

Scalp fibroblasts have a shared expression profile in monogenic craniosynostosis

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ABSTRACT

Background Craniosynostosis can be caused by both genetic and environmental factors, the relative contributions of which vary between patients. Genetic testing identifies a pathogenic mutation or chromosomal abnormality in ~21% of cases, but it is likely that further causative mutations remain to be discovered.

Objective To identify a shared signature of genetically determined craniosynostosis by comparing the expression patterns in three monogenic syndromes with a control group of patients with non-syndromic sagittal synostosis.

Methods Fibroblasts from 10 individuals each with Apert syndrome (FGFR2 substitution S252W), Muenke syndrome (FGFR3 substitution P250R), Saethre–Chotzen syndrome (various mutations in *TWIST1*) and non-syndromic sagittal synostosis (no mutation detected) were cultured. The relative expression of ~47 000 transcripts was quantified on Affymetrix arrays.

Results 435, 45 and 46 transcripts were identified in the Apert, Muenke and Saethre–Chotzen groups, respectively, that differed significantly from the controls. Forty-six of these transcripts were shared between two or more syndromes and, in all but one instance, showed the same direction of altered expression level compared with controls. Pathway analysis showed over-representation of the shared transcripts in core modules involving cell-to-cell communication and signal transduction. Individual samples from the Apert syndrome cases could be reliably distinguished from non-syndromic samples based on the gene expression profile, but this was not possible for samples from patients with Muenke and Saethre–Chotzen syndromes.

Conclusions Common modules of altered gene expression shared by genetically distinct forms of craniosynostosis were identified. Although the expression profiles cannot currently be used to classify individual patients, this may be overcome by using more sensitive assays and sampling additional tissues.

Craniosynostosis (CRS), the premature fusion of one or more of the cranial sutures, affects 1 in every 2100–2500 children and requires multidisciplinary management to address potential complications, which include raised intracranial pressure, problems with vision, hearing, breathing and feeding, learning difficulties, and significant cosmetic deformity.¹

CRS is very heterogeneous, in both presentation and aetiology. Patients may variously be classified according to which sutures are fused, the association with identified genetic or environmental risk factors, the presence of additional clinical features suggestive of a syndrome, or the identification of

a causative genetic mutation or chromosomal abnormality. About two-thirds of patients have non-syndromic synostosis affecting a single suture, the sagittal suture being most commonly involved (accounting for up to 50% of all individuals with CRS).¹ Non-syndromic sagittal synostosis (NSS) occurs in males about four times as often as in females, but no other genetic risk factors have been consistently demonstrated, and epidemiological evidence indicates that the genetic contribution to this disorder is largely polygenic.^{2–4} Although intrauterine fetal head constraint is suspected to represent an important risk factor for sagittal synostosis,^{3, 5} it is challenging to prove this in individual cases because objective data on fetal head constraint are difficult to obtain.

At the other end of the spectrum of causation, a specific genetic aetiology (either single gene mutation or chromosome abnormality) can be identified in ~21% of patients, the majority of whom have additional clinical features indicating the presence of a syndrome.⁶ Heterozygous mutations in the fibroblast growth factor receptor type 2 (*FGFR2*) and type 3 (*FGFR3*) genes, and the *TWIST1* gene, are most commonly identified.⁷ The *FGFR2* and *FGFR3* mutations usually encode specific missense substitutions that confer gain-of-function to the mutant receptor tyrosine kinase, whereas the *TWIST1* mutations are heterogeneous and result in loss-of-function (haploinsufficiency) of the encoded basic helix–loop–helix transcription factor. The most common individual CRS-related substitutions are S252W and P253R in *FGFR2* (causing Apert syndrome; AS) and P250R in *FGFR3* (causing Muenke syndrome; MS)^{6, 8}; *TWIST1* mutations are diagnostic of Saethre–Chotzen syndrome (SCS).⁹

Genetic counselling for families affected with CRS is straightforward when the proband has either non-syndromic midline suture synostosis (risks are relatively low and empiric data can be used) or an identified genetic alteration (genetic testing identifies those individuals at risk). However, it is much more challenging in the minority of cases (~15–20%)⁶ in whom either a syndrome is suspected (based on positive family history, additional dysmorphic features or learning disability), or multiple cranial sutures are fused, but where all currently available genetic tests are negative. This situation is clearly unsatisfactory as the various aetiological possibilities in this situation (dominant, recessive, polygenic) are associated with very different recurrence risks.

To provide an alternative approach to the investigation of causation, we sought here to identify a characteristic signature, based on finding altered



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patterns of mRNA expression in fibroblasts, that could potentially provide a biological marker of genetically mediated CRS. We chose to analyse fibroblasts for two reasons. Firstly, these can readily be cultured at the time of craniofacial surgery from a small biopsy sample of scalp skin, enabling the standardisation of the sampling protocol and greater simplicity for diagnostic purposes. Secondly, fibroblasts are developmentally related to osteoblasts, which have been described as 'sophisticated fibroblasts',¹⁰ and therefore represent a particularly relevant cell type in the context of CRS. By comparing the expression patterns in three of the most common genetic types of CRS with NSS cases, we have identified shared modules of altered gene expression in the syndromic groups that indicate a common pathogenetic pathway involving cell-to-cell communication and signal transduction. These results provide a starting point for a new functional method of classifying CRS based on the mRNA expression profile.

SUBJECTS AND METHODS

Patients and samples

Ethics approval for the work was obtained from the Oxfordshire Research Ethics Committee (C02.143). Patients with suspected diagnoses of AS, MS and SCS were screened for mutations in *FGFR2*, *FGFR3* and *TWIST1*, respectively, by restriction digest, denaturing high-performance liquid chromatography (Transgenomic WAVE System) and DNA sequencing of appropriate PCR products.⁸ Patients with *TWIST1* mutations from whom we obtained samples were all reported on previously.¹¹ Patients with NSS were screened for all common mutations in *FGFR1*, *FGFR2*, *FGFR3* and *TWIST1*.⁶ At operation, a transverse incision was made across the vertex of the scalp, and a strip of skin (~2 cm × 0.3 cm) was removed from the incision site before closure. In two cases of AS, skin was taken from the hand at the time of a corrective procedure. Online supplementary table 1 summarises the mutational data, site of tissue sampling, and age of the patient when each sample was obtained. For the microarray studies, the average age at sampling ranged from 1.40 years for the NSS group to 3.96 years for the MS group, the difference in age was not statistically significant for any of the groups (t test).

Skin was cultured at 37°C with 5% CO₂ in Dulbecco's modified Eagle's medium (Invitrogen, Paisley, UK) supplemented with 10% fetal calf serum (FCS; catalogue Nos A15-041 and A15-043, PAA Laboratories GmbH, Pasching, Austria) and frozen in 50% FCS for storage. Frozen cells were thawed and grown to ~70% confluency in a 75 cm³ flask before RNA extraction. All analyses were conducted on cells passaged between three and five times.

RNA extraction and microarray processing

Total RNA was extracted using TRIzol (Invitrogen) following the manufacturer's protocol. The quality of RNA samples was evaluated using the Agilent Bioanalyzer 2100 (Agilent Technologies, South Queensferry, UK). Only samples with preserved rRNA ratio (28S/18S) and no evidence for RNA degradation were analysed further.

RNA labelling and hybridisation used protocols, reagents and equipment supplied by Affymetrix, High Wycombe, UK. A 2 µg portion of total RNA from each sample was labelled with the One-Cycle cDNA Synthesis and One-Cycle Target Labelling and Control Reagent kits. Then 10 µg of the resulting biotin-labelled fragmented cRNA was hybridised to GeneChip Human Genome U133 Plus 2.0 arrays, which identify over 47 000 transcripts.

After hybridisation at 45°C for 16 h (Hybridisation Oven 640), microarrays were washed and stained with streptavidin-phycoerythrin conjugate in a Fluidics Station 450, and scanned with a GeneChip Scanner 3000.

Microarray data analysis

After array scanning, quality control (QC) was performed with GCOS software (Affymetrix). All QC measures (scaling factor ≤3-fold difference within a study; 3'/5' ratio for probe sets for *GAPDH* ≤3; present (P) calls in the same range for all samples in the study and RawQ below 100) were in the acceptable range for all samples. The .CEL data files have been deposited in ArrayExpress (accession No E-MEXP-2236).

Affymetrix GeneChip .CEL files were analysed in R (see <http://www.r-project.org>) using the Bioconductor packages (<http://www.bioconductor.org>) for QC analysis, data normalisation, hierarchical clustering, and identification of differentially expressed transcripts. Specifically, the data were normalised using Robust MultiChip Analysis,¹² and differentially expressed genes were identified using Statistical Analysis for Microarrays (SAM) with a false discovery rate cut-off of 5%.¹³ Prediction Analysis for Microarrays (PAM) was implemented to determine if a gene set could be identified that classified the arrays correctly when cross-validation was applied.¹⁴ Both unsupervised and supervised two-way (genes against samples) hierarchical clustering methods were used to establish the relationships among samples and to check if the individual samples clustered together according to similarity in their expression signatures. Hierarchical clustering was performed with Genesis software using complete linkage clustering.¹⁵

Gene lists produced using the above methods were subsequently imported into Ingenuity and mined by Ingenuity Pathways Analysis (IPA) (Ingenuity Systems, US; <http://www.ingenuity.com>). This core gene list was analysed for gene annotation enrichment using the Database for Annotation, Visualisation and Integrated Discovery (DAVID) 2008; the enriched functional annotation terms associated with each gene were identified and listed according to their enrichment p value (<http://niaid.abcc.ncicrf.gov/>).^{16 17}

Quantitative real-time PCR

To validate the gene expression measurements independently, we performed quantitative reverse transcription PCR (RT-PCR) on three genes (*HLA-DPA1*, *MMP1* and *TGFBR2*) using pre-designed ABI Taqman primers, probes and amplification reagents (Assays-on-Demand; Applied Biosystems, Warrington, UK), according to the manufacturer's instructions. Firstly, 2 µg total RNA from each subject was reverse-transcribed with the RETROscript kit (Ambion, Warrington, UK), and the cDNA was amplified by quantitative real-time PCR in an ABI 7500 PCR system (Applied Biosystems). Amplification of the *GAPDH* gene served as a normalisation control for each sample to correct for minor differences in RNA quality and quantity. The expression ratio was calculated using the 2^{-ΔΔCT} method.¹⁸ t Tests were performed to determine significant differences in gene expression, and Fisher exact tests to compare data in 2×2 tables.

RESULTS

Expression profiling of syndromic CRS

We established primary skin fibroblast cell lines derived from scalp skin, from subjects with confirmed diagnoses of AS, MS and SCS, and control subjects with NSS. Ten samples from each diagnostic category were chosen for investigation by expression profiling

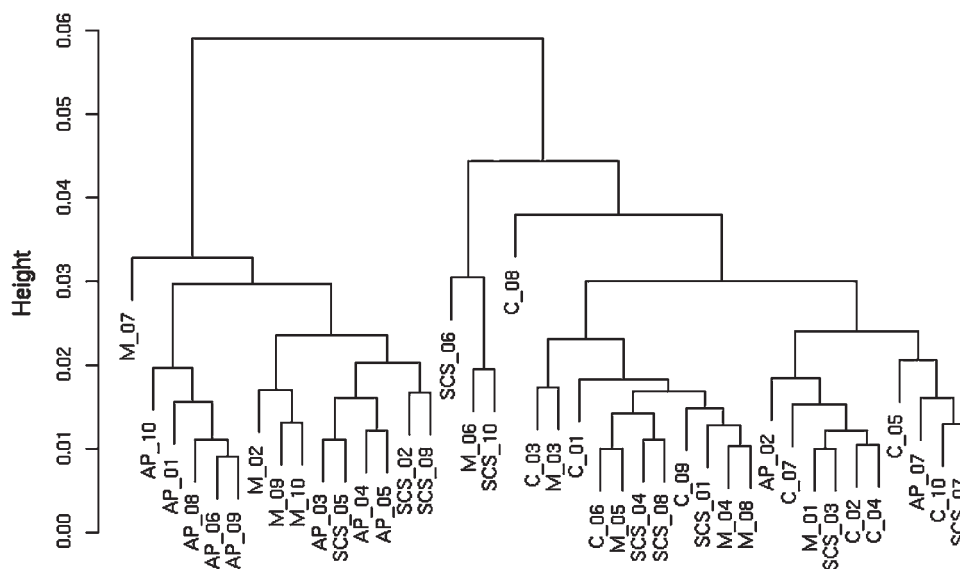
(online supplementary table 1). RNA from the 40 subjects was hybridised to Affymetrix GeneChip U133 Plus 2.0 microarrays, which comprehensively cover the human transcriptome.

For the first stage of the analysis, we asked whether the samples could be clustered by disease category. Unsupervised clustering of all samples, based on all transcripts on the microarray, produced the dendrogram shown in figure 1. Eight of 10 AS samples located to a cluster that did not contain any NSS controls ($p=0.0007$), indicating that AS has the most distinctive expression profile among the four patient groups studied. By contrast, the MS and SCS samples clustered poorly, and only a minority (four MS, three SCS) were clearly discriminated from the NSS controls.

To identify the transcripts that best discriminated the syndromic patients as a whole from the NSS controls, we used SAM analysis. A total of 1044 independent probe sets, representing 863 different genes, were found to be significantly differentially expressed (online supplementary table 2). Of the 141 genes represented by two or more probe sets, the direction of change in transcription was concordant for the different probe sets in 139 cases, indicating that the great majority of changes observed are real rather than the result of statistical noise. However, supervised clustering using this gene set provided only modest improvement over unsupervised analysis, with nine of 10 AS samples clustered in a single group that contained one MS sample in addition, but no major change in the clustering of MS or SCS samples (online supplementary figure 1).

One factor that might have impeded clustering of syndromic cases from NSS controls is that the different syndromic diagnoses were associated with different expression signatures. We therefore repeated the SAM analysis, comparing each syndromic group (AS, MS, SCS) individually with the NSS controls. This analysis identified 547 (AS), 52 (MS) and 56 (SCS) independent probe sets, representing, respectively, 435 (AS), 45 (MS) and 46 (SCS) differentially expressed genes between the syndromic cases and the NSS controls (online supplementary table 3). In the previous SAM analysis of all syndromic versus NSS controls, 163 of the unique gene entries were also represented. The much larger number of probe sets identified for the AS fibroblasts presumably reflects a more widespread disturbance in cellular homeostasis, and correlates with the greater phenotypic severity of AS, with regard to both CRS and other skeletal features, compared with either MS or SCS.

Figure 1 Cluster analysis of gene expression in craniosynostosis (CRS). The dendrogram shows the results of unsupervised clustering analysis of 10 samples each of Apert syndrome (AS) (AP_01–AP_10), Muenke syndrome (MS) (M_01–M_10), Saethre–Chotzen syndrome (SCS) (SCS_01–SCS_10), and 10 non-syndromic sagittal synostosis (NSS) controls (C_01–C_10), using information from all the probe sets of the Affymetrix U133 Plus 2.0 arrays.



Discrimination of individual syndromic samples from controls

As an alternative approach to testing the use of these data for sample classification, we used PAM analysis for each of the syndromes compared with controls. In the case of AS, satisfactory discrimination from NSS controls (misclassification error ≤ 0.1) could be achieved by the measurement of 91 transcripts representing 73 genes (figure 2A). Figure 2B shows the heat map obtained when clustering using these genes. However, similar PAM analyses of MS and SCS gave unacceptably high misclassification error (>0.2) and hence poor classification potential (online supplementary figure 2).

These results indicate that, while our analytical procedure was able to distinguish individual AS from NSS samples with good confidence, it was not reliable in the case of individual MS or SCS samples.

