0.02	9.39E-01	9.83E-01	---	---	---	230268_at	---

3.22	3.24	0.02	9.39E-01	9.83E-01	DENND3	DENN/MADD domain containing 3	chr8q24.3	212974_at	NM_014957
4.37	4.38	0.01	9.39E-01	9.83E-01	MAP7	microtubule-associated protein 7	chr6q23.3	215471_s_at	NM_003980
1.94	1.95	0.01	9.39E-01	9.83E-01	---	---	---	1559725_at	---
2.30	2.31	0.01	9.39E-01	9.83E-01	LOC643623	hypothetical LOC643623	chr6q22.31	1569647_at	XR_041847 /// XR_041848 /// XR_041849
5.71	5.73	0.02	9.39E-01	9.83E-01	UTP14C	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	chr13q14.2	203614_at	NM_021645
10.62	10.64	0.02	9.39E-01	9.83E-01	HMGB1	high-mobility group box 1	chr13q12	200680_x_at	NM_002128
4.04	4.06	0.02	9.39E-01	9.83E-01	INSL3 /// JAK3	insulin-like 3 (Leydig cell) /// Janus kinase 3 (a protein tyrosine kinase, leukocyte)	chr19p13.1 /// chr19p13.2-p12	1553594_a_at	NM_000215 /// NM_005543
11.93	11.94	0.01	9.39E-01	9.83E-01	RPS6	ribosomal protein S6	chr9p21	209134_s_at	NM_001010
5.35	5.36	0.01	9.39E-01	9.83E-01	MGC33894	transcript expressed during hematopoiesis 2	chr17p11.2	1553872_at	NM_152914
3.18	3.20	0.02	9.40E-01	9.83E-01	SCARF2	scavenger receptor class F, member 2	chr22q11.21	239454_at	NM_153334 /// NM_182895
3.76	3.77	0.01	9.39E-01	9.83E-01	ANKRD11	ankyrin repeat domain 11	chr16q24.3	231999_at	NM_013275
2.20	2.21	0.01	9.39E-01	9.83E-01	MACROD2	MACRO domain containing 2	chr20p12.1	1561677_at	NM_001033087 /// NM_080676
2.89	2.90	0.01	9.39E-01	9.83E-01	SAMD14	sterile alpha motif domain containing 14	chr17q21.33	1559996_s_at	NM_174920
2.21	2.22	0.01	9.40E-01	9.83E-01	CMYA5	cardiomyopathy associated 5	chr5q14.1	237981_at	NM_153610
2.27	2.28	0.01	9.40E-01	9.83E-01	ZEB2	Zinc finger E-box binding homeobox 2	chr2q22	233033_at	NM_014795
2.60	2.61	0.01	9.40E-01	9.83E-01	LBX1	ladybird homeobox 1	chr10q24	208380_at	NM_006562
2.94	2.95	0.01	9.40E-01	9.83E-01	TTC22	tetratricopeptide repeat domain 22	chr1p32.3	215106_at	NM_001114108 /// NM_017904
4.46	4.46	0.01	9.40E-01	9.83E-01	CXorf56	chromosome X open reading frame 56	chrXq23	239444_at	NM_022101
3.63	3.65	0.02	9.40E-01	9.83E-01	CBS	cystathionine-beta-synthase	chr21q22.3	1553972_a_at	NM_000071
3.35	3.37	0.02	9.40E-01	9.83E-01	RBBP9	retinoblastoma binding protein 9	chr20p11.2	221440_s_at	NM_006606
3.05	3.06	0.01	9.40E-01	9.83E-01	C15orf24	Chromosome 15 open reading frame 24	chr15q14	227535_at	NM_020154
3.05	3.06	0.01	9.40E-01	9.83E-01	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	chr5q23-q31	202335_s_at	NM_003337
3.55	3.57	0.01	9.40E-01	9.83E-01	GEMIN8	gem (nuclear organelle) associated protein 8	chrXp22.2	219252_s_at	NM_001042479 /// NM_001042480 /// NM_017856
3.70	3.71	0.01	9.40E-01	9.83E-01	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	chr17q11.2	1316_at	NM_003250 /// NM_199334
3.15	3.16	0.01	9.40E-01	9.83E-01	ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	chr22q13.1	1563108_at	NM_052906
1.97	1.99	0.01	9.40E-01	9.83E-01	VPS26A	Vacuolar protein sorting 26 homolog A (S. pombe)	chr10q21.1	243316_x_at	NM_001035260 /// NM_004896
2.02	2.03	0.01	9.40E-01	9.83E-01	---	---	---	222246_at	---
3.43	3.44	0.02	9.40E-01	9.83E-01	---	---	---	240233_at	---
2.67	2.68	0.01	9.40E-01	9.83E-01	---	---	---	1561683_at	---
1.99	2.00	0.01	9.40E-01	9.83E-01	---	---	---	242708_at	---
2.13	2.14	0.01	9.40E-01	9.83E-01	---	---	---	1556521_a_at	---
2.17	2.19	0.01	9.40E-01	9.83E-01	NASP	Nuclear autoantigenic sperm protein (histone-binding)	chr1p34.1	242918_at	NM_002482 /// NM_152298 /// NM_172164
2.56	2.57	0.01	9.40E-01	9.83E-01	KLHDC7A	kelch domain containing 7A	chr1p36.13	1556012_at	NM_152375
3.90	3.92	0.02	9.40E-01	9.83E-01	FYCO1	FYVE and coiled-coil domain containing 1	chr3p21.31	1555523_a_at	NM_024513
1.99	2.00	0.01	9.40E-01	9.84E-01	---	---	---	244031_at	---
3.08	3.10	0.02	9.41E-01	9.84E-01	CCDC117	coiled-coil domain containing 117	chr22q12.1	235330_at	NM_173510
2.78	2.79	0.01	9.40E-01	9.84E-01	CLCNKA /// CLCNKB	chloride channel Ka /// chloride channel Kb	chr1p36	207047_s_at	NM_000085 /// NM_001042704 /// NM_004070
2.42	2.43	0.01	9.40E-01	9.84E-01	CDC25C	cell division cycle 25 homolog C (S. pombe)	chr5q31	205167_s_at	NM_001790 /// NM_022809
6.46	6.49	0.03	9.41E-01	9.84E-01	TM4SF1	transmembrane 4 L six family member 1	chr3q21-q25	215034_s_at	NM_014220
2.46	2.47	0.01	9.41E-01	9.84E-01	DMRT3	doublesex and mab-3 related transcription factor 3	chr9p24.3	233930_at	NM_021240
3.86	3.87	0.01	9.41E-01	9.84E-01	KLHL35	Kelch-like 35 (Drosophila)	chr11q13.4	214208_at	NM_001039548
2.18	2.19	0.01	9.41E-01	9.84E-01	KRT34	keratin 34	chr17q12-q21	206969_at	NM_021013
1.92	1.93	0.01	9.41E-01	9.84E-01	---	---	---	1569577_x_at	---
3.22	3.24	0.01	9.41E-01	9.84E-01	PNPLA5	patatin-like phospholipase domain containing 5	chr22q13.31	233597_at	NM_138814
6.57	6.60	0.03	9.41E-01	9.84E-01	CNOT8	CCR4-NOT transcription complex, subunit 8	chr5q31-q33	202162_s_at	NM_004779
2.93	2.95	0.01	9.41E-01	9.84E-01	---	---	---	1566949_at	---
2.09	2.10	0.01	9.41E-01	9.84E-01	---	---	---	1563038_at	---
3.37	3.38	0.01	9.41E-01	9.84E-01	---	---	---	239941_at	---
1.99	2.00	0.01	9.41E-01	9.84E-01	---	---	---	242815_x_at	---
3.07	3.08	0.01	9.41E-01	9.84E-01	---	---	---	241286_at	---
2.22	2.23	0.01	9.41E-01	9.84E-01	WDR88	WD repeat domain 88	chr19q13.11	1552453_a_at	NM_173479

3.04	3.05	0.01	9.41E-01	9.84E-01	ACSM3	acyl-CoA synthetase medium-chain family member 3	chr16p13.11	205942_s_at	NM_005622 /// NM_202000
2.02	2.03	0.01	9.41E-01	9.84E-01	---	---	---	239501_at	---
2.35	2.36	0.01	9.41E-01	9.84E-01	UNC93A	unc-93 homolog A (C. elegans)	chr6q27	214640_at	NM_018974
6.92	6.97	0.05	9.42E-01	9.84E-01	NNMT	nicotinamide N-methyltransferase	chr11q23.1	202238_s_at	NM_006169
2.64	2.66	0.02	9.41E-01	9.84E-01	FBXO40	F-box protein 40	chr3q13.33	222954_at	NM_016298
3.41	3.42	0.01	9.41E-01	9.84E-01	CD300LB	CD300 molecule-like family member b	chr17q25.1	1554175_at	NM_174892
5.70	5.71	0.01	9.41E-01	9.84E-01	---	---	---	244429_at	---
2.98	2.99	0.01	9.41E-01	9.84E-01	FRMPD4	FERM and PDZ domain containing 4	chrXp22.2	239290_at	NM_014728
2.54	2.55	0.01	9.42E-01	9.84E-01	EMR2	egf-like module containing, mucin-like, hormone receptor-like 2	chr19p13.1	232009_at	NM_013447 /// NM_152916 /// NM_152917 /// NM_152918 /// NM_152919 /// NM_152920 /// NM_152921
2.62	2.63	0.01	9.41E-01	9.84E-01	INHBC	inhibin, beta C	chr12q13.1	207687_at	NM_005538
2.16	2.17	0.01	9.42E-01	9.84E-01	TRIP11	Thyroid hormone receptor interactor 11	chr14q31-q32	235973_at	NM_004239
7.11	7.13	0.02	9.42E-01	9.84E-01	SMAD2	SMAD family member 2	chr18q21.1	203075_at	NM_001003652 /// NM_005901
3.13	3.14	0.02	9.42E-01	9.84E-01	DIO2	deiodinase, iodothyronine, type II	chr14q24.2-q24.3	210819_x_at	NM_000793 /// NM_001007023 /// NM_013989
5.96	5.98	0.02	9.42E-01	9.84E-01	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	chr11q13.4	221845_s_at	NM_030813
5.72	5.73	0.01	9.42E-01	9.84E-01	TFEB	transcription factor EB	chr6p21	221866_at	NM_007162
6.62	6.64	0.01	9.42E-01	9.84E-01	NCAPH2	non-SMC condensin II complex, subunit H2	chr22q13.33	209718_at	NM_014551 /// NM_152299
4.83	4.84	0.01	9.42E-01	9.84E-01	ZNF232	zinc finger protein 232	chr17p13-p12	219123_at	NM_014519
2.82	2.83	0.01	9.42E-01	9.84E-01	---	---	---	242219_at	---
2.61	2.61	0.01	9.42E-01	9.84E-01	LOC286114	hypothetical protein LOC286114	chr8p21.3	244255_at	---
2.03	2.04	0.01	9.42E-01	9.84E-01	SYCP2	synaptonemal complex protein 2	chr20q13.33	206546_at	NM_014258
2.59	2.59	0.01	9.42E-01	9.84E-01	S100A6	S100 calcium binding protein A6	chr1q21	228923_at	NM_014624
1.89	1.90	0.01	9.42E-01	9.84E-01	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	chr8q22.2	211078_s_at	NM_006281
10.02	10.03	0.01	9.42E-01	9.84E-01	CSTB	cystatin B (stefin B)	chr21q22.3	201201_at	NM_000100
4.83	4.85	0.01	9.42E-01	9.84E-01	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	chr8p11.1	227564_at	NM_152419
2.34	2.35	0.01	9.43E-01	9.84E-01	LRCH1	Leucine-rich repeats and calponin homology (CH) domain containing 1	chr13q14.13-q14.2	214936_at	NM_015116
4.36	4.38	0.02	9.43E-01	9.84E-01	KCTD20	potassium channel tetramerisation domain containing 20	chr6p21.31	214849_at	NM_173562
4.12	4.14	0.02	9.43E-01	9.84E-01	ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl	chr4p15.3	204241_at	NM_001101667 /// NM_003501
3.95	3.97	0.02	9.43E-01	9.84E-01	LOC339988	hypothetical protein LOC339988	chr4p16.1	1562698_x_at	---
2.76	2.77	0.02	9.43E-01	9.84E-01	KHDC1	KH homology domain containing 1	chr6q13	230055_at	NM_030568
2.98	3.00	0.01	9.43E-01	9.84E-01	---	---	---	237174_at	---
2.48	2.50	0.01	9.43E-01	9.84E-01	---	---	---	238198_at	---
2.46	2.47	0.01	9.43E-01	9.84E-01	---	---	---	1569999_at	---
2.15	2.16	0.01	9.43E-01	9.84E-01	---	---	---	234600_at	---
3.34	3.36	0.01	9.43E-01	9.84E-01	LOC154822	hypothetical LOC154822	chr7q36.3	236753_at	---
6.08	6.13	0.05	9.43E-01	9.84E-01	LOC205251	LOC205251	chr2q13	228614_at	XR_017711 /// XR_017795 /// XR_041295
4.55	4.58	0.03	9.43E-01	9.84E-01	---	---	---	242461_at	---
7.29	7.32	0.03	9.43E-01	9.84E-01	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	chr10pter-q25.3	202524_s_at	NM_001134434 /// NM_014767
2.59	2.61	0.02	9.43E-01	9.84E-01	LIMS1	LIM and senescent cell antigen-like domains 1	chr2q12.3-q13	1570259_at	NM_004987
3.95	3.96	0.02	9.43E-01	9.84E-01	SCT	secretin	chr11p15.5	221198_at	NM_021920
3.18	3.19	0.01	9.43E-01	9.84E-01	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	chr7p13	240014_at	NR_003655 /// XR_042143 /// XR_042182
3.33	3.34	0.01	9.43E-01	9.84E-01	---	---	---	1565920_at	---
4.66	4.67	0.01	9.43E-01	9.84E-01	---	---	---	230176_at	---
2.04	2.05	0.01	9.43E-01	9.84E-01	COL25A1	collagen, type XXV, alpha 1	chr4q25	224389_s_at	NM_032518 /// NM_198721
2.04	2.05	0.01	9.43E-01	9.84E-01	FBXO34	F-box protein 34	chr14q22.3	1570183_at	NM_017943 /// NM_152231
2.27	2.28	0.01	9.43E-01	9.84E-01	C12orf42	chromosome 12 open reading frame 42	chr12q23.2-q23.3	1561378_at	NM_001099336 /// NM_198521
2.51	2.52	0.01	9.43E-01	9.84E-01	TCP11	t-complex 11 homolog (mouse)	chr6p21.3-p21.2	220378_at	NM_001093728 /// NM_018679
1.93	1.94	0.01	9.43E-01	9.84E-01	LOC283516	hypothetical protein LOC283516	chr13q14.11	1557345_at	---
3.81	3.86	0.04	9.43E-01	9.84E-01	UBA6	ubiquitin-like modifier activating enzyme 6	chr4q13.2	218340_s_at	NM_018227

2.46	2.48	0.01	9.44E-01	9.84E-01	PRKCB	protein kinase C, beta	chr16p11.2	207957_s_at	NM_002738 /// NM_212535
2.12	2.12	0.01	9.44E-01	9.84E-01	PARP15	poly (ADP-ribose) polymerase family, member 15	chr3q21.1	1553380_at	NM_001113523 /// NM_152615
1.88	1.88	0.01	9.44E-01	9.84E-01	C1orf99	chromosome 1 open reading frame 99	chr1q31.1	1561331_at	NM_001012274
2.02	2.03	0.01	9.44E-01	9.84E-01	---	---	---	1562414_at	---
5.15	5.17	0.02	9.44E-01	9.84E-01	ANKFY1	ankyrin repeat and FYVE domain containing 1	chr17p13.3	219868_s_at	NM_016376 /// NM_020740
1.83	1.84	0.01	9.44E-01	9.85E-01	---	---	---	1555519_at	---
4.91	4.94	0.03	9.44E-01	9.85E-01	LOC728806	Similar to Vesicle-fusing ATPase (Vesicular-fusion protein NSF) (N-ethylmaleimide sensitive fusion protein) (NEM-sensitive fusion protein)	chr17q21.31-q21.32	1566785_x_at	XM_001128535
4.04	4.06	0.02	9.44E-01	9.85E-01	---	---	---	220375_s_at	---
5.46	5.48	0.01	9.44E-01	9.85E-01	LIMK1	LIM domain kinase 1	chr7q11.23	204357_s_at	NM_002314
2.71	2.72	0.01	9.44E-01	9.85E-01	LOC644450	hypothetical protein LOC644450	chr1q12	1566145_s_at	XM_927590
2.67	2.68	0.01	9.44E-01	9.85E-01	LOC284757	hypothetical protein LOC284757	chr20q13.33	236846_at	XR_041615 /// XR_041616 /// XR_041617
2.70	2.71	0.01	9.44E-01	9.85E-01	PCBP2 /// PCBP2P2	poly(rC) binding protein 2 /// poly(rC) binding protein 2, pseudogene 2	chr12q13.12-q13.13 /// chr8q21-q22	237813_at	NM_001098620 /// NM_001128911 /// NM_001128912 /// NM_001128913 /// NM_001128914 /// NM_005016 /// NM_031989 /// XR_038597 /// XR_038598 /// XR_038608
2.09	2.10	0.01	9.44E-01	9.85E-01	---	---	---	244390_at	---
6.41	6.44	0.03	9.44E-01	9.85E-01	ZRANB2	zinc finger, RAN-binding domain containing 2	chr1p31	223016_x_at	NM_005455 /// NM_203350
7.56	7.59	0.03	9.45E-01	9.85E-01	RABGGTB	Rab geranylgeranyltransferase, beta subunit	chr1p31	209180_at	NM_004582
4.75	4.77	0.02	9.44E-01	9.85E-01	---	---	---	229841_at	---
3.79	3.80	0.01	9.44E-01	9.85E-01	C21orf30	chromosome 21 open reading frame 30	chr21q22.3	232536_at	XM_001720003 /// XM_001722905 /// XM_001726311
2.81	2.82	0.01	9.44E-01	9.85E-01	C21orf129	chromosome 21 open reading frame 129	chr21q22.3	1553918_at	XR_040346 /// XR_040347 /// XR_040348
2.04	2.05	0.01	9.45E-01	9.85E-01	---	---	---	241502_x_at	---
3.20	3.21	0.01	9.45E-01	9.85E-01	ITGB1BP1	Integrin beta 1 binding protein 1	chr2p25.2	228227_at	NM_004763 /// NM_022334
3.12	3.14	0.02	9.45E-01	9.85E-01	C1orf25	chromosome 1 open reading frame 25	chr1q25.2	223404_s_at	NM_030934
2.44	2.45	0.02	9.45E-01	9.85E-01	---	---	---	1558385_at	---
3.78	3.79	0.01	9.45E-01	9.85E-01	---	---	---	1562081_a_at	---
3.58	3.59	0.01	9.45E-01	9.85E-01	---	---	---	241361_at	---
2.62	2.63	0.01	9.45E-01	9.85E-01	TMEM133	transmembrane protein 133	chr11q22.1	223595_at	NM_032021
2.15	2.16	0.01	9.45E-01	9.85E-01	LOC152742	hypothetical protein LOC152742	chr4p15.33	240167_at	XM_001128848 /// XM_001131702 /// XM_001723200
4.97	5.01	0.03	9.45E-01	9.85E-01	COL4A4	collagen, type IV, alpha 4	chr2q35-q37	214602_at	NM_000092
5.13	5.15	0.02	9.45E-01	9.85E-01	ARL4A	ADP-ribosylation factor-like 4A	chr7p21-p15.3	205020_s_at	NM_001037164 /// NM_005738 /// NM_212460
3.55	3.56	0.02	9.45E-01	9.85E-01	HYAL3 /// NAT6	hyaluronoglucosaminidase 3 /// N-acetyltransferase 6	chr3p21.3	211728_s_at	NM_003549 /// NM_012191
8.46	8.47	0.01	9.45E-01	9.85E-01	COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	chr3q13.33	203880_at	NM_005694
3.26	3.27	0.01	9.45E-01	9.85E-01	RASGRP4	RAS guanyl releasing protein 4	chr19q13.1	240862_at	NM_170604
3.00	3.02	0.01	9.45E-01	9.85E-01	C1orf159	chromosome 1 open reading frame 159	chr1p36.33	219337_at	NM_017891
3.16	3.17	0.01	9.45E-01	9.85E-01	---	---	---	243098_at	---
2.63	2.64	0.01	9.45E-01	9.85E-01	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	chr1q43	235504_at	NM_022469
2.05	2.06	0.01	9.45E-01	9.85E-01	CDC6	cell division cycle 6 homolog (S. cerevisiae)	chr17q21.3	203967_at	NM_001254