Identification of a common CRS syndromic expression profile

We next asked whether the lists of unique transcripts generated using the separate SAM analyses of each syndrome compared with NSS controls, described above (online supplementary table 3), showed significant overlap. Of a total of 477 transcripts in these lists, 43 featured in two of the lists and three in all three lists (figure 3). All except one of these 46 multiply listed transcripts showed the same direction of change in the different syndromic CRS disorders relative to the NSS group, indicating that these trends were highly non-random ($p=10^{-7}$). We randomly selected three transcripts significantly altered at least in the AS group for independent assessment by real-time RT-PCR; the genes chosen were *HLA-DPA1* (major histocompatibility complex, class II, DP α 1), *MMP1* (matrix metalloproteinase 1, interstitial collagenase; also significantly altered in SCS) and *TGFBR2* (transforming growth factor beta receptor II (70/80 kDa); also significantly altered in SCS). We analysed both the original samples used in the Affymetrix microarray experiment (not shown), and—for further validation on an independent set of samples—five different AS patients with P253R FGFR2 mutations and five further NSS controls (figure 4). In all cases, the results confirmed the trends originally identified in the microarray analysis, indicating that they were independent of changes in the sample, time of culture, and method of mRNA quantification.

To assess whether particular regulatory networks were enriched in the lists of discriminating transcripts for the three

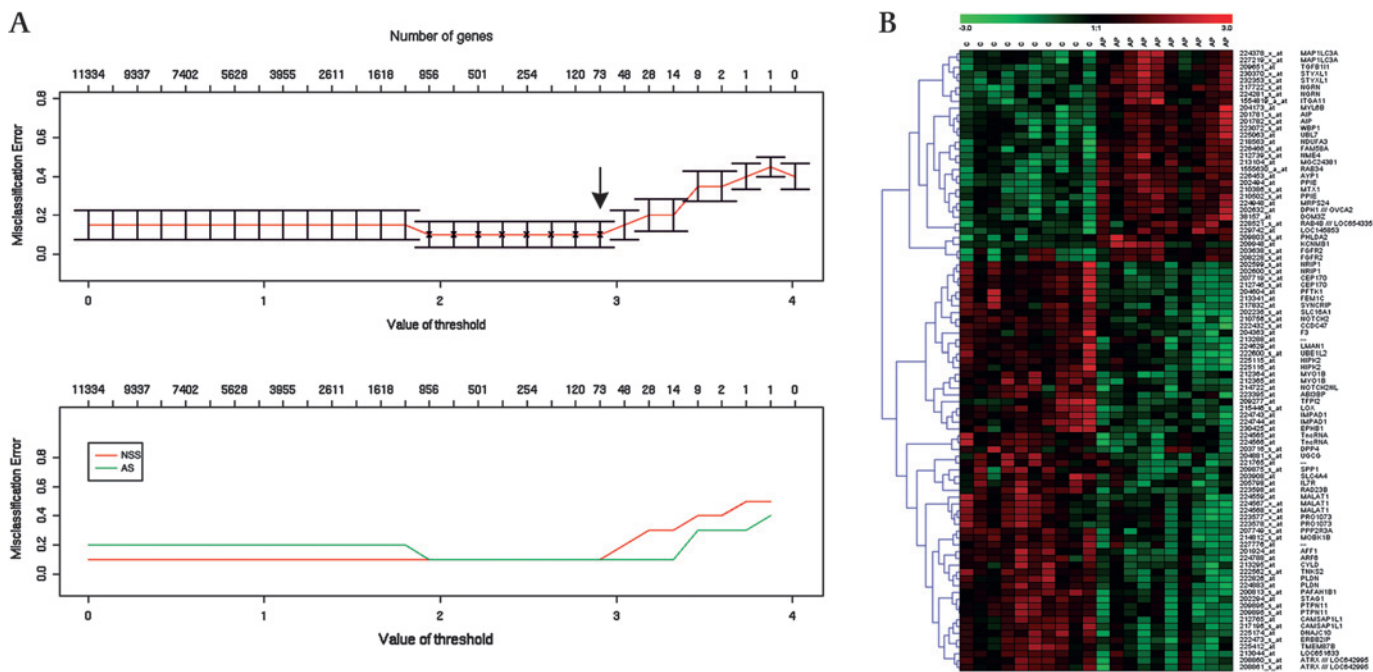


Figure 2 Fibroblast expression signature distinguishes Apert syndrome (AS) samples from non-syndromic sagittal synostosis (NSS) controls. (A) Prediction Analysis for Microarrays (PAM) analysis. The upper panel shows the predictive power (measured by misclassification error on the y axis) of the full list of genes (extreme left on the x axis) to a single classifying gene (extreme right of the x axis). The best predictive power, hence smallest misclassification error, is achieved with the top 73 classifying genes (arrow). The lower panel shows the misclassification error for each diagnosis, with the NSS controls in red and AS cases in green. (B) Supervised clustering and heat map generated with the top 73 AS-classifying genes.

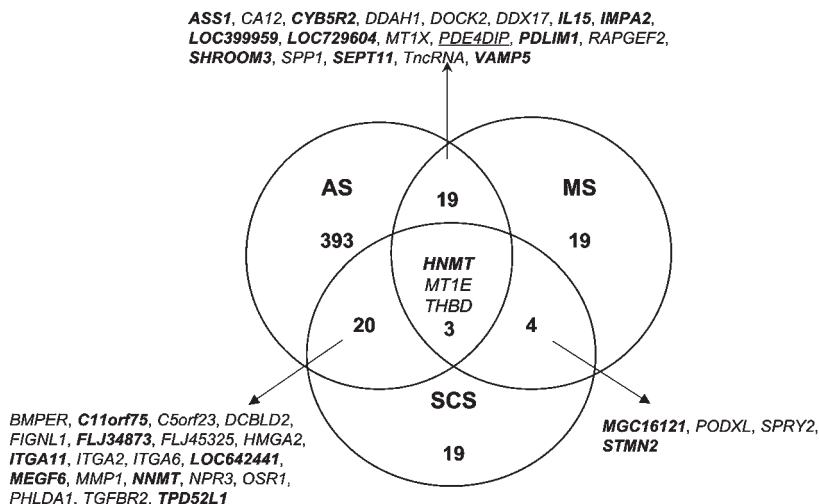
syndromic conditions, we used IPA. This highlighted 22 of the 46 transcripts that had shown differential changes in more than one CRS syndrome compared with NSS controls (figure 3) as belonging to core conserved networks. ‘Network’ genes that showed increased expression in syndromic CRS are *ASS1*, *IL15*, *ITGA11*, *PDLIM1*, *SHROOM3*, *STMN2* and *TPD52L1*, and those that showed decreased expression are *CA12*, *DCBLD2*, *DDX17*, *DOCK2*, *HMGA2*, *ITGA2*, *ITGA6*, *MMP1*, *MT1E*, *NPR3*, *PHLDA1*, *PODXL*, *RAPGEF2*, *SPRY2* and *THBD*. This core list was analysed for gene annotation enrichment using the DAVID algorithm. Highly significant enrichment was identified for encoded proteins involved in cell-to-cell communication and signal transduction (*DCBLD2*, *IL15*, *ITGA2*, *ITGA6*, *ITGA11*, *NPR3*, *RAPGEF2*, *SPRY2*, *STMN2*) ($p=0.036$), with nine of the

proteins integral to the plasma membrane (*DCBLD2*, *IL15*, *ITGA2*, *ITGA6*, *ITGA11*, *PODXL*, *RAPGEF2*, *SHROOM3*, *THBD*) ($p=0.0032$).

DISCUSSION

In this work we have identified a shared alteration in expression profile in scalp fibroblasts obtained from patients with mutations in the three genes that are most commonly mutated in CRS—*FGFR2*, *FGFR3* and *TWIST1*. We would expect this profile to indicate common perturbations in gene networks downstream of the mutations, providing insights into the shared pathogenesis of genetically determined CRS (as opposed to NSS, which in most cases has a different, multifactorial origin).

Figure 3 Comparison of syndromic craniosynostosis (CRS) expression profiles. A Venn diagram of the lists from the Statistical Analysis for Microarrays (SAM) analysis corresponding to the three conditions (Apert syndrome (AS), Muenke syndrome (MS) and Saethre–Chotzen syndrome (SCS)) is shown. Genes showing significant alterations in two or more conditions are identified individually; upregulated genes are shown in bold, and downregulated genes in normal type. A single gene (*PDE4DIP*, underlined) showed an inconsistent direction of change, with upregulation in MS and downregulation in AS.



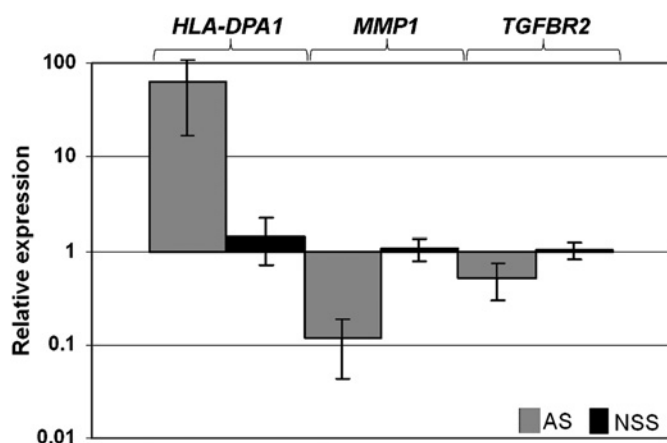


Figure 4 Real-time PCR (RT-PCR) validation of the expression of *HLA-DPA1*, *MMP1* and *TGFBR2* genes in five further AS cases (P253R mutation) and five further NSS controls. The values presented are log-transformed and normalised to *GAPDH* control gene expression. All the data reached statistical significance (Student t test, $p < 0.05$).

The shared networks identified are likely to reflect the interconnectedness of *FGFR2*, *FGFR3* and *TWIST1* in signal transduction events, with similar downstream consequences for cellular phenotype. In the mouse, all three orthologous genes are expressed in different zones of the definitive coronal suture at embryonic day (E)16.¹⁹ *Twist1* appears to have an earlier role at E14.5 in maintaining the boundary between neural crest and cephalic mesoderm at the site of the developing coronal suture,²⁰ whereas *Fgfr2* expression is characteristic of actively dividing cells in the definitive suture.²¹ The presence of *TWIST1* binding sites adjacent to the *FGFR2* gene indicates direct transcriptional regulation²²; in addition, the sutural mesenchyme of *Twist1*^{+/-} mice shows greater responsiveness to fibroblast growth factors (FGFs).²³ The role of *FGFR3* in the cranial sutures is less well defined, but it has been proposed that *TWIST1* negatively regulates *FGFR3* transcriptional activation induced by its binding partner E2A.²⁴

When considering the genes showing altered expression in more than one CRS syndrome compared with NSS controls (figure 3), we found highly significant trends both in sharing of the direction of altered expression and in the classes of encoded protein affected by these alterations. Together with the replication, using real-time PCR (RT-PCR), of selected expression alterations in samples from fibroblasts of a different set of patients and cultured at a different time (figure 4), this indicates that our findings are robust and point to important biological differences between the fibroblasts of patients with defined CRS syndromes and those with NSS. Of note, it is essential to use a consistent source of FCS during fibroblast culture; in contrast with the data presented here, when we grew fibroblasts in serum sourced from a different manufacturer, expression profiles on microarray analysis appeared dampened, and we observed few significant differences even between the AS sample group and NSS controls (data not shown).

Assessment of the genes showing shared alterations in expression using a combination of IPA and DAVID classification indicates that fibroblasts from the syndromic patients have altered characteristics for cell recognition and signalling. Among genes exhibiting increased expression in syndromic CRS (online supplementary tables 2 and 3), several encode proteins with cytoarchitectural functions. Prominent examples are *STMN2* (encoding stathmin-like 2), which showed the highest upregulation of any transcript in both MS and SCS (average of 8.7-fold

and 12.0-fold increase respectively), as well as the highest upregulation overall, and *SHROOM3* (encoding shroom family member 3), which was upregulated 3.07/3.93-fold in AS and 3.48/4.03-fold in MS. Stathmin-like 2 is a cytosolic phosphoprotein that controls microtubule assembly and dynamics, and is a marker of osteogenesis in mesenchymal stem cells²⁵; shroom 3 is an actin-binding protein that regulates the apical constriction of epithelial cells.²⁶ Genes influencing cell adhesion and extracellular matrix are also prominent. *ITGA11*, upregulated 3.78-fold in SCS and 2.38/3.37-fold in AS, encodes half of a heterodimeric integrin ($\alpha 11\beta 1$) that functions as a collagen receptor²⁷; by contrast, genes encoding two other integrin subunits, *ITGA2* and *ITGA6*, as well as *MMP1* (encoding matrix metalloproteinase 1 (an interstitial collagenase)), were downregulated in the same two disorders. *SPP1* encoding osteopontin, the principal phosphorylated glycoprotein of bone, was downregulated fourfold in AS and 3.1-fold in MS, and *SPRY2*, encoding sprouty 2, a negative regulator of FGF signalling, was downregulated 2.0-fold in MS and 2.9-fold in SCS.

Whereas these data point to a major influence of CRS mutations on downstream gene expression, the SAM analysis did not highlight any significant changes in expression of the mutated genes themselves (*TWIST1*, *FGFR2* or *FGFR3*) in these samples. In the PAM analysis, however, two *FGFR2* probe sets were selected among the 73 genes giving the best discrimination of AS from NSS controls (figure 1). Interestingly, *FGFR2* showed relative upregulation in AS cells, which contrasts with previous reports that *FGFR2/Fgfr2* expression is either unchanged or reduced in the cranial sutures of AS individuals or mouse models.^{28–31} Clearly fibroblast culture represents a different cellular milieu from the cranial suture, and we do not expect a simple equivalence of gene expression profiles between the two situations. Nevertheless, it is likely that the altered cellular properties of fibroblasts reflect endogenous properties of the suture, hence the genes that show altered expression are plausible candidates in which mutations may cause CRS. Supporting this, heterozygous mutations in *TGFBR2*, which showed reduced expression in AS (2.17–2.94-fold; figure 4) and MS (2.08-fold), cause Loeys–Dietz syndrome, in which CRS sometimes occurs.³²

Previously, three other studies have profiled gene expression in CRS using microarray analysis of transcripts.^{31 33 34} These studies investigated different cell types compared with the present work and used diverse array platforms. Carinci *et al*³³ studied periosteal fibroblasts of three patients (AS with *FGFR2* P253R mutation, Crouzon syndrome with *FGFR2* G338R mutation, and Crouzon syndrome without an identified mutation), using a 19K cDNA array platform. Fanganiello *et al*³⁴ studied periosteal fibroblasts in seven AS patients with the *FGFR2* S252W mutation, using the CodeLink array platform. Coussens *et al*³¹ used tissue samples from a combination of fused, fusing and unfused sutures in five patients (AS with S252W mutation, and three sagittal and one unicoronal synostosis without identified mutations), using the same Affymetrix platform as in the present work. By contrast, we chose to undertake expression profiling in fibroblasts (see the Introduction); the relative simplicity of harvesting and culture enabled us to sample a much larger number of patients than described in the previous studies.

We compared the gene lists generated from the two larger previously published studies (262 genes in Fanganiello *et al*³⁴ and 651 in Coussens *et al*³¹) with our list of 863 differentially expressed genes between monogenic CRS and NSS controls (online supplementary table 2). No genes were found in common to all of the lists, and the overlap of genes shared by

any two lists was modest (online supplementary figure 3). In none of the three comparisons did the shared transcripts show changes in a consistent direction for syndromic cases or fusing sutures more often than expected by chance. Hence we conclude that, presumably owing to substantial differences in sample sources and methodology, it is not appropriate to combine the results of any of these studies. Notably, our experimental design used fibroblasts from patients with NSS as the 'control' comparator group; we did not explore whether these NSS samples might themselves show consistent differences from a non-CRS population. Such an effect could have obscured some of the features of the monogenic CRS expression profile compared with the normal state.

In summary, we have identified an expression profile of syndromic CRS in scalp fibroblasts that exhibits shared features across three of the most common genetically determined syndromes (AS, MS, SCS) that distinguish these samples from NSS controls. As well as demonstrating shared signalling modules in these three syndromes, this observation supports our original reasoning that NSS has a distinct pathological origin. The syndromic CRS profile is robust, based on the consistent direction of change in expression, and replication in independent samples. Although, with the exception of AS, this profile cannot currently distinguish individual samples from NSS, improved sensitivity of the cDNA assay (for example, using deep sequencing methods) should increase signal specificity. Further refinements to this approach may provide a method of classifying individual samples into dichotomous groups with either high or low genetic load, which would assist genetic counselling even when a causative mutation has not been found.

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Competing interests None.

Ethical approval This study was conducted with the approval of the Oxfordshire Research Ethics Committee (CO2.143).

Contributors EB designed experiments, analysed data, wrote the paper. SS analysed data, SAW coordinated obtaining samples, AOMW designed the study, analysed data and wrote the paper.

Provenance and peer review Not commissioned; externally peer reviewed.

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Supplemental table 2. List of differentially expressed genes identified by SAM analysis (5% FDR) for combined CRS syndromes compared with NSS controls.

Probe Set ID	Gene Symbol	Gene Title	Fold cha	Entrez Gen	Cytoband
1555623_at	DERP12	dermal papilla derived protein 12	-100	---	---
233847_x_at	ZA31P	---	-33.33	---	---
1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-5.88	5743	1q25.2-q25.3
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-5	5743	1q25.2-q25.3
206204_at	GRB14	growth factor receptor-bound protein 14	-3.85	2888	2q22-q24
236824_at	TMEM132B	transmembrane protein 132B	-3.85	114795	12q24.31-q24.32
230135_at	---	---	-3.7	---	---
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-3.12	4883	5p14-p13
209277_at	TFPI2	tissue factor pathway inhibitor 2	-3.12	7980	7q22
203887_s_at	THBD	thrombomodulin	-3.12	7056	20p11.2
208719_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-3.03	10521	22q13.1
227314_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-3.03	3673	5q23-q31
228964_at	PRDM1	PR domain containing 1, with ZNF domain	-2.94	639	6q21-q22.1
204614_at	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	-2.86	5055	18q21.3
203888_at	THBD	thrombomodulin	-2.78	7056	20p11.2
236468_at	---	---	-2.7	---	---
230425_at	EPHB1	EPH receptor B1	-2.7	2047	3q21-q23
209278_s_at	TFPI2	tissue factor pathway inhibitor 2	-2.7	7980	7q22
205428_s_at	CALB2	calbindin 2, 29kDa (calretinin)	-2.63	794	16q22.2
208151_x_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-2.63	10521	22q13.1
208394_x_at	ESM1	endothelial cell-specific molecule 1	-2.63	11082	5q11.2
219054_at	C5orf23	chromosome 5 open reading frame 23	-2.56	79614	5p13.3
201578_at	PODXL	podocalyxin-like	-2.56	5420	7q32-q33
212859_x_at	MT1E	metallothionein 1E	-2.38	4493	16q13
229070_at	C6orf105	chromosome 6 open reading frame 105	-2.33	84830	6p24.1
209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	-2.33	6696	4q21-q25
239331_at	---	---	-2.27	---	---
230560_at	STXBP6	syntaxin binding protein 6 (amisyn)	-2.27	29091	14q12
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	-2.22	64919	14q32.2
208893_s_at	DUSP6	dual specificity phosphatase 6	-2.17	1848	12q22-q23
208581_x_at	MT1X	metallothionein 1X	-2.17	4501	16q13
228399_at	OSR1	odd-skipped related 1 (Drosophila)	-2.17	130497	2p24.1
205828_at	MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	-2.13	4314	11q22.3
204326_x_at	MT1X	metallothionein 1X	-2.13	4501	16q13
236718_at	MYO10	myosin X	-2.13	4651	5p15.1-p14.3
203908_at	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	-2.13	8671	4q21
237252_at	THBD	thrombomodulin	-2.13	7056	20p11.2
235236_at	---	---	-2.08	---	---
204475_at	MMP1	matrix metalloproteinase 1 (interstitial collagenase)	-2.08	4312	11q22.3
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	-2.08	10253	13q31.1
226218_at	IL7R	interleukin 7 receptor	-2.04	3575	5p13
219790_s_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-2.04	4883	5p14-p13

229576_s_at	TBX3	T-box 3 (ulnar mammary syndrome)	-2.04	6926	12q24.1
211814_s_at	CCNE2	cyclin E2	-2	9134	8q22.1
215177_s_at	ITGA6	integrin, alpha 6	-2	3655	2q31.1
218340_s_at	UBA6	ubiquitin-like modifier activating enzyme 6	-2	55236	4q13.2
229824_at	---	---	-1.96	---	---
225750_at	---	---	-1.96	---	---
213865_at	DCBLD2	discoïdin, CUB and LCCL domain containing 2	-1.96	131566	3q12.1 3
217165_x_at	MT1F	metallothionein 1F	-1.96	4494	16q13
206461_x_at	MT1H	metallothionein 1H	-1.96	4496	16q13
227082_at	---	---	-1.92	---	---
216336_x_at	MT1E	metallothionein 1E	-1.92	4493	16q13
207334_s_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	-1.92	7048	3p22
223395_at	ABI3BP	ABI gene family, member 3 (NESH) binding protein	-1.89	25890	3q12
227084_at	DTNA	dystrobrevin, alpha	-1.89	1837	18q12
1567224_at	HMGA2	high mobility group AT-hook 2	-1.89	8091	12q15
206172_at	IL13RA2	interleukin 13 receptor, alpha 2	-1.89	3598	Xq13.1-q28
205798_at	IL7R	interleukin 7 receptor	-1.89	3575	5p13
211456_x_at	MT1P2	metallothionein 1 pseudogene 2	-1.89	645745	1q43
212185_x_at	MT2A	metallothionein 2A	-1.89	4502	16q13
227354_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-1.89	55824	8q21.13
235046_at	---	---	-1.85	---	---
203180_at	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-1.85	220	15q26.3
210735_s_at	CA12	carbonic anhydrase XII	-1.85	771	15q22
213998_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-1.85	10521	22q13.1
202600_s_at	NRIP1	nuclear receptor interacting protein 1	-1.85	8204	21q11.2
212240_s_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	-1.85	5295	5q13.1
1555326_a_at	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	-1.82	8754	8p11.23
218498_s_at	ERO1L	ERO1-like (<i>S. cerevisiae</i>)	-1.82	30001	14q22.1
217999_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-1.82	22822	12q15
218782_s_at	ATAD2	ATPase family, AAA domain containing 2	-1.79	29028	8q24.13
217523_at	CD44	CD44 molecule (Indian blood group)	-1.79	960	11p13
223533_at	LRRC8C	leucine rich repeat containing 8 family, member C	-1.79	84230	1p22.2
242677_at	NRP1	Neuropilin 1	-1.79	8829	10p12
217998_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-1.79	22822	12q15
228483_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	-1.79	51616	Xq13.1-q21.1
229011_at	---	---	-1.75	---	---
228314_at	---	---	-1.75	---	---
225847_at	AADA1	arylacetamide deacetylase-like 1	-1.75	57552	3q26.31
204508_s_at	CA12	carbonic anhydrase XII	-1.75	771	15q22
203963_at	CA12	carbonic anhydrase XII	-1.75	771	15q22
1552921_a_at	FIGL1	figetin-like 1	-1.75	63979	7p12.2
208025_s_at	HMGA2	high mobility group AT-hook 2	-1.75	8091	12q15
213629_x_at	MT1F	metallothionein 1F	-1.75	4494	16q13
225173_at	ARHGAP18	Rho GTPase activating protein 18	-1.72	93663	6q22.33
227404_s_at	EGR1	Early growth response 1	-1.72	1958	5q31.1
200637_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	-1.72	5792	1p34
228250_at	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	-1.72	51735	5q23.3
214895_s_at	ADAM10	ADAM metallopeptidase domain 10	-1.69	102	15q2

202604_x_at	ADAM10	ADAM metallopeptidase domain 10	-1.69	102	15q2
205410_s_at	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	-1.69	493	1q32.1
213895_at	EMP1	epithelial membrane protein 1	-1.69	2012	12p12.3
201976_s_at	MYO10	myosin X	-1.69	4651	5p15.1-p14.3
223661_at	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	-1.69	64710	1q32.1
218000_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-1.69	22822	12q15
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	-1.69	9693	4q32.1
240991_at	---	---	-1.67	---	---
227529_s_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-1.67	9590	6q24-q25
210896_s_at	ASPH	aspartate beta-hydroxylase	-1.67	444	8q12.1
241986_at	BMPER	BMP binding endothelial regulator	-1.67	168667	7p14.3
224911_s_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	-1.67	131566	3q12.1 3
222889_at	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, <i>S. cerevisiae</i>)	-1.67	64858	1p13.2
216250_s_at	LPXN	leupaxin	-1.67	9404	11q12.1
228262_at	MAP7D2	MAP7 domain containing 2	-1.67	256714	Xp22.12
232431_at	---	---	-1.64	---	---
227530_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-1.64	9590	6q24-q25
225919_s_at	C9orf72	chromosome 9 open reading frame 72	-1.64	203228	9p21.2
215867_x_at	CA12	carbonic anhydrase XII	-1.64	771	15q22
214164_x_at	CA12	carbonic anhydrase XII	-1.64	771	15q22
226545_at	CD109	CD109 molecule	-1.64	135228	6q13
210311_at	FGF5	fibroblast growth factor 5	-1.64	2250	4q21
225842_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-1.64	22822	12q15
210807_s_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-1.64	9194	12q13
242629_at	---	---	-1.61	---	---
203526_s_at	APC	adenomatous polyposis coli	-1.61	324	5q21-q22
225171_at	ARHGAP18	Rho GTPase activating protein 18	-1.61	93663	6q22.33
221703_at	BRIP1	BRCA1 interacting protein C-terminal helicase 1	-1.61	83990	17q22-q24
208711_s_at	CCND1	cyclin D1	-1.61	595	11q13
239719_at	CD109	CD109 molecule	-1.61	135228	6q13
224829_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	-1.61	80315	5q21
233655_s_at	FAM29A	family with sequence similarity 29, member A	-1.61	54801	9p22.1
225116_at	HIPK2	homeodomain interacting protein kinase 2	-1.61	28996	7q32-q34
217997_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-1.61	22822	12q15
204612_at	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-1.61	5569	8q21.12
227340_s_at	RGMB	RGM domain family, member B	-1.61	285704	5q21.1
222088_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-1.61	6515	12p13.3
212286_at	ANKRD12	ankyrin repeat domain 12	-1.59	23253	18p11.22
219558_at	ATP13A3	ATPase type 13A3	-1.59	79572	3q29
244852_at	DSEL	dermatan sulfate epimerase-like	-1.59	92126	18q22.1
226810_at	OGFRL1	opioid growth factor receptor-like 1	-1.59	79627	6q13
212239_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	-1.59	5295	5q13.1
212629_s_at	PKN2	protein kinase N2	-1.59	5586	1p22.2
200636_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	-1.59	5792	1p34
236834_at	SCFD2	sec1 family domain containing 2	-1.59	152579	4q12
207057_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-1.59	9194	12q13
208944_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	-1.59	7048	3p22
1558733_at	ZBTB38	zinc finger and BTB domain containing 38	-1.59	253461	3q23

233506_at	---	---	-1.56	---	---
221823_at	C5orf30	chromosome 5 open reading frame 30	-1.56	90355	5q21.1
212746_s_at	CEP170	centrosomal protein 170kDa	-1.56	9859	1q44
1552717_s_at	CEP170	centrosomal protein 170kDa	-1.56	645455	1q44
206806_at	DGKI	diacylglycerol kinase, iota	-1.56	9162	7q32.3-q33
232080_at	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	-1.56	57520	2q32.3-q33.1
200635_s_at	PTPRF	protein tyrosine phosphatase, receptor type, F	-1.56	5792	1p34
1569269_s_at	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	-1.56	57522	12q14.2
222735_at	TMEM38B	transmembrane protein 38B	-1.56	55151	9q31.2
213107_at	TNIK	TRAF2 and NCK interacting kinase	-1.56	23043	3q26.2-q26.31
222600_s_at	UBA6	ubiquitin-like modifier activating enzyme 6	-1.56	55236	4q13.2
238587_at	UBASH3B	ubiquitin associated and SH3 domain containing, B	-1.56	84959	11q24.1
219062_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	-1.56	54877	18q21.33
230175_s_at	---	---	-1.54	---	---
205808_at	ASPH	aspartate beta-hydroxylase	-1.54	444	8q12.1
226463_at	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	-1.54	528	8q22.3
202873_at	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	-1.54	528	8q22.3
235486_at	C11orf41	chromosome 11 open reading frame 41	-1.54	25758	11p13
228728_at	C7orf58	chromosome 7 open reading frame 58	-1.54	79974	7q31.31
228555_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.54	817	4q26
219279_at	DOCK10	dedicator of cytokinesis 10	-1.54	55619	2q36.2
221773_at	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	-1.54	2004	12q23
218748_s_at	EXOC5	exocyst complex component 5	-1.54	10640	14q23.1
202599_s_at	NRIP1	nuclear receptor interacting protein 1	-1.54	8204	21q11.2
216236_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-1.54	144195	12p13.3
233827_s_at	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	-1.54	11198	14q11.2
216228_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	-1.54	11169	14q22.3
223542_at	ANKRD32	ankyrin repeat domain 32	-1.52	84250	5q15
212135_s_at	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	-1.52	493	1q32.1
203482_at	C10orf6	chromosome 10 open reading frame 6	-1.52	55719	10q24.31
231793_s_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.52	817	4q26
208712_at	CCND1	cyclin D1	-1.52	595	11q13
203641_s_at	COBLL1	COBL-like 1	-1.52	22837	2q24.3
206127_at	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	-1.52	2004	12q23
225115_at	HIPK2	homeodomain interacting protein kinase 2	-1.52	28996	7q32-q34
210261_at	KCNK2	potassium channel, subfamily K, member 2	-1.52	3776	1q41
225752_at	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	-1.52	123606	15q11.2
222719_s_at	PDGFC	platelet derived growth factor C	-1.52	56034	4q32
204835_at	POLA1	polymerase (DNA directed), alpha 1	-1.52	5422	Xp22.1-p21.3
222846_at	RAB8B	RAB8B, member RAS oncogene family	-1.52	51762	15q22.2
226989_at	RGMB	RGM domain family, member B	-1.52	285704	5q21.1
222536_s_at	ZNF395	zinc finger protein 395	-1.52	55893	8p21.1
226186_at	---	---	-1.49	---	---
1558517_s_at	---	---	-1.49	---	---
224797_at	ARRDC3	arrestin domain containing 3	-1.49	57561	5q14.3
213295_at	CYLD	cylindromatosis (turban tumor syndrome)	-1.49	1540	16q12.1
225368_at	HIPK2	homeodomain interacting protein kinase 2	-1.49	28996	7q32-q34
225097_at	HIPK2	homeodomain interacting protein kinase 2	-1.49	28996	7q32-q34