2.36	2.37	0.01	9.45E-01	9.85E-01	MGC39584	hypothetical gene supported by BC029568	chr4q35.2	240814_at	XR_017735 /// XR_017787 /// XR_041937																					
2.22	2.23	0.01	9.45E-01	9.85E-01	FMN2	formin 2	chr1q43	223618_at	NM_020066																					
2.47	2.47	0.01	9.45E-01	9.85E-01	---	---	---	1561354_at	---																					
1.85	1.86	0.01	9.45E-01	9.85E-01	---	---	---	1562616_at	---																					
3.30	3.31	0.01	9.46E-01	9.85E-01	LOC645733	similar to hCG1812929	chr2q14.2	241234_at	XM_001130623 /// XM_374004																					
3.94	3.95	0.01	9.46E-01	9.85E-01	KRT7	keratin 7	chr12q12-q13	1558393_at	NM_005556																					
3.14	3.15	0.01	9.45E-01	9.85E-01	---	---	---	1560942_at	---																					
4.13	4.16	0.03	9.46E-01	9.85E-01	RNF144B	ring finger 144B	chr6p22.3	228153_at	NM_182757																					
5.50	5.52	0.02	9.46E-01	9.85E-01	RANBP10	RAN binding protein 10	chr16q22.1	53987_at	NM_020850																					
3.92	3.95	0.02	9.46E-01	9.85E-01	ZFAND6	Zinc finger, AN1-type domain 6	chr15q25.1	222186_at	NM_019006																					
4.33	4.35	0.02	9.46E-01	9.85E-01	SMAD6	SMAD family member 6	chr15q21-q22	207069_s_at	NM_005585																					
8.32	8.34	0.02	9.46E-01	9.85E-01	PRKCSH	protein kinase C substrate 80K-H	chr19p13.2	214080_x_at	NM_001001329 /// NM_002743																					
4.25	4.26	0.01	9.46E-01	9.85E-01	NRG1	neuregulin 1	chr8p12	208230_s_at	NM_004495 /// NM_013956 /// NM_013957 /// NM_013958 /// NM_013959 /// NM_013960 /// NM_013961 /// NM_013962 /// NM_013964																					
2.27	2.28	0.01	9.46E-01	9.85E-01	---	---	---	238184_at	---																					
2.29	2.30	0.01	9.46E-01	9.85E-01	---	---	---	240296_at	---																					
2.70	2.71	0.01	9.46E-01	9.85E-01	---	---	---	244800_x_at	---																					
2.64	2.65	0.01	9.46E-01	9.85E-01	CADM1	cell adhesion molecule 1	chr11q23.2	232767_at	NM_001098517 /// NM_014333																					
2.14	2.15	0.01	9.46E-01	9.85E-01	CCDC15	coiled-coil domain containing 15	chr11q24.2	241360_at	NM_025004																					
7.37	7.39	0.01	9.46E-01	9.85E-01	TPRG1L	tumor protein p63 regulated 1-like	chr1p36.32	224871_at	NM_182752																					
2.24	2.25	0.01	9.47E-01	9.85E-01	TRIM55	tripartite motif-containing 55	chr8q13.1	232721_at	NM_033058 /// NM_184085 /// NM_184086 /// NM_184087																					
6.99	7.01	0.02	9.47E-01	9.85E-01	GDE1	glycerophosphodiester phosphodiesterase 1	chr16p12-p11.2	202593_s_at	NM_016641																					
8.89	8.90	0.01	9.47E-01	9.85E-01	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	chr9q12	216308_x_at	NM_012203																					
8.49	8.49	0.01	9.47E-01	9.85E-01	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	chr7p22.1	200699_at	NM_001100603 /// NM_006854																					
3.84	3.86	0.02	9.47E-01	9.85E-01	C4orf15	chromosome 4 open reading frame 15	chr4p16.3	210054_at	NM_024511																					
9.10	9.11	0.02	9.47E-01	9.85E-01	APP	amyloid beta (A4) precursor protein	chr21q21.2|21q21.3	214953_s_at	NM_000484 /// NM_201413 /// NM_201414																					
3.29	3.31	0.01	9.47E-01	9.85E-01	---	---	---	239784_at	---																					
2.30	2.31	0.01	9.47E-01	9.85E-01	---	---	---	1560870_a_at	---																					
2.56	2.57	0.01	9.47E-01	9.85E-01	LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	chr19q13.4	215838_at	NM_021250 /// NM_181879 /// NM_181985 /// NM_181986																					
2.04	2.04	0.01	9.47E-01	9.85E-01	GPR88	G protein-coupled receptor 88	chr1p21.3	220313_at	NM_022049																					
8.55	8.57	0.01	9.47E-01	9.86E-01	FUNDC2	FUN14 domain containing 2	chrXq28	223042_s_at	NM_023934																					
3.59	3.60	0.01	9.47E-01	9.86E-01	---	---	---	1556806_at	---																					
3.72	3.74	0.01	9.47E-01	9.86E-01	---	---	---	237843_at	---																					
2.21	2.22	0.01	9.47E-01	9.86E-01	---	---	---	1560148_at	---																					
2.56	2.57	0.01	9.47E-01	9.86E-01	CYB5R1	cytochrome b5 reductase 1	chr1p36.13-q41	1560043_at	NM_016243																					
3.08	3.10	0.02	9.47E-01	9.86E-01	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	chr11q23.3	208455_at	NM_002855 /// NM_203285 /// NM_203286																					
2.40	2.41	0.01	9.48E-01	9.86E-01	---	---	---	1565917_at	---																					
3.50	3.51	0.01	9.48E-01	9.86E-01	C14orf176	Chromosome 14 open reading frame 176	chr14q11.2	1558594_at	XM_001714742 /// XM_001716718 /// XM_001716933																					
2.00	2.01	0.01	9.48E-01	9.86E-01	---	---	---	238398_s_at	---																					
2.05	2.06	0.01	9.48E-01	9.86E-01	MBL2	mannose-binding lectin (protein C) 2, soluble (opsonic defect)	chr10q11.2-q21	207256_at	NM_000242																					
3.70	3.71	0.01	9.48E-01	9.86E-01	TBX3	T-box 3	chr12q24.1	228344_s_at	NM_005996 /// NM_016569																					
3.00	3.01	0.01	9.48E-01	9.86E-01	---	---	---	1561995_at	---																					
7.02	7.04	0.02	9.48E-01	9.86E-01	---	---	---	217653_x_at	---																					

2.92	2.94	0.01	9.48E-01	9.86E-01	TGFBR1	transforming growth factor, beta receptor 1	chr9q22	206943_at	NM_001130916 /// NM_004612
2.35	2.36	0.01	9.48E-01	9.86E-01	LOC401312	LOC401318	chr7p15.3	1560520_at	---
3.92	3.93	0.01	9.48E-01	9.86E-01	TRIM46	tripartite motif-containing 46	chr1q22	238147_at	NM_025058
2.02	2.03	0.01	9.48E-01	9.86E-01	---	---	---	240773_at	---
7.98	8.00	0.02	9.48E-01	9.86E-01	WAC	WW domain containing adaptor with coiled-coil	---	222390_at	NM_016628 /// NM_100264 /// NM_100486
3.04	3.06	0.02	9.48E-01	9.86E-01	HERC4	hect domain and RLD 4	chr10q21.3	208055_s_at	NM_015601 /// NM_022079
4.50	4.51	0.02	9.48E-01	9.86E-01	DUSP4	dual specificity phosphatase 4	chr8p12-p11	204014_at	NM_001394 /// NM_057158
3.03	3.04	0.01	9.48E-01	9.86E-01	---	---	---	241046_at	---
2.91	2.92	0.01	9.48E-01	9.86E-01	ATP8B3	ATPase, class I, type 8B, member 3	chr19p13.3	239457_at	NM_138813
2.11	2.12	0.01	9.48E-01	9.86E-01	---	---	---	239566_at	---
1.99	2.00	0.01	9.48E-01	9.86E-01	---	---	---	1566694_at	---
2.13	2.14	0.01	9.48E-01	9.86E-01	MCART6	mitochondrial carrier triple repeat 6	chrXq22.2	1561578_s_at	NM_001012755
2.52	2.53	0.01	9.48E-01	9.86E-01	---	---	---	240923_at	---
2.87	2.88	0.02	9.48E-01	9.86E-01	SETD2	SET domain containing 2	chr3p21.31	220946_s_at	NM_014159
3.24	3.26	0.01	9.49E-01	9.86E-01	---	---	---	237255_at	---
2.68	2.70	0.01	9.49E-01	9.86E-01	GABBR1 /// UBD	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D	chr6p21.3 /// chr6p21.31	205890_s_at	NM_001470 /// NM_006398 /// NM_021903 /// NM_021904 /// NM_021905
2.80	2.81	0.01	9.49E-01	9.86E-01	ATAD5	ATPase family, AAA domain containing 5	chr17q11.2	220223_at	NM_024857
2.60	2.61	0.01	9.49E-01	9.86E-01	GRIK1	glutamate receptor, ionotropic, kainate 1	chr21q22.11	214611_at	NM_000830 /// NM_175611
3.56	3.58	0.02	9.49E-01	9.86E-01	ZNF280B	zinc finger protein 280B	chr22q11.22	230789_at	NM_080764
6.47	6.50	0.03	9.49E-01	9.86E-01	PSME4	proteasome (prosome, macropain) activator subunit 4	chr2p16.2	212219_at	NM_014614
2.22	2.23	0.01	9.49E-01	9.86E-01	---	---	---	1562597_at	---
4.90	4.92	0.02	9.49E-01	9.86E-01	UBA6	ubiquitin-like modifier activating enzyme 6	chr4q13.2	222601_at	NM_018227
3.33	3.34	0.01	9.49E-01	9.86E-01	---	---	---	232460_at	---
2.11	2.11	0.01	9.49E-01	9.86E-01	---	---	---	1564561_at	---
5.94	5.96	0.02	9.49E-01	9.86E-01	SCYL2	SCY1-like 2 (S. cerevisiae)	chr12q23.1	224960_at	NM_017988
6.84	6.86	0.02	9.49E-01	9.86E-01	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	chr2p15-p13	212810_s_at	NM_003038
3.62	3.63	0.01	9.49E-01	9.86E-01	BMP8A	bone morphogenetic protein 8a	chr1p34.2	220204_s_at	NM_181809
2.24	2.25	0.01	9.49E-01	9.86E-01	FANCD2	Fanconi anemia, complementation group D2	chr3p26	1568891_x_at	NM_001018115 /// NM_033084
2.30	2.31	0.01	9.49E-01	9.86E-01	AAA1	asthma-associated alternatively spliced gene 1	chr7p14.3	234117_at	NM_207283 /// NM_207284 /// NM_207285 /// NM_207286 /// NM_207287 /// NM_207288 /// NM_207289 /// NM_207290 /// NR_015356
1.94	1.95	0.01	9.49E-01	9.86E-01	DES	desmin	chr2q35	216947_at	NM_001927
2.74	2.75	0.01	9.49E-01	9.86E-01	LOC151877	hypothetical protein LOC151877	chr3p14.3	1561301_at	---
1.98	1.99	0.01	9.49E-01	9.86E-01	---	---	---	243211_at	---
2.50	2.51	0.01	9.49E-01	9.86E-01	TRPA1	transient receptor potential cation channel, subfamily A, member 1	chr8q13	208349_at	NM_007332
2.45	2.45	0.01	9.49E-01	9.86E-01	MYLK4	myosin light chain kinase family, member 4	chr6p25.2	1556136_at	NM_001012418
5.76	5.79	0.03	9.50E-01	9.86E-01	TMEM38B	transmembrane protein 38B	chr9q31.2	222736_s_at	NM_018112
4.15	4.17	0.02	9.50E-01	9.86E-01	SMCR7	Smith-Magenis syndrome chromosome region, candidate 7	chr17p11.2	235896_s_at	NM_139162 /// NM_148886
4.83	4.85	0.02	9.50E-01	9.86E-01	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	chrXq13.2-q13.3	205198_s_at	NM_000052
6.25	6.27	0.01	9.50E-01	9.86E-01	LOC100128443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	chr5q12.3	210958_s_at	NM_015183 /// NM_198828 /// XM_001720470 /// XM_001720479 /// XM_001722488
6.52	6.53	0.01	9.50E-01	9.86E-01	ZNF828	zinc finger protein 828	chr13q34	226194_at	NM_032436

7.17	7.20	0.03	9.50E-01	9.86E-01	TGFB1I1	transforming growth factor beta 1 induced transcript 1	chr16p11.2	209651_at	NM_001042454 /// NM_015927																					
4.91	4.92	0.01	9.50E-01	9.86E-01	PTCH1	patched homolog 1 (Drosophila)	chr9q22.3	209815_at	NM_000264 /// NM_001083602 /// NM_001083603 /// NM_001083604 /// NM_001083605 /// NM_001083606 /// NM_001083607																					
3.67	3.69	0.01	9.50E-01	9.86E-01	ALMS1	Alstrom syndrome 1	chr2p13	214220_s_at	NM_015120																					
3.33	3.34	0.01	9.50E-01	9.86E-01	LUZP1	leucine zipper protein 1	chr1p36	1558173_a_at	NM_033631																					
6.17	6.18	0.01	9.50E-01	9.86E-01	MRPL2	mitochondrial ribosomal protein L2	chr6p21.3	218887_at	NM_015950																					
2.29	2.30	0.01	9.50E-01	9.86E-01	---	---	---	241365_at	---																					
2.43	2.44	0.01	9.50E-01	9.86E-01	---	---	---	242152_at	---																					
2.46	2.47	0.01	9.50E-01	9.86E-01	C10orf118	chromosome 10 open reading frame 118	chr10q25.3	219844_at	NM_018017																					
3.01	3.02	0.01	9.50E-01	9.86E-01	---	---	---	1561530_at	---																					
2.69	2.72	0.02	9.50E-01	9.86E-01	---	---	---	234650_at	---																					
4.23	4.25	0.02	9.50E-01	9.86E-01	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	chr15q15.1	225164_s_at	NM_001013703																					
2.94	2.96	0.01	9.50E-01	9.86E-01	LOC100131795 /// NMNAT2	hypothetical protein LOC100131795 /// nicotinamide nucleotide adenylyltransferase 2	chr15q21.3 /// chr1q25	209755_at	NM_015039 /// NM_170706 /// XM_001722686 /// XM_001726267 /// XM_001726271																					
2.63	2.65	0.01	9.50E-01	9.86E-01	SYCN	syncollin	chr19q13.2	229995_at	NM_001080468																					
4.55	4.56	0.01	9.51E-01	9.86E-01	GCNT7	Glucosaminyl (N-acetyl) transferase family member 7	chr20q13.2	242040_at	NM_001128614 /// NM_080615 /// XM_001723312 /// XM_001723344 /// XM_001723681																					
2.58	2.60	0.01	9.50E-01	9.86E-01	PDZK1	PDZ domain containing 1	chr1q21	205380_at	NM_002614																					
2.18	2.19	0.01	9.50E-01	9.86E-01	---	---	---	1556911_at	---																					
2.80	2.81	0.01	9.50E-01	9.86E-01	---	---	---	238571_at	---																					
2.84	2.85	0.01	9.50E-01	9.86E-01	HCRT	hypocretin (orexin) neuropeptide precursor	chr17q21	207642_at	NM_001524																					
2.84	2.85	0.01	9.51E-01	9.86E-01	FUBP1	far upstream element (FUSE) binding protein 1	chr1p31.1	214094_at	NM_003902																					
2.41	2.42	0.01	9.51E-01	9.86E-01	---	---	---	1569399_at	---																					
2.61	2.62	0.01	9.51E-01	9.86E-01	GPR107	G protein-coupled receptor 107	chr9q34.11	220265_at	NM_020960																					
2.06	2.06	0.01	9.50E-01	9.86E-01	---	---	---	1558595_at	---																					
2.49	2.49	0.01	9.51E-01	9.87E-01	COX4NB	COX4 neighbor	chr16q24	227323_at	NM_006067																					
4.98	5.01	0.02	9.51E-01	9.87E-01	UBE3A	ubiquitin protein ligase E3A	chr15q11-q13	211575_s_at	NM_000462 /// NM_130838 /// NM_130839																					
2.58	2.59	0.01	9.51E-01	9.87E-01	---	---	---	1565807_at	---																					
2.71	2.72	0.01	9.51E-01	9.87E-01	KRT1	keratin 1	chr12q12-q13	205900_at	NM_006121																					
2.11	2.12	0.01	9.51E-01	9.87E-01	FLJ16686	FLJ16686 protein	chr4p14	1564160_at	XM_001713945 /// XM_379262 /// XM_940851																					
4.19	4.22	0.03	9.51E-01	9.87E-01	WDR26	WD repeat domain 26	chr1q42.11	224898_at	NM_001115113 /// NM_025160																					
3.90	3.92	0.02	9.51E-01	9.87E-01	C14orf135 /// LOC100130173	chromosome 14 open reading frame 135 /// hypothetical protein LOC100130173	chr14q23.1	219972_s_at	NM_022495 /// XM_001719623 /// XM_001723734																					
3.87	3.88	0.02	9.51E-01	9.87E-01	---	---	---	228778_at	---																					
2.86	2.87	0.01	9.51E-01	9.87E-01	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	chr6p21.2-p21.1	221661_at	NM_006672 /// NM_153320																					
3.80	3.81	0.01	9.51E-01	9.87E-01	TMEM44	transmembrane protein 44	chr3q29	1560275_at	NM_001011655 /// NM_138399																					

3.14	3.15	0.01	9.51E-01	9.87E-01	CCDC77	coiled-coil domain containing 77	chr12p13.33	224521_s_at	NM_001130146 /// NM_001130147 /// NM_001130148 /// NM_032358																				
2.28	2.29	0.01	9.51E-01	9.87E-01	---	---	---	232824_at	---																				
2.31	2.32	0.01	9.51E-01	9.87E-01	C10orf99	chromosome 10 open reading frame 99	chr10q23.1	227735_s_at	NM_207373																				
3.82	3.83	0.01	9.51E-01	9.87E-01	---	---	---	237878_at	---																				
2.42	2.43	0.01	9.51E-01	9.87E-01	---	---	---	241589_at	---																				
2.79	2.79	0.01	9.51E-01	9.87E-01	---	---	---	1561834_a_at	---																				
6.65	6.66	0.01	9.51E-01	9.87E-01	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	chr1q42.11	203794_at	NM_003607 /// NM_014826																				
1.97	1.97	0.01	9.52E-01	9.87E-01	CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	chr8q11-q12	207406_at	NM_000780																				
2.91	2.92	0.01	9.52E-01	9.87E-01	---	---	---	1569578_at	---																				
2.01	2.01	0.01	9.52E-01	9.87E-01	---	---	---	1570076_at	---																				
4.23	4.24	0.01	9.52E-01	9.87E-01	DBP	D site of albumin promoter (albumin D-box) binding protein	chr19q13.3	209783_at	NM_001352																				
2.35	2.36	0.01	9.52E-01	9.87E-01	---	---	---	234657_at	---																				
2.10	2.11	0.01	9.52E-01	9.87E-01	LOC90246	hypothetical protein LOC90246	chr3q21.3	233830_at	---																				
1.97	1.98	0.01	9.52E-01	9.87E-01	POLR3G	Polymerase (RNA) III (DNA directed) polypeptide G (32kD)	chr5q14.3	231544_s_at	NM_006467																				
2.03	2.03	0.01	9.52E-01	9.87E-01	TMEM146	transmembrane protein 146	chr19p13.3	237020_at	NM_152784																				
4.91	4.94	0.03	9.52E-01	9.87E-01	---	---	---	228603_at	---																				
3.54	3.56	0.02	9.52E-01	9.87E-01	CSF2RA /// LOC100133516	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) /// hypothetical protein LOC100133516	chrXp22.32 and Yp11.3	207085_x_at	NM_006140 /// NM_172245 /// NM_172246 /// NM_172247 /// NM_172249 /// XM_001714505																				
3.56	3.58	0.01	9.52E-01	9.87E-01	C9orf164	chromosome 9 open reading frame 164	chr9q22.2	228891_at	NM_182635																				
4.86	4.87	0.01	9.52E-01	9.87E-01	LOC283140	hypothetical protein LOC283140	chr11q23.1	1563800_at	---																				
5.64	5.65	0.01	9.52E-01	9.87E-01	STX6	syntaxin 6	chr1q25.3	212799_at	NM_005819																				
2.59	2.60	0.01	9.52E-01	9.87E-01	CCNA2	cyclin A2	chr4q25-q31	203418_at	NM_001237																				
2.71	2.72	0.01	9.52E-01	9.87E-01	LOC286059	hypothetical protein LOC286059	chr8p21.2	234147_at	---																				
2.14	2.15	0.01	9.52E-01	9.87E-01	---	---	---	243877_at	---																				
2.13	2.13	0.01	9.52E-01	9.87E-01	---	---	---	241319_at	---																				
2.78	2.79	0.01	9.52E-01	9.87E-01	---	---	---	1566688_at	---																				
2.13	2.14	0.01	9.52E-01	9.87E-01	LOC440345	hypothetical protein LOC440345	chr16p12.1	214984_at	XR_015786																				
2.27	2.28	0.01	9.52E-01	9.87E-01	STK4	serine/threonine kinase 4	chr20q11.2-q13.2	1569791_at	NM_006282																				
2.86	2.87	0.01	9.52E-01	9.87E-01	C8orf39	chromosome 8 open reading frame 39	chr8q22.1	220222_at	XR_040452 /// XR_040453 /// XR_040454																				
2.26	2.26	0.01	9.52E-01	9.87E-01	---	---	---	241145_at	---																				
2.20	2.21	0.01	9.52E-01	9.87E-01	ZNF19	zinc finger protein 19	chr16q22	240836_at	NM_006961																				
3.47	3.48	0.01	9.53E-01	9.87E-01	NMNAT1	nicotinamide nucleotide adenylyltransferase 1	chr1p32-p35	229852_at	NM_022787																				
4.09	4.10	0.01	9.53E-01	9.87E-01	RPLP2	ribosomal protein, large, P2	chr11p15.5-p15.4	200908_s_at	NM_001004																				
2.10	2.11	0.01	9.53E-01	9.87E-01	SUFU	suppressor of fused homolog (Drosophila)	chr10q24.32	224202_at	NM_016169																				
1.91	1.91	0.01	9.53E-01	9.87E-01	---	---	---	216151_at	---																				
2.76	2.77	0.01	9.53E-01	9.87E-01	---	---	---	1560435_at	---																				
6.62	6.64	0.02	9.53E-01	9.87E-01	NBL1	neuroblastoma, suppression of tumorigenicity 1	chr1p36.13|1p36.13-p36.11	201621_at	NM_005380 /// NM_182744																				
2.59	2.60	0.01	9.53E-01	9.87E-01	GINS4	GINS complex subunit 4 (Sld5 homolog)	chr8p11.21	240778_at	NM_032336																				
2.35	2.36	0.01	9.53E-01	9.87E-01	TMEM185A	Transmembrane protein 185A	chrXq28	231326_s_at	NM_032508																				
3.04	3.05	0.01	9.53E-01	9.87E-01	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	chr17q11.2	204996_s_at	NM_003885																				
6.12	6.14	0.02	9.53E-01	9.87E-01	GCOM1 /// GRINL1A	GRINL1A complex locus /// glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	chr15q21.3 /// chr15q22.1	212244_at	NM_001018090 /// NM_001018091 /// NM_001018100 /// NM_001018102 /// NM_001018103 /// NM_015532 /// NM_152451																				
3.22	3.24	0.01	9.53E-01	9.87E-01	---	---	---	1564753_at	---																				
2.09	2.10	0.01	9.53E-01	9.87E-01	COL4A6	collagen, type IV, alpha 6	chrXq22	210945_at	NM_001847 /// NM_033641																				
2.25	2.26	0.01	9.53E-01	9.87E-01	LOC100128570	hypothetical protein LOC100128570	chr15q25.1	239747_s_at	XM_001720242 /// XM_001720250 /// XM_001726884																				