209512_at	HSDL2	hydroxysteroid dehydrogenase like 2	-1.49	84263	9q32
213640_s_at	LOX	lysyl oxidase	-1.49	4015	5q23.2
218273_s_at	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	-1.49	54704	8q22.1
201647_s_at	SCARB2	scavenger receptor class B, member 2	-1.49	950	4q21.1
226416_at	THEX1	three prime histone mRNA exonuclease 1	-1.49	90459	8p23.1
222562_s_at	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-1.49	80351	10q23.3
1566968_at	---	---	-1.47	---	---
213805_at	ABHD5	abhydrolase domain containing 5	-1.47	51099	3p21
226893_at	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	-1.47	27	1q24-q25
202760_s_at	AKAP2	PALM2-AKAP2	-1.47	445815	9q31-q33
212253_x_at	DST	dystonin	-1.47	667	6p12.1
205021_s_at	FOXN3	forkhead box N3	-1.47	1112	14q31.3
229055_at	GPR68	G protein-coupled receptor 68	-1.47	8111	14q31
213446_s_at	IQGAP1	IQ motif containing GTPase activating protein 1	-1.47	8826	15q26.1
201465_s_at	JUN	jun oncogene	-1.47	3725	1p32-p31
227638_at	KIAA1632	KIAA1632	-1.47	57724	18q12.3-q21.1
227761_at	MYO5A	myosin VA (heavy chain 12, myoxin)	-1.47	4644	15q21
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	-1.47	9975	3p24.2
204082_at	PBX3	pre-B-cell leukemia homeobox 3	-1.47	5090	9q33-q34
1557918_s_at	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	-1.47	6566	1p12
221765_at	UGCG	UDP-glucose ceramide glucosyltransferase	-1.47	7357	9q31
219221_at	ZBTB38	zinc finger and BTB domain containing 38	-1.47	253461	3q23
242366_at	---	---	-1.45	---	---
1555977_at	---	---	-1.45	---	---
208703_s_at	APLP2	amyloid beta (A4) precursor-like protein 2	-1.45	334	11q23-q25
201101_s_at	BCLAF1	BCL2-associated transcription factor 1	-1.45	9774	6q22-q23
1553108_at	C5orf24	chromosome 5 open reading frame 24	-1.45	134553	5q31.1
210310_s_at	FGF5	fibroblast growth factor 5	-1.45	2250	4q21
238539_at	HPS3	Hermansky-Pudlak syndrome 3	-1.45	84343	3q24
236108_at	KIAA1632	KIAA1632	-1.45	57724	18q12.3-q21.1
228986_at	OSBPL8	oxysterol binding protein-like 8	-1.45	114882	12q14
205991_s_at	PRRX1	paired related homeobox 1	-1.45	5396	1q24
202497_x_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-1.45	6515	12p13.3
222736_s_at	TMEM38B	transmembrane protein 38B	-1.45	55151	9q31.2
222601_at	UBA6	ubiquitin-like modifier activating enzyme 6	-1.45	55236	4q13.2
1564053_a_at	YTHDF3	YTH domain family, member 3	-1.45	253943	8q12.3
209049_s_at	ZMYND8	zinc finger, MYND-type containing 8	-1.45	23613	20q13.12
241925_x_at	---	---	-1.43	---	---
226550_at	---	---	-1.43	---	---
200727_s_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	-1.43	10097	2p14
209135_at	ASPH	aspartate beta-hydroxylase	-1.43	444	8q12.1
203481_at	C10orf6	chromosome 10 open reading frame 6	-1.43	55719	10q24.31
230739_at	C18orf19	chromosome 18 open reading frame 19	-1.43	125228	18p11.21
208853_s_at	CANX	calnexin	-1.43	821	5q35
207719_x_at	CEP170	centrosomal protein 170kDa	-1.43	9859	1q44
223249_at	CLDN12	claudin 12	-1.43	9069	7q21
39582_at	CYLD	cylindromatosis (turban tumor syndrome)	-1.43	1540	16q12.1
213645_at	ENOSF1	enolase superfamily member 1	-1.43	55556	18p11.32

235202_x_at	IKIP	IKK interacting protein	-1.43	121457	12q23.1
228453_at	KIAA1632	KIAA1632	-1.43	57724	18q12.3-q21.1
203294_s_at	LMAN1	lectin, mannose-binding, 1	-1.43	3998	18q21.3-q22
210756_s_at	NOTCH2	Notch homolog 2 (Drosophila)	-1.43	4853	1p13-p11
225768_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	-1.43	9975	3p24.2
221045_s_at	PER3	period homolog 3 (Drosophila)	-1.43	8863	1p36.23
210568_s_at	RECQL	RecQ protein-like (DNA helicase Q1-like)	-1.43	5965	12p12
1557078_at	SLFN5	schlafen family member 5	-1.43	162394	17q12
209447_at	SYNE1	spectrin repeat containing, nuclear envelope 1	-1.43	23345	6q25
1554878_a_at	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	-1.41	5825	1p22-p21
218096_at	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	-1.41	55326	8p23.1
210858_x_at	ATM	ataxia telangiectasia mutated	-1.41	472	11q22-q23
205095_s_at	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	-1.41	535	17q21
229900_at	CD109	CD109 molecule	-1.41	135228	6q13
208499_s_at	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	-1.41	5611	13q32
230263_s_at	DOCK5	Dedicator of cytokinesis 5	-1.41	80005	8p21.2
242422_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	-1.41	10146	5q33.1
224744_at	IMPAD1	inositol monophosphatase domain containing 1	-1.41	54928	8q12.1
224743_at	IMPAD1	inositol monophosphatase domain containing 1	-1.41	54928	8q12.1
1552611_a_at	JAK1	Janus kinase 1 (a protein tyrosine kinase)	-1.41	3716	1p32.3-p31.3
238490_at	KIAA2026	KIAA2026	-1.41	158358	9p24.1
224410_s_at	LMBR1	limb region 1 homolog (mouse)	-1.41	64327	7q36
211599_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	-1.41	4233	7q31
225997_at	MOBK1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)	-1.41	92597	4q13.3
209629_s_at	NXT2	nuclear transport factor 2-like export factor 2	-1.41	55916	Xq22.3
212214_at	OPA1	optic atrophy 1 (autosomal dominant)	-1.41	4976	3q28-q29
200730_s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	-1.41	7803	6q12
226923_at	SCFD2	sec1 family domain containing 2	-1.41	152579	4q12
212577_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	-1.41	23347	18p11.32
221727_at	SUB1	SUB1 homolog (S. cerevisiae)	-1.41	10923	5p13.3
201730_s_at	TPR	translocated promoter region (to activated MET oncogene)	-1.41	7175	1q25
203690_at	TUBGCP3	tubulin, gamma complex associated protein 3	-1.41	10426	13q34
238420_at	---	---	-1.39	---	---
202759_s_at	AKAP2	A kinase (PRKA) anchor protein 2	-1.39	11217	9q31-q33
208248_x_at	APLP2	amyloid beta (A4) precursor-like protein 2	-1.39	334	11q23-q25 11q24
222538_s_at	APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	-1.39	26060	3p21.1-p14.3
216266_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	-1.39	10565	8q13
212136_at	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	-1.39	493	1q32.1
228748_at	CD59	CD59 molecule, complement regulatory protein	-1.39	966	11p13
204662_at	CP110	CP110 protein	-1.39	9738	16p12.3
203302_at	DCK	deoxycytidine kinase	-1.39	1633	4q13.3-q21.1
222665_at	FAM82B	family with sequence similarity 82, member B	-1.39	51115	8q21.3
224933_s_at	JMJD1C	jumonji domain containing 1C	-1.39	221037	10q21.2-q21.3
226534_at	KITLG	KIT ligand	-1.39	4254	12q22
224606_at	KLF6	Kruppel-like factor 6	-1.39	1316	10p15
1555832_s_at	KLF6	Kruppel-like factor 6	-1.39	1316	10p15
215446_s_at	LOX	lysyl oxidase	-1.39	4015	5q23.2
201299_s_at	MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	-1.39	55233	2p13.1

219321_at	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	-1.39	64398	14q23.3
211547_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	-1.39	5048	17p13.3
224883_at	PLDN	pallidin homolog (mouse)	-1.39	26258	15q21.1
238020_at	PSMC2	Proteasome (prosome, macropain) 26S subunit, ATPase, 2	-1.39	5701	7q22.1-q22.3
200731_s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	-1.39	7803	6q12
201646_at	SCARB2	scavenger receptor class B, member 2	-1.39	950	4q21.1
233888_s_at	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	-1.39	57522	12q14.2
208097_s_at	TXNDC1	thioredoxin domain containing 1	-1.39	81542	14q22.1
208704_x_at	APLP2	amyloid beta (A4) precursor-like protein 2	-1.37	334	11q23-q25
214483_s_at	ARFIP1	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	-1.37	27236	4q31.3
201971_s_at	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	-1.37	523	3q13.2-q13.31
217196_s_at	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	-1.37	23271	1q32.1
217814_at	CCDC47	coiled-coil domain containing 47	-1.37	57003	17q23.3
230426_at	DLD	dihydroliipoamide dehydrogenase	-1.37	1738	7q31-q32
212467_at	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.37	23317	3q22.1
211607_x_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	-1.37	1956	7p12
201325_s_at	EMP1	epithelial membrane protein 1	-1.37	2012	12p12.3
203285_s_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	-1.37	9653	1p31.1-p22.1
203202_at	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	-1.37	11103	12q21.2
213457_at	MFHAS1	malignant fibrous histiocytoma amplified sequence 1	-1.37	9258	8p23.1
204837_at	MTMR9	myotubularin related protein 9	-1.37	66036	8p23-p22
222393_s_at	NAT13	N-acetyltransferase 13	-1.37	80218	3q13.2
211090_s_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-1.37	8899	6p25.2
235484_at	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-1.37	375743	9q21.11
223028_s_at	SNX9	sorting nexin 9	-1.37	51429	6q25.1-q26
225492_at	TMEM33	transmembrane protein 33	-1.37	55161	4p13
218772_x_at	TMEM38B	transmembrane protein 38B	-1.37	55151	9q31.2
222502_s_at	UFM1	ubiquitin-fold modifier 1	-1.37	51569	13q13.3
230177_at	---	---	-1.35	---	---
227623_at	---	---	-1.35	---	---
227539_at	---	---	-1.35	---	---
226834_at	---	---	-1.35	---	---
224755_at	---	---	-1.35	---	---
202955_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-1.35	10565	8q13
214499_s_at	BCLAF1	BCL2-associated transcription factor 1	-1.35	9774	6q22-q23
211985_s_at	CALM1	calmodulin 1 (phosphorylase kinase, delta)	-1.35	801	14q24-q31
206788_s_at	CBFB	core-binding factor, beta subunit	-1.35	865	16q22.1
208866_at	CSNK1A1	casein kinase 1, alpha 1	-1.35	1452	5q32
225549_at	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	-1.35	1656	11q23.3
210984_x_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	-1.35	1956	7p12
211998_at	H3F3A	H3 histone, family 3A	-1.35	3020	17q25
208055_s_at	HERC4	hect domain and RLD 4	-1.35	26091	10q21.3
226395_at	HOOK3	hook homolog 3 (Drosophila)	-1.35	84376	8p11.21
209513_s_at	HSDL2	hydroxysteroid dehydrogenase like 2	-1.35	84263	9q32
209185_s_at	IRS2	insulin receptor substrate 2	-1.35	8660	13q34
216908_x_at	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	-1.35	730092	16p12.1
225479_at	LRRC58	leucine rich repeat containing 58	-1.35	116064	3q13.33
212076_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	-1.35	4297	11q23

1553551_s_at	ND2	NADH dehydrogenase, subunit 2 (complex I)	-1.35	4536	---
204049_s_at	PHACTR2	phosphatase and actin regulator 2	-1.35	9749	6q24.2
208995_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	-1.35	9360	2q31.1
200732_s_at	PTP4A1	protein tyrosine phosphatase type IVA, member 1	-1.35	7803	6q12
1552790_a_at	SEC62	SEC62 homolog (S. cerevisiae)	-1.35	7095	3q26.2
243999_at	SLFN5	schlafen family member 5	-1.35	162394	17q12
207983_s_at	STAG2	stromal antigen 2	-1.35	10735	Xq25
238604_at	---	---	-1.33	---	---
225269_s_at	C2orf12	chromosome 2 open reading frame 12	-1.33	192137	2q24.3
204489_s_at	CD44	CD44 molecule (Indian blood group)	-1.33	960	11p13
200984_s_at	CD59	CD59 molecule, complement regulatory protein	-1.33	966	11p13
225077_at	CHD2	chromodomain helicase DNA binding protein 2	-1.33	1106	15q26
202444_s_at	ERLIN1	ER lipid raft associated 1	-1.33	10613	10q21-q22
201514_s_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	-1.33	10146	5q33.1
221480_at	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-1.33	3184	4q21.1-q21.2
208936_x_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	-1.33	3964	1q42-q43
213807_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	-1.33	4233	7q31
1554414_a_at	OSGIN2	oxidative stress induced growth inhibitor family member 2	-1.33	734	8q21
212720_at	PAPOLA	poly(A) polymerase alpha	-1.33	10914	14q32.31
222565_s_at	PRKD3	protein kinase D3	-1.33	23683	2p21
210543_s_at	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	-1.33	5591	8q11
220368_s_at	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	-1.33	55671	14q32.12
235074_at	SPRED1	sprouty-related, EVH1 domain containing 1	-1.33	161742	15q14
216100_s_at	TOR1AIP1	torsin A interacting protein 1	-1.33	26092	1q24.2
203476_at	TPBG	trophoblast glycoprotein	-1.33	7162	6q14-q15
224895_at	YAP1	Yes-associated protein 1, 65kDa	-1.33	10413	11q13
227978_s_at	ZADH2	zinc binding alcohol dehydrogenase, domain containing 2	-1.33	284273	18q22.3
202654_x_at	MARCH7	membrane-associated ring finger (C3HC4) 7	-1.33	64844	2q24.2
213935_at	ABHD5	abhydrolase domain containing 5	-1.32	51099	3p21
200776_s_at	BZW1	basic leucine zipper and W2 domains 1	-1.32	9689	3q13.31
208852_s_at	CANX	calnexin	-1.32	821	5q35
212586_at	CAST	calpastatin	-1.32	831	5q15
212014_x_at	CD44	CD44 molecule (Indian blood group)	-1.32	960	11p13
213548_s_at	CDV3	CDV3 homolog (mouse)	-1.32	55573	3q22.1
214030_at	DKFZp667G2110	hypothetical protein DKFZp667G2110	-1.32	131544	3q11.2
226970_at	FBXO33	F-box protein 33	-1.32	254170	14q21.1
206920_s_at	GLE1	GLE1 RNA export mediator homolog (yeast)	-1.32	2733	9q34.11
212223_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	-1.32	3423	Xq28
1556186_s_at	KIAA0090	KIAA0090	-1.32	23065	1p36.13
214577_at	MAP1B	microtubule-associated protein 1B	-1.32	4131	5q13
206473_at	MBTPS2	membrane-bound transcription factor peptidase, site 2	-1.32	51360	Xp22.1-p22.2
217279_x_at	MMP14	matrix metalloproteinase 14 (membrane-inserted)	-1.32	4323	14q11-q12
225563_at	PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-1.32	255967	13q12.2
222826_at	PLDN	pallidin homolog (mouse)	-1.32	26258	15q21.1
207749_s_at	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	-1.32	5523	3q22.1
209896_s_at	PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	-1.32	5781	12q24
201087_at	PXN	paxillin	-1.32	5829	12q24.31
202129_s_at	RIOK3	RIO kinase 3 (yeast)	-1.32	8780	18q11.2

201070_x_at	SF3B1	splicing factor 3b, subunit 1, 155kDa	-1.32	23451	2q33.1
213600_at	SIPA1L3	signal-induced proliferation-associated 1 like 3	-1.32	23094	19q13.13
201894_s_at	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	-1.32	6745	6p24.3
214007_s_at	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	-1.32	5756	12q12
202316_x_at	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	-1.32	10277	1p36.3
233559_s_at	WDFY1	WD repeat and FYVE domain containing 1	-1.32	57590	2q36.1
226280_at	---	---	-1.3	---	---
1559822_s_at	---	---	-1.3	---	---
211986_at	AHNAK	AHNAK nucleoprotein	-1.3	79026	11q12.2
216521_s_at	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	-1.3	79184	Xq28
200777_s_at	BZW1	basic leucine zipper and W2 domains 1	-1.3	9689	2q33
224311_s_at	CAB39	calcium binding protein 39	-1.3	51719	2q37.1
212765_at	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	-1.3	23271	1q32.1
1559954_s_at	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	-1.3	11325	17q23.3
204077_x_at	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	-1.3	9583	8p21.3
222726_s_at	EXOC5	exocyst complex component 5	-1.3	10640	14q23.1
211299_s_at	FLOT2	flotillin 2	-1.3	2319	17q11-q12
238959_at	LARP4	La ribonucleoprotein domain family, member 4	-1.3	113251	12q13.13
201866_s_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	-1.3	2908	5q31.3
222394_at	PDCD6IP	programmed cell death 6 interacting protein	-1.3	10015	3p22.3
213405_at	RAB22A	RAB22A, member RAS oncogene family	-1.3	57403	20q13.32
201870_at	TOMM34	translocase of outer mitochondrial membrane 34	-1.3	10953	---
222579_at	UBA5	ubiquitin-like modifier activating enzyme 5	-1.3	79876	3q22.1
201378_s_at	UBAP2L	ubiquitin associated protein 2-like	-1.3	9898	1q21.3
224691_at	---	---	-1.28	---	---
201686_x_at	API5	apoptosis inhibitor 5	-1.28	8539	11p11.2
211984_at	CALM1	calmodulin 1 (phosphorylase kinase, delta)	-1.28	801	---
200985_s_at	CD59	CD59 molecule, complement regulatory protein	-1.28	966	11p13
225805_at	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	-1.28	3192	1q44
202419_at	KDSR	3-ketodihydrosphingosine reductase	-1.28	2531	18q21.3
225556_at	LOC203547	hypothetical protein LOC203547	-1.28	203547	Xq28
201251_at	PKM2	pyruvate kinase, muscle	-1.28	5315	15q22
233080_s_at	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	-1.28	55660	2q23.3
223598_at	RAD23B	RAD23 homolog B (S. cerevisiae)	-1.28	5887	9q31.2
224880_at	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	-1.28	5898	7p15-p13
235747_at	SLC25A16	Solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	-1.28	8034	10q21.3
223197_s_at	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	-1.28	56916	4q22-q23
217832_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	-1.28	10492	6q14-q15
204147_s_at	TFDP1	transcription factor Dp-1	-1.28	7027	13q34
215533_s_at	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	-1.28	10277	1p36.3
208884_s_at	UBR5	ubiquitin protein ligase E3 component n-recognin 5	-1.28	51366	8q22
203855_at	WDR47	WD repeat domain 47	-1.28	22911	1p13.3
1554159_a_at	ZMYND11	zinc finger, MYND domain containing 11	-1.28	10771	10p14
232808_at	---	---	-1.27	---	---
1556121_at	---	---	-1.27	---	---
214959_s_at	API5	apoptosis inhibitor 5	-1.27	8539	11p11.2
212815_at	ASCC3	activating signal cointegrator 1 complex subunit 3	-1.27	10973	6q16.1-q16.3
225677_at	BCAP29	B-cell receptor-associated protein 29	-1.27	55973	7q22-q31

225019_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.27	817	4q26
222432_s_at	CCDC47	coiled-coil domain containing 47	-1.27	57003	17q23.3
209835_x_at	CD44	CD44 molecule (Indian blood group)	-1.27	960	11p13
200983_x_at	CD59	CD59 molecule, complement regulatory protein	-1.27	966	11p13
1555278_a_at	CKAP5	cytoskeleton associated protein 5	-1.27	9793	11p11.2
200861_at	CNOT1	CCR4-NOT transcription complex, subunit 1	-1.27	23019	16q21
222409_at	CORO1C	coronin, actin binding protein, 1C	-1.27	23603	12q24.1
203079_s_at	CUL2	cullin 2	-1.27	8453	10p11.21
227521_at	FBXO33	F-box protein 33	-1.27	254170	14q21.1
222570_at	FREQ	frequenin homolog (Drosophila)	-1.27	23413	9q34
225007_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	-1.27	10146	5q33.1
224863_at	GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide	-1.27	2776	9q21
224316_at	KCTD9	potassium channel tetramerisation domain containing 9	-1.27	54793	8p21.1
212248_at	MTDH	Metadherin	-1.27	92140	8q22.1
225673_at	MYADM	myeloid-associated differentiation marker	-1.27	91663	19q13.41
202780_at	OXCT1	3-oxoacid CoA transferase 1	-1.27	5019	5p13.1
200813_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	-1.27	5048	17p13.3
209780_at	PHTF2	putative homeodomain transcription factor 2	-1.27	57157	7q11.23-q21
216153_x_at	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	-1.27	8434	9p13-p12
235390_at	SFRS12IP1	SFRS12-interacting protein 1	-1.27	285672	5q12.3
221483_s_at	ARPP-19	cyclic AMP phosphoprotein, 19 kD	-1.25	10776	15q21.2
202370_s_at	CBFB	core-binding factor, beta subunit	-1.25	865	16q22.1
212063_at	CD44	CD44 molecule (Indian blood group)	-1.25	960	11p13
209092_s_at	GLOD4	glyoxalase domain containing 4	-1.25	51031	17p13.3
202544_at	GMFB	glia maturation factor, beta	-1.25	2764	14q22.2
222403_at	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	-1.25	23788	11p11.2
212365_at	MYO1B	myosin IB	-1.25	4430	2q12-q34
209798_at	NPAT	nuclear protein, ataxia-telangiectasia locus	-1.25	4863	11q22-q23
224956_at	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	-1.25	57532	17q11.2
202614_at	SLC30A9	solute carrier family 30 (zinc transporter), member 9	-1.25	10463	4p13-p12
1558249_s_at	STX16	syntaxin 16	-1.25	8675	20q13.32
224908_s_at	TTL	tubulin tyrosine ligase	-1.25	150465	2q13
208459_s_at	XPO7	exportin 7	-1.25	23039	8p21
212285_s_at	AGRN	agrin	-1.23	375790	1p36.33
201012_at	ANXA1	annexin A1	-1.23	301	9q12-q21.2
222834_s_at	GNG12	guanine nucleotide binding protein (G protein), gamma 12	-1.23	55970	1p31.3
218091_at	HRB	HIV-1 Rev binding protein	-1.23	3267	2q36.3
200691_s_at	HSPA9	heat shock 70kDa protein 9 (mortalin)	-1.23	3313	5q31.1
200791_s_at	IQGAP1	IQ motif containing GTPase activating protein 1	-1.23	8826	15q26.1
207121_s_at	MAPK6	mitogen-activated protein kinase 6	-1.23	5597	15q21
218109_s_at	MFSD1	major facilitator superfamily domain containing 1	-1.23	64747	3q25.33
214812_s_at	MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	-1.23	55233	2p13.1
210510_s_at	NRP1	neuropilin 1	-1.23	8829	10p12
206323_x_at	OPHN1	oligophrenin 1	-1.23	4983	Xq12
233873_x_at	PAPD1	PAP associated domain containing 1	-1.23	55149	10p11.23
229517_at	PTPDC1	protein tyrosine phosphatase domain containing 1	-1.23	138639	9q22.32
201529_s_at	RPA1	replication protein A1, 70kDa	-1.23	6117	17p13.3
201528_at	RPA1	replication protein A1, 70kDa	-1.23	6117	17p13.3

211769_x_at	SERINC3	serine incorporator 3	-1.23	10955	20q13.1-q13.3
218228_s_at	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-1.23	80351	10q23.3
225179_at	UBE2K	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	-1.23	3093	4p14
226719_at	---	---	-1.22	---	---
200068_s_at	CANX	calnexin	-1.22	821	5q35
208624_s_at	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	-1.22	1981	3q27-qter
223248_at	HSDL1	hydroxysteroid dehydrogenase like 1	-1.22	83693	16q24.1
211961_s_at	RAB7A	RAB7A, member RAS oncogene family	-1.22	7879	3q21.3
221473_x_at	SERINC3	serine incorporator 3	-1.22	10955	20q13.1-q13.3
208920_at	SRI	sorcin	-1.22	6717	7q21.1
1555841_at	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	-1.22	8577	9q31
222976_s_at	TPM3	tropomyosin 3	-1.22	7170	1q21.2
226567_at	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	-1.22	9097	18p11.32
242857_at	---	---	-1.2	---	---
214726_x_at	ADD1	adducin 1 (alpha)	-1.2	118	4p16.3
208683_at	CAPN2	calpain 2, (m/II) large subunit	-1.2	824	1q41-q42
225697_at	CRKRS	Cdc2-related kinase, arginine/serine-rich	-1.2	51755	17q12
201219_at	CTBP2	C-terminal binding protein 2	-1.2	1488	10q26.13
225132_at	FBXL3	F-box and leucine-rich repeat protein 3	-1.2	26224	13q22
238701_x_at	FLJ45803	FLJ45803 protein	-1.2	399948	11q23.1
200745_s_at	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	-1.2	2782	1p36.33
212597_s_at	HMG2L1	high-mobility group protein 2-like 1	-1.2	10042	22q13.1
41386_i_at	JMJD3	jumonji domain containing 3, histone lysine demethylase	-1.2	23135	17p13.1
217725_x_at	SERBP1	SERPINE1 mRNA binding protein 1	-1.2	26135	1p31
224636_at	ZFP91	zinc finger protein 91 homolog (mouse)	-1.2	80829	11q12
1554747_a_at	SEPT2	septin 2	-1.2	4735	2q37
224893_at	ATL3	atlastin 3	-1.19	25923	11q13.1
208625_s_at	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	-1.19	1981	3q27-qter
223073_at	HIATL1	hippocampus abundant transcript-like 1	-1.19	84641	9q22.32
225506_at	KIAA1468	KIAA1468	-1.19	57614	18q21.33
224958_at	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	-1.19	57532	17q11.2
225494_at	---	---	-1.18	---	---
1556442_x_at	---	---	-1.18	---	---
203142_s_at	AP3B1	adaptor-related protein complex 3, beta 1 subunit	-1.18	8546	5q14.1
202100_at	RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	-1.18	5899	2cen-q13
225198_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	-1.18	9218	18p11.22
208374_s_at	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	-1.15	829	1p13.2
223420_at	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	-1.15	85406	12q13.2
210570_x_at	MAPK9	mitogen-activated protein kinase 9	-1.14	5601	5q35
219108_x_at	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	1.09	55661	20q13.13
211956_s_at	EIF1	eukaryotic translation initiation factor 1	1.11	10209	17q21.2
226091_s_at	MRFAP1	Mof4 family associated protein 1	1.11	93621	4p16.1
225554_s_at	ANAPC7	anaphase promoting complex subunit 7	1.13	51434	12q24.11
217768_at	C14orf166	chromosome 14 open reading frame 166	1.13	51637	14q22.1
201837_s_at	SUPT7L	suppressor of Ty 7 (S. cerevisiae)-like	1.13	9913	2pter-p25.1
202349_at	TOR1A	torsin family 1, member A (torsin A)	1.13	1861	9q34
207812_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa	1.14	26003	2q31.1-q31.2
225808_at	LOC124512	hypothetical protein LOC124512	1.14	124512	17q25.2

223356_s_at	MTIF3	mitochondrial translational initiation factor 3	1.15	219402	13q12.2
219133_at	OXSM	3-oxoacyl-ACP synthase, mitochondrial	1.15	54995	3p24.2
221475_s_at	RPL15	ribosomal protein L15	1.15	6138	3p24.2
217801_at	ATP5E	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	1.16	514	20q13.32
200086_s_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	1.16	1327	16q22-qter
201956_s_at	GNPAT	glyceronephosphate O-acyltransferase	1.16	8443	1q42
210633_x_at	KRT10	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	1.16	3858	17q21
219598_s_at	RWDD1	RWD domain containing 1	1.16	51389	6q13-q22.33
203588_s_at	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	1.16	7029	3q23
205849_s_at	UQCRB	ubiquinol-cytochrome c reductase binding protein	1.16	7381	8q22
224696_s_at	WDR22	WD repeat domain 22	1.16	8816	14q23-q24.1
211793_s_at	ABI2	abl interactor 2	1.17	10152	2q33
213099_at	ANGEL1	angel homolog 1 (Drosophila)	1.17	23357	14q24.3
207335_x_at	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	1.17	521	4p16.3
221821_s_at	C12orf41	chromosome 12 open reading frame 41	1.17	54934	12q13.11
204215_at	C7orf23	chromosome 7 open reading frame 23	1.17	79161	7q21.1-q21.2
201134_x_at	COX7C	cytochrome c oxidase subunit VIIc	1.17	1350	5q14
222997_s_at	MRPS21	mitochondrial ribosomal protein S21	1.17	148523	1q21
203396_at	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	1.17	5685	15q25.1
217492_s_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	1.17	5728	10q23.3
202640_s_at	RANBP3	RAN binding protein 3	1.17	8498	19p13.3
217457_s_at	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	1.17	5910	4q23-q25
218254_s_at	SAR1B	SAR1 gene homolog B (S. cerevisiae)	1.17	51128	5q31.1
218470_at	YARS2	tyrosyl-tRNA synthetase 2, mitochondrial	1.17	51067	12p11.21
226386_at	C7orf30	chromosome 7 open reading frame 30	1.18	115416	7p15.3
210114_at	INVS	inversin	1.18	27130	9q31
207023_x_at	KRT10	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	1.18	3858	17q21
221847_at	LOC100129361	hypothetical protein LOC100129361	1.18	100129361	12p13.2
222992_s_at	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	1.18	4715	8q13.3
209222_s_at	OSBPL2	oxysterol binding protein-like 2	1.18	9885	20q13.3
223269_at	POLR3GL	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	1.18	84265	1q21.1
209444_at	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	1.18	5910	4q23-q25
209545_s_at	RIPK2	receptor-interacting serine-threonine kinase 2	1.18	8767	8q21
217256_x_at	RPL36A	ribosomal protein L36a	1.18	6173	19p12
225783_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	1.18	140739	2q37.3
226242_at	C1orf131	chromosome 1 open reading frame 131	1.19	128061	1q42.2
213846_at	COX7C	cytochrome c oxidase subunit VIIc	1.19	1350	5q14
204756_at	MAP2K5	mitogen-activated protein kinase kinase 5	1.19	5607	15q23
217980_s_at	MRPL16	mitochondrial ribosomal protein L16	1.19	54948	11q12-q13.1
210212_x_at	MTCP1	mature T-cell proliferation 1	1.19	4515	Xq28
202244_at	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	1.19	5692	1q21
201705_at	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	1.19	5713	16q23-q24
204053_x_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	1.19	5728	10q23.3
1569895_at	---	---	1.2	---	---
208822_s_at	DAP3	death associated protein 3	1.2	7818	1q21-q22
218799_at	GPN2	GPN-loop GTPase 2	1.2	54707	1p36.11
213287_s_at	KRT10	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	1.2	3858	17q21
221274_s_at	LMAN2L	lectin, mannose-binding 2-like	1.2	81562	2q11.2

208771_s_at	LTA4H	leukotriene A4 hydrolase	1.2	4048	12q22
218163_at	MCTS1	malignant T cell amplified sequence 1	1.2	28985	Xq22-q24
204091_at	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	1.2	5147	2q35-q36
225849_s_at	SFT2D1	SFT2 domain containing 1	1.2	113402	6q27
202682_s_at	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	1.2	7375	3p21.3
202144_s_at	ADSL	adenylosuccinate lyase	1.21	158	22q13.1
200042_at	C22orf28	chromosome 22 open reading frame 28	1.21	51493	22q12
226011_at	CCDC12	coiled-coil domain containing 12	1.21	151903	3p21.31
218970_s_at	CUTC	cutC copper transporter homolog (E. coli)	1.21	51076	10q24.2
225359_at	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	1.21	131118	3q26.33
218100_s_at	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	1.21	55081	3q13.12
218982_s_at	MRPS17	mitochondrial ribosomal protein S17	1.21	51373	7p11
203616_at	POLB	polymerase (DNA directed), beta	1.21	5423	8p11.2
218286_s_at	RNF7	ring finger protein 7	1.21	9616	3q22-q24
1554555_a_at	SETD6	SET domain containing 6	1.21	79918	16q21
221702_s_at	TM2D3	TM2 domain containing 3	1.21	80213	15q26.3
207268_x_at	ABI2	abl interactor 2	1.22	10152	2q33
212645_x_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	1.22	9577	2p23.2
211566_x_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	1.22	9577	2p23.2
202279_at	C14orf2	chromosome 14 open reading frame 2	1.22	9556	14q32.33
228135_at	C1orf52	chromosome 1 open reading frame 52	1.22	148423	1p22.3
227086_at	C22orf39	chromosome 22 open reading frame 39	1.22	128977	22q11.21
203450_at	CBY1	chibby homolog 1 (Drosophila)	1.22	25776	22q12
225331_at	CCDC50	coiled-coil domain containing 50	1.22	152137	3q28
203522_at	CCS	copper chaperone for superoxide dismutase	1.22	9973	11q13
217491_x_at	COX7C	cytochrome c oxidase subunit VIIc	1.22	1350	5q14
201738_at	EIF1B	eukaryotic translation initiation factor 1B	1.22	10289	3p22.1
218154_at	GSDMDC1	gasdermin domain containing 1	1.22	79792	8q24.3
209075_s_at	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	1.22	23479	12q24.1
223428_s_at	ISY1	ISY1 splicing factor homolog (S. cerevisiae)	1.22	57461	3q21.3
223104_at	JAGN1	jagunal homolog 1 (Drosophila)	1.22	84522	3p25.2
78383_at	LOC100129250	similar to hCG1811779	1.22	100129250	9p21.1
203478_at	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	1.22	4717	4q28.2-q31.1
218946_at	NFU1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	1.22	27247	2p15-p13
211033_s_at	PEX7	peroxisomal biogenesis factor 7	1.22	5191	6q21-q22.2
223808_s_at	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	1.22	114971	11p11.2
217846_at	QARS	glutamyl-tRNA synthetase	1.22	5859	3p21.3-p21.1
224395_s_at	RNF7	ring finger protein 7	1.22	9616	3q22-q24
223917_s_at	SLC39A3	solute carrier family 39 (zinc transporter), member 3	1.22	29985	19p13.3
227356_at	---	---	1.23	---	---
1555970_at	---	---	1.23	---	---
210250_x_at	ADSL	adenylosuccinate lyase	1.23	158	22q13.1 22q13.2
226414_s_at	ANAPC11	APC11 anaphase promoting complex subunit 11 homolog (yeast)	1.23	51529	17q25.3
223023_at	BET1L	blocked early in transport 1 homolog (S. cerevisiae)-like	1.23	51272	11p15.5
209112_at	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1.23	1027	12p13.1-p12
218648_at	CRTC3	CREB regulated transcription coactivator 3	1.23	64784	15q26.1
212541_at	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	1.23	80308	1q21.3
213357_at	GTF2H5	general transcription factor IIH, polypeptide 5	1.23	404672	6q25.3