4.93	4.94	0.02	9.53E-01	9.87E-01	TMEM198	transmembrane protein 198	chr2q35	227890_at	NM_001005209
5.98	5.99	0.01	9.53E-01	9.87E-01	---	---	---	229384_at	---
9.92	9.94	0.02	9.54E-01	9.87E-01	CNBP	CCHC-type zinc finger, nucleic acid binding protein	chr3q21	206158_s_at	NM_001127192 /// NM_001127193 /// NM_001127194 /// NM_001127195 /// NM_001127196 /// NM_003418
2.62	2.64	0.02	9.54E-01	9.87E-01	HNT	neurotrimin	chr11q25	227566_at	NM_001048209 /// NM_016522
3.32	3.33	0.01	9.54E-01	9.87E-01	C7orf51	chromosome 7 open reading frame 51	chr7q22.1	1553288_a_at	NM_173564
2.60	2.61	0.01	9.54E-01	9.87E-01	---	---	---	240674_at	---
2.23	2.24	0.01	9.54E-01	9.87E-01	---	---	---	240007_at	---
3.19	3.20	0.01	9.54E-01	9.87E-01	LOC253842 /// NR6A1	hypothetical protein LOC253842 /// nuclear receptor subfamily 6, group A, member 1	chr9q33-q34.1 /// chr9q34.11	227496_at	NM_001489 /// NM_033334
2.33	2.34	0.01	9.54E-01	9.87E-01	OR2A20P /// OR2A5 /// OR2A9P	olfactory receptor, family 2, subfamily A, member 20 pseudogene /// olfactory receptor, family 2, subfamily A, member 5 /// olfactory receptor, family 2, subfamily A, member 9 pseudogene	chr7q35	222290_at	NM_012365 /// NR_002157 /// NR_002158
1.97	1.98	0.01	9.54E-01	9.87E-01	LOC255130	hypothetical LOC255130	chr4q12	1557395_at	XR_041369 /// XR_041370 /// XR_041371
2.18	2.19	0.01	9.54E-01	9.87E-01	---	---	---	1563121_at	---
3.71	3.74	0.03	9.54E-01	9.87E-01	PLIN	perilipin	chr15q26	205913_at	NM_002666
2.38	2.39	0.01	9.54E-01	9.87E-01	---	---	---	1558765_a_at	---
2.27	2.28	0.01	9.54E-01	9.87E-01	PRIM2	primase, DNA, polypeptide 2 (58kDa)	chr6p12-p11.1	1554885_a_at	NM_000947
2.01	2.02	0.01	9.54E-01	9.87E-01	SPP1	Secreted phosphoprotein 1	chr4q21-q25	1568574_x_at	NM_000582 /// NM_001040058 /// NM_001040060
2.16	2.17	0.01	9.54E-01	9.88E-01	CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	chr4q31.1	1554283_at	NM_012118
2.10	2.10	0.01	9.54E-01	9.88E-01	---	---	---	1566266_at	---
7.07	7.09	0.02	9.55E-01	9.88E-01	ZMAT3	zinc finger, matrin type 3	chr3q26.3-q27	219628_at	NM_022470 /// NM_152240
5.16	5.18	0.01	9.55E-01	9.88E-01	RGAG4	retrotransposon gag domain containing 4	chrXq13.1	227823_at	NM_001024455
2.61	2.63	0.02	9.55E-01	9.88E-01	FZD3	frizzled homolog 3 (Drosophila)	chr8p21	219683_at	NM_017412
2.82	2.83	0.01	9.55E-01	9.88E-01	---	---	---	236596_at	---
2.14	2.15	0.01	9.55E-01	9.88E-01	C17orf69	Chromosome 17 open reading frame 69	chr17q21.31	1558611_at	XR_040436 /// XR_040437 /// XR_040438
3.11	3.12	0.01	9.55E-01	9.88E-01	---	---	---	237678_at	---
4.36	4.38	0.02	9.55E-01	9.88E-01	CEP68	centrosomal protein 68kDa	chr2p14	207971_s_at	NM_015147
2.02	2.02	0.01	9.55E-01	9.88E-01	SEDLP /// TRAPPC2	spondyloepiphyseal dysplasia, late, pseudogene /// trafficking protein particle complex 2	chr19q13.4 /// chrXp22	1562349_at	NM_001011658 /// NM_001128835 /// NM_014563 /// NR_002166
2.46	2.47	0.01	9.55E-01	9.88E-01	SMC1B	structural maintenance of chromosomes 1B	chr22q13.31	1553249_at	NM_148674
5.22	5.24	0.01	9.55E-01	9.88E-01	WDR44	WD repeat domain 44	chrXq24	219297_at	NM_019045
1.90	1.91	0.01	9.55E-01	9.88E-01	---	---	---	1561340_at	---
3.90	3.92	0.02	9.55E-01	9.88E-01	PICALM	phosphatidylinositol binding clathrin assembly protein	chr11q14	212511_at	NM_001008660 /// NM_007166
6.59	6.60	0.01	9.55E-01	9.88E-01	UNC119	unc-119 homolog (C. elegans)	chr17q11.2	203271_s_at	NM_005148 /// NM_054035
2.43	2.43	0.01	9.55E-01	9.88E-01	---	---	---	243652_at	---
2.18	2.19	0.01	9.55E-01	9.88E-01	KIAA0774	KIAA0774	chr13q12.3	214961_at	NM_001033602 /// NM_015233
2.11	2.12	0.01	9.55E-01	9.88E-01	---	---	---	233721_x_at	---
2.65	2.66	0.01	9.55E-01	9.88E-01	AKR1CL2	aldo-keto reductase family 1, member C-like 2	chr10p15.1	1555220_a_at	NM_001040177
2.74	2.75	0.01	9.55E-01	9.88E-01	---	---	---	231894_at	---
3.36	3.37	0.01	9.56E-01	9.88E-01	GTSF1L	gametocyte specific factor 1-like	chr20q13.12	232820_s_at	NM_001008901 /// NM_176791
2.72	2.73	0.01	9.55E-01	9.88E-01	---	---	---	235031_at	---
2.19	2.20	0.01	9.55E-01	9.88E-01	---	---	---	242909_at	---

2.96	2.97	0.01	9.55E-01	9.88E-01	---	---	---	230584_at	---
2.17	2.17	0.01	9.56E-01	9.88E-01	TSHR	thyroid stimulating hormone receptor	chr14q31	215442_s_at	NM_000369 /// NM_001018036
2.13	2.14	0.01	9.56E-01	9.88E-01	CCDC108	coiled-coil domain containing 108	chr2q35	1553886_at	NM_152389 /// NM_194302
6.56	6.57	0.02	9.56E-01	9.88E-01	SNTA1	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	chr20q11.2	203516_at	NM_003098
8.80	8.81	0.01	9.56E-01	9.88E-01	STUB1	STIP1 homology and U-box containing protein 1	chr16p13.3	217934_x_at	NM_005861
2.90	2.91	0.01	9.56E-01	9.88E-01	---	---	---	236898_at	---
4.10	4.11	0.01	9.56E-01	9.88E-01	---	---	---	242749_at	---
2.70	2.71	0.01	9.56E-01	9.88E-01	---	---	---	216075_at	---
3.41	3.42	0.01	9.56E-01	9.88E-01	HSFX1 /// HSFX2 /// LOC100130086	heat shock transcription factor family, X linked 1 /// heat shock transcription factor family, X linked 2 /// hypothetical protein LOC100130086	chrXq28	220314_at	NM_016153 /// XM_001126546 /// XM_001713713
3.51	3.52	0.01	9.56E-01	9.88E-01	CRYM	crystallin, mu	chr16p13.11-p12.3	205489_at	NM_001014444 /// NM_001888
3.63	3.64	0.01	9.56E-01	9.88E-01	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	chr11q23.2	222351_at	NM_002716 /// NM_181699
2.92	2.93	0.01	9.56E-01	9.88E-01	HJURP	Holliday junction recognition protein	chr2q37.1	218726_at	NM_018410
2.29	2.30	0.01	9.56E-01	9.88E-01	LOC732096	Similar to hCG2040240	chr12q23.1	1564533_at	XM_001720784 /// XM_001725388 /// XR_016064
2.97	2.98	0.01	9.56E-01	9.88E-01	PPM1L	Protein phosphatase 1 (formerly 2C)-like	chr3q26.1	239855_at	NM_139245
2.20	2.21	0.01	9.56E-01	9.88E-01	CACNA1A	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	chr19p13.2-p13.1	1558944_at	NM_000068 /// NM_001127221 /// NM_001127222 /// NM_023035
2.28	2.29	0.01	9.56E-01	9.88E-01	---	---	---	230910_s_at	---
3.79	3.80	0.01	9.56E-01	9.88E-01	LOC100129951 /// LOC100134638	hypothetical protein LOC100129951 /// hypothetical protein LOC100134638	chr7q36.3	236357_at	XM_001714763 /// XM_001715187 /// XM_001715862 /// XM_001719382
2.35	2.35	0.01	9.56E-01	9.88E-01	FAM120A	family with sequence similarity 120A	chr9q22.31	1555947_at	NM_014612
7.48	7.51	0.02	9.56E-01	9.88E-01	STAB1	stabilin 1	chr3p21.1	204150_at	NM_015136
3.98	3.99	0.01	9.56E-01	9.88E-01	NENF	Neuron derived neurotrophic factor	chr1q32.3	214072_x_at	NM_013349
2.27	2.28	0.01	9.56E-01	9.88E-01	---	---	---	1557520_a_at	---
2.76	2.78	0.01	9.56E-01	9.88E-01	CDC20B	cell division cycle 20 homolog B (S. cerevisiae)	chr5q11.2	1564674_a_at	NM_152623
6.54	6.54	0.01	9.57E-01	9.88E-01	AK2	adenylate kinase 2	chr1p34	212175_s_at	NM_001625 /// NM_013411
3.21	3.26	0.05	9.57E-01	9.88E-01	DDX3Y /// LOC100130220	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked /// hypothetical protein LOC100130220	chrYq11	205001_s_at	NM_001122665 /// NM_004660 /// XM_001713697
3.95	3.97	0.02	9.57E-01	9.88E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	214855_s_at	NM_014990 /// NM_194301
3.77	3.78	0.01	9.57E-01	9.88E-01	ZNF555	zinc finger protein 555	chr19p13.3	1553286_at	NM_152791
3.31	3.32	0.01	9.57E-01	9.88E-01	ASRGL1	asparaginase like 1	chr11q12.3	222764_at	NM_001083926 /// NM_025080
2.44	2.45	0.01	9.57E-01	9.88E-01	KLRD1	killer cell lectin-like receptor subfamily D, member 1	chr12p13	207796_x_at	NM_001114396 /// NM_002262 /// NM_007334
3.87	3.88	0.01	9.57E-01	9.88E-01	---	---	---	235984_at	---
8.00	8.02	0.02	9.57E-01	9.88E-01	SRP72	signal recognition particle 72kDa	chr4q11	208801_at	NM_006947
2.74	2.75	0.01	9.57E-01	9.88E-01	---	---	---	235523_at	---
2.89	2.90	0.01	9.57E-01	9.88E-01	KIAA1462	KIAA1462	chr10p11.23	231842_at	NM_020848
2.33	2.34	0.01	9.57E-01	9.88E-01	CAND1	cullin-associated and neddylation-dissociated 1	chr12q14	239771_at	NM_018448
2.52	2.52	0.01	9.57E-01	9.88E-01	---	---	---	239644_at	---
2.35	2.35	0.01	9.57E-01	9.88E-01	---	---	---	244072_at	---
5.69	5.70	0.01	9.57E-01	9.88E-01	HPS3	Hermansky-Pudlak syndrome 3	chr3q24	227139_s_at	NM_032383
3.59	3.60	0.01	9.57E-01	9.88E-01	LZTS1	leucine zipper, putative tumor suppressor 1	chr8p22	219042_at	NM_021020

2.11	2.11	0.01	9.57E-01	9.88E-01	P4HA3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III	chr11q13.4	1560715_at	NM_182904																					
4.97	4.98	0.01	9.57E-01	9.89E-01	YIPF2	Yip1 domain family, member 2	chr19p13.2	219075_at	NM_024029																					
5.06	5.10	0.04	9.58E-01	9.89E-01	---	---	---	232776_at	---																					
6.68	6.70	0.02	9.58E-01	9.89E-01	RAB21	RAB21, member RAS oncogene family	chr12q21.1	203885_at	NM_014999																					
4.97	4.98	0.02	9.58E-01	9.89E-01	MRTO4	mRNA turnover 4 homolog (S. cerevisiae)	chr1p36.13	235783_at	NM_016183																					
3.83	3.84	0.02	9.58E-01	9.89E-01	TUBGCP5	tubulin, gamma complex associated protein 5	chr15q11.2	214876_s_at	NM_001102610 /// NM_052903																					
6.90	6.92	0.02	9.58E-01	9.89E-01	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	chr10q24	212593_s_at	NM_014456 /// NM_145341																					
8.13	8.14	0.01	9.58E-01	9.89E-01	NINJ1	ninjurin 1	chr9q22	203045_at	NM_004148																					
6.83	6.84	0.01	9.58E-01	9.89E-01	PGPEP1	pyroglutamyl-peptidase I	chr19p13.11	237202_at	NM_017712																					
2.44	2.45	0.01	9.58E-01	9.89E-01	DARC	Duffy blood group, chemokine receptor	chr1q21-q22	226953_at	NM_001122951 /// NM_002036																					
2.80	2.81	0.01	9.58E-01	9.89E-01	CCDC4	Coiled-coil domain containing 4	chr4p13	238101_at	NM_207406																					
5.15	5.16	0.01	9.58E-01	9.89E-01	SREBF1	sterol regulatory element binding transcription factor 1	chr17p11.2	1558875_at	NM_001005291 /// NM_004176																					
2.41	2.42	0.01	9.58E-01	9.89E-01	KLHDC6	kelch domain containing 6	chr3q21.3	244771_at	NM_207335																					
2.40	2.41	0.01	9.58E-01	9.89E-01	PLCG2	Phospholipase C, gamma 2 (phosphatidylinositol-specific)	chr16q24.1	1563263_at	NM_002661																					
2.13	2.14	0.01	9.58E-01	9.89E-01	AICDA	activation-induced cytidine deaminase	chr12p13	219841_at	NM_020661																					
2.47	2.48	0.01	9.58E-01	9.89E-01	TMEM171	transmembrane protein 171	chr5q13.2	1553559_at	NM_173490																					
2.92	2.94	0.02	9.58E-01	9.89E-01	ANKRD28	ankyrin repeat domain 28	chr3p24.3	1561079_at	NM_015199																					
4.51	4.52	0.01	9.59E-01	9.89E-01	---	---	---	217625_x_at	---																					
5.47	5.48	0.01	9.59E-01	9.89E-01	LOC440456 /// PLEKHM1	similar to pleckstrin homology domain containing, family M (with RUN domain) member 1; adapter protein 162 /// pleckstrin homology domain containing, family M (with RUN domain) member 1	chr17q21.31 /// chr17q24.1	212700_x_at	NM_014798 /// XM_001724417 /// XM_935188 /// XM_940040																					
3.37	3.38	0.01	9.59E-01	9.89E-01	MRPL23	Mitochondrial ribosomal protein L23	chr11p15.5-p15.4	1562392_at	NM_021134																					
3.37	3.38	0.01	9.59E-01	9.89E-01	---	---	---	1557319_at	---																					
3.53	3.53	0.01	9.59E-01	9.89E-01	KIAA1467	KIAA1467	chr12p13.1	1559302_at	NM_020853																					
2.16	2.17	0.01	9.59E-01	9.89E-01	---	---	---	237682_at	---																					
2.10	2.11	0.01	9.59E-01	9.89E-01	PTPRB	Protein tyrosine phosphatase, receptor type, B	chr12q15-q21	1560105_at	NM_001109754 /// NM_002837																					
2.32	2.33	0.01	9.59E-01	9.89E-01	---	---	---	1556654_at	---																					
2.58	2.59	0.01	9.59E-01	9.89E-01	DLG1	Discs, large homolog 1 (Drosophila)	chr3q29	229703_at	NM_001098424 /// NM_004087																					
2.99	3.00	0.01	9.59E-01	9.89E-01	---	---	---	241898_at	---																					
2.09	2.10	0.01	9.59E-01	9.89E-01	CTNNA3	catenin (cadherin-associated protein), alpha 3	chr10q22.2	1554235_at	NM_001127384 /// NM_013266																					
3.19	3.20	0.01	9.59E-01	9.89E-01	ZNF438	zinc finger protein 438	chr10p11.23	244752_at	NM_182755																					
2.56	2.56	0.01	9.59E-01	9.89E-01	ZNF224	zinc finger protein 224	chr19q13.2	216991_at	NM_013398																					
1.91	1.91	0.01	9.59E-01	9.89E-01	---	---	---	1565809_x_at	---																					
3.29	3.36	0.07	9.59E-01	9.89E-01	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	chrYq11	205000_at	NM_001122665 /// NM_004660																					
4.42	4.45	0.02	9.60E-01	9.89E-01	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	chr7q21.1	205999_x_at	NM_017460																					
3.20	3.22	0.02	9.59E-01	9.89E-01	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	chr18q22.1	238846_at	NM_003839																					
3.74	3.75	0.02	9.59E-01	9.89E-01	FBXW7	F-box and WD repeat domain containing 7	chr4q31.3	222729_at	NM_001013415 /// NM_018315 /// NM_033632																					
7.86	7.88	0.01	9.59E-01	9.89E-01	RAP2B	RAP2B, member of RAS oncogene family	chr3q25.2	227897_at	NM_002886																					
2.61	2.62	0.01	9.59E-01	9.89E-01	CASP2	caspase 2, apoptosis-related cysteine peptidase	chr7q34-q35	226036_x_at	NM_032982 /// NM_032983																					
3.21	3.22	0.01	9.59E-01	9.89E-01	UBXN10	UBX domain protein 10	chr1p36.12	238657_at	NM_152376																					
2.25	2.26	0.01	9.59E-01	9.89E-01	ZNF141	zinc finger protein 141	chr4p16.3	206931_at	NM_003441																					
2.53	2.54	0.01	9.59E-01	9.89E-01	---	---	---	1563157_at	---																					
2.28	2.29	0.01	9.59E-01	9.89E-01	MPL	myeloproliferative leukemia virus oncogene	chr1p34	207550_at	NM_005373																					
3.02	3.03	0.01	9.59E-01	9.89E-01	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	chr5q22.2	220119_at	NM_022140																					
2.72	2.72	0.01	9.59E-01	9.89E-01	ACR /// LOC645529	acrosin /// similar to OTTHUMP00000045489	chr22q13-qter|22q13.33 /// chr2q14.1	207427_at	NM_001097 /// XM_001716670 /// XM_001716815																					
3.03	3.04	0.01	9.59E-01	9.89E-01	---	---	---	239240_at	---																					
2.58	2.59	0.01	9.59E-01	9.89E-01	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	chr16q22.1	201130_s_at	NM_004360																					
1.95	1.96	0.01	9.59E-01	9.89E-01	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	chrXq26.2	1552766_at	NM_001077188 /// NM_147175																					

2.41	2.42	0.01	9.59E-01	9.89E-01	KLHL35	Kelch-like 35 (Drosophila)	chr11q13.4	215748_at	NM_001039548
2.69	2.69	0.01	9.59E-01	9.89E-01	---	---	---	233723_at	---
1.87	1.88	0.01	9.59E-01	9.89E-01	---	---	---	240133_x_at	---
2.11	2.12	0.01	9.59E-01	9.89E-01	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	chr2q11.1-q11.2	211470_s_at	NM_001056 /// NM_176825
2.05	2.06	0.01	9.59E-01	9.89E-01	SIAE	sialic acid acetylesterase	chr11q24	1554355_a_at	NM_170601
1.97	1.98	0.01	9.60E-01	9.89E-01	LOC732096	similar to hCG2040240	chr12q23.1	1570009_at	XM_001720784 /// XM_001725388 /// XR_016064
6.01	6.02	0.01	9.60E-01	9.89E-01	LOC100134082	hypothetical protein LOC100134082	---	239026_x_at	XM_001719649
6.78	6.79	0.02	9.60E-01	9.89E-01	MEF2A	myocyte enhancer factor 2A	chr15q26	212535_at	NM_001130926 /// NM_001130927 /// NM_001130928 /// NM_005587
2.94	2.95	0.01	9.60E-01	9.89E-01	C17orf28	chromosome 17 open reading frame 28	chr17q25.1	244593_at	NM_030630
2.54	2.54	0.01	9.60E-01	9.89E-01	LOC285147	hypothetical protein LOC285147	chr2p25.2	242852_at	---
4.03	4.05	0.02	9.60E-01	9.89E-01	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	chr1p13.2	222889_at	NM_022836
2.37	2.38	0.01	9.60E-01	9.89E-01	LOC100129828	hypothetical protein LOC100129828	chr1p36.33	236584_at	XM_001714962 /// XM_001724980
3.96	3.98	0.03	9.60E-01	9.89E-01	---	---	---	220612_at	---
4.95	4.98	0.03	9.60E-01	9.89E-01	---	---	---	240502_at	---
4.46	4.47	0.01	9.60E-01	9.89E-01	ADM2	adrenomedullin 2	chr22q13.33	220538_at	NM_024866
3.07	3.08	0.02	9.60E-01	9.89E-01	---	---	---	1569521_s_at	---
3.56	3.57	0.01	9.60E-01	9.89E-01	DCAKD	dephospho-CoA kinase domain containing	chr17q21.31	221225_at	NM_001128631 /// NM_024819
2.57	2.58	0.01	9.60E-01	9.89E-01	NEFL	neurofilament, light polypeptide 68kDa	chr8p21	221916_at	NM_006158
4.27	4.28	0.01	9.60E-01	9.89E-01	---	---	---	239842_x_at	---
2.21	2.22	0.01	9.60E-01	9.89E-01	C12orf48	chromosome 12 open reading frame 48	chr12q23.2	220060_s_at	NM_017915
2.36	2.37	0.01	9.60E-01	9.89E-01	---	---	---	233628_at	---
2.22	2.23	0.00	9.60E-01	9.89E-01	C10orf122	chromosome 10 open reading frame 122	chr10q26.13	244789_at	NM_001128202 /// XM_370582 /// XM_926761 /// XM_942118 /// XM_945727
4.29	4.30	0.02	9.61E-01	9.89E-01	TMCC3	transmembrane and coiled-coil domain family 3	chr12q22	235146_at	NM_020698
3.45	3.46	0.01	9.61E-01	9.89E-01	CCDC48	coiled-coil domain containing 48	chr3q21.3	220006_at	NM_024768
4.70	4.71	0.01	9.61E-01	9.89E-01	NHSL1	NHS-like 1	chr6q23.3	234922_s_at	XM_001723403 /// XM_496826 /// XM_941807
2.30	2.31	0.01	9.61E-01	9.89E-01	LETM2	leucine zipper-EF-hand containing transmembrane protein 2	chr8p12	1557415_s_at	NM_144652
2.53	2.53	0.01	9.61E-01	9.89E-01	FAM126A	family with sequence similarity 126, member A	chr7p15.3	244115_at	NM_032581
2.42	2.43	0.01	9.61E-01	9.89E-01	SLC30A4	solute carrier family 30 (zinc transporter), member 4	chr15q11.2-q21.3|15q21.1	238845_at	NM_013309
3.08	3.09	0.01	9.61E-01	9.89E-01	RLN3	relaxin 3	chr19p13.2	1553403_at	NM_080864
3.28	3.29	0.01	9.61E-01	9.89E-01	MYL4	myosin, light chain 4, alkali; atrial, embryonic	chr17q21-qter	210395_x_at	NM_001002841 /// NM_002476
2.12	2.13	0.01	9.61E-01	9.89E-01	LOC149643	hypothetical LOC149643	chr1q32.3	1559390_a_at	NM_001024601
2.03	2.04	0.01	9.61E-01	9.89E-01	---	---	---	244188_at	---
2.42	2.42	0.01	9.61E-01	9.89E-01	LOC643837	Hypothetical LOC643837	chr1p36.33	237011_at	NR_015368 /// XM_927114
4.98	4.99	0.01	9.61E-01	9.89E-01	SLC2A4RG	SLC2A4 regulator	chr20q13.33	222650_s_at	NM_020062
2.26	2.26	0.01	9.61E-01	9.89E-01	DBC1	deleted in bladder cancer 1	chr9q32-q33	1555457_at	NM_014618
3.95	3.96	0.02	9.61E-01	9.89E-01	LIG4	ligase IV, DNA, ATP-dependent	chr13q33-q34	206235_at	NM_001098268 /// NM_002312 /// NM_206937
6.37	6.39	0.02	9.61E-01	9.89E-01	HECA	headcase homolog (Drosophila)	chr6q23-q24	218603_at	NM_016217
5.20	5.21	0.01	9.61E-01	9.89E-01	ELF4	E74-like factor 4 (ets domain transcription factor)	chrXq26	203490_at	NM_001127197 /// NM_001421
1.95	1.96	0.01	9.61E-01	9.89E-01	C14orf85	chromosome 14 open reading frame 85	chr14q32.12	1563524_a_at	NR_002808
2.72	2.73	0.01	9.61E-01	9.89E-01	---	---	---	1558938_at	---
1.87	1.87	0.01	9.61E-01	9.89E-01	---	---	---	241853_at	---
2.14	2.15	0.01	9.61E-01	9.90E-01	---	---	---	1556334_s_at	---