201035_s_at	HADH	hydroxyacyl-Coenzyme A dehydrogenase	1.23	3033	4q22-q26
231865_at	KIAA1602	KIAA1602	1.23	57701	12q13.13
231319_x_at	KIF9	kinesin family member 9	1.23	64147	3p21.31
213127_s_at	MED8	mediator complex subunit 8	1.23	112950	1p34.2
224948_at	MRPS24	mitochondrial ribosomal protein S24	1.23	64951	7p14
218654_s_at	MRPS33	mitochondrial ribosomal protein S33	1.23	51650	7q32-q34
209578_s_at	POFUT2	protein O-fucosyltransferase 2	1.23	23275	21q22.3
226150_at	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	1.23	84513	8p12
224710_at	RAB34	RAB34, member RAS oncogene family	1.23	83871	17q11.2
205037_at	RABL4	RAB, member of RAS oncogene family-like 4	1.23	11020	22q13.1
219816_s_at	RBM23	RNA binding motif protein 23	1.23	55147	14q11.2
225547_at	SNHG6	small nucleolar RNA host gene (non-protein coding) 6	1.23	641638	8q13
209358_at	TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	1.23	6882	6p21.31
212910_at	THAP11	THAP domain containing 11	1.23	57215	16q22.1
1552426_a_at	TM2D3	TM2 domain containing 3	1.23	80213	15q26.3
223113_at	TMEM138	transmembrane protein 138	1.23	51524	11q12.2
217797_at	UFC1	ubiquitin-fold modifier conjugating enzyme 1	1.23	51506	1q23.3
212747_at	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	1.24	23294	6p21.31
202641_at	ARL3	ADP-ribosylation factor-like 3	1.24	403	10q23.3
227904_at	AZI2	5-azacytidine induced 2	1.24	64343	3p24.1
210817_s_at	CALCOCO2	calcium binding and coiled-coil domain 2	1.24	10241	17q21.32
222609_s_at	EXOSC1	exosome component 1	1.24	51013	10q24
224885_s_at	KRTCAP2	keratinocyte associated protein 2	1.24	200185	1q22
219119_at	LSM8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.24	51691	7q31.1-q31.3
212748_at	MKL1	megakaryoblastic leukemia (translocation) 1	1.24	57591	22q13
218869_at	MLYCD	malonyl-CoA decarboxylase	1.24	23417	16q24
209609_s_at	MRPL9	mitochondrial ribosomal protein L9	1.24	65005	1q21
221027_s_at	PLA2G12A	phospholipase A2, group XIIA	1.24	81579	4q25
225251_at	RAB24	RAB24, member RAS oncogene family	1.24	53917	5q35.3
217756_x_at	SERF2	small EDRK-rich factor 2	1.24	10169	15q15.3
223277_at	TMEM103	transmembrane protein 103	1.24	54859	3p21.31
226752_at	TMEM157	transmembrane protein 157	1.24	345757	5q21.1
1729_at	TRADD	TNFRSF1A-associated via death domain	1.24	8717	16q22
202090_s_at	UQCR	ubiquinol-cytochrome c reductase, 6.4kDa subunit	1.24	10975	19p13.3
222503_s_at	WDR41	WD repeat domain 41	1.24	55255	5q14.1
208906_at	BSCL2	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)	1.25	221092	11q12-q13.5
226165_at	C8orf59	chromosome 8 open reading frame 59	1.25	401466	8q21.2
204264_at	CPT2	carnitine palmitoyltransferase II	1.25	1376	1p32
218845_at	DUSP22	dual specificity phosphatase 22	1.25	56940	6p25.3
226466_s_at	FAM58A	family with sequence similarity 58, member A	1.25	92002	Xq28
221515_s_at	LCMT1	leucine carboxyl methyltransferase 1	1.25	51451	16p12.3-p12.1
213220_at	LOC92482	hypothetical LOC92482	1.25	92482	10q25.2
203781_at	MRPL33	mitochondrial ribosomal protein L33	1.25	9553	2p21
226616_s_at	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	1.25	4731	21q22.3
225418_at	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	1.25	5819	19q13.2
231059_x_at	SCAND1	SCAN domain containing 1	1.25	51282	20q11.1-q11.23
224751_at	SLC13A4	Solute carrier family 13 (sodium/sulfate symporters), member 4	1.25	26266	7q33
218822_s_at	STX16	syntaxin 16	1.25	79716	20q13.32

223170_at	TMEM98	transmembrane protein 98	1.25	26022	17q11.2
226546_at	---	---	1.26	---	---
224756_s_at	BAT5	HLA-B associated transcript 5	1.26	7920	6p21.3
209836_x_at	BOLA2	bolA homolog 2 (E. coli)	1.26	552900	16p11.2
219022_at	C12orf43	chromosome 12 open reading frame 43	1.26	64897	12q
45526_g_at	FLJ14154	hypothetical protein FLJ14154	1.26	79903	16p13.3
217990_at	GMPR2	guanosine monophosphate reductase 2	1.26	51292	14q12
203776_at	GPKOW	G patch domain and KOW motifs	1.26	27238	Xp11.23
52159_at	HEMK1	HemK methyltransferase family member 1	1.26	51409	3p21.3
209575_at	IL10RB	interleukin 10 receptor, beta	1.26	3588	21q22.1-q22.2
48825_at	ING4	inhibitor of growth family, member 4	1.26	51147	12p13.31
220160_s_at	KPTN	kaptin (actin binding protein)	1.26	11133	19q13.32
203897_at	LYRM1	LYR motif containing 1	1.26	57149	16p11.2
224302_s_at	MRPS36	mitochondrial ribosomal protein S36	1.26	92259	5q13.2
209303_at	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	1.26	4724	5q11.1
225844_at	POLE4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	1.26	56655	2p12
225143_at	SFXN4	sideroflexin 4	1.26	119559	10q26.11
65630_at	TMEM80	transmembrane protein 80	1.26	283232	11p15.5
226787_at	ZNF18	zinc finger protein 18	1.26	7566	17p11.2
219603_s_at	ZNF226	zinc finger protein 226	1.26	7769	19q13.2
222064_s_at	AARSD1	alanyl-tRNA synthetase domain containing 1	1.27	80755	17q21.31
204290_s_at	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	1.27	4329	14q24.3
213995_at	ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	1.27	27109	14q22.1
230326_s_at	C11orf73	chromosome 11 open reading frame 73	1.27	51501	11q14.2
228249_at	C11orf74	chromosome 11 open reading frame 74	1.27	119710	11p12
230871_at	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	1.27	22907	3p21.31
224163_s_at	DMAP1	DNA methyltransferase 1 associated protein 1	1.27	55929	1p34
227166_at	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	1.27	202052	5q31.2
203562_at	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	1.27	9638	11q24.2
205661_s_at	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	1.27	80308	1q21.3
217751_at	GSTK1	glutathione S-transferase kappa 1	1.27	373156	---
1555866_a_at	HEXDC	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	1.27	284004	17q25.3
210927_x_at	JTB	jumping translocation breakpoint	1.27	10899	1q21
209971_x_at	JTV1	JTV1 gene	1.27	7965	7p22
207170_s_at	LETMD1	LETM1 domain containing 1	1.27	25875	12q13.13
201871_s_at	LOC51035	SAPK substrate protein 1	1.27	51035	11q12.3
226958_s_at	MED11	mediator complex subunit 11	1.27	400569	17p13.2
226209_at	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	1.27	4731	21q22.3
218556_at	ORMDL2	ORM1-like 2 (S. cerevisiae)	1.27	29095	12q13.2
208454_s_at	PGCP	plasma glutamate carboxypeptidase	1.27	10404	8q22.2
218667_at	PJA1	praja 1	1.27	64219	Xq13.1
35156_at	R3HCC1	R3H domain and coiled-coil containing 1	1.27	203069	8p21.3
225743_at	RPUSD3	RNA pseudouridylation synthase domain containing 3	1.27	285367	3p25.3
222493_s_at	ZFAND3	zinc finger, AN1-type domain 3	1.27	60685	6pter-p22.3
219345_at	BOLA1	bolA homolog 1 (E. coli)	1.28	51027	1p36.13-q31.3
205550_s_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	1.28	9577	2p23.2
217780_at	C19orf56	chromosome 19 open reading frame 56	1.28	51398	19p13.13
224968_at	CCDC104	coiled-coil domain containing 104	1.28	112942	2p16.1

209501_at	CDR2	cerebellar degeneration-related protein 2, 62kDa	1.28	1039	16p12.3
222701_s_at	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	1.28	79145	8q12.1
209549_s_at	DGUOK	deoxyguanosine kinase	1.28	1716	2p13
218620_s_at	HEMK1	HemK methyltransferase family member 1	1.28	51409	3p21.3
202138_x_at	JTV1	JTV1 gene	1.28	7965	7p22
225014_at	LOC389203	hypothetical gene supported by BC032431	1.28	389203	4p15.2
228355_s_at	NDUFAF2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	1.28	91942	5q12.1
219680_at	NLRX1	NLR family member X1	1.28	79671	11q23.3
51146_at	PIGV	phosphatidylinositol glycan anchor biosynthesis, class V	1.28	55650	1p36.11
224857_s_at	POLR1D	polymerase (RNA) I polypeptide D, 16kDa	1.28	51082	13q12.2
204839_at	POP5	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	1.28	51367	12q24.31
225901_at	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	1.28	114971	11p11.2
203150_at	RABEPK	Rab9 effector protein with kelch motifs	1.28	10244	9q33.3
221827_at	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	1.28	10616	20p13
229009_at	SIX5	SIX homeobox 5	1.28	147912	19q13.32
210242_x_at	ST20	suppressor of tumorigenicity 20	1.28	400410	15q25.1
201812_s_at	TOMM7	translocase of outer mitochondrial membrane 7 homolog (yeast)	1.28	201725	4q32.1
217958_at	TRAPPC4	trafficking protein particle complex 4	1.28	51399	11q23.3
220261_s_at	ZDHC4	zinc finger, DHHC-type containing 4	1.28	55146	7p22.1
218213_s_at	C11orf10	chromosome 11 open reading frame 10	1.29	746	11q12-q13.1
203257_s_at	C11orf49	chromosome 11 open reading frame 49	1.29	79096	11p11.2
205530_at	ETFDH	electron-transferring-flavoprotein dehydrogenase	1.29	2110	4q32-q35
217168_s_at	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	1.29	9709	16q12.2-q13
210719_s_at	HMG20B	high-mobility group 20B	1.29	10362	19p13.3
210434_x_at	JTB	jumping translocation breakpoint	1.29	10899	1q21
218253_s_at	LGTN	ligatin	1.29	1939	1q31-q32
222512_at	NUB1	negative regulator of ubiquitin-like proteins 1	1.29	51667	7q36
1553587_a_at	POLE4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	1.29	56655	2p12
209817_at	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	1.29	5532	10q21-q22
1560587_s_at	PRDX5	peroxiredoxin 5	1.29	25824	11q13
212922_s_at	SMYD2	SET and MYND domain containing 2	1.29	56950	1q41
33736_at	STOML1	stomatin (EPB72)-like 1	1.29	9399	15q24-q25
231948_s_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	1.29	140739	2q37.3
230257_s_at	C1orf19	chromosome 1 open reading frame 19	1.3	116461	1q25
225195_at	DPH3	DPH3, KTI11 homolog (S. cerevisiae)	1.3	285381	3p24.3
225591_at	FBXO25	F-box protein 25	1.3	26260	8p23.3
202105_at	IGBP1	immunoglobulin (CD79A) binding protein 1	1.3	3476	Xq13.1-q13.3
205055_at	ITGAE	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	1.3	3682	17p13
202595_s_at	LEPROTL1	leptin receptor overlapping transcript-like 1	1.3	23484	8p21.2-p21.1
214083_at	LOC100132532	hypothetical protein LOC100132532	1.3	100132532	14q32.31
208682_s_at	MAGED2	melanoma antigen family D, 2	1.3	10916	Xp11.2
204173_at	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle	1.3	140465	12q13.13
202891_at	NIT1	nitrilase 1	1.3	4817	1q21-q22
34187_at	RBMS2	RNA binding motif, single stranded interacting protein 2	1.3	5939	12q13.3
218206_x_at	SCAND1	SCAN domain containing 1	1.3	51282	20q11.1-q11.23
224752_at	SLC13A4	Solute carrier family 13 (sodium/sulfate symporters), member 4	1.3	26266	7q33
202811_at	STAMPB	STAM binding protein	1.3	10617	2p13.1
224670_at	SYS1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	1.3	90196	20q13.12

225787_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	1.3	140739	2q37.3
218645_at	ZNF277	zinc finger protein 277	1.3	11179	7q31.1
226519_s_at	AGXT2L2	alanine-glyoxylate aminotransferase 2-like 2	1.31	85007	5q35.3
224665_at	C10orf104	chromosome 10 open reading frame 104	1.31	119504	10q22.1
221600_s_at	C11orf67	chromosome 11 open reading frame 67	1.31	28971	11q14.1
218214_at	C12orf44	chromosome 12 open reading frame 44	1.31	60673	12q13.13
209177_at	C3orf60	chromosome 3 open reading frame 60	1.31	25915	3p21.31
226723_at	CCDC23	coiled-coil domain containing 23	1.31	374969	1p34.2
218504_at	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	1.31	51011	2p24.3-p11.2
213896_x_at	FAM149B1	family with sequence similarity 149, member B1	1.31	317662	10q22.2
227479_at	KIAA1244	KIAA1244	1.31	57221	6q23.3
230435_at	LOC375190	hypothetical LOC375190	1.31	375190	2p23.3
234875_at	LOC729926	similar to rCG45476	1.31	729926	19p12
204784_s_at	MLF1	myeloid leukemia factor 1	1.31	4291	3q25.1
210386_s_at	MTX1	metaxin 1	1.31	4580	1q21
220311_at	N6AMT1	N-6 adenine-specific DNA methyltransferase 1 (putative)	1.31	29104	21q21.3
211711_s_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	1.31	5728	10q23.3
218526_s_at	RANGRF	RAN guanidine nucleotide release factor	1.31	29098	17p13
218836_at	RPP21	ribonuclease P/MRP 21kDa subunit	1.31	79897	6p21.33
201522_x_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	1.31	6638	15q11.2
209770_at	BTN3A1	butyrophilin, subfamily 3, member A1	1.32	11119	6p22.1
204820_s_at	BTN3A3	butyrophilin, subfamily 3, member A3	1.32	10384	6p21.3
225419_at	C7orf11	chromosome 7 open reading frame 11	1.32	136647	7p14.1
222702_x_at	CRIP1	cysteine-rich PDZ-binding protein	1.32	9419	2p21
226402_at	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	1.32	113612	4q25
202262_x_at	DDAH2	dimethylarginine dimethylaminohydrolase 2	1.32	23564	6p21.3
224060_s_at	DPH5	DPH5 homolog (S. cerevisiae)	1.32	51611	1p21.2
203430_at	HEBP2	heme binding protein 2	1.32	23593	6q24
224981_at	LOC124446	hypothetical protein BC017488	1.32	124446	16p11.2
226236_at	LOC388789	hypothetical LOC388789	1.32	388789	20p11.23
204027_s_at	METTL1	methyltransferase like 1	1.32	4234	12q13
209845_at	MKRN1	makorin, ring finger protein, 1	1.32	23608	7q34
223650_s_at	NRBF2	nuclear receptor binding factor 2	1.32	29982	10q21.2
217499_x_at	OR7E37P	olfactory receptor, family 7, subfamily E, member 37 pseudogene	1.32	26636	13q14.11
232902_s_at	RARS2	arginyl-tRNA synthetase 2, mitochondrial	1.32	57038	6q16.1
205228_at	RBMS2	RNA binding motif, single stranded interacting protein 2	1.32	5939	12q13.3
1554076_s_at	TMEM136	transmembrane protein 136	1.32	219902	11q23.3
224298_s_at	UBAC2	UBA domain containing 2	1.32	337867	13q32.3
223072_s_at	WBP1	WW domain binding protein 1	1.32	83444	2p12
227942_s_at	CRIP1	cysteine-rich PDZ-binding protein	1.33	9419	2p21
204257_at	FADS3	fatty acid desaturase 3	1.33	3995	11q12-q13.1
222105_s_at	NKIRAS2	NFKB inhibitor interacting Ras-like 2	1.33	28511	17q21.2
219489_s_at	NXN	nucleoredoxin	1.33	64359	17p13.3
210502_s_at	PPIE	peptidylprolyl isomerase E (cyclophilin E)	1.33	10450	1p32
222742_s_at	RABL5	RAB, member RAS oncogene family-like 5	1.33	64792	7q22.1
225264_at	RARS2	arginyl-tRNA synthetase 2, mitochondrial	1.33	57038	6q16.1
232652_x_at	SCAND1	SCAN domain containing 1	1.33	51282	20q11.1-q11.23
214096_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	1.33	6472	12q12-q14