2.71	2.72	0.01	9.61E-01	9.90E-01	---	---	---	242452_at	---
2.79	2.80	0.01	9.61E-01	9.90E-01	PAQR3	progestin and adipoQ receptor family member III	chr4q21.21	213372_at	NM_001040202
2.72	2.73	0.01	9.62E-01	9.90E-01	KRT31	keratin 31	chr17q12-q21	206677_at	NM_002277
3.06	3.07	0.01	9.62E-01	9.90E-01	CCDC108	coiled-coil domain containing 108	chr2q35	1556969_at	NM_152389 /// NM_194302
6.81	6.82	0.01	9.62E-01	9.90E-01	---	---	---	231818_x_at	---
3.63	3.64	0.01	9.62E-01	9.90E-01	---	---	---	237875_at	---
3.28	3.30	0.01	9.62E-01	9.90E-01	---	---	---	1562323_at	---
2.39	2.40	0.01	9.62E-01	9.90E-01	LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	chr19q13.4	1555643_s_at	NM_021250 /// NM_181879 /// NM_181985 /// NM_181986
2.72	2.74	0.02	9.62E-01	9.90E-01	PDE5A	phosphodiesterase 5A, cGMP-specific	chr4q25-q27	1553175_s_at	NM_001083 /// NM_033430 /// NM_033437
5.28	5.29	0.01	9.62E-01	9.90E-01	---	---	---	1569415_at	---
5.66	5.67	0.01	9.62E-01	9.90E-01	JMJD2B	jumonji domain containing 2B	chr19p13.3	215616_s_at	NM_015015
6.74	6.75	0.01	9.62E-01	9.90E-01	GLG1	golgi apparatus protein 1	chr16q22-q23	212045_at	NM_012201
3.47	3.49	0.01	9.62E-01	9.90E-01	SPATA18	spermatogenesis associated 18 homolog (rat)	chr4q12	229331_at	NM_145263
2.66	2.67	0.01	9.62E-01	9.90E-01	RSAD2	radical S-adenosyl methionine domain containing 2	chr2p25.2	242625_at	NM_080657
3.23	3.24	0.01	9.62E-01	9.90E-01	---	---	---	215036_at	---
2.22	2.23	0.01	9.62E-01	9.90E-01	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	chr2p23-p22	1564985_a_at	NM_001112800 /// NM_001112801 /// NM_001112802 /// NM_021097
3.18	3.19	0.01	9.62E-01	9.90E-01	---	---	---	217385_at	---
2.60	2.61	0.01	9.62E-01	9.90E-01	ZNF365	zinc finger protein 365	chr10q21.2	206448_at	NM_014951 /// NM_199450 /// NM_199451 /// NM_199452
2.09	2.09	0.01	9.62E-01	9.90E-01	IQGAP3	IQ motif containing GTPase activating protein 3	chr1q22-q23.1	1569062_s_at	NM_178229
3.71	3.72	0.01	9.62E-01	9.90E-01	TRIM7	tripartite motif-containing 7	chr5q35.3	223694_at	NM_033342 /// NM_203293 /// NM_203294 /// NM_203295 /// NM_203296 /// NM_203297
2.94	2.95	0.01	9.62E-01	9.90E-01	SAP30L	SAP30-like	chr5q33.2	239802_at	NM_001131062 /// NM_001131063 /// NM_024632 /// NR_024084
3.17	3.17	0.01	9.62E-01	9.90E-01	KIAA0515	KIAA0515	chr9q34.13	223793_at	NM_013318
2.24	2.25	0.01	9.62E-01	9.90E-01	LOC728543	hypothetical protein LOC728543	chr12q24.13	233718_at	XR_041705 /// XR_041706 /// XR_041707
2.52	2.53	0.01	9.63E-01	9.90E-01	LRRC58	leucine rich repeat containing 58	chr3q13.33	238506_at	NM_001099678
10.16	10.17	0.01	9.63E-01	9.90E-01	PGAM1	phosphoglycerate mutase 1 (brain)	chr10q25.3	200886_s_at	NM_002629
2.17	2.17	0.01	9.63E-01	9.90E-01	LOC728804	Hypothetical LOC728804	chr16p11.2	237556_at	XM_001133002 /// XM_001719468 /// XM_001732827
2.26	2.27	0.01	9.63E-01	9.90E-01	---	---	---	1562821_a_at	---
2.31	2.32	0.01	9.63E-01	9.90E-01	LIMS1	LIM and senescent cell antigen-like domains 1	chr2q12.3-q13	1566127_at	NM_004987
3.89	3.92	0.03	9.63E-01	9.90E-01	NARG2	NMDA receptor regulated 2	chr15q22.2	235189_at	NM_001018089 /// NM_024611
9.03	9.06	0.03	9.64E-01	9.90E-01	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	chr6p21.3	201137_s_at	NM_002121
6.05	6.07	0.02	9.63E-01	9.90E-01	SESN2	sestrin 2	chr1p35.3	223195_s_at	NM_031459

6.50	6.51	0.01	9.63E-01	9.90E-01	MITF	microphthalmia-associated transcription factor	chr3p14.2-p14.1	226066_at	NM_000248 /// NM_006722 /// NM_198158 /// NM_198159 /// NM_198177 /// NM_198178																				
6.31	6.33	0.01	9.64E-01	9.90E-01	BCL2L1	BCL2-like 1	chr20q11.21	212312_at	NM_001191 /// NM_138578																				
3.22	3.23	0.01	9.63E-01	9.90E-01	---	---	---	227431_at	---																				
5.70	5.71	0.01	9.63E-01	9.90E-01	SORBS2	sorbin and SH3 domain containing 2	chr4q35.1	237285_at	NM_003603 /// NM_021069																				
4.21	4.22	0.01	9.63E-01	9.90E-01	---	---	---	1559917_a_at	---																				
3.76	3.76	0.01	9.64E-01	9.90E-01	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	chr17p13	206405_x_at	NM_004505																				
3.10	3.11	0.01	9.64E-01	9.90E-01	---	---	---	1566484_at	---																				
2.29	2.30	0.01	9.63E-01	9.90E-01	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	chr5q11	234474_x_at	NM_002184 /// NM_175767																				
2.11	2.12	0.01	9.63E-01	9.90E-01	SLC5A7	solute carrier family 5 (choline transporter), member 7	chr2q12	222967_at	NM_021815																				
2.28	2.29	0.01	9.63E-01	9.90E-01	LOC93432	maltase-glucoamylase-like pseudogene	chr7q34	216666_at	NR_003715																				
3.97	3.98	0.01	9.63E-01	9.90E-01	PDCD6	Aryl-hydrocarbon receptor repressor	chr5p15.33	222381_at	NM_013232 /// XM_001714855 /// XM_001720072 /// XM_001723249																				
2.52	2.52	0.01	9.63E-01	9.90E-01	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	chr22q11.21	223999_at	NM_014337 /// NM_148175 /// NM_148176																				
2.17	2.18	0.01	9.64E-01	9.90E-01	FASLG	Fas ligand (TNF superfamily, member 6)	chr1q23	211333_s_at	NM_000639																				
2.14	2.15	0.01	9.64E-01	9.90E-01	psiTPTE22	TPTE pseudogene	chr22q11.2	1569348_at	NR_001591 /// XR_042159																				
2.46	2.46	0.01	9.63E-01	9.90E-01	DLEU7	Deleted in lymphocytic leukemia, 7	chr13q14.3	233277_at	NM_198989																				
2.90	2.90	0.01	9.63E-01	9.90E-01	OSGIN2	Oxidative stress induced growth inhibitor family member 2	chr8q21	41553_at	NM_001126111 /// NM_004337																				
2.21	2.21	0.01	9.63E-01	9.90E-01	RNF152	ring finger protein 152	chr18q21.33	1553721_at	NM_173557																				
1.98	1.98	0.00	9.63E-01	9.90E-01	RBM34	RNA binding motif protein 34	chr1q42.3	214942_at	NM_015014																				
2.11	2.12	0.01	9.64E-01	9.90E-01	ZPBP2	zona pellucida binding protein 2	chr17q12	231442_at	NM_198844 /// NM_199321																				
2.34	2.34	0.01	9.64E-01	9.90E-01	---	---	---	1559304_at	---																				
2.08	2.08	0.01	9.64E-01	9.90E-01	C14orf81	chromosome 14 open reading frame 81	chr14q32.33	1564499_at	XR_040163																				
5.89	5.90	0.01	9.64E-01	9.90E-01	XPO4	exportin 4	chr13q11	222649_at	NM_022459																				
5.38	5.41	0.03	9.64E-01	9.90E-01	APOLD1	apolipoprotein L domain containing 1	chr12p13.1	221031_s_at	NM_001130415 /// NM_030817																				
3.02	3.02	0.01	9.64E-01	9.90E-01	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	chr11q21	209892_at	NM_002033																				
2.69	2.70	0.01	9.64E-01	9.90E-01	---	---	---	1563065_at	---																				
3.43	3.44	0.01	9.64E-01	9.90E-01	SLC26A10	solute carrier family 26, member 10	chr12q13	214951_at	NM_133489																				
3.82	3.82	0.01	9.64E-01	9.90E-01	SPG11	spastic paraplegia 11 (autosomal recessive)	chr15q14	232403_at	NM_025137																				
6.98	6.99	0.01	9.64E-01	9.90E-01	MAPK6	mitogen-activated protein kinase 6	chr15q21	207121_s_at	NM_002748																				
2.13	2.13	0.01	9.64E-01	9.90E-01	POLI	polymerase (DNA directed) iota	chr18q21.1	238992_at	NM_007195																				
2.73	2.74	0.01	9.64E-01	9.90E-01	PATE	expressed in prostate and testis	chr11q24.2	243468_at	NM_138294																				
9.53	9.53	0.01	9.64E-01	9.90E-01	SQSTM1	sequestosome 1	chr5q35	201471_s_at	NM_003900																				
6.64	6.65	0.01	9.64E-01	9.90E-01	KLHL36	kelch-like 36 (Drosophila)	chr16q24.1	238523_at	NM_024731																				
1.98	1.99	0.00	9.64E-01	9.90E-01	---	---	---	1569122_at	---																				
2.52	2.53	0.01	9.64E-01	9.90E-01	KCNE1	potassium voltage-gated channel, Isk-related family, member 1	chr21q22.1-q22.2|21q22.12	208514_at	NM_000219 /// NM_001127668 /// NM_001127669 /// NM_001127670																				
2.19	2.19	0.01	9.64E-01	9.90E-01	HOPX	HOP homeobox	chr4q11-q12	1566139_at	NM_032495 /// NM_139211 /// NM_139212																				
5.83	5.85	0.02	9.65E-01	9.90E-01	---	---	---	227117_at	---																				
5.81	5.83	0.02	9.65E-01	9.90E-01	TSN	translin	chr2q21.1	201504_s_at	NM_004622																				
6.02	6.03	0.01	9.65E-01	9.90E-01	NCBP2	nuclear cap binding protein subunit 2, 20kDa	chr3q29	201521_s_at	NM_001042540 /// NM_007362																				
4.05	4.06	0.01	9.65E-01	9.90E-01	CEP70	centrosomal protein 70kDa	chr3q22-q23	219036_at	NM_024491																				
3.12	3.13	0.01	9.65E-01	9.90E-01	---	---	---	241388_at	---																				
2.56	2.57	0.01	9.64E-01	9.90E-01	DLX4	distal-less homeobox 4	chr17q21.33	208216_at	NM_001934 /// NM_138281																				
2.11	2.11	0.01	9.65E-01	9.90E-01	---	---	---	1559274_at	---																				
11.27	11.28	0.01	9.65E-01	9.90E-01	OAZ1	ornithine decarboxylase antizyme 1	chr19p13.3	200077_s_at	NM_004152																				

2.54	2.55	0.01	9.65E-01	9.90E-01	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	chr7p13	210965_x_at	NM_003718 /// NM_031267
2.44	2.44	0.01	9.65E-01	9.90E-01	---	---	---	1561612_at	---
2.06	2.06	0.01	9.65E-01	9.90E-01	---	---	---	1555498_at	---
2.29	2.30	0.01	9.65E-01	9.90E-01	FAM48A	Family with sequence similarity 48, member A	chr13q13.3	216717_at	NM_001014286 /// NM_017569
2.03	2.04	0.01	9.65E-01	9.90E-01	LOC645513	Hypothetical LOC645513	chr4q26-q27	1561759_at	XM_001714125 /// XM_001714854 /// XM_001717939
2.01	2.01	0.01	9.65E-01	9.90E-01	---	---	---	1559543_at	---
5.60	5.63	0.03	9.65E-01	9.90E-01	FMO1	flavin containing monooxygenase 1	chr1q23-q25	205666_at	NM_002021
8.32	8.33	0.01	9.65E-01	9.90E-01	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	chr1q32.1	215171_s_at	NM_006335
2.56	2.57	0.01	9.65E-01	9.90E-01	BLZF1	basic leucine zipper nuclear factor 1	chr1q24	203840_at	NM_003666
2.19	2.19	0.01	9.65E-01	9.90E-01	FLJ14213	protor-2	chr11p13-p12	219383_at	NM_024841
2.64	2.65	0.01	9.65E-01	9.90E-01	LOR	loricrin	chr1q21	207720_at	NM_000427
2.05	2.06	0.01	9.65E-01	9.90E-01	---	---	---	244767_at	---
2.09	2.10	0.01	9.65E-01	9.90E-01	CCDC41	coiled-coil domain containing 41	chr12q22	239282_at	NM_001042399 /// NM_016122
5.45	5.46	0.01	9.65E-01	9.90E-01	---	---	---	237643_at	---
3.50	3.50	0.01	9.65E-01	9.90E-01	---	---	---	221717_at	---
8.65	8.66	0.01	9.65E-01	9.90E-01	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr19p13.11	202736_s_at	NM_012321
3.30	3.31	0.01	9.65E-01	9.90E-01	LOC100128500	hypothetical protein LOC100128500	chr3p26.2	243837_x_at	XM_001719603 /// XM_001720777 /// XM_001720893
6.19	6.20	0.01	9.65E-01	9.90E-01	AKT1S1	AKT1 substrate 1 (proline-rich)	chr19q13.33	224982_at	NM_001098632 /// NM_001098633 /// NM_032375
2.48	2.49	0.01	9.65E-01	9.90E-01	---	---	---	238181_at	---
2.83	2.84	0.01	9.65E-01	9.90E-01	---	---	---	1567105_at	---
2.56	2.56	0.01	9.65E-01	9.90E-01	---	---	---	216355_at	---
2.45	2.46	0.01	9.65E-01	9.90E-01	---	---	---	243379_at	---
2.64	2.65	0.01	9.65E-01	9.90E-01	---	---	---	239581_at	---
4.00	4.01	0.01	9.65E-01	9.90E-01	CSNK1G3	casein kinase 1, gamma 3	chr5q23	227767_at	NM_001031812 /// NM_001044722 /// NM_001044723 /// NM_004384
7.09	7.10	0.02	9.66E-01	9.90E-01	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	chr1p36.23	201337_s_at	NM_004781
3.20	3.21	0.01	9.66E-01	9.90E-01	---	---	---	230570_at	---
6.74	6.75	0.01	9.66E-01	9.90E-01	CTSD	cathepsin D	chr11p15.5	227863_at	NM_001909
6.49	6.50	0.01	9.66E-01	9.90E-01	PAIP1	poly(A) binding protein interacting protein 1	chr5p12	209063_x_at	NM_006451 /// NM_182789 /// NM_183323
2.95	2.96	0.01	9.66E-01	9.90E-01	USP31	ubiquitin specific peptidase 31	chr16p12.1	227256_at	NM_020718
2.91	2.92	0.01	9.66E-01	9.90E-01	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	chr14q32.3-qter|14q32	244768_at	NM_001376
2.58	2.59	0.01	9.66E-01	9.90E-01	---	---	---	214854_at	---
2.42	2.42	0.01	9.66E-01	9.90E-01	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	chr1q42.3	1553691_at	NM_152490
3.82	3.83	0.01	9.65E-01	9.90E-01	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	chr6q27	1557970_s_at	NM_001006932 /// NM_021135
2.91	2.92	0.01	9.65E-01	9.90E-01	BMP2K	BMP2 inducible kinase	chr4q21.21	219546_at	NM_017593 /// NM_198892
3.09	3.09	0.01	9.66E-01	9.90E-01	---	---	---	241006_at	---
2.28	2.29	0.01	9.66E-01	9.90E-01	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	chrXp21.2	1552927_at	NM_152787
2.16	2.17	0.01	9.66E-01	9.90E-01	---	---	---	1562811_at	---
2.96	2.97	0.00	9.66E-01	9.90E-01	TRIM36	tripartite motif-containing 36	chr5q22.3	1565812_at	NM_001017397 /// NM_001017398 /// NM_018700

2.79	2.80	0.01	9.66E-01	9.91E-01	FAM164B /// LTV1	family with sequence similarity 164, member B /// LTV1 homolog (S. cerevisiae)	chr6q24.2	239212_at	NM_001013623 /// NM_032860 /// XM_001723038 /// XM_928657 /// XM_941265
2.85	2.86	0.01	9.66E-01	9.91E-01	---	---	---	234088_at	---
2.61	2.62	0.01	9.66E-01	9.91E-01	---	---	---	241349_at	---
2.02	2.03	0.01	9.66E-01	9.91E-01	PTGER3	prostaglandin E receptor 3 (subtype EP3)	chr1p31.2	210375_at	NM_000957 /// NM_001126044 /// NM_198712 /// NM_198713 /// NM_198714 /// NM_198715 /// NM_198716 /// NM_198717 /// NM_198718 /// NM_198719
5.71	5.72	0.01	9.66E-01	9.91E-01	ATN1	atrophin 1	chr12p13.31	40489_at	NM_001007026 /// NM_001940
1.99	1.99	0.00	9.66E-01	9.91E-01	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	chr1p13.2	217392_at	NM_006135
3.30	3.31	0.01	9.66E-01	9.91E-01	CIDEA	cell death-inducing DFFA-like effector a	chr18p11.21|18	221295_at	NM_001279 /// NM_198289
5.38	5.40	0.02	9.66E-01	9.91E-01	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	chr5q12.3	213483_at	NM_015342
3.45	3.46	0.01	9.67E-01	9.91E-01	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	chr22q13.1	207419_s_at	NM_002872
6.64	6.66	0.02	9.67E-01	9.91E-01	PHF3	PHD finger protein 3	chr6q12	217952_x_at	NM_015153
2.02	2.02	0.01	9.67E-01	9.91E-01	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	chr1q31	232238_at	NM_018136
5.63	5.64	0.01	9.67E-01	9.91E-01	RARA	retinoic acid receptor, alpha	chr17q21	203749_s_at	NM_000964 /// NM_001024809
3.84	3.86	0.01	9.67E-01	9.91E-01	MKNK1	MAP kinase interacting serine/threonine kinase 1	chr1p33	243256_at	NM_003684 /// NM_198973
2.83	2.83	0.01	9.67E-01	9.91E-01	MIST	mast cell immunoreceptor signal transducer	chr4p16.1	1570239_a_at	NM_052964
2.19	2.20	0.01	9.67E-01	9.91E-01	SFRS11	Splicing factor, arginine/serine-rich 11	chr1p31	237746_at	NM_004768
3.64	3.65	0.01	9.67E-01	9.91E-01	LCN6	lipocalin 6	chr9q34.3	1559864_at	NM_198946
3.11	3.12	0.01	9.67E-01	9.91E-01	ZBED5	zinc finger, BED-type containing 5	chr11p15.3	242552_x_at	XR_041298 /// XR_041299 /// XR_041300
12.41	12.42	0.00	9.67E-01	9.91E-01	RPLP1	ribosomal protein, large, P1	chr15q22	200763_s_at	NM_001003 /// NM_213725
5.91	5.92	0.01	9.67E-01	9.91E-01	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	chr1p36.13	216381_x_at	NM_012067
5.52	5.53	0.01	9.67E-01	9.91E-01	GTF2F2	general transcription factor IIF, polypeptide 2, 30kDa	chr13q14	209595_at	NM_004128
4.29	4.30	0.01	9.68E-01	9.91E-01	PRLR	prolactin receptor	chr5p14-p13	210476_s_at	NM_000949
2.44	2.45	0.01	9.67E-01	9.91E-01	RIPPLY1	ripply1 homolog (zebrafish)	chrXq22.3	1560291_at	NM_138382
5.23	5.24	0.01	9.67E-01	9.91E-01	CTBP2	C-terminal binding protein 2	chr10q26.13	215377_at	NM_001083914 /// NM_001329 /// NM_022802
2.72	2.73	0.01	9.67E-01	9.91E-01	CD6	CD6 molecule	chr11q13	208602_x_at	NM_006725
2.26	2.27	0.01	9.68E-01	9.91E-01	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	chr9q22.33	1554923_at	NM_173551
5.63	5.64	0.01	9.67E-01	9.91E-01	ADD1	adducin 1 (alpha)	chr4p16.3	214726_x_at	NM_001119 /// NM_014189 /// NM_014190 /// NM_176801
3.30	3.31	0.01	9.67E-01	9.91E-01	BCL3	B-cell CLL/lymphoma 3	chr19q13.1-q13.2	204907_s_at	NM_005178
2.85	2.85	0.01	9.67E-01	9.91E-01	TNFRSF18	tumor necrosis factor receptor superfamily, member 18	chr1p36.3	224553_s_at	NM_004195 /// NM_148901 /// NM_148902
2.09	2.09	0.01	9.67E-01	9.91E-01	FLJ31958	hypothetical protein FLJ31958	chr10q11.23	232803_at	---
2.52	2.52	0.01	9.67E-01	9.91E-01	C11orf54	Chromosome 11 open reading frame 54	chr11q21	1559623_at	NM_014039
2.25	2.25	0.00	9.67E-01	9.91E-01	---	---	---	234593_at	---
3.74	3.75	0.01	9.68E-01	9.91E-01	LRRC6	leucine rich repeat containing 6	chr8q24.22	206483_at	NM_012472
2.37	2.38	0.01	9.68E-01	9.91E-01	---	---	---	241251_at	---
2.50	2.51	0.01	9.68E-01	9.91E-01	---	---	---	237505_at	---
2.15	2.15	0.01	9.68E-01	9.91E-01	FAM62C	family with sequence similarity 62 (C2 domain containing), member C	chr3q22.3	239770_at	NM_031913
3.70	3.70	0.00	9.68E-01	9.91E-01	PWP2	PWP2 periodic tryptophan protein homolog (yeast)	chr21q22.3	1565604_at	NM_005049