210886_x_at	TP53AP1	TP53 activated protein 1	1.33	11257	7q21.1
1294_at	UBA7	ubiquitin-like modifier activating enzyme 7	1.33	7318	3p21
219609_at	WDR25	WD repeat domain 25	1.33	79446	14q32.2
223639_s_at	ZNRD1	zinc ribbon domain containing 1	1.33	30834	6p21.3
225702_at	C8orf76	chromosome 8 open reading frame 76	1.34	84933	8q24.13
203880_at	COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	1.34	10063	3q13.33
204008_at	DNAL4	dynein, axonemal, light chain 4	1.34	10126	22q13.1
53071_s_at	FLJ22222	hypothetical protein FLJ22222	1.34	79701	17q25.3
200048_s_at	JTB	jumping translocation breakpoint	1.34	10899	1q21
209363_s_at	MED21	mediator complex subunit 21	1.34	9412	12p11.23
214075_at	NENF	neuron derived neurotrophic factor	1.34	29937	1q32.3
204436_at	PLEKHO2	pleckstrin homology domain containing, family O member 2	1.34	80301	15q22.1
202494_at	PPIE	peptidylprolyl isomerase E (cyclophilin E)	1.34	10450	1p32
202659_at	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	1.34	5699	16q22.1
242139_s_at	---	---	1.35	---	---
205775_at	FAM50B	family with sequence similarity 50, member B	1.35	26240	6p25-pter
213249_at	FBXL7	F-box and leucine-rich repeat protein 7	1.35	23194	5p15.1
201977_s_at	KIAA0141	KIAA0141	1.35	9812	5q31.3
230588_s_at	LOC285074	hypothetical protein LOC285074	1.35	285074	2p11.2
225441_x_at	LSMD1	LSM domain containing 1	1.35	84316	17p13.1
204168_at	MGST2	microsomal glutathione S-transferase 2	1.35	4258	4q28.3
218563_at	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	1.35	4696	19q13.42
221803_s_at	NRBF2	nuclear receptor binding factor 2	1.35	29982	10q21.2
218291_at	RP11-336K24.9	mitogen-activated protein-binding protein-interacting protein	1.35	28956	1q22
223538_at	SERF1A	small EDRK-rich factor 1A (telomeric)	1.35	8293	5q12.2-q13.3
218321_x_at	STYXL1	serine/threonine/tyrosine interacting-like 1	1.35	51657	7q11.23
228606_at	TM4SF19	transmembrane 4 L six family member 19	1.35	116211	3q29
204254_s_at	VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor	1.35	7421	12q13.11
227092_at	---	---	1.36	---	---
204821_at	BTN3A3	butyrophilin, subfamily 3, member A3	1.36	10384	6p21.3
223773_s_at	C1orf79	chromosome 1 open reading frame 79	1.36	85028	1p35.3
225951_s_at	CHD2	Chromodomain helicase DNA binding protein 2	1.36	1106	15q26
207843_x_at	CYB5A	cytochrome b5 type A (microsomal)	1.36	1528	18q23
203979_at	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	1.36	1593	2q33-qter
214909_s_at	DDAH2	dimethylarginine dimethylaminohydrolase 2	1.36	23564	6p21.3
222854_s_at	GEMIN8	gem (nuclear organelle) associated protein 8	1.36	54960	Xp22.2
217266_at	LOC100130624	hypothetical LOC100130624	1.36	100130624	22q12.1
224512_s_at	LSMD1	LSM domain containing 1	1.36	84316	17p13.1
218543_s_at	PARP12	poly (ADP-ribose) polymerase family, member 12	1.36	64761	7q34
226361_at	TMEM42	transmembrane protein 42	1.36	131616	3p21.31
210241_s_at	TP53AP1	TP53 activated protein 1	1.36	11257	7q21.1
203227_s_at	TSPAN31	tetraspanin 31	1.36	6302	12q13.3
219348_at	USE1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	1.36	55850	19p13.11
202418_at	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	1.36	10897	11q13
228009_x_at	ZNRD1	zinc ribbon domain containing 1	1.36	30834	6p21.3
229493_at	---	---	1.37	---	---
219979_s_at	C11orf73	chromosome 11 open reading frame 73	1.37	51501	11q14.2
219709_x_at	C16orf24	chromosome 16 open reading frame 24	1.37	65990	16p13.3

218945_at	C16orf68	chromosome 16 open reading frame 68	1.37	79091	16p13.2
228291_s_at	C20orf19	chromosome 20 open reading frame 19	1.37	55857	20pter-q11.23
225723_at	C6orf129	chromosome 6 open reading frame 129	1.37	154467	6p21.2
226434_at	C7orf47	chromosome 7 open reading frame 47	1.37	221908	7q22.1
221951_at	TMEM80	transmembrane protein 80	1.37	283232	11p15.5
225651_at	UBE2E2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	1.37	7325	3p24.2
227674_at	ZNF585A	zinc finger protein 585A	1.37	199704	19q13.12
228275_at	---	---	1.38	---	---
221599_at	C11orf67	chromosome 11 open reading frame 67	1.38	28971	11q14.1
225312_at	COMMD6	COMM domain containing 6	1.38	170622	---
222056_s_at	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	1.38	51011	2p24.3-p11.2
225806_at	JUB	jub, ajuba homolog (Xenopus laevis)	1.38	84962	14q11.2
218773_s_at	MSRB2	methionine sulfoxide reductase B2	1.38	22921	10p12
209739_s_at	PNPLA4	patatin-like phospholipase domain containing 4	1.38	8228	Xp22.3
204078_at	SC65	synaptonemal complex protein SC65	1.38	10609	17q21.2
213571_s_at	EIF4E2	eukaryotic translation initiation factor 4E family member 2	1.39	9470	2q37.1
238021_s_at	hCG_1815491	hCG1815491	1.39	643911	16q12.2
210312_s_at	IFT20	intraflagellar transport 20 homolog (Chlamydomonas)	1.39	90410	17q11.2
230405_at	LOC441108	hypothetical gene supported by AK128882	1.39	441108	5q31.1
201475_x_at	MARS	methionyl-tRNA synthetase	1.39	4141	12q13.2
224574_at	RNASEK	ribonuclease, RNase K	1.39	440400	17p13.1
209111_at	RNF5	ring finger protein 5	1.39	6048	6p21.3
230370_x_at	STYXL1	serine/threonine/tyrosine interacting-like 1	1.39	51657	7q11.23
203281_s_at	UBA7	ubiquitin-like modifier activating enzyme 7	1.39	7318	3p21
223186_at	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	1.39	7335	20q13.2
212669_at	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	1.4	818	10q22
205361_s_at	PFDN4	prefoldin subunit 4	1.4	5203	20q13.2
204517_at	PPIC	peptidylprolyl isomerase C (cyclophilin C)	1.4	5480	5q23.2
226674_at	SHISA4	shisa homolog 4 (Xenopus laevis)	1.4	149345	1q32.1
223478_at	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	1.4	26521	11q23.1-q23.2
204985_s_at	TRAPPC6A	trafficking protein particle complex 6A	1.4	79090	19q13.32
209538_at	ZNF32	zinc finger protein 32	1.4	7580	10q22-q25
204175_at	ZNF593	zinc finger protein 593	1.4	51042	1p36.11
219506_at	C1orf54	chromosome 1 open reading frame 54	1.41	79630	1q21.2
205008_s_at	CIB2	calcium and integrin binding family member 2	1.41	10518	15q24
216080_s_at	FADS3	fatty acid desaturase 3	1.41	3995	11q12-q13.1
202967_at	GSTA4	glutathione S-transferase A4	1.41	2941	6p12.1
236075_s_at	LOC100129673	similar to hCG2042915	1.41	100129673	17p13.2
205760_s_at	OGG1	8-oxoguanine DNA glycosylase	1.41	4968	3p26.2
244050_at	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	1.41	401494	9p21.3
207836_s_at	RBPMS	RNA binding protein with multiple splicing	1.41	11030	8p12-p11
217977_at	SEPX1	selenoprotein X, 1	1.41	51734	16p13.3
228044_at	SERP2	stress-associated endoplasmic reticulum protein family member 2	1.41	387923	13q14.11
219147_s_at	C9orf95	chromosome 9 open reading frame 95	1.42	54981	9q21.13
201642_at	IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	1.42	3460	21q22.11
226453_at	RNASEH2C	ribonuclease H2, subunit C	1.42	84153	11q13.1
214838_at	SFT2D2	SFT2 domain containing 2	1.42	375035	1q24.2
203787_at	SSBP2	single-stranded DNA binding protein 2	1.42	23635	5q14.1

218818_at	FHL3	four and a half LIM domains 3	1.43	2275	1p34
202531_at	IRF1	interferon regulatory factor 1	1.43	3659	5q31.1
217722_s_at	NGRN	neugrin, neurite outgrowth associated	1.43	51335	15q26.1
57540_at	RBKS	ribokinase	1.43	64080	2p23.3
213223_at	RPL28	ribosomal protein L28	1.43	6158	19q13.4
232353_s_at	STYXL1	serine/threonine/tyrosine interacting-like 1	1.43	51657	7q11.23
242140_at	---	---	1.44	---	---
225841_at	C1orf59	chromosome 1 open reading frame 59	1.44	113802	1p13.3
212923_s_at	C6orf145	chromosome 6 open reading frame 145	1.44	221749	6p25.2
215726_s_at	CYB5A	cytochrome b5 type A (microsomal)	1.44	1528	18q23
209366_x_at	CYB5A	cytochrome b5 type A (microsomal)	1.44	1528	18q23
228622_s_at	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	1.44	3338	11q13
218450_at	HEBP1	heme binding protein 1	1.44	50865	12p13.1
235191_at	LOC148189	Hypothetical protein LOC148189	1.44	148189	19q12
227488_at	MGC16121	hypothetical protein MGC16121	1.44	84848	Xq26.3
224281_s_at	NGRN	neugrin, neurite outgrowth associated	1.44	51335	15q26.1
225220_at	SNHG8	small nucleolar RNA host gene (non-protein coding) 8	1.44	100093630	4q26
62212_at	C1orf50	chromosome 1 open reading frame 50	1.45	79078	1p34.2
238022_at	hCG_1815491	hCG1815491	1.45	643911	16q12.2
213671_s_at	MARS	methionyl-tRNA synthetase	1.45	4141	12q13.2
226074_at	PPM1M	protein phosphatase 1M (PP2C domain containing)	1.45	132160	3p21.1
217336_at	RPS10	ribosomal protein S10	1.45	158104	15q22.2
34408_at	RTN2	reticulin 2	1.45	6253	19q13.32
200670_at	XBP1	X-box binding protein 1	1.45	7494	22q12.1 22q12
202982_s_at	ACOT2	stathmin-like 2	1.46	10965	14q24.3
235721_at	DTX3	deltex 3 homolog (Drosophila)	1.46	196403	12q13.3
204773_at	IL11RA	interleukin 11 receptor, alpha	1.46	3590	9p13
210239_at	IRX5	iroquois homeobox 5	1.46	10265	16q11.2-q13
218388_at	PGLS	6-phosphogluconolactonase	1.46	25796	19p13.2
219406_at	C1orf50	chromosome 1 open reading frame 50	1.47	79078	1p34.2
212757_s_at	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	1.47	818	10q22
228661_s_at	---	---	1.48	---	---
225807_at	JUB	jub, ajuba homolog (Xenopus laevis)	1.48	84962	14q11.2
223305_at	MGC13379	HSPC244	1.48	51259	11q13.1
212647_at	RRAS	related RAS viral (r-ras) oncogene homolog	1.48	6237	19q13.3-qter
223318_s_at	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	1.49	84266	19p13.3
1553987_at	C12orf47	chromosome 12 open reading frame 47	1.49	51275	12q24.12
204025_s_at	PDCD2	programmed cell death 2	1.49	5134	6q27
206600_s_at	SLC16A5	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	1.49	9121	17q25.1
203919_at	TCEA2	transcription elongation factor A (SII), 2	1.49	6919	20q13.33
208868_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	1.5	23710	12p13.2
225800_at	JAZF1	JAZF zinc finger 1	1.5	221895	7p15.2-p15.1
204279_at	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	1.5	5698	6p21.3
227878_s_at	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	1.51	84266	19p13.3
214724_at	DIXDC1	DIX domain containing 1	1.51	85458	---
218387_s_at	PGLS	6-phosphogluconolactonase	1.51	25796	19p13.2
223179_at	YPEL3	yippee-like 3 (Drosophila)	1.51	83719	16p11.2
212841_s_at	PPFIBP2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	1.52	8495	11p15.4