2.10	2.11	0.01	9.68E-01	9.91E-01	PIGX	phosphatidylinositol glycan anchor biosynthesis, class X	chr3q29	227403_at	NM_017861
2.01	2.02	0.00	9.68E-01	9.91E-01	---	---	---	241207_at	---
3.36	3.37	0.01	9.68E-01	9.91E-01	---	---	---	238854_at	---
3.90	3.91	0.01	9.68E-01	9.91E-01	EFR3B	EFR3 homolog B (S. cerevisiae)	chr2p23.3	227283_at	NM_014971 /// XM_001717587 /// XM_039733 /// XM_940464
8.93	8.94	0.01	9.68E-01	9.91E-01	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	chr8q23.1	200639_s_at	NM_003406 /// NM_145690
5.07	5.08	0.01	9.68E-01	9.91E-01	TBCE	tubulin folding cofactor E	chr1q42.3	203714_s_at	NM_001079515 /// NM_003193
2.61	2.61	0.01	9.68E-01	9.91E-01	RREB1	ras responsive element binding protein 1	chr6p25	216648_s_at	NM_001003698 /// NM_001003699 /// NM_002955
2.45	2.45	0.01	9.69E-01	9.91E-01	---	---	---	234599_at	---
3.50	3.52	0.02	9.69E-01	9.91E-01	MAN2A1	mannosidase, alpha, class 2A, member 1	chr5q21-q22	235103_at	NM_002372
6.21	6.22	0.01	9.69E-01	9.91E-01	NMT1	N-myristoyltransferase 1	chr17q21.31	201158_at	NM_021079
2.56	2.57	0.01	9.69E-01	9.91E-01	---	---	---	240628_at	---
2.58	2.59	0.01	9.69E-01	9.91E-01	---	---	---	240124_at	---
1.97	1.98	0.00	9.69E-01	9.91E-01	---	---	---	233845_at	---
2.23	2.23	0.00	9.69E-01	9.91E-01	LOC285401	hypothetical protein LOC285401	chr3p14.2	1557369_a_at	---
2.01	2.01	0.00	9.69E-01	9.91E-01	CLEC2D	C-type lectin domain family 2, member D	chr12p13	220132_s_at	NM_001004419 /// NM_013269
3.30	3.31	0.01	9.69E-01	9.91E-01	PPP1R14D	protein phosphatase 1, regulatory (inhibitor) subunit 14D	chr15q15.1	220082_at	NM_001130143 /// NM_017726
6.32	6.33	0.01	9.69E-01	9.91E-01	SLC38A10	solute carrier family 38, member 10	chr17q25.3	212890_at	NM_001037984 /// NM_138570
3.50	3.51	0.01	9.69E-01	9.91E-01	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	chr22q13.31-q13.33	224188_s_at	NM_022098
3.67	3.67	0.01	9.69E-01	9.91E-01	FAM105B	family with sequence similarity 105, member B	chr5p15.2	228382_at	NM_138348
1.94	1.95	0.00	9.69E-01	9.91E-01	C2orf15	chromosome 2 open reading frame 15	chr2q11.2	1552740_at	NM_144706
2.02	2.03	0.00	9.69E-01	9.91E-01	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	chr7q22.3	206370_at	NM_002649
2.02	2.02	0.00	9.69E-01	9.91E-01	C13orf38	chromosome 13 open reading frame 38	chr13q13.3	233297_s_at	XM_001130109 /// XM_001133689 /// XM_001719885
6.64	6.67	0.03	9.69E-01	9.91E-01	NR1H4	nuclear receptor subfamily 1, group H, member 4	chr12q23.1	1554375_a_at	NM_005123
2.93	2.94	0.01	9.69E-01	9.91E-01	C9orf167	chromosome 9 open reading frame 167	chr9q34.3	233589_x_at	NM_017723
3.39	3.39	0.01	9.69E-01	9.91E-01	ANKRD60	ankyrin repeat domain 60	chr20q13.32	234511_at	XM_001134442 /// XM_001134462 /// XM_001717339
6.38	6.39	0.02	9.69E-01	9.91E-01	AMIGO1	adhesion molecule with Ig-like domain 1	chr1p13.3	226718_at	NM_020703
3.70	3.71	0.01	9.69E-01	9.91E-01	RTN4	reticulon 4	chr2p16.3	1556049_at	NM_007008 /// NM_020532 /// NM_153828 /// NM_207520 /// NM_207521
5.44	5.46	0.01	9.69E-01	9.91E-01	ABI1	abl-interactor 1	chr10p11.2	209028_s_at	NM_001012750 /// NM_001012751 /// NM_001012752 /// NM_005470
4.94	4.95	0.01	9.69E-01	9.91E-01	NFYA	nuclear transcription factor Y, alpha	chr6p21.3	204108_at	NM_002505 /// NM_021705 /// XM_001716589 /// XM_001717592 /// XM_001718396
4.39	4.40	0.01	9.69E-01	9.91E-01	CD7	CD7 molecule	chr17q25.2-q25.3	214049_x_at	NM_006137
6.82	6.83	0.01	9.69E-01	9.91E-01	SETD3	SET domain containing 3	chr14q32.2	212465_at	NM_032233 /// NM_199123
7.23	7.24	0.01	9.69E-01	9.91E-01	---	---	---	222207_x_at	---

7.94	7.95	0.01	9.69E-01	9.91E-01	NOMO1 /// NOMO2 /// NOMO3	NODAL modulator 1 /// NODAL modulator 2 /// NODAL modulator 3	chr16p12.3 /// chr16p13 /// chr16p13.11	221853_s_at	NM_001004060 /// NM_001004067 /// NM_014287 /// NM_173614 /// XM_001716489 /// XM_001716493
3.25	3.26	0.01	9.70E-01	9.91E-01	ERICH1	glutamate-rich 1	chr8p23.3	227016_at	NM_207332
2.53	2.54	0.01	9.69E-01	9.91E-01	---	---	---	244524_at	---
4.72	4.72	0.01	9.70E-01	9.91E-01	MGC50722	hypothetical MGC50722	---	1554683_a_at	NM_203348
2.26	2.26	0.00	9.69E-01	9.91E-01	LASS5	LAG1 homolog, ceramide synthase 5	chr12q13.13	239491_at	NM_147190
2.09	2.09	0.00	9.69E-01	9.91E-01	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	chr9p22.3	206543_at	NM_003070 /// NM_139045
4.66	4.68	0.03	9.70E-01	9.91E-01	CAV1	caveolin 1, caveolae protein, 22kDa	chr7q31.1	212097_at	NM_001753
1.97	1.98	0.00	9.70E-01	9.91E-01	---	---	---	216529_at	---
2.58	2.59	0.01	9.70E-01	9.91E-01	MEX3C	Mex-3 homolog C (C. elegans)	chr18q21.2	227275_at	NM_016626
5.14	5.15	0.02	9.70E-01	9.91E-01	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	chr16q23	225754_at	NM_001030007 /// NM_001128
5.51	5.52	0.01	9.70E-01	9.91E-01	---	---	---	238612_at	---
2.42	2.43	0.00	9.70E-01	9.91E-01	---	---	---	217172_at	---
2.40	2.41	0.01	9.70E-01	9.92E-01	WISP3	WNT1 inducible signaling pathway protein 3	chr6q21	226182_s_at	NM_003880 /// NM_130396 /// NM_198239
4.06	4.07	0.01	9.70E-01	9.92E-01	ADAMTSL3	ADAMTS-like 3	chr15q25.2	213974_at	NM_207517
3.73	3.74	0.01	9.70E-01	9.92E-01	PDXDC2	Pyridoxal-dependent decarboxylase domain containing 2	chr16q22.1	1565845_at	NR_003610
3.15	3.15	0.01	9.70E-01	9.92E-01	IRAK2	interleukin-1 receptor-associated kinase 2	chr3p25.3	1553740_a_at	NM_001570
2.75	2.76	0.01	9.70E-01	9.92E-01	HIVEP3	Human immunodeficiency virus type I enhancer binding protein 3	chr1p34	244764_at	NM_001127714 /// NM_024503
2.28	2.29	0.00	9.70E-01	9.92E-01	---	---	---	229147_at	---
5.78	5.79	0.02	9.70E-01	9.92E-01	UBA5	ubiquitin-like modifier activating enzyme 5	chr3q22.1	222579_at	NM_024818 /// NM_198329
6.99	7.00	0.01	9.70E-01	9.92E-01	COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	chr10q24	219547_at	NM_004376 /// NM_078470
2.34	2.35	0.01	9.70E-01	9.92E-01	TET2	tet oncogene family member 2	chr4q24	1569385_s_at	NM_001127208 /// NM_017628
2.61	2.62	0.00	9.71E-01	9.92E-01	GPX5	glutathione peroxidase 5 (epididymal androgen-related protein)	chr6p22.1	208028_s_at	NM_001509 /// NM_003996
2.45	2.46	0.01	9.71E-01	9.92E-01	OR2J2	olfactory receptor, family 2, subfamily J, member 2	chr6p22.2-p21.31	216818_s_at	NM_030905
2.25	2.26	0.01	9.71E-01	9.92E-01	SENP7	SUMO1/sentrin specific peptidase 7	chr3q12	220735_s_at	NM_001077203 /// NM_020654
5.52	5.52	0.01	9.71E-01	9.92E-01	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	chr22q12|7p14.3-p14.1	34846_at	NM_001220 /// NM_172078 /// NM_172079 /// NM_172080 /// NM_172081 /// NM_172082 /// NM_172083 /// NM_172084
3.19	3.20	0.01	9.71E-01	9.92E-01	LOC148145	hypothetical protein LOC148145	chr19q12	1557550_at	---
2.72	2.72	0.01	9.71E-01	9.92E-01	C9orf70	chromosome 9 open reading frame 70	chr9p24.2	1553756_at	XM_001721481 /// XM_001723928 /// XM_001724353
2.03	2.03	0.00	9.71E-01	9.92E-01	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	chr18q21.31	208065_at	NM_015879
2.02	2.02	0.00	9.71E-01	9.92E-01	SCGB1D1	secretoglobin, family 1D, member 1	chr11q13	207910_at	NM_006552
5.08	5.09	0.01	9.71E-01	9.92E-01	HDAC4	histone deacetylase 4	chr2q37.3	228813_at	NM_006037
6.82	6.84	0.01	9.71E-01	9.92E-01	RNF135	ring finger protein 135	chr17q11.2	223592_s_at	NM_032322 /// NM_197939
4.82	4.83	0.01	9.71E-01	9.92E-01	TRPM2	transient receptor potential cation channel, subfamily M, member 2	chr21q22.3	205708_s_at	NM_003307
2.60	2.61	0.01	9.72E-01	9.92E-01	---	---	---	240524_x_at	---
2.16	2.16	0.00	9.72E-01	9.92E-01	SFRS15	splicing factor, arginine/serine-rich 15	chr21q22.1	233753_at	NM_020706
2.09	2.09	0.00	9.72E-01	9.92E-01	---	---	---	1556810_a_at	---
2.85	2.85	0.00	9.72E-01	9.92E-01	TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	chr6p21.31	1558135_at	NM_005643
1.80	1.80	0.00	9.72E-01	9.92E-01	---	---	---	233683_at	---

9.21	9.22	0.01	9.72E-01	9.92E-01	CDC42	Cell division cycle 42 (GTP binding protein, 25kDa)	chr1p36.1	226400_at	NM_001039802 /// NM_001791 /// NM_044472
2.10	2.10	0.00	9.72E-01	9.92E-01	NKAIN2	Na+/K+ transporting ATPase interacting 2	chr6q21	242002_at	NM_001040214
1.98	1.98	0.01	9.72E-01	9.92E-01	---	---	---	241052_at	---
2.89	2.89	0.00	9.72E-01	9.92E-01	POU3F4	POU class 3 homeobox 4	chrXq21.1	207694_at	NM_000307
3.76	3.77	0.01	9.72E-01	9.92E-01	CARS	cysteinyl-tRNA synthetase	chr11p15.5	240983_s_at	NM_001014437 /// NM_001014438 /// NM_001751 /// NM_139273
3.38	3.39	0.01	9.72E-01	9.92E-01	---	---	---	238859_at	---
1.94	1.94	0.00	9.72E-01	9.92E-01	CRISP1	cysteine-rich secretory protein 1	chr6p21.3	216314_at	NM_001131 /// NM_170609
6.09	6.11	0.02	9.72E-01	9.92E-01	RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1	chr3q12.3	223267_at	NM_017819
2.99	2.99	0.01	9.72E-01	9.92E-01	C3orf70	chromosome 3 open reading frame 70	chr3q27.2	242447_at	NM_001025266
3.73	3.73	0.00	9.72E-01	9.93E-01	---	---	---	214871_x_at	---
2.42	2.43	0.00	9.72E-01	9.93E-01	---	---	---	217449_at	---
6.64	6.65	0.01	9.73E-01	9.93E-01	DLC1	deleted in liver cancer 1	chr8p22	224822_at	NM_006094 /// NM_024767 /// NM_182643
2.82	2.83	0.02	9.73E-01	9.93E-01	RASSF9	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	chr12q21.31	210335_at	NM_005447
2.28	2.29	0.00	9.73E-01	9.93E-01	RRAGC	Ras-related GTP binding C	chr1p34	242531_at	NM_022157
6.61	6.62	0.01	9.73E-01	9.93E-01	PLDN	pallidin homolog (mouse)	chr15q21.1	224892_at	NM_012388
1.88	1.88	0.00	9.73E-01	9.93E-01	---	---	---	207461_at	---
2.04	2.04	0.00	9.73E-01	9.93E-01	WDR69	WD repeat domain 69	chr2q36.3	242162_at	NM_178821
2.22	2.23	0.01	9.73E-01	9.93E-01	STRN	striatin, calmodulin binding protein	chr2p22-p21	1569813_at	NM_003162
3.00	3.00	0.01	9.73E-01	9.93E-01	---	---	---	222167_at	---
6.56	6.57	0.01	9.73E-01	9.93E-01	CIRH1A	cirrhosis, autosomal recessive 1A (cirhin)	chr16q22.1	230656_s_at	NM_032830
2.57	2.58	0.00	9.73E-01	9.93E-01	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	chr2q24.1	211613_s_at	NM_000408 /// NM_001083112
6.93	6.94	0.01	9.73E-01	9.93E-01	MOCS2	molybdenum cofactor synthesis 2	chr5q11	218212_s_at	NM_004531 /// NM_176806
2.01	2.01	0.00	9.73E-01	9.93E-01	---	---	---	237723_at	---
2.23	2.24	0.00	9.73E-01	9.93E-01	---	---	---	1561556_at	---
2.37	2.38	0.00	9.73E-01	9.93E-01	---	---	---	241773_at	---
2.18	2.18	0.00	9.74E-01	9.93E-01	CCL7	chemokine (C-C motif) ligand 7	chr17q11.2-q12	208075_s_at	NM_006273
2.45	2.46	0.00	9.74E-01	9.93E-01	CLDN18	claudin 18	chr3q22.3	221132_at	NM_001002026 /// NM_016369
1.95	1.96	0.00	9.74E-01	9.93E-01	---	---	---	242309_at	---
3.54	3.55	0.01	9.74E-01	9.93E-01	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	chr3p14.3	210108_at	NM_000720 /// NM_001128839 /// NM_001128840
4.91	4.91	0.01	9.74E-01	9.93E-01	WEE1	WEE1 homolog (S. pombe)	chr11p15.3-p15.1	212533_at	NM_003390
2.51	2.52	0.01	9.74E-01	9.93E-01	---	---	---	239668_at	---
4.11	4.12	0.01	9.74E-01	9.93E-01	BCOR	BCL6 co-repressor	chrXp21.2-p11.4	223916_s_at	NM_001123383 /// NM_001123384 /// NM_001123385 /// NM_001130139 /// NM_017745 /// NM_020926
2.59	2.60	0.01	9.74E-01	9.93E-01	PCDHGB7	protocadherin gamma subfamily B, 7	chr5q31	1552662_a_at	NM_018927 /// NM_032101
2.43	2.44	0.00	9.74E-01	9.93E-01	---	---	---	244040_at	---
2.10	2.11	0.00	9.74E-01	9.93E-01	---	---	---	1559240_at	---
3.77	3.78	0.01	9.74E-01	9.93E-01	ATP11B	ATPase, class VI, type 11B	chr3q27	1564064_a_at	NM_014616
7.25	7.26	0.00	9.74E-01	9.93E-01	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	chr17q11.2	208777_s_at	NM_002815
2.65	2.65	0.00	9.74E-01	9.93E-01	DPP6	dipeptidyl-peptidase 6	chr7q36.2	207789_s_at	NM_001039350 /// NM_001936 /// NM_130797
2.25	2.26	0.00	9.74E-01	9.93E-01	FAM45A	Family with sequence similarity 45, member A	chr10q25	1562919_at	NM_207009

2.29	2.29	0.01	9.74E-01	9.93E-01	---	---	---	236996_at	---
2.51	2.51	0.00	9.74E-01	9.93E-01	---	---	---	1565826_at	---
2.48	2.49	0.00	9.74E-01	9.93E-01	---	---	---	1557825_at	---
6.70	6.72	0.02	9.74E-01	9.93E-01	KIAA1702	KIAA1702 protein	chr6p11	1556060_a_at	XM_001722675 /// XM_001724453 /// XM_001726133
4.28	4.30	0.01	9.75E-01	9.93E-01	SPAG9	sperm associated antigen 9	chr17q21.33	206748_s_at	NM_001130528 /// NM_003971
4.48	4.48	0.01	9.75E-01	9.93E-01	---	---	---	232002_at	---
4.46	4.46	0.01	9.75E-01	9.93E-01	MECP2	methyl CpG binding protein 2 (Rett syndrome)	chrXq28	202616_s_at	NM_001110792 /// NM_004992
5.31	5.32	0.01	9.75E-01	9.93E-01	CX3CL1	chemokine (C-X3-C motif) ligand 1	chr16q13	203687_at	NM_002996
6.20	6.20	0.01	9.74E-01	9.93E-01	ARHGAP23	Rho GTPase activating protein 23	chr17q12	226638_at	XM_001714948 /// XM_001716606 /// XM_290799
7.58	7.59	0.01	9.75E-01	9.93E-01	ECE1	endothelin converting enzyme 1	chr1p36.1	201749_at	NM_001113347 /// NM_001113348 /// NM_001113349 /// NM_001397
4.41	4.42	0.01	9.75E-01	9.93E-01	---	---	---	234466_at	---
3.27	3.27	0.01	9.75E-01	9.93E-01	CADM4	Cell adhesion molecule 4	chr19q13.31	214267_s_at	NM_145296
3.52	3.53	0.01	9.75E-01	9.93E-01	TAF3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa	chr10p15.1	235119_at	NM_031923
2.77	2.77	0.00	9.75E-01	9.93E-01	---	---	---	234181_at	---
2.86	2.87	0.00	9.75E-01	9.93E-01	C1orf168	chromosome 1 open reading frame 168	chr1p32.2	231073_at	NM_001004303
2.37	2.37	0.00	9.75E-01	9.93E-01	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	chr15q21.1	233882_s_at	NM_020858 /// NM_024966 /// NM_153616 /// NM_153617 /// NM_153618 /// NM_153619
3.30	3.31	0.00	9.75E-01	9.93E-01	---	---	---	235676_at	---
2.16	2.17	0.00	9.75E-01	9.93E-01	---	---	---	1569770_x_at	---
1.84	1.84	0.00	9.74E-01	9.93E-01	---	---	---	238391_at	---
8.30	8.31	0.01	9.75E-01	9.93E-01	PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	chr5q31.1	208652_at	NM_002715
3.64	3.65	0.01	9.75E-01	9.93E-01	FSD1	fibronectin type III and SPRY domain containing 1	chr19p13.3	219170_at	NM_024333
3.58	3.59	0.01	9.75E-01	9.93E-01	CALD1	caldesmon 1	chr7q33	243084_at	NM_004342 /// NM_033138 /// NM_033139 /// NM_033140 /// NM_033157
4.50	4.51	0.01	9.75E-01	9.93E-01	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	chr5q23.1	210260_s_at	NM_001077654 /// NM_014350
3.30	3.31	0.01	9.75E-01	9.93E-01	COL4A5	collagen, type IV, alpha 5	chrXq22	213110_s_at	NM_000495 /// NM_033380 /// NM_033381
1.94	1.94	0.00	9.75E-01	9.93E-01	---	---	---	1570579_at	---
3.44	3.45	0.01	9.75E-01	9.93E-01	C8orf56	chromosome 8 open reading frame 56	chr8q22.3	1554228_a_at	---
3.04	3.04	0.00	9.75E-01	9.94E-01	---	---	---	244866_at	---
2.02	2.03	0.01	9.76E-01	9.94E-01	ST18	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	chr8q11.23	206135_at	NM_014682
2.08	2.08	0.00	9.75E-01	9.94E-01	---	---	---	233858_at	---
2.30	2.31	0.00	9.76E-01	9.94E-01	C6orf12	HLA complex group 8	chr6p21.33	242557_at	XR_041144 /// XR_041145
2.15	2.15	0.00	9.75E-01	9.94E-01	---	---	---	211459_at	---
2.07	2.07	0.00	9.76E-01	9.94E-01	---	---	---	241967_at	---
4.03	4.04	0.01	9.76E-01	9.94E-01	SLAMF8	SLAM family member 8	chr1q23.2	219385_at	NM_020125

3.89	3.90	0.01	9.76E-01	9.94E-01	EIF4E /// LOC100131565 /// LOC100132918	eukaryotic translation initiation factor 4E /// similar to Eukaryotic translation initiation factor 4E /// similar to hCG1777996	chr3q26.33 /// chr4q21-q25 /// chr8p22	201436_at	NM_001130678 /// NM_001130679 /// NM_001968 /// XR_038724 /// XR_038758 /// XR_038877 /// XR_039697 /// XR_042313 /// XR_042380																				
6.56	6.57	0.01	9.76E-01	9.94E-01	MRPS31	mitochondrial ribosomal protein S31	chr13q14.11	212603_at	NM_005830																				
3.52	3.53	0.01	9.76E-01	9.94E-01	---	---	---	233833_at	---																				
5.97	5.97	0.01	9.76E-01	9.94E-01	POMT2	protein-O-mannosyltransferase 2	chr14q24	220632_s_at	NM_013382																				
2.53	2.53	0.00	9.76E-01	9.94E-01	---	---	---	1556211_a_at	---																				
1.90	1.91	0.00	9.76E-01	9.94E-01	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	chr18q21.3	209720_s_at	NM_006919																				
2.02	2.02	0.00	9.76E-01	9.94E-01	ST7OT2	ST7 overlapping transcript 2 (antisense non-coding RNA)	chr7q31.1-q31.2	237808_at	NR_002331																				
8.86	8.87	0.01	9.76E-01	9.94E-01	TFE3	transcription factor binding to IGHM enhancer 3	chrXp11.22	212457_at	NM_006521																				
2.48	2.48	0.00	9.76E-01	9.94E-01	---	---	---	240903_at	---																				
1.97	1.98	0.00	9.76E-01	9.94E-01	TRPC4	transient receptor potential cation channel, subfamily C, member 4	chr13q13.1-q13.2	220817_at	NM_016179																				
5.67	5.68	0.02	9.76E-01	9.94E-01	C5orf23	chromosome 5 open reading frame 23	chr5p13.3	219054_at	NM_024563																				
4.57	4.58	0.01	9.76E-01	9.94E-01	C14orf142	chromosome 14 open reading frame 142	chr14q32.12	223273_at	NM_032490																				
4.49	4.50	0.01	9.76E-01	9.94E-01	PRCD	progressive rod-cone degeneration	chr17q25.1	1556727_at	NM_001077620																				
3.05	3.05	0.01	9.76E-01	9.94E-01	ITGB4	integrin, beta 4	chr17q25	204989_s_at	NM_000213 /// NM_001005619 /// NM_001005731																				
2.77	2.78	0.00	9.76E-01	9.94E-01	---	---	---	216150_at	---																				
2.07	2.07	0.00	9.76E-01	9.94E-01	MLNR	motilin receptor	chr13q14-q21	221365_at	NM_001507																				
2.46	2.46	0.01	9.76E-01	9.94E-01	---	---	---	1564763_at	---																				
8.59	8.60	0.01	9.76E-01	9.94E-01	BLOC1S1	biogenesis of lysosomal organelles complex-1, subunit 1	chr12q13-q14	202592_at	NM_001487																				
3.34	3.34	0.00	9.76E-01	9.94E-01	---	---	---	236319_at	---																				
2.41	2.42	0.00	9.76E-01	9.94E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	1554147_s_at	NM_033364																				
2.04	2.05	0.00	9.77E-01	9.94E-01	PDXDC2	Pyridoxal-dependent decarboxylase domain containing 2	chr16q22.1	238957_at	NR_003610																				
3.43	3.43	0.01	9.77E-01	9.94E-01	---	---	---	240162_at	---																				
11.73	11.74	0.01	9.77E-01	9.94E-01	RPS6	ribosomal protein S6	chr9p21	201254_x_at	NM_001010																				
6.90	6.91	0.01	9.77E-01	9.94E-01	N4BP1	NEDD4 binding protein 1	chr16q12.1	48612_at	NM_153029																				
2.34	2.35	0.01	9.77E-01	9.94E-01	---	---	---	241593_x_at	---																				
2.43	2.43	0.00	9.77E-01	9.94E-01	LOC100131014	similar to hCG2045213	chr18q23	231356_at	XM_001715758 /// XM_001721462 /// XM_001721478																				
2.69	2.70	0.00	9.77E-01	9.94E-01	ANKAR	ankyrin and armadillo repeat containing	chr2q32.2	1556653_at	NM_144708																				
3.77	3.78	0.01	9.77E-01	9.94E-01	FLJ14311	hypothetical gene FLJ14311	---	233358_at	---																				
2.56	2.57	0.01	9.77E-01	9.94E-01	---	---	---	235361_at	---																				
2.96	2.97	0.01	9.77E-01	9.94E-01	CABLES1	Cdk5 and Abl enzyme substrate 1	chr18q11.2	1558621_at	NM_001100619 /// NM_138375 /// NR_023359																				
2.22	2.22	0.00	9.77E-01	9.94E-01	---	---	---	244678_at	---																				
3.12	3.14	0.02	9.77E-01	9.94E-01	---	---	---	216093_at	---																				
4.52	4.53	0.01	9.77E-01	9.94E-01	COG5	component of oligomeric golgi complex 5	chr7q22-q31	203629_s_at	NM_006348 /// NM_181733																				
4.06	4.07	0.01	9.77E-01	9.94E-01	FAM182B /// RP13-401N8.2	family with sequence similarity 182, member B /// hypothetical gene supported by BC042812	chr20p11.1 /// chr20p11.21-p11.1	215487_x_at	XM_001132551 /// XM_001133521 /// XM_001718365 /// XM_933752																				
2.33	2.34	0.00	9.77E-01	9.94E-01	---	---	---	215059_at	---																				
3.79	3.80	0.00	9.77E-01	9.94E-01	TBX3	T-box 3	chr12q24.1	229565_x_at	NM_005996 /// NM_016569																				
2.57	2.57	0.01	9.77E-01	9.94E-01	---	---	---	240641_at	---																				
6.31	6.32	0.01	9.77E-01	9.94E-01	PLXND1	plexin D1	chr3q21.3	212235_at	NM_015103																				
3.40	3.40	0.01	9.77E-01	9.94E-01	---	---	---	243252_at	---																				
3.22	3.23	0.01	9.77E-01	9.94E-01	SPRR2B	small proline-rich protein 2B	chr1q21-q22	208539_x_at	NM_001017418																				
2.08	2.08	0.00	9.77E-01	9.94E-01	GAFA3	FGF-2 activity-associated protein 3	chr4p14	1555726_at	XM_001715321 /// XM_001722922 /// XM_001723636																				
2.44	2.44	0.00	9.77E-01	9.94E-01	CHRM5	cholinergic receptor, muscarinic 5	chr15q26	221347_at	NM_012125																				

2.09	2.10	0.00	9.77E-01	9.94E-01	RAD51L1	RAD51-like 1 (S. cerevisiae)	chr14q23-q24.2	216880_at	NM_002877 /// NM_133509 /// NM_133510																				
2.17	2.18	0.00	9.77E-01	9.94E-01	RG9MTD2	RNA (guanine-9-) methyltransferase domain containing 2	chr4q23	231877_at	NM_001134665 /// NM_001134666 /// NM_152292																				
2.35	2.35	0.00	9.77E-01	9.94E-01	UBE3A	Ubiquitin protein ligase E3A	chr15q11-q13	234166_at	NM_000462 /// NM_130838 /// NM_130839																				
1.88	1.88	0.00	9.78E-01	9.94E-01	---	---	---	222330_at	---																				
2.03	2.03	0.00	9.78E-01	9.94E-01	C17orf57	chromosome 17 open reading frame 57	chr17q21.32	1553627_s_at	NM_152347																				
4.78	4.79	0.01	9.78E-01	9.94E-01	TEK	TEK tyrosine kinase, endothelial	chr9p21	206702_at	NM_000459																				
1.94	1.94	0.00	9.78E-01	9.94E-01	DPYD	dihydropyrimidine dehydrogenase	chr1p22	1554536_at	NM_000110																				
5.47	5.47	0.01	9.78E-01	9.94E-01	RAB30	RAB30, member RAS oncogene family	chr11q12-q14	228003_at	NM_014488																				
2.83	2.83	0.00	9.78E-01	9.94E-01	---	---	---	237734_s_at	---																				
3.03	3.03	0.00	9.78E-01	9.94E-01	---	---	---	238268_at	---																				
3.64	3.65	0.01	9.78E-01	9.94E-01	RPESP	RPE-spondin	chr8q21.11	235209_at	NM_153225																				
2.27	2.28	0.00	9.78E-01	9.94E-01	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	chr13q14.3	1561585_at	NM_001268																				
2.17	2.18	0.00	9.78E-01	9.94E-01	---	---	---	1558948_a_at	---																				
6.56	6.58	0.02	9.78E-01	9.94E-01	---	---	---	243395_at	---																				
2.58	2.59	0.01	9.78E-01	9.94E-01	CNR1	cannabinoid receptor 1 (brain)	chr6q14-q15	208243_s_at	NM_016083 /// NM_033181																				
2.81	2.81	0.00	9.78E-01	9.94E-01	---	---	---	240620_at	---																				
2.84	2.85	0.00	9.78E-01	9.94E-01	CYP2A7P1	cytochrome P450, family 2, subfamily A, polypeptide 7 pseudogene 1	chr19q13.2	216334_s_at	---																				
3.10	3.11	0.01	9.78E-01	9.94E-01	LOC283745	hypothetical protein LOC283745	chr15q14	1557628_s_at	---																				
2.23	2.23	0.00	9.79E-01	9.94E-01	---	---	---	1565856_at	---																				
2.14	2.14	0.00	9.79E-01	9.95E-01	C13orf30	chromosome 13 open reading frame 30	chr13q14.11	1556711_at	NM_182508																				
4.49	4.50	0.01	9.79E-01	9.95E-01	LOC285086	hypothetical protein LOC285086	chr2q36.3	226561_at	---																				
3.37	3.38	0.01	9.79E-01	9.95E-01	BAG4	BCL2-associated athanogene 4	chr8p12	222909_s_at	NM_004874																				
2.19	2.19	0.00	9.79E-01	9.95E-01	---	---	---	239503_at	---																				
3.62	3.62	0.00	9.79E-01	9.95E-01	CARHSP1	calcium regulated heat stable protein 1, 24kDa	chr16p13.2	1566135_at	NM_001042476 /// NM_014316																				
3.87	3.87	0.00	9.79E-01	9.95E-01	C19orf43	chromosome 19 open reading frame 43	chr19p13.13	230213_at	NM_024038																				
2.40	2.40	0.00	9.79E-01	9.95E-01	MOS	v-mos Moloney murine sarcoma viral oncogene homolog	chr8q11	221367_at	NM_005372																				
6.66	6.67	0.01	9.79E-01	9.95E-01	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	chr7q36.1	222414_at	NM_170606																				
2.43	2.44	0.00	9.79E-01	9.95E-01	SETD7	SET domain containing (lysine methyltransferase) 7	chr4q28	244653_at	NM_030648																				
2.04	2.05	0.00	9.79E-01	9.95E-01	KIAA1622	KIAA1622	chr14q32.13	233002_at	NM_020958 /// NM_058237																				
1.89	1.90	0.00	9.79E-01	9.95E-01	C9orf11	chromosome 9 open reading frame 11	chr9p21	1554981_at	NM_020641																				
2.48	2.49	0.00	9.79E-01	9.95E-01	MGC5566	Hypothetical protein LOC100128040	chr20q13.12	241759_at	XM_926767 /// XM_938022																				
2.03	2.03	0.00	9.79E-01	9.95E-01	---	---	---	234872_at	---																				
5.27	5.28	0.00	9.79E-01	9.95E-01	---	---	---	228478_at	---																				
2.80	2.81	0.00	9.79E-01	9.95E-01	---	---	---	216118_at	---																				
3.00	3.00	0.00	9.79E-01	9.95E-01	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	chr3q26.1	210079_x_at	NM_003471 /// NM_172159 /// NM_172160																				
1.89	1.89	0.00	9.79E-01	9.95E-01	NEGR1	neuronal growth regulator 1	chr1p31.1	239548_at	NM_173808																				
2.35	2.36	0.00	9.80E-01	9.95E-01	LOC653166 /// OR1D4 /// OR1D5	olfactory receptor pseudogene /// olfactory receptor, family 1, subfamily D, member 4 /// olfactory receptor, family 1, subfamily D, member 5	chr17p13.3	221341_s_at	NM_003552 /// NM_014566																				
5.42	5.42	0.01	9.80E-01	9.95E-01	SERTAD2	SERTA domain containing 2	chr2p14	202657_s_at	NM_014755																				
2.77	2.77	0.00	9.80E-01	9.95E-01	FBXO43	F-box protein 43	chr8q22.2	236852_at	NM_001029860 /// NM_001077528																				
1.98	1.98	0.00	9.80E-01	9.95E-01	RUNX1	runt-related transcription factor 1	chr21q22.3	211179_at	NM_001001890 /// NM_001122607 /// NM_001754																				
1.90	1.90	0.00	9.80E-01	9.95E-01	ZC3H12C	zinc finger CCCH-type containing 12C	chr11q22.3	1559763_at	NM_033390																				
2.02	2.03	0.00	9.80E-01	9.95E-01	MYO3A	myosin IIIA	chr10p11.1	1569186_at	NM_017433																				
3.85	3.86	0.01	9.80E-01	9.95E-01	ATP13A3	ATPase type 13A3	chr3q29	219558_at	NM_024524																				
6.52	6.53	0.01	9.80E-01	9.95E-01	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	chr17q24.3	213353_at	NM_018672 /// NM_172232																				
5.47	5.47	0.01	9.80E-01	9.95E-01	CLN5	ceroid-lipofuscinosis, neuronal 5	chr13q21.1-q32	204084_s_at	NM_006493																				
3.02	3.03	0.01	9.80E-01	9.95E-01	NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	chr4q25-q26	208334_at	NM_022569																				
3.68	3.69	0.00	9.80E-01	9.95E-01	---	---	---	237443_at	---																				
1.91	1.91	0.00	9.80E-01	9.95E-01	---	---	---	1566428_at	---																				

2.64	2.64	0.00	9.80E-01	9.95E-01	LOC642587	NPC-A-5	chr1q32.2	1555942_a_at	NM_001104548																					
2.47	2.48	0.00	9.80E-01	9.95E-01	LOC201617	hypothetical protein LOC201617	chr3p14.2	1557602_at	---																					
7.79	7.80	0.01	9.80E-01	9.95E-01	DCTN4	dynactin 4 (p62)	chr5q31-q32	222488_s_at	NM_016221																					
3.56	3.57	0.01	9.80E-01	9.95E-01	LOC606495	hypothetical protein LOC606495	chr1p32.3	235991_at	NM_001031672																					
3.06	3.07	0.01	9.80E-01	9.95E-01	---	---	---	1570439_at	---																					
6.75	6.76	0.00	9.80E-01	9.95E-01	PLEKHM1	pleckstrin homology domain containing, family M (with RUN domain) member 1	chr17q21.31	212717_at	NM_014798																					
4.07	4.07	0.00	9.80E-01	9.95E-01	OLFM1	olfactomedin 1	chr9q34.3	210924_at	NM_006334 /// NM_014279																					
2.11	2.11	0.00	9.80E-01	9.95E-01	ZMYM6	zinc finger, MYM-type 6	chr1p34.2	1561892_at	NM_007167																					
2.62	2.62	0.00	9.80E-01	9.95E-01	ARMC3	armadillo repeat containing 3	chr10p12.31	240275_at	NM_173081																					
2.27	2.27	0.00	9.80E-01	9.95E-01	INPP5F	inositol polyphosphate-5-phosphatase F	chr10q26.11	230363_s_at	NM_014937 /// NR_003251 /// NR_003252																					
5.68	5.69	0.01	9.80E-01	9.95E-01	WDSOF1	WD repeats and SOF1 domain containing	chr8q22.3	225676_s_at	NM_015420																					
2.02	2.02	0.00	9.80E-01	9.95E-01	ATXN3	ataxin 3	chr14q24.3-q32.2	216657_at	NM_001127696 /// NM_001127697 /// NM_004993 /// NM_030660																					
8.34	8.35	0.01	9.80E-01	9.95E-01	C11orf67	chromosome 11 open reading frame 67	chr11q14.1	221599_at	NM_024684																					
2.72	2.72	0.00	9.81E-01	9.95E-01	BMP8A /// BMP8B	bone morphogenetic protein 8a /// bone morphogenetic protein 8b	chr1p34.2 /// chr1p35-p32	221615_at	NM_001720 /// NM_181809																					
5.41	5.42	0.00	9.81E-01	9.95E-01	POGZ	pogo transposable element with ZNF domain	chr1q21.3	215281_x_at	NM_015100 /// NM_145796 /// NM_207171																					
2.99	3.00	0.01	9.81E-01	9.95E-01	---	---	---	222316_at	---																					
2.64	2.64	0.00	9.81E-01	9.95E-01	---	---	---	242530_at	---																					
4.74	4.75	0.00	9.81E-01	9.95E-01	---	---	---	233319_x_at	---																					
2.06	2.06	0.00	9.81E-01	9.95E-01	---	---	---	244612_at	---																					
3.05	3.06	0.01	9.81E-01	9.95E-01	---	---	---	1557689_at	---																					
3.41	3.42	0.00	9.81E-01	9.95E-01	LGALS8	lectin, galactoside-binding, soluble, 8	chr1q42-q43	210731_s_at	NM_006499 /// NM_201543 /// NM_201544 /// NM_201545																					
2.20	2.21	0.00	9.81E-01	9.95E-01	---	---	---	1561143_at	---																					
3.03	3.04	0.00	9.81E-01	9.95E-01	C1orf111	chromosome 1 open reading frame 111	chr1q23.3	231163_at	NM_182581																					
2.31	2.31	0.00	9.81E-01	9.95E-01	C21orf42	chromosome 21 open reading frame 42	chr21q21.3	231303_at	NM_058184 /// NR_024027																					
6.35	6.36	0.01	9.82E-01	9.95E-01	C7orf47	chromosome 7 open reading frame 47	chr7q22.1	226434_at	NM_145030																					
4.49	4.49	0.01	9.81E-01	9.95E-01	---	---	---	231305_at	---																					
2.78	2.78	0.00	9.82E-01	9.95E-01	NSUN6	NOL1/NOP2/Sun domain family, member 6	chr10p12.33	1569354_at	NM_182543																					
2.30	2.30	0.00	9.82E-01	9.95E-01	---	---	---	1560963_a_at	---																					
7.54	7.55	0.00	9.82E-01	9.95E-01	GDE1	glycerophosphodiester phosphodiesterase 1	chr16p12-p11.2	226214_at	NM_016641																					
3.15	3.15	0.00	9.81E-01	9.95E-01	---	---	---	239531_at	---																					
2.34	2.34	0.00	9.81E-01	9.95E-01	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	chr1p21	210742_at	NM_003672 /// NM_033312 /// NM_033313																					
2.88	2.88	0.00	9.82E-01	9.95E-01	CNGB3	cyclic nucleotide gated channel beta 3	chr8q21-q22	220304_s_at	NM_019098																					
1.98	1.99	0.00	9.82E-01	9.95E-01	FAM12B	family with sequence similarity 12, member B (epididymal)	chr14q11.2	220759_at	NM_022360																					
3.41	3.42	0.01	9.82E-01	9.95E-01	CEP70	centrosomal protein 70kDa	chr3q22-q23	1554489_a_at	NM_024491																					
4.90	4.90	0.00	9.82E-01	9.95E-01	KIAA1303	raptor	chr17q25.3	225715_at	NM_020761																					
2.41	2.41	0.00	9.82E-01	9.95E-01	---	---	---	1561443_at	---																					
3.72	3.73	0.01	9.82E-01	9.95E-01	KBTBD7	kelch repeat and BTB (POZ) domain containing 7	chr13q14.11	223412_at	NM_032138																					
11.85	11.85	0.00	9.82E-01	9.95E-01	RPL5	ribosomal protein L5	chr1p22.1	213080_x_at	NM_000969																					
2.94	2.94	0.00	9.82E-01	9.95E-01	SLC4A5	solute carrier family 4, sodium bicarbonate cotransporter, member 5	chr2p13	221723_s_at	NM_021196 /// NM_133478																					
4.70	4.71	0.01	9.82E-01	9.95E-01	RLF	rearranged L-myc fusion	chr1p32	204243_at	NM_012421																					
7.24	7.24	0.00	9.82E-01	9.95E-01	---	---	---	229420_at	---																					
4.96	4.97	0.00	9.82E-01	9.95E-01	CNTD2	cyclin N-terminal domain containing 2	chr19q13.2	220323_at	NM_024877																					
5.12	5.13	0.00	9.82E-01	9.95E-01	FLJ36208	hypothetical protein FLJ36208	chr16p13.3	1558431_at	NM_176677																					
2.21	2.22	0.00	9.82E-01	9.95E-01	---	---	---	1558858_at	---																					
2.62	2.62	0.00	9.82E-01	9.95E-01	UBE2Q1	ubiquitin-conjugating enzyme E2Q family member 1	chr1q21.3	231816_s_at	NM_017582																					
2.47	2.47	0.00	9.82E-01	9.95E-01	---	---	---	1565897_at	---																					

2.59	2.59	0.00	9.82E-01	9.95E-01	CDY1 /// CDY1B /// CDY2A /// CDY2B	chromodomain protein, Y-linked, 1 /// chromodomain protein, Y-linked, 1B /// chromodomain protein, Y-linked, 2A /// chromodomain protein, Y-linked, 2B	chrYq11.221 /// chrYq11.223 /// chrYq11.23	207646_s_at	NM_001001722 /// NM_001003894 /// NM_001003895 /// NM_004680 /// NM_004825 /// NM_170723																				
2.64	2.65	0.00	9.82E-01	9.95E-01	SLC9A11	solute carrier family 9, member 11	chr1q25.1	1563495_at	NM_178527																				
2.63	2.63	0.00	9.82E-01	9.95E-01	---	---	---	236669_at	---																				
1.94	1.95	0.00	9.82E-01	9.95E-01	TEX15	testis expressed 15	chr8p12	232760_at	NM_031271																				
2.01	2.02	0.00	9.82E-01	9.95E-01	LOC286467	hypothetical protein LOC286467	chrXq26.2	1558791_at	XR_015266 /// XR_015395 /// XR_042075																				
6.38	6.38	0.01	9.83E-01	9.95E-01	KIAA1468	KIAA1468	chr18q21.33	225506_at	NM_020854																				
1.99	1.99	0.00	9.83E-01	9.95E-01	---	---	---	224107_at	---																				
5.34	5.35	0.01	9.83E-01	9.96E-01	MED21	mediator complex subunit 21	chr12p11.23	209363_s_at	NM_004264																				
3.49	3.50	0.01	9.83E-01	9.96E-01	CDA	cytidine deaminase	chr1p36.2-p35	205627_at	NM_001785																				
4.07	4.08	0.00	9.83E-01	9.96E-01	PLB1	phospholipase B1	chr2p23.2	235703_at	NM_153021																				
2.20	2.21	0.00	9.83E-01	9.96E-01	---	---	---	1557645_at	---																				
1.98	1.98	0.00	9.83E-01	9.96E-01	C21orf94	chromosome 21 open reading frame 94	chr21q21.3	1553519_at	XR_017891 /// XR_017990 /// XR_041774																				
2.66	2.66	0.00	9.83E-01	9.96E-01	C6orf122	chromosome 6 open reading frame 122	chr6q27	1561327_at	XR_040753 /// XR_040754 /// XR_040755																				
2.49	2.49	0.00	9.83E-01	9.96E-01	---	---	---	238743_at	---																				
3.04	3.05	0.00	9.83E-01	9.96E-01	LOC644613	hypothetical protein LOC644613	chr11q13.1	1563426_a_at	XM_927728																				
2.38	2.38	0.00	9.83E-01	9.96E-01	---	---	---	240477_at	---																				
6.55	6.56	0.01	9.83E-01	9.96E-01	RCN2	reticulocalbin 2, EF-hand calcium binding domain	chr15q23	201485_s_at	NM_002902																				
4.32	4.32	0.01	9.83E-01	9.96E-01	DMBT1	deleted in malignant brain tumors 1	chr10q25.3-q26.1	208250_s_at	NM_004406 /// NM_007329 /// NM_017579																				
2.73	2.73	0.00	9.83E-01	9.96E-01	MPZ	myelin protein zero	chr1q23.3	210280_at	NM_000530																				
2.29	2.29	0.00	9.83E-01	9.96E-01	PAQR9	progestin and adipoQ receptor family member IX	chr3q23	1558322_a_at	NM_198504																				
2.03	2.04	0.00	9.83E-01	9.96E-01	MME	membrane metallo-endopeptidase	chr3q25.1-q25.2	203434_s_at	NM_000902 /// NM_007287 /// NM_007288 /// NM_007289																				
2.52	2.52	0.00	9.83E-01	9.96E-01	IPO5	Importin 5	chr13q32.2	236906_x_at	NM_002271																				
3.72	3.72	0.00	9.83E-01	9.96E-01	POMP	proteasome maturation protein	chr13q12.3	222402_at	NM_015932																				
5.48	5.49	0.00	9.83E-01	9.96E-01	LOC286260	hypothetical protein LOC286260	chr9q34.3	232420_x_at	XM_001723591																				
3.77	3.78	0.00	9.83E-01	9.96E-01	BANK1	B-cell scaffold protein with ankyrin repeats 1	chr4q24	222915_s_at	NM_001083907 /// NM_001127507 /// NM_017935																				
2.11	2.11	0.00	9.83E-01	9.96E-01	SPINLW1	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	chr20q12-q13.2	206318_at	NM_020398 /// NM_181502																				
2.07	2.08	0.00	9.83E-01	9.96E-01	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	chr20q12-q13	1558210_at	NM_005417 /// NM_198291																				
6.03	6.04	0.01	9.83E-01	9.96E-01	ASB3	ankyrin repeat and SOCS box-containing 3	chr2p16-p14	224524_s_at	NM_016115 /// NM_145863																				
5.41	5.42	0.00	9.84E-01	9.96E-01	ANKS3	ankyrin repeat and sterile alpha motif domain containing 3	chr16p13.3	227303_at	NM_133450																				
2.17	2.17	0.00	9.84E-01	9.96E-01	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	chr11q12.1	1554892_a_at	NM_001031666 /// NM_001031809 /// NM_006138																				
4.09	4.09	0.00	9.84E-01	9.96E-01	HES2	hairy and enhancer of split 2 (Drosophila)	chr1p36.31-p36.11	231928_at	NM_019089																				
3.83	3.83	0.00	9.84E-01	9.96E-01	MMP19	matrix metallopeptidase 19	chr12q14	204575_s_at	NM_002429																				
2.39	2.40	0.00	9.84E-01	9.96E-01	---	---	---	242892_at	---																				
2.03	2.03	0.00	9.84E-01	9.96E-01	---	---	---	243347_at	---																				
3.00	3.00	0.00	9.84E-01	9.96E-01	SV2B	synaptic vesicle glycoprotein 2B	chr15q26.1	244717_x_at	NM_014848																				
2.02	2.02	0.00	9.84E-01	9.96E-01	---	---	---	1560739_a_at	---																				
2.75	2.76	0.00	9.84E-01	9.96E-01	BPIL2	bactericidal/permeability-increasing protein-like 2	chr22q12.3	1555773_at	NM_174932																				
5.88	5.89	0.01	9.84E-01	9.96E-01	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	chr1q43-q44	212607_at	NM_005465 /// NM_181690																				
4.32	4.32	0.00	9.84E-01	9.96E-01	C3orf15	chromosome 3 open reading frame 15	chr3q12-q13.3	236222_at	NM_033364																				

8.01	8.02	0.01	9.84E-01	9.96E-01	C16orf52	Chromosome 16 open reading frame 52	chr16p12.1	230296_at	NR_024104 /// XM_001126460 /// XM_001132387 /// XM_001724381
6.42	6.42	0.01	9.84E-01	9.96E-01	---	---	---	226485_at	---
2.31	2.31	0.00	9.84E-01	9.96E-01	---	---	---	1562822_at	---
2.40	2.41	0.00	9.84E-01	9.96E-01	LOC641798	hypothetical protein LOC641798	---	244322_at	XM_935966
2.07	2.07	0.00	9.84E-01	9.96E-01	FNBP4	Formin binding protein 4	chr11p11.2	242472_x_at	NM_015308
9.16	9.17	0.01	9.84E-01	9.96E-01	SORBS2	sorbin and SH3 domain containing 2	chr4q35.1	225728_at	NM_003603 /// NM_021069
3.23	3.24	0.00	9.84E-01	9.96E-01	SRPK2	SFRS protein kinase 2	chr7q22-q31.1	217517_x_at	NM_182691 /// NM_182692
2.18	2.19	0.00	9.84E-01	9.96E-01	C18orf20	chromosome 18 open reading frame 20	chr18q22.1	1553934_at	XR_039927 /// XR_039928 /// XR_039929 /// XR_039930
2.20	2.20	0.00	9.85E-01	9.96E-01	---	---	---	1562879_at	---
3.80	3.80	0.00	9.85E-01	9.96E-01	UGT1A1 /// UGT1A10 /// UGT1A3 /// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A1 /// UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 family, polypeptide A3 /// UDP glucuronosyltransferase 1 family, polypeptide A4 /// UDP glucuronosyltransferase 1 family, polypeptide A5 /// UDP glucuronosyltransferase 1 family, polypeptide A6 /// UDP glucuronosyltransferase 1 family, polypeptide A7 /// UDP glucuronosyltransferase 1 family, polypeptide A8 /// UDP glucuronosyltransferase 1 family, polypeptide A9	chr2q37	206094_x_at	NM_000463 /// NM_001072 /// NM_007120 /// NM_019075 /// NM_019076 /// NM_019077 /// NM_019078 /// NM_019093 /// NM_021027 /// NM_205862
2.74	2.74	0.00	9.85E-01	9.96E-01	ELA3A	elastase 3A, pancreatic	chr1p36.12	210080_x_at	NM_005747
3.32	3.32	0.00	9.85E-01	9.96E-01	MYO7A	myosin VIIA	chr11q13.5	211103_at	NM_000260 /// NM_001127179 /// NM_001127180
5.81	5.82	0.00	9.85E-01	9.96E-01	---	---	---	217619_x_at	---
2.81	2.81	0.00	9.85E-01	9.96E-01	MAP4	microtubule-associated protein 4	chr3p21	200835_s_at	NM_001134364 /// NM_001134365 /// NM_002375 /// NM_030884 /// NM_030885
6.78	6.79	0.01	9.85E-01	9.96E-01	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	chr2q36-q37	222073_at	NM_000091 /// NM_031362 /// NM_031365 /// NM_031366
2.70	2.70	0.01	9.85E-01	9.96E-01	TMEM161B	transmembrane protein 161B	chr5q14.3	236227_at	NM_153354
2.30	2.30	0.00	9.85E-01	9.96E-01	---	---	---	216664_at	---
4.14	4.14	0.00	9.85E-01	9.96E-01	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	chr10q24.1	216360_x_at	NM_015179
4.46	4.46	0.00	9.85E-01	9.96E-01	---	---	---	216371_at	---
2.37	2.37	0.00	9.85E-01	9.96E-01	---	---	---	1558402_at	---
3.81	3.81	0.00	9.85E-01	9.96E-01	ZNF135	zinc finger protein 135	chr19q13.4	1567410_at	NM_003436
4.66	4.67	0.00	9.85E-01	9.96E-01	---	---	---	1556662_at	---
2.10	2.10	0.00	9.85E-01	9.96E-01	MYO1H	myosin IH	chr12q24.11	1553452_at	NM_001101421
1.77	1.78	0.00	9.85E-01	9.96E-01	DEPDC4	DEP domain containing 4	chr12q23.1	1561114_a_at	NM_152317
2.30	2.31	0.00	9.85E-01	9.96E-01	TUBGCP3	tubulin, gamma complex associated protein 3	chr13q34	1554086_at	NM_006322
3.18	3.18	0.00	9.85E-01	9.96E-01	GPA33	glycoprotein A33 (transmembrane)	chr1q24.1	205929_at	NM_005814
6.03	6.04	0.01	9.85E-01	9.96E-01	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	chr4p14	212138_at	NM_001100399 /// NM_001100400 /// NM_015200
5.45	5.45	0.00	9.85E-01	9.96E-01	C9orf9	chromosome 9 open reading frame 9	chr9q34	220050_at	NM_018956
2.85	2.85	0.00	9.85E-01	9.96E-01	OR10D3P	olfactory receptor, family 10, subfamily D, member 3 pseudogene	chr11q24.2	1567252_at	---
4.83	4.84	0.01	9.86E-01	9.96E-01	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	chr2q14.1	208896_at	NM_006773
2.87	2.87	0.00	9.86E-01	9.96E-01	ZNF81	zinc finger protein 81	chrXp11.23	1561038_at	NM_007137
2.77	2.77	0.00	9.86E-01	9.96E-01	PSG7	pregnancy specific beta-1-glycoprotein 7	chr19q13.2	205602_x_at	NM_002783
7.35	7.36	0.01	9.86E-01	9.96E-01	MSH6	mutS homolog 6 (E. coli)	chr2p16	202911_at	NM_000179
3.36	3.36	0.00	9.86E-01	9.96E-01	---	---	---	243145_at	---
2.56	2.56	0.00	9.86E-01	9.96E-01	---	---	---	241573_at	---
5.75	5.75	0.00	9.86E-01	9.96E-01	CCDC93	coiled-coil domain containing 93	chr2q14.1	209689_at	NM_019044
5.45	5.45	0.00	9.86E-01	9.96E-01	PCDHB18	protocadherin beta 18 pseudogene	chr5q31	234724_x_at	NR_001281

5.56	5.56	0.00	9.86E-01	9.96E-01	BMPR1A	bone morphogenetic protein receptor, type IA	chr10q22.3	213578_at	NM_004329
2.16	2.17	0.00	9.86E-01	9.96E-01	KLHDC1	kelch domain containing 1	chr14q22.1	1564273_at	NM_172193
6.67	6.68	0.01	9.87E-01	9.96E-01	PRELP	proline/arginine-rich end leucine-rich repeat protein	chr1q32	204223_at	NM_002725 /// NM_201348
6.08	6.08	0.01	9.87E-01	9.96E-01	IAH1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	chr2p25.1	230621_at	NM_001039613
5.30	5.31	0.01	9.87E-01	9.96E-01	RSF1	remodeling and spacing factor 1	chr11q14.1	222541_at	NM_016578
4.96	4.97	0.01	9.87E-01	9.96E-01	GAB1	GRB2-associated binding protein 1	chr4q31.21	225998_at	NM_002039 /// NM_207123
4.31	4.32	0.00	9.87E-01	9.96E-01	---	---	---	235733_at	---
2.95	2.95	0.00	9.86E-01	9.96E-01	IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	chr16p13.3	244585_at	NM_014714
3.77	3.77	0.00	9.87E-01	9.96E-01	FMNL3	formin-like 3	chr12q13.12	232249_at	NM_175736 /// NM_198900
5.37	5.38	0.00	9.87E-01	9.96E-01	UCK1	uridine-cytidine kinase 1	chr9q34.13	223142_s_at	NM_031432
5.50	5.50	0.00	9.87E-01	9.96E-01	BRF1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	chr14q	203754_s_at	NM_001519 /// NM_145685
2.35	2.35	0.00	9.87E-01	9.96E-01	XPA	Xeroderma pigmentosum, complementation group A	chr9q22.3	232967_at	NM_000380
3.10	3.10	0.00	9.87E-01	9.96E-01	C4orf23	chromosome 4 open reading frame 23	chr4p16.1	235097_at	NM_152544
4.51	4.51	0.00	9.87E-01	9.96E-01	---	---	---	233274_at	---
5.48	5.48	0.00	9.87E-01	9.96E-01	MCM4	minichromosome maintenance complex component 4	chr8q11.2	212141_at	NM_005914 /// NM_182746
2.62	2.62	0.00	9.87E-01	9.96E-01	TMEM92	transmembrane protein 92	chr17q21.33	231408_at	NM_153229
2.66	2.66	0.00	9.87E-01	9.96E-01	C9orf5	chromosome 9 open reading frame 5	chr9q31	227831_at	NM_001099734 /// NM_032012
2.59	2.60	0.00	9.87E-01	9.96E-01	DSG2	desmoglein 2	chr18q12.1	217901_at	NM_001943
2.24	2.24	0.00	9.87E-01	9.96E-01	---	---	---	242620_at	---
2.33	2.34	0.00	9.86E-01	9.96E-01	PBX3	pre-B-cell leukemia homeobox 3	chr9q33-q34	234145_at	NM_006195
2.03	2.04	0.00	9.86E-01	9.96E-01	TMPRSS12	transmembrane protease, serine 12	chr12q13.13	1569176_at	NM_182559
2.68	2.68	0.00	9.87E-01	9.96E-01	BFSP2	beaded filament structural protein 2, phakinin	chr3q21-q25	207399_at	NM_003571
2.23	2.23	0.00	9.87E-01	9.96E-01	---	---	---	240067_at	---
2.56	2.56	0.00	9.86E-01	9.96E-01	PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	chr6q21	1560910_at	NM_001111298 /// NM_173672
2.24	2.24	0.00	9.87E-01	9.96E-01	KITLG	KIT ligand	chr12q22	211124_s_at	NM_000899 /// NM_003994
2.55	2.55	0.00	9.86E-01	9.96E-01	WFDC13	WAP four-disulfide core domain 13	chr20q13.12	1553052_at	NM_172005
2.60	2.60	0.00	9.87E-01	9.96E-01	---	---	---	242354_at	---
2.00	2.00	0.00	9.87E-01	9.96E-01	TNP2	transition protein 2 (during histone to protamine replacement)	chr16p13.13	217460_at	NM_005425
2.33	2.33	0.00	9.87E-01	9.96E-01	ADCYAP1	adenylate cyclase activating polypeptide 1 (pituitary)	chr18p11	230237_at	NM_001099733 /// NM_001117
1.98	1.98	0.00	9.87E-01	9.96E-01	---	---	---	234009_at	---
2.31	2.31	0.00	9.87E-01	9.96E-01	CA1	carbonic anhydrase I	chr8q13-q22.1	205949_at	NM_001128829 /// NM_001128830 /// NM_001128831 /// NM_001738
2.12	2.12	0.00	9.87E-01	9.96E-01	---	---	---	1557139_at	---
2.10	2.10	0.00	9.86E-01	9.96E-01	---	---	---	1561609_at	---
4.42	4.42	0.00	9.87E-01	9.96E-01	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	chr4p16-p15.3	219991_at	NM_001001290 /// NM_020041
2.34	2.34	0.00	9.87E-01	9.96E-01	---	---	---	1561883_at	---
2.00	2.00	0.00	9.87E-01	9.96E-01	---	---	---	244773_at	---
5.58	5.58	0.00	9.88E-01	9.97E-01	---	---	---	202648_at	---
7.63	7.63	0.00	9.88E-01	9.97E-01	FLNA	filamin A, alpha (actin binding protein 280)	chrXq28	214752_x_at	NM_001110556 /// NM_001456
2.17	2.17	0.00	9.88E-01	9.97E-01	LOC255480	hypothetical protein LOC255480	chr12q24.21	233965_at	XM_001134335 /// XM_001719855 /// XM_001723369
2.25	2.25	0.00	9.88E-01	9.97E-01	---	---	---	240610_at	---
7.94	7.95	0.01	9.88E-01	9.97E-01	RNF139	ring finger protein 139	chr8q24	209510_at	NM_007218
6.01	6.01	0.00	9.88E-01	9.97E-01	CXorf39	Chromosome X open reading frame 39	chrXq22.2	225216_at	NM_207318
3.46	3.46	0.00	9.88E-01	9.97E-01	TDRG1	testis development related protein 1	chr6p21.2	230236_at	NR_024015 /// XM_001132383 /// XM_001724507 /// XM_001725310
2.19	2.19	0.00	9.88E-01	9.97E-01	---	---	---	240974_at	---
2.01	2.01	0.00	9.88E-01	9.97E-01	---	---	---	1563299_at	---

2.53	2.53	0.00	9.88E-01	9.97E-01	ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	chr2p13.1	205473_at	NM_001692
4.14	4.14	0.00	9.88E-01	9.97E-01	FBF1	Fas (TNFRSF6) binding factor 1	chr17q25.1	1556131_s_at	NM_001080542
5.36	5.37	0.01	9.88E-01	9.97E-01	CD48	CD48 molecule	chr1q21.3-q22	204118_at	NM_001778
2.19	2.20	0.00	9.88E-01	9.97E-01	---	---	---	1566438_at	---
7.04	7.04	0.00	9.88E-01	9.97E-01	KIAA1430	KIAA1430	chr4q35.1	226254_s_at	NM_020827
2.70	2.70	0.00	9.89E-01	9.97E-01	PKLR	pyruvate kinase, liver and RBC	chr1q21	210451_at	NM_000298 /// NM_181871
2.24	2.25	0.00	9.88E-01	9.97E-01	---	---	---	1559255_a_at	---
2.54	2.54	0.00	9.89E-01	9.97E-01	FAM106A	family with sequence similarity 106, member A	chr17p11.2	220575_at	XR_017880 /// XR_040965 /// XR_040966
2.03	2.03	0.00	9.88E-01	9.97E-01	FETUB	fetuin B	chr3q27	210521_s_at	NM_014375
1.94	1.94	0.00	9.89E-01	9.97E-01	---	---	---	237233_at	---
7.00	7.00	0.00	9.89E-01	9.97E-01	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	chr17q25.3	201168_x_at	NM_004309
3.29	3.29	0.00	9.89E-01	9.97E-01	LOC723809	LOC723809	---	239656_at	---
2.76	2.76	0.01	9.89E-01	9.97E-01	HIPK3	homeodomain interacting protein kinase 3	chr11p13	210148_at	NM_001048200 /// NM_005734
4.52	4.52	0.01	9.89E-01	9.97E-01	OSBPL10	oxysterol binding protein-like 10	chr3p22.3	219073_s_at	NM_017784
5.63	5.63	0.00	9.89E-01	9.97E-01	CSE1L	CSE1 chromosome segregation 1-like (yeast)	chr20q13	201111_at	NM_001316
2.69	2.69	0.00	9.89E-01	9.97E-01	DDIT4L	DNA-damage-inducible transcript 4-like	chr4q23	228057_at	NM_145244
2.41	2.41	0.00	9.89E-01	9.97E-01	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	chr19q13.3-q13.4	243893_at	NM_004977
2.50	2.50	0.00	9.89E-01	9.97E-01	---	---	---	232779_at	---
2.33	2.33	0.00	9.89E-01	9.97E-01	---	---	---	231392_at	---
4.42	4.42	0.01	9.89E-01	9.97E-01	FJX1	four jointed box 1 (Drosophila)	chr11p13	219522_at	NM_014344
4.75	4.75	0.00	9.89E-01	9.97E-01	C14orf118	chromosome 14 open reading frame 118	chr14q22.1-q24.3	229520_s_at	NM_017926 /// NM_017972
2.57	2.57	0.00	9.89E-01	9.97E-01	---	---	---	1557908_at	---
3.05	3.05	0.00	9.89E-01	9.97E-01	LOC728163	hypothetical protein LOC728163	chr15q25.3	229783_at	XM_001715315
2.76	2.76	0.00	9.90E-01	9.97E-01	---	---	---	242728_at	---
3.23	3.24	0.00	9.90E-01	9.97E-01	FLJ38717	FLJ38717 protein	chr6p21.1	1559964_at	XR_040734 /// XR_040735 /// XR_040736
4.08	4.09	0.01	9.90E-01	9.97E-01	---	---	---	243659_at	---
3.58	3.59	0.01	9.90E-01	9.97E-01	LOC400713	zinc finger-like	chr19q13.33	232315_at	XR_039381 /// XR_039390 /// XR_039621
3.02	3.02	0.00	9.90E-01	9.97E-01	IRS4	insulin receptor substrate 4	chrXq22.3	207403_at	NM_003604
7.59	7.59	0.00	9.90E-01	9.97E-01	DPH5	DPH5 homolog (S. cerevisiae)	chr1p21.2	223671_x_at	NM_001077394 /// NM_001077395 /// NM_015958
2.05	2.05	0.00	9.90E-01	9.97E-01	---	---	---	241130_at	---
2.32	2.32	0.00	9.90E-01	9.97E-01	---	---	---	242024_at	---
2.21	2.21	0.00	9.90E-01	9.97E-01	LOC647323	hypothetical protein LOC647323	chr3q29	1564539_at	XM_930391
2.45	2.46	0.00	9.90E-01	9.97E-01	ZNF3	zinc finger protein 3	chr7q22.1	219605_at	NM_017715 /// NM_032924
3.17	3.17	0.00	9.90E-01	9.97E-01	LOC143678	hypothetical LOC143678	chr11p11.2	240029_at	NM_001080446
3.45	3.45	0.00	9.90E-01	9.97E-01	NRP2	neuropilin 2	chr2q33.3	223510_at	NM_003872 /// NM_018534 /// NM_201264 /// NM_201266 /// NM_201267 /// NM_201279
8.25	8.26	0.01	9.90E-01	9.97E-01	PCOLCE	procollagen C-endopeptidase enhancer	chr7q22	202465_at	NM_002593
4.94	4.95	0.01	9.90E-01	9.97E-01	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	chr16p13.1	214033_at	NM_001079528 /// NM_001171
5.68	5.69	0.00	9.91E-01	9.97E-01	SLK	STE20-like kinase (yeast)	chr10q25.1	206875_s_at	NM_014720
5.77	5.77	0.00	9.90E-01	9.97E-01	SPAG9	sperm associated antigen 9	chr17q21.33	212470_at	NM_001130528 /// NM_003971
5.39	5.40	0.00	9.91E-01	9.97E-01	GATC	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	chr12q24.31	214711_at	NM_176818
6.45	6.45	0.00	9.90E-01	9.97E-01	OXSR1	oxidative-stress responsive 1	chr3p22-p21.3	202696_at	NM_005109
4.94	4.94	0.00	9.91E-01	9.97E-01	PCTK3	PCTAIRE protein kinase 3	chr1q31-q32	214797_s_at	NM_002596 /// NM_212502 /// NM_212503
5.09	5.09	0.00	9.91E-01	9.97E-01	PCGF2	polycomb group ring finger 2	chr17q12	203792_x_at	NM_007144
2.19	2.19	0.00	9.91E-01	9.97E-01	CLRN1	clarin 1	chr3q25	1555035_a_at	NM_052995 /// NM_174878
3.22	3.22	0.00	9.91E-01	9.97E-01	hCG_1645220	hCG1645220	chr2p21	241710_at	NM_001101330

4.36	4.36	0.00	9.91E-01	9.97E-01	ACAN	aggrecan	chr15q26.1	217161_x_at	NM_001135 /// NM_013227
3.55	3.55	0.00	9.91E-01	9.97E-01	---	---	---	216179_x_at	---
2.74	2.74	0.00	9.90E-01	9.97E-01	---	---	---	1561844_at	---
2.72	2.72	0.00	9.90E-01	9.97E-01	RGS11	regulator of G-protein signaling 11	chr16p13.3	1554643_at	NM_003834 /// NM_183337
2.33	2.33	0.00	9.91E-01	9.97E-01	CASD1	CAS1 domain containing 1	chr7q21.3	231244_at	NM_022900
2.33	2.34	0.00	9.91E-01	9.97E-01	---	---	---	215965_at	---
3.15	3.15	0.00	9.91E-01	9.97E-01	TNK2	tyrosine kinase, non-receptor, 2	chr3q29	1565783_at	NM_001010938 /// NM_005781
1.95	1.95	0.00	9.91E-01	9.97E-01	---	---	---	241537_at	---
5.80	5.80	0.00	9.91E-01	9.97E-01	REV1	REV1 homolog (S. cerevisiae)	chr2q11.1-q11.2	222628_s_at	NM_001037872 /// NM_016316
3.55	3.56	0.00	9.91E-01	9.97E-01	AKT2	v-akt murine thymoma viral oncogene homolog 2	chr19q13.1-q13.2	203809_s_at	NM_001626
2.68	2.68	0.00	9.91E-01	9.97E-01	---	---	---	234838_at	---
2.23	2.23	0.00	9.91E-01	9.97E-01	CRHR2	corticotropin releasing hormone receptor 2	chr7p15.1	211510_s_at	NM_001883
3.78	3.78	0.00	9.91E-01	9.97E-01	ASPH	Aspartate beta-hydroxylase	chr8q12.1	242037_at	NM_004318 /// NM_020164 /// NM_032466 /// NM_032467 /// NM_032468
3.75	3.75	0.00	9.91E-01	9.97E-01	C18orf1	chromosome 18 open reading frame 1	chr18p11.2	207996_s_at	NM_001003674 /// NM_001003675 /// NM_004338 /// NM_181481 /// NM_181482 /// NM_181483
3.83	3.83	0.00	9.91E-01	9.97E-01	---	---	---	229592_at	---
4.94	4.94	0.00	9.91E-01	9.97E-01	---	---	---	236961_at	---
5.99	6.00	0.00	9.92E-01	9.97E-01	CEP350	centrosomal protein 350kDa	chr1p36.13-q41	213165_at	NM_014810
3.09	3.09	0.00	9.91E-01	9.97E-01	ZMYM6	zinc finger, MYM-type 6	chr1p34.2	227594_at	NM_007167
3.04	3.05	0.00	9.91E-01	9.97E-01	CLCN4	chloride channel 4	chrXp22.3	205148_s_at	NM_001830
5.41	5.41	0.00	9.91E-01	9.97E-01	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	chr2q23.3	228254_at	NM_005843
3.13	3.13	0.00	9.91E-01	9.97E-01	KIAA1407	KIAA1407	chr3q13.31	228476_at	NM_020817
3.75	3.75	0.00	9.92E-01	9.97E-01	NKX1-1	NK1 homeobox 1	chr4p16.3	1565537_at	XM_001715809 /// XM_926341 /// XM_937659
6.11	6.11	0.00	9.92E-01	9.97E-01	FAM33A	family with sequence similarity 33, member A	chr17q22	225684_at	NM_001100595 /// NM_182620
2.08	2.08	0.00	9.92E-01	9.97E-01	DIRAS2	DIRAS family, GTP-binding RAS-like 2	chr9q22.2	240122_at	NM_017594
2.68	2.68	0.00	9.91E-01	9.97E-01	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	chr3p21.3	214187_x_at	NM_001008392 /// NM_005808
2.75	2.75	0.00	9.91E-01	9.97E-01	ALK	anaplastic lymphoma receptor tyrosine kinase	chr2p23	208212_s_at	NM_004304
2.59	2.59	0.00	9.91E-01	9.97E-01	GNL1	Guanine nucleotide binding protein-like 1	chr6p21.3	233544_at	NM_005275
4.10	4.10	0.00	9.91E-01	9.97E-01	BMP8B	Bone morphogenetic protein 8b	chr1p35-p32	235275_at	NM_001720
2.71	2.71	0.00	9.91E-01	9.97E-01	CEP110	centrosomal protein 110kDa	chr9q33-q34	205642_at	NM_007018
2.73	2.73	0.00	9.91E-01	9.97E-01	PCNXL2	pecanex-like 2 (Drosophila)	chr1q42.2	39650_s_at	NM_014801
2.33	2.33	0.00	9.92E-01	9.97E-01	---	---	---	1560900_a_at	---
2.08	2.08	0.00	9.91E-01	9.97E-01	---	---	---	241662_x_at	---
2.04	2.04	0.00	9.91E-01	9.97E-01	CCDC85A	coiled-coil domain containing 85A	chr2p16.1	235228_at	NM_001080433
2.00	2.00	0.00	9.91E-01	9.97E-01	---	---	---	242976_at	---
2.03	2.03	0.00	9.91E-01	9.97E-01	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	chr6q14	244623_at	NM_019842
3.24	3.24	0.00	9.92E-01	9.97E-01	---	---	---	235748_s_at	---
2.36	2.36	0.00	9.92E-01	9.97E-01	LOC100128840	hypothetical protein LOC100128840	chr12q24.33	1562783_at	XM_001719971 /// XM_001722553 /// XM_001726768
3.17	3.17	0.00	9.92E-01	9.97E-01	IRF6	interferon regulatory factor 6	chr1q32.3-q41	1552477_a_at	NM_006147
2.32	2.32	0.00	9.92E-01	9.97E-01	MAPRE2	microtubule-associated protein, RP/EB family, member 2	chr18q12.1	211556_at	NM_014268
8.22	8.23	0.00	9.92E-01	9.97E-01	TBC1D4	TBC1 domain family, member 4	chr13q22.2	203386_at	NM_014832
3.16	3.16	0.00	9.92E-01	9.97E-01	NOTCH3	Notch homolog 3 (Drosophila)	chr19p13.2-p13.1	203237_s_at	NM_000435
11.41	11.41	0.00	9.92E-01	9.97E-01	RPL22	ribosomal protein L22	chr1p36.3-p36.2	208768_x_at	NM_000983

4.20	4.21	0.00	9.92E-01	9.97E-01	ZNF706	zinc finger protein 706	chr8q22.3	227132_at	NM_001042510 /// NM_001042511 /// NM_016096																				
2.62	2.62	0.00	9.92E-01	9.97E-01	---	---	---	239030_at	---																				
3.42	3.42	0.00	9.92E-01	9.97E-01	CSF1	colony stimulating factor 1 (macrophage)	chr1p21-p13	207082_at	NM_000757 /// NM_172210 /// NM_172211 /// NM_172212																				
3.58	3.58	0.00	9.92E-01	9.97E-01	NDOR1	NADPH dependent diflavin oxidoreductase 1	chr9q34.3	234935_at	NM_014434 /// XM_001716570																				
2.83	2.83	0.00	9.92E-01	9.97E-01	PLCXD2	phosphatidylinositol-specific phospholipase C, X domain containing 2	chr3q13.2	1553281_at	NM_001134478 /// NM_153268																				
3.68	3.68	0.00	9.92E-01	9.97E-01	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	chr3p22.1	235120_at	NM_004206 /// NM_032970																				
2.93	2.93	0.00	9.92E-01	9.97E-01	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	chr3q22.1	1560020_at	NM_015268																				
4.43	4.43	0.00	9.92E-01	9.97E-01	PRDM1	PR domain containing 1, with ZNF domain	chr6q21-q22.1	217192_s_at	NM_001198 /// NM_182907																				
2.43	2.43	0.00	9.92E-01	9.97E-01	WFDC8	WAP four-disulfide core domain 8	chr20q13.12	1554157_a_at	NM_130896 /// NM_181510																				
2.99	2.99	0.00	9.92E-01	9.97E-01	---	---	---	238238_at	---																				
2.56	2.56	0.00	9.92E-01	9.97E-01	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	chr11q23.3	206607_at	NM_005188																				
4.36	4.36	0.00	9.92E-01	9.97E-01	GPC6	glypican 6	chr13q32	223730_at	NM_005708																				
1.94	1.95	0.00	9.93E-01	9.98E-01	---	---	---	241044_x_at	---																				
7.99	7.99	0.00	9.93E-01	9.98E-01	WDR40A	WD repeat domain 40A	chr9p13.3	224789_at	NM_015397																				
2.83	2.83	0.00	9.93E-01	9.98E-01	LOC728192	hypothetical protein LOC728192	chr13q33.3	1558930_at	XM_001128662																				
2.54	2.54	0.00	9.93E-01	9.98E-01	ANKHD1	ankyrin repeat and KH domain containing 1	chr5q31.3	229457_at	NM_017747 /// NM_017978 /// NM_024668																				
2.06	2.06	0.00	9.93E-01	9.98E-01	CNKSR2	connector enhancer of kinase suppressor of Ras 2	chrXp22.12	1554607_at	NM_014927																				
1.88	1.88	0.00	9.93E-01	9.98E-01	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	chr11q23	1559856_s_at	NM_005933																				
2.65	2.65	0.00	9.93E-01	9.98E-01	HMGB4	high-mobility group box 4	chr1p35.1	230473_s_at	NM_001008728 /// NM_145205																				
2.33	2.33	0.00	9.93E-01	9.98E-01	---	---	---	243872_at	---																				
6.33	6.34	0.01	9.93E-01	9.98E-01	---	---	---	233442_at	---																				
2.03	2.03	0.00	9.93E-01	9.98E-01	CLCA2	CLCA family member 2, chloride channel regulator	chr1p31-p22	206165_s_at	NM_006536																				
2.07	2.07	0.00	9.93E-01	9.98E-01	CENPK	centromere protein K	chr5p15.2-q12.3	222848_at	NM_022145																				
2.19	2.19	0.00	9.93E-01	9.98E-01	---	---	---	216148_at	---																				
2.11	2.11	0.00	9.93E-01	9.98E-01	GARNL1	GTPase activating Rap/RanGAP domain-like 1	chr14q13.2	1566271_x_at	NM_014990 /// NM_194301																				
2.51	2.51	0.00	9.94E-01	9.98E-01	---	---	---	233709_at	---																				
6.38	6.38	0.00	9.94E-01	9.98E-01	FAM114A1	family with sequence similarity 114, member A1	chr4p14	226697_at	NM_138389																				
3.87	3.87	0.00	9.94E-01	9.98E-01	RNF157	ring finger protein 157	chr17q25.1	1569775_at	NM_052916																				
2.48	2.48	0.00	9.94E-01	9.98E-01	YOD1	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	chr1q32.1	215150_at	NM_018566																				
2.49	2.49	0.00	9.94E-01	9.98E-01	NTN1	netrin 1	chr17p13-p12	208005_at	NM_004822																				
7.42	7.42	0.00	9.94E-01	9.98E-01	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	chr20q13.3	204540_at	NM_001958																				
4.26	4.26	0.00	9.94E-01	9.98E-01	---	---	---	229607_at	---																				
2.54	2.54	0.00	9.94E-01	9.98E-01	UQCRC2	ubiquinol-cytochrome c reductase core protein II	chr16p12	241755_at	NM_003366																				
2.07	2.07	0.00	9.94E-01	9.98E-01	---	---	---	242018_at	---																				
2.14	2.14	0.00	9.94E-01	9.98E-01	LOC255480	hypothetical protein LOC255480	chr12q24.21	233947_s_at	XM_001134335 /// XM_001719855 /// XM_001723369																				
2.78	2.78	0.00	9.94E-01	9.98E-01	LAMC2	laminin, gamma 2	chr1q25-q31	202267_at	NM_005562 /// NM_018891																				
4.56	4.56	0.00	9.94E-01	9.98E-01	---	---	---	227565_at	---																				
2.46	2.46	0.00	9.95E-01	9.98E-01	FRZB	Frizzled-related protein	chr2qter	231273_x_at	NM_001463																				
6.93	6.94	0.00	9.95E-01	9.98E-01	---	---	---	1562529_s_at	---																				
2.01	2.01	0.00	9.95E-01	9.98E-01	USP25	Ubiquitin specific peptidase 25	chr21q11.2	1555558_at	NM_013396																				
2.12	2.13	0.00	9.95E-01	9.98E-01	ZFP42	zinc finger protein 42 homolog (mouse)	chr4q35.2	1554776_at	NM_174900																				
5.63	5.63	0.00	9.95E-01	9.99E-01	---	---	---	227991_x_at	---																				
3.18	3.18	0.00	9.95E-01	9.99E-01	ERGIC2	ERGIC and golgi 2	chr12p11.22	226418_at	NM_016570																				
2.43	2.43	0.00	9.95E-01	9.99E-01	---	---	---	231925_at	---																				
2.86	2.86	0.00	9.95E-01	9.99E-01	ABHD3	abhydrolase domain containing 3	chr18q11.2	213017_at	NM_138340																				
1.95	1.95	0.00	9.95E-01	9.99E-01	---	---	---	234352_x_at	---																				

2.40	2.40	0.00	9.95E-01	9.99E-01	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	chr9q22.1	229463_at	NM_001007097 /// NM_001018064 /// NM_001018065 /// NM_001018066 /// NM_006180
6.14	6.15	0.00	9.95E-01	9.99E-01	PIGF	phosphatidylinositol glycan anchor biosynthesis, class F	chr2p21-p16	205078_at	NM_002643 /// NM_173074
2.24	2.24	0.00	9.95E-01	9.99E-01	LOC730034	Hypothetical LOC730034	chr14q31.3	1559970_at	XM_001133186 /// XM_001134172 /// XM_001720905
6.61	6.61	0.00	9.95E-01	9.99E-01	---	---	---	216858_x_at	---
3.13	3.13	0.00	9.95E-01	9.99E-01	LOC284408	hypothetical protein LOC284408	chr19q13.13	1558809_s_at	---
2.25	2.25	0.00	9.95E-01	9.99E-01	---	---	---	233330_s_at	---
2.27	2.27	0.00	9.95E-01	9.99E-01	CHEK1	CHK1 checkpoint homolog (S. pombe)	chr11q24-q24	205393_s_at	NM_001114121 /// NM_001114122 /// NM_001274
2.14	2.14	0.00	9.95E-01	9.99E-01	---	---	---	1561033_at	---
4.30	4.30	0.00	9.95E-01	9.99E-01	TBC1D26 /// ZNF286A	TBC1 domain family, member 26 /// zinc finger protein 286A	chr17p11.2	240576_at	NM_001130842 /// NM_020652 /// NM_178571
2.95	2.95	0.00	9.96E-01	9.99E-01	OTUD4	OTU domain containing 4	chr4q31.21	203479_s_at	NM_001102653 /// NM_017493 /// NM_199324
3.36	3.36	0.00	9.96E-01	9.99E-01	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	chr7q21	207702_s_at	NM_012301
6.10	6.10	0.00	9.96E-01	9.99E-01	TUG1	taurine upregulated gene 1	chr22q12.2	212337_at	NR_002323
1.99	1.99	0.00	9.96E-01	9.99E-01	---	---	---	241761_at	---
1.94	1.94	0.00	9.96E-01	9.99E-01	---	---	---	241340_at	---
3.83	3.83	0.00	9.96E-01	9.99E-01	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	chr1p36	206933_s_at	NM_004285
2.21	2.21	0.00	9.96E-01	9.99E-01	PHF3	PHD finger protein 3	chr6q12	217953_at	NM_015153
2.95	2.95	0.00	9.96E-01	9.99E-01	MAP2K7	mitogen-activated protein kinase kinase 7	chr19p13.3-p13.2	209951_s_at	NM_145185
2.18	2.18	0.00	9.96E-01	9.99E-01	MGC14738	hypothetical protein MGC14738	---	1562107_at	---
2.06	2.06	0.00	9.96E-01	9.99E-01	DKK2	dickkopf homolog 2 (Xenopus laevis)	chr4q25	219908_at	NM_014421
3.27	3.27	0.00	9.96E-01	9.99E-01	CLDN4	claudin 4	chr7q11.23	201428_at	NM_001305
3.29	3.29	0.00	9.96E-01	9.99E-01	MUC1	mucin 1, cell surface associated	chr1q21	207847_s_at	NM_001018016 /// NM_001018017 /// NM_001044390 /// NM_001044391 /// NM_001044392 /// NM_001044393 /// NM_002456
5.36	5.36	0.00	9.96E-01	9.99E-01	C10orf76	chromosome 10 open reading frame 76	chr10q24.32	218891_at	NM_024541
2.49	2.49	0.00	9.96E-01	9.99E-01	LOC642313	hypothetical LOC642313	chr9p24.3	1559810_at	XR_041113
2.22	2.22	0.00	9.96E-01	9.99E-01	NPSA	novel prostate-specific antigen	---	1555502_at	---
3.59	3.59	0.00	9.96E-01	9.99E-01	---	---	---	234195_at	---
3.22	3.22	0.00	9.96E-01	9.99E-01	OR7C2	olfactory receptor, family 7, subfamily C, member 2	chr19p13.1	208507_at	NM_012377
2.94	2.94	0.00	9.96E-01	9.99E-01	CCBP2	chemokine binding protein 2	chr3p21.3	206887_at	NM_001296
4.26	4.26	0.00	9.96E-01	9.99E-01	---	---	---	227665_at	---
2.34	2.35	0.00	9.96E-01	9.99E-01	---	---	---	237527_at	---
4.71	4.71	0.00	9.97E-01	9.99E-01	PHF19	PHD finger protein 19	chr9q33.2	227212_s_at	NM_001009936 /// NM_015651
2.28	2.28	0.00	9.97E-01	9.99E-01	VASH2	vasohibin 2	chr1q32.3	219740_at	NM_024749
2.12	2.12	0.00	9.97E-01	9.99E-01	RHOJ	ras homolog gene family, member J	chr14q23.2	243481_at	NM_020663
4.79	4.79	0.00	9.97E-01	9.99E-01	AXIN2	axin 2	chr17q23-q24	224176_s_at	NM_004655
6.00	6.00	0.00	9.97E-01	9.99E-01	ZEB1	zinc finger E-box binding homeobox 1	chr10p11.2	212764_at	NM_001128128 /// NM_030751
1.98	1.98	0.00	9.97E-01	9.99E-01	---	---	---	1562352_at	---

4.62	4.62	0.00	9.97E-01	9.99E-01	SLC16A8	solute carrier family 16, member 8 (monocarboxylic acid transporter 3)	chr22q12.3-q13.2	220455_at	NM_013356
4.21	4.21	0.00	9.97E-01	9.99E-01	C16orf74	chromosome 16 open reading frame 74	chr16q24.1	227806_at	NM_206967
2.19	2.19	0.00	9.97E-01	9.99E-01	---	---	---	230444_at	---
5.01	5.01	0.00	9.97E-01	9.99E-01	SIPA1L3	signal-induced proliferation-associated 1 like 3	chr19q13.13	37831_at	NM_015073
2.05	2.05	0.00	9.97E-01	9.99E-01	---	---	---	1561795_at	---
6.67	6.67	0.00	9.97E-01	9.99E-01	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	chr5q31.1	202462_s_at	NM_014829
5.89	5.89	0.00	9.98E-01	9.99E-01	HLA-B /// HLA-C /// MICA /// MICB /// XXbac-BPG181B23.1	major histocompatibility complex, class I, B /// major histocompatibility complex, class I, C /// MHC class I polypeptide-related sequence A /// MHC class I polypeptide-related sequence B /// MHC class I polypeptide-related sequence A	chr6p21.3 /// chr6p21.33	205905_s_at	NM_000247 /// NM_002117 /// NM_005514 /// NM_005931 /// XM_001713607 /// XM_001715881 /// XM_001717045 /// XM_001719879
3.45	3.45	0.00	9.97E-01	9.99E-01	NASP	nuclear autoantigenic sperm protein (histone-binding)	chr1p34.1	201969_at	NM_002482 /// NM_152298 /// NM_172164
1.99	1.99	0.00	9.97E-01	9.99E-01	---	---	---	237751_x_at	---
3.37	3.37	0.00	9.98E-01	9.99E-01	PRDM16	PR domain containing 16	chr1p36.23-p33	220928_s_at	NM_022114 /// NM_199454 /// XM_936932
3.17	3.17	0.00	9.98E-01	9.99E-01	---	---	---	238038_at	---
3.53	3.54	0.00	9.97E-01	9.99E-01	---	---	---	1566157_x_at	---
2.54	2.54	0.00	9.98E-01	9.99E-01	LOC255177	hypothetical protein LOC255177	chr15q22.2	1562501_at	---
2.72	2.72	0.00	9.98E-01	9.99E-01	---	---	---	1570110_at	---
2.71	2.71	0.00	9.97E-01	9.99E-01	RICH2	Rho-type GTPase-activating protein RICH2	chr17p12	215232_at	NM_014859
3.82	3.82	0.00	9.97E-01	9.99E-01	---	---	---	228178_s_at	---
2.60	2.60	0.00	9.97E-01	9.99E-01	IL18R1	interleukin 18 receptor 1	chr2q12	206618_at	NM_003855
2.19	2.19	0.00	9.97E-01	9.99E-01	BNC1	basonuclin 1	chr15q25.2	206581_at	NM_001717
2.26	2.27	0.00	9.97E-01	9.99E-01	SLC17A2	solute carrier family 17 (sodium phosphate), member 2	chr6p21.3	207097_s_at	NM_005835
2.64	2.64	0.00	9.97E-01	9.99E-01	ERVWE1	endogenous retroviral family W, env(C7), member 1	chr7q21-q22	1553352_x_at	NM_001130925 /// NM_014590
2.04	2.04	0.00	9.98E-01	9.99E-01	PDE9A	phosphodiesterase 9A	chr21q22.3	237139_at	NM_001001567 /// NM_001001568 /// NM_001001569 /// NM_001001570 /// NM_001001571 /// NM_001001572 /// NM_001001573 /// NM_001001574 /// NM_001001575 /// NM_001001576 /// NM_001001577 /// NM_001001578 /// NM_001001579 /// NM_001001580 /// NM_001001581 /// NM_001001582 /// NM_001001583 /// NM_001001584 /// NM_001001585 /// NM_002606

7.35	7.35	0.00	9.98E-01	9.99E-01	TFRC	transferrin receptor (p90, CD71)	chr3q29	207332_s_at	NM_001128148 /// NM_003234
5.31	5.31	0.00	9.98E-01	9.99E-01	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	chr4q12	212851_at	NM_001040402 /// NM_015115
4.87	4.88	0.00	9.98E-01	9.99E-01	GSTM4	glutathione S-transferase M4	chr1p13.3	204149_s_at	NM_000850 /// NM_147148
3.57	3.57	0.00	9.98E-01	9.99E-01	ALOXE3	arachidonate lipoxygenase 3	chr17p13.1	207708_at	NM_021628
3.39	3.39	0.00	9.98E-01	9.99E-01	---	---	---	1562869_at	---
4.10	4.10	0.00	9.98E-01	9.99E-01	ZFP36L2	Zinc finger protein 36, C3H type-like 2	chr2p22.3-p21	227681_at	NM_006887
2.23	2.23	0.00	9.98E-01	9.99E-01	SLC38A11	solute carrier family 38, member 11	chr2q24.3	243231_at	NM_173512
2.88	2.88	0.00	9.98E-01	9.99E-01	HOXB13	homeobox B13	chr17q21.2	230105_at	NM_006361
1.97	1.97	0.00	9.98E-01	9.99E-01	---	---	---	1563310_a_at	---
2.52	2.52	0.00	9.98E-01	9.99E-01	ZNF215	zinc finger protein 215	chr11p15.4	220214_at	NM_013250
2.51	2.52	0.00	9.98E-01	9.99E-01	---	---	---	237959_at	---
2.29	2.29	0.00	9.98E-01	9.99E-01	SENP7	SUMO1/sentrin specific peptidase 7	chr3q12	223444_at	NM_001077203 /// NM_020654
3.26	3.26	0.00	9.98E-01	9.99E-01	MSL3L1	male-specific lethal 3-like 1 (Drosophila)	chrXp22.3	236165_at	NM_006800 /// NM_078628 /// NM_078629 /// NM_078630
2.33	2.33	0.00	9.98E-01	9.99E-01	ZBTB45	zinc finger and BTB domain containing 45	chr19q13.43	240551_at	NM_032792
2.16	2.16	0.00	9.98E-01	9.99E-01	---	---	---	1566771_at	---
1.83	1.83	0.00	9.98E-01	9.99E-01	---	---	---	1569277_at	---
4.95	4.95	0.00	9.98E-01	9.99E-01	ADA	adenosine deaminase	chr20q12-q13.11	204639_at	NM_000022
2.96	2.96	0.00	9.98E-01	9.99E-01	TCP10L	t-complex 10 (mouse)-like	chr21q22.11	230394_at	NM_144659
2.27	2.27	0.00	9.98E-01	9.99E-01	SH2D3A	SH2 domain containing 3A	chr19p13.3	219513_s_at	NM_005490
2.01	2.01	0.00	9.98E-01	9.99E-01	---	---	---	231598_x_at	---
2.79	2.79	0.00	9.99E-01	1.00E+00	GJB3	gap junction protein, beta 3, 31kDa	chr1p34	205491_s_at	NM_001005752 /// NM_024009
6.92	6.92	0.00	9.99E-01	1.00E+00	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	chr3p21.3	202520_s_at	NM_000249
3.19	3.19	0.00	9.99E-01	1.00E+00	---	---	---	233212_at	---
2.29	2.29	0.00	9.99E-01	1.00E+00	CORIN	corin, serine peptidase	chr4p13-p12	239260_at	NM_006587
3.52	3.52	0.00	9.99E-01	1.00E+00	ZNF45	zinc finger protein 45	chr19q13.2	207304_at	NM_003425
2.61	2.61	0.00	9.99E-01	1.00E+00	C7orf33	chromosome 7 open reading frame 33	chr7q36.1	1553927_at	NM_145304
2.24	2.24	0.00	9.99E-01	1.00E+00	CEP290	Centrosomal protein 290kDa	chr12q21.32	1556850_at	NM_025114
2.62	2.62	0.00	9.99E-01	1.00E+00	ASB11	ankyrin repeat and SOCS box-containing 11	chrXp22.31	1553074_at	NM_001012428 /// NM_080873
5.42	5.42	0.00	9.99E-01	1.00E+00	DKFZP564O0823	DKFZP564O0823 protein	chr4q13.3-q21.3	204687_at	NM_015393
2.32	2.32	0.00	9.99E-01	1.00E+00	FA2H	fatty acid 2-hydroxylase	chr16q23	219429_at	NM_024306
5.15	5.15	0.00	9.99E-01	1.00E+00	C9orf95	chromosome 9 open reading frame 95	chr9q21.13	219147_s_at	NM_001127603 /// NM_017881 /// NR_023352
2.83	2.83	0.00	9.99E-01	1.00E+00	---	---	---	1563138_at	---
2.44	2.44	0.00	9.99E-01	1.00E+00	MED4	mediator complex subunit 4	chr13q14.2	222438_at	NM_014166
2.95	2.96	0.00	9.99E-01	1.00E+00	---	---	---	215545_at	---
2.40	2.40	0.00	9.99E-01	1.00E+00	PHF20L1	PHD finger protein 20-like 1	chr8q24.22	219606_at	NM_016018 /// NM_032205 /// NM_198513
2.76	2.76	0.00	9.99E-01	1.00E+00	SFRS1	splicing factor, arginine/serine-rich 1	chr17q21.3-q22	201741_x_at	NM_001078166 /// NM_006924
2.17	2.17	0.00	9.99E-01	1.00E+00	TSHR	thyroid stimulating hormone receptor	chr14q31	210055_at	NM_000369 /// NM_001018036
2.03	2.03	0.00	9.99E-01	1.00E+00	---	---	---	1561663_at	---
6.78	6.78	0.00	1.00E+00	1.00E+00	PXN	paxillin	chr12q24.31	201087_at	NM_001080855 /// NM_002859 /// NM_025157
2.23	2.23	0.00	1.00E+00	1.00E+00	TRAF5	TNF receptor-associated factor 5	chr1q32	1569861_at	NM_001033910 /// NM_004619 /// NM_145759
4.99	4.99	0.00	1.00E+00	1.00E+00	LOC203274	Hypothetical protein LOC203274	chr9q21.11	1554517_x_at	---
2.35	2.35	0.00	1.00E+00	1.00E+00	---	---	---	242573_at	---

6.00	6.00	0.00	1.00E+00	1.00E+00	PLA2G12A	Phospholipase A2, group XIIA	chr4q25	242323_at	NM_030821																				
2.91	2.91	0.00	1.00E+00	1.00E+00	---	---	---	1561413_at	---																				
4.27	4.27	0.00	1.00E+00	1.00E+00	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	chr15q25	1557795_s_at	NM_001007156 /// NM_001012338 /// NM_002530																				