219366_at	AVEN	apoptosis, caspase activation inhibitor	1.53	57099	15q13.1
223401_at	C17orf48	chromosome 17 open reading frame 48	1.53	56985	17p13.1
220755_s_at	C6orf48	chromosome 6 open reading frame 48	1.53	50854	6p21.3
223340_at	SPG3A	spastic paraplegia 3A (autosomal dominant)	1.53	51062	14q22.1
220387_s_at	HHLA3	HERV-H LTR-associating 3	1.54	11147	1p31.1
201212_at	LGMN	legumain	1.54	5641	14q32.1
205194_at	PSPH	phosphoserine phosphatase	1.54	5723	7p15.2-p15.1
213170_at	GPX7	glutathione peroxidase 7	1.55	2882	1p32
229742_at	LOC145853	hypothetical LOC145853	1.55	145853	15q23
202150_s_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	1.55	4739	6p25-p24
226196_s_at	C14orf179	chromosome 14 open reading frame 179	1.56	112752	14q24.3
209448_at	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	1.56	10553	11p15.1
223063_at	C1orf198	chromosome 1 open reading frame 198	1.57	84886	1q42.13-q43
211458_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	1.57	23710	12p13.2
205872_x_at	PDE4DIP	phosphodiesterase 4D interacting protein (myomegalin)	1.57	9659	1q12
224719_s_at	C12orf57	chromosome 12 open reading frame 57	1.58	113246	12p13.31
201605_x_at	CNN2	calponin 2	1.58	1265	19p13.3
209759_s_at	DCI	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	1.58	1632	16p13.3
226552_at	IER5L	immediate early response 5-like	1.58	389792	9q34.11
204964_s_at	SSPN	sarcospan (Kras oncogene-associated gene)	1.58	8082	12p11.2
235173_at	---	---	1.59	---	---
217988_at	CCNB1IP1	cyclin B1 interacting protein 1	1.59	57820	14q11.2
1598_g_at	GAS6	growth arrest-specific 6	1.59	2621	13q34
205174_s_at	QPCT	glutaminy-peptide cyclotransferase (glutaminy cyclase)	1.59	25797	2p22.2
226504_at	FAM109B	family with sequence similarity 109, member B	1.6	150368	22q13.2
202237_at	NNMT	nicotinamide N-methyltransferase	1.6	4837	11q23.1
204545_at	PEX6	peroxisomal biogenesis factor 6	1.6	5190	6p21.1
205687_at	UBFD1	ubiquitin family domain containing 1	1.6	56061	16p12
226195_at	C14orf179	chromosome 14 open reading frame 179	1.61	112752	14q24.3
206595_at	CST6	cystatin E/M	1.61	1474	11q13
1553672_at	ENAH	enabled homolog (Drosophila)	1.61	55740	1q42.12
205752_s_at	GSTM5	glutathione S-transferase M5	1.61	2949	1p13.3
201397_at	PHGDH	phosphoglycerate dehydrogenase	1.62	26227	1p12
204929_s_at	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	1.62	10791	2p11.2
229874_x_at	---	---	1.63	---	---
204079_at	TPST2	tyrosylprotein sulfotransferase 2	1.63	8459	22q12.1
208869_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	1.64	23710	12p13.2
220606_s_at	C17orf48	chromosome 17 open reading frame 48	1.65	56985	17p13.1
229429_x_at	FAM91A2	family with sequence similarity 91, member A2	1.65	57234	1q21.1
209917_s_at	TP53AP1	TP53 activated protein 1	1.65	11257	7q21.1
220230_s_at	CYB5R2	cytochrome b5 reductase 2	1.67	51700	11p15.4
229638_at	IRX3	iroquois homeobox 3	1.68	79191	16q12.2
205807_s_at	TUFT1	tuftelin 1	1.68	7286	1q21
209885_at	RHOD	ras homolog gene family, member D	1.7	29984	11q14.3
230963_at	EMX2OS	empty spiracles homeobox 2 opposite strand	1.71	196047	10q26.1
224741_x_at	GAS5	growth arrest-specific 5	1.71	60674	1q25.1
224841_x_at	GAS5	growth arrest-specific 5	1.72	60674	1q25.1
202177_at	GAS6	growth arrest-specific 6	1.73	2621	13q34

219044_at	THNSL2	threonine synthase-like 2 (<i>S. cerevisiae</i>)	1.73	55258	2p11.2
217127_at	CTH	cystathionase (cystathionine gamma-lyase)	1.74	1491	1p31.1
232531_at	EMX2OS	empty spiracles homeobox 2 opposite strand	1.75	196047	10q26.1
222001_x_at	FAM91A2	family with sequence similarity 91, member A2	1.77	57234	1q21.1
223499_at	MFRP	membrane frizzled-related protein	1.78	83552	11q23
225698_at	C5orf26	chromosome 5 open reading frame 26	1.79	114915	5q21-q22
229693_at	LOC388335	RIKEN cDNA A730055C05-like	1.79	388335	17p13.1
205047_s_at	ASNS	asparagine synthetase	1.8	440	7q21.3
203973_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	1.8	1052	8p11.2-p11.1
202238_s_at	NNMT	nicotinamide N-methyltransferase	1.8	4837	11q23.1
225895_at	SYNPO2	synaptopodin 2	1.8	171024	4q26
218706_s_at	GRAMD3	GRAM domain containing 3	1.83	65983	5q23.2
213942_at	MEGF6	multiple EGF-like-domains 6	1.85	1953	1p36.3
219806_s_at	C11orf75	chromosome 11 open reading frame 75	1.89	56935	11q13.3-q23.3
225767_at	---	---	1.9	---	---
214293_at	SEPT11	Septin 11	1.9	55752	4q21.1
229872_s_at	LOC100132999	hypothetical protein LOC100132999	1.93	100132999	1q21.1
213845_at	GRIK2	glutamate receptor, ionotropic, kainate 2	1.95	2898	6q16.3-q21
207076_s_at	ASS1	argininosuccinate synthetase 1	2.04	445	9q34.1
236313_at	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	2.1	1030	9p21
240382_at	LOC100131914	hypothetical protein LOC100131914	2.11	100131914	6p24.3
204983_s_at	GPC4	glypican 4	2.19	2239	Xq26.1
211732_x_at	HNMT	histamine N-methyltransferase	2.2	3176	2q22.1
204984_at	GPC4	glypican 4	2.21	2239	Xq26.1
223734_at	OSAP	ovary-specific acidic protein	2.24	84709	4q31.1
205992_s_at	IL15	interleukin 15	2.28	3600	4q31
222899_at	ITGA11	integrin, alpha 11	2.31	22801	15q23
236640_at	LOC399959	Hypothetical gene supported by BX647608	2.38	399959	11q24.1
204112_s_at	HNMT	histamine N-methyltransferase	2.4	3176	2q22.1
229566_at	LOC645638	similar to WDNM1-like protein	2.44	645638	17q23.1
202149_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	2.44	4739	6p25-p24
205439_at	GSTT2	glutathione S-transferase theta 2	2.6	2953	22q11.2
211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	2.74	3113	6p21.3
203126_at	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	2.75	3613	18p11.2
225548_at	SHROOM3	shroom family member 3	2.76	57619	4q21.1
210372_s_at	TPD52L1	tumor protein D52-like 1	3.1	7164	6q22-q23
227099_s_at	LOC387763	hypothetical LOC387763	3.2	387763	11p11.2
203786_s_at	TPD52L1	tumor protein D52-like 1	3.26	7164	6q22-q23
229296_at	LOC100128501	hypothetical protein LOC100128501	3.36	100128501	9q34.11
218332_at	BEX1	brain expressed, X-linked 1	3.67	55859	Xq21-q23
203000_at	STMN2	stathmin-like 2	5.62	11075	8q21.13
203001_s_at	STMN2	stathmin-like 2	6.9	11075	8q21.13

Supplemental table 3. List of differentially expressed genes identified by SAM analysis (5% FDR) for each separate CRS syndrome compared with NSS controls.

AS

Probe Set ID	Gene Symbol	Gene Title	Fold ch	Entrez Gene	Chromosomal Location
227510_x_at	PRO1073	PRO1073 protein	-7.69	29005	11cen-q12.3
224568_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-7.69	378938	11q13.1
209277_at	TFPI2	tissue factor pathway inhibitor 2	-7.14	7980	7q22
238320_at	TncRNA	trophoblast-derived noncoding RNA	-6.67	283131	11q13.1
228964_at	PRDM1	PR domain containing 1, with ZNF domain	-6.67	639	6q21-q22.1
223940_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-6.67	378938	11q13.1
229070_at	C6orf105	chromosome 6 open reading frame 105	-6.67	84830	6p24.1
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-6.25	4883	5p14-p13
209278_s_at	TFPI2	tissue factor pathway inhibitor 2	-5.88	7980	7q22
208719_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-5.88	10521	22q13.1
227461_at	STON2	stonin 2	-5.56	85439	14q31.1
206172_at	IL13RA2	interleukin 13 receptor, alpha 2	-5.56	3598	Xq13.1-q28
230425_at	EPHB1	EPH receptor B1	-5.56	2047	3q21-q23
208798_x_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	-5.26	23015	15q11.2
214657_s_at	TncRNA	Trophoblast-derived noncoding RNA	-4.76	283131	11q13.1
223578_x_at	PRO1073	PRO1073 protein	-4.76	29005	11cen-q12.3
203888_at	THBD	thrombomodulin	-4.55	7056	20p11.2
205798_at	IL7R	interleukin 7 receptor	-4.55	3575	5p13
239331_at	FLJ43663	Transcribed locus	-4.55	---	---
227082_at	DKFZp586K1922	DKFZp586K1922	-4.55	---	---
227062_at	TncRNA	trophoblast-derived noncoding RNA	-4.35	283131	11q13.1
219054_at	C5orf23	chromosome 5 open reading frame 23	-4.35	79614	5p13.3
203887_s_at	THBD	thrombomodulin	-4.17	7056	20p11.2
238185_at	RBMS1	Transcribed locus	-4.17	---	---
226218_at	IL7R	interleukin 7 receptor	-4.17	3575	5p13
213107_at	TNIK	TRAF2 and NCK interacting kinase	-4	23043	3q26.2-q26.31
224566_at	TncRNA	trophoblast-derived noncoding RNA	-4	283131	11q13.1
209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	-4	6696	4q21-q25
238619_at	FLJ43663	FLJ26188	-4	---	---
232541_at	EGFR	FLJ20099	-4	---	---
208151_x_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-4	10521	22q13.1
1555938_x_at	VIM	vimentin	-3.85	7431	10p13
1556641_at	FLJ37228	hypothetical protein FLJ37228	-3.85	285264	3q26.2
222895_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	-3.85	64919	14q32.2
242110_at	ARHGAP5	Transcribed locus	-3.85	---	---
218340_s_at	UBA6	ubiquitin-like modifier activating enzyme 6	-3.7	55236	4q13.2
203908_at	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	-3.7	8671	4q21
215206_at	EXT1	FLJ21490	-3.7	---	---
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	-3.7	64919	14q32.2
223395_at	ABI3BP	ABI gene family, member 3 (NESH) binding protein	-3.7	25890	3q12
228582_x_at	---	Transcribed locus, moderately similar to XP_001103824.1 PREDICTED: similar to 60S ribosomal protein L39 [Macaca mulatta]	-3.7	---	---
232138_at	MBNL2	Muscleblind-like 2 (Drosophila)	-3.57	10150	13q32.1

228030_at	---	Transcribed locus, strongly similar to NP_005768.1 RNA binding motif protein 6	-3.57	---	---
235046_at	---	Transcribed locus	-3.57	---	---
234989_at	TncRNA	trophoblast-derived noncoding RNA	-3.45	283131	11q13.1
232748_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	-3.45	5069	9q33.2
229437_at	MIRN155, BIC	microRNA 155	-3.45	114614	21q21.3
1558678_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.45	378938	11q13.1
224567_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.45	378938	11q13.1
226675_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.45	378938	11q13.1
228250_at	FNIP1	folliculin interacting protein 1	-3.45	96459	5q23.3
235009_at	FAM44A	family with sequence similarity 44, member A	-3.45	259282	4p16.1
204363_at	F3	coagulation factor III (thromboplastin, tissue factor)	-3.45	2152	1p22-p21
211478_s_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-3.45	1803	2q24.3
242476_at	---	Transcribed locus	-3.45	---	---
240395_at	---	FLJ42406	-3.45	---	---
230130_at	SLIT2	Transcribed locus	-3.33	---	---
238317_x_at	RBMS1	---	-3.33	---	---
231735_s_at	PRO1073	PRO1073 protein	-3.33	29005	11cen-q12.3
243683_at	MORF4L2	Mortality factor 4 like 2	-3.33	9643	Xq22
235567_at	LOC283666	Hypothetical protein LOC283666	-3.33	283666	15q21.3
211958_at	IGFBP5	insulin-like growth factor binding protein 5	-3.33	3488	2q33-q36
213359_at	HNRPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-3.33	3184	4q21.1-q21.2
244026_at	ELL2	Transcribed locus	-3.33	---	---
1561123_at	PRRX1	Full length insert cDNA clone ZD75H02	-3.23	---	---
233286_at	PDZRN3	FLJ12196	-3.23	---	---
205828_at	MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	-3.23	4314	11q22.3
227314_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-3.23	3673	5q23-q31
204863_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-3.23	3572	5q11
213865_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	-3.23	131566	3q12.1 3
242693_at	CDC2L5	Transcribed locus	-3.23	---	---
237252_at	THBD	thrombomodulin	-3.12	7056	20p11.2
212240_s_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-3.12	5295	5q13.1
203434_s_at	MME	membrane metallo-endopeptidase	-3.12	4311	3q25.1-q25.2
203435_s_at	MME	membrane metallo-endopeptidase	-3.12	4311	3q25.1-q25.2
224559_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.12	378938	11q13.1
211000_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-3.12	3572	5q11
225107_at	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	-3.12	3181	7p15
220085_at	HELLS	helicase, lymphoid-specific	-3.12	3070	10q24.2
223730_at	GPC6	glypican 6	-3.12	10082	13q32
229800_at	DCLK1	Doublecortin-like kinase 1	-3.12	9201	13q13
226810_at	C6orf155	MRNA full length insert cDNA clone EUROIMAGE 1509279	-3.12	---	---
226663_at	ANKRD10	ankyrin repeat domain 10	-3.12	55608	13q34
225750_at	---	FLJ14162	-3.12	---	---
244433_at	---	---	-3.12	---	---
228157_at	ZNF207	zinc finger protein 207	-3.03	7756	17q11.2
230560_at	STXBP6	syntaxin binding protein 6 (amisyn)	-3.03	29091	14q12
243768_at	SENP6	Transcribed locus	-3.03	---	---
202600_s_at	NRIP1	nuclear receptor interacting protein 1	-3.03	8204	21q11.2
242059_at	ETNK1	Transcribed locus	-3.03	---	---
230180_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-3.03	10521	22q13.1
205830_at	CLGN	calmegin	-3.03	1047	4q28.3-q31.1
230319_at	C4orf31	Chromosome 4 open reading frame 31	-3.03	79625	4q27
231205_at	---	---	-3.03	---	---

1556035_s_at	ZNF207	zinc finger protein 207	-2.94	7756	17q11.2
229765_at	ZNF207	zinc finger protein 207	-2.94	7756	17q11.2
224565_at	TncRNA	trophoblast-derived noncoding RNA	-2.94	283131	11q13.1
207334_s_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	-2.94	7048	3p22
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	-2.94	9693	4q32.1
240450_at	PAPPA	Transcribed locus	-2.94	---	---
223533_at	LRRC8C	leucine rich repeat containing 8 family, member C	-2.94	84230	1p22.2
203716_s_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-2.94	1803	2q24.3
243514_at	---	Transcribed locus	-2.94	---	---
235138_at	VPS35	Transcribed locus	-2.86	---	---
226864_at	PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-2.86	5569	8q21.12
243993_at	PCTK2	---	-2.86	---	---
243296_at	PBEF1	Pre-B-cell colony enhancing factor 1	-2.86	10135	7q22.2
228399_at	OSR1	odd-skipped related 1 (Drosophila)	-2.86	130497	2p24.1
1558111_at	MBNL1	muscleblind-like (Drosophila)	-2.86	4154	3q25
244341_at	MAK3	Transcribed locus	-2.86	---	---
202156_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	-2.86	10659	10p13
235333_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	-2.86	9331	18q11
203788_s_at	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	-2.78	10512	7q21-q31
1555878_at	RPS24	Ribosomal protein S24	-2.78	6229	10q22-q23
223577_x_at	PRO1073	PRO1073 protein	-2.78	29005	11cen-q12.3
214375_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	-2.78	729222	12p11.23
220940_at	KIAA1641	KIAA1641	-2.78	57730	2q11.2
239835_at	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	-2.78	84541	3p14
242126_at	EXT1	Transcribed locus	-2.78	---	---
218498_s_at	ERO1L	ERO1-like (<i>S. cerevisiae</i>)	-2.78	30001	14q22.1
240038_at	ELL2	Transcribed locus	-2.78	---	---
1570351_at	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	-2.78	11174	5q12
213805_at	ABHD5	abhydrolase domain containing 5	-2.78	51099	3p21
202566_s_at	SVIL	supervillin	-2.7	6840	10p11.2
230494_at	SLC20A1	Solute carrier family 20 (phosphate transporter), member 1	-2.7	6574	2q11-q14
221768_at	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	-2.7	6421	1p34.3
213459_at	RPL37A	ribosomal protein L37a	-2.7	6168	2q35
232431_at	NR3C1	Glucocorticoid receptor alpha mRNA, variant 3' UTR	-2.7	---	---
1558028_x_at	LOC647979	hypothetical protein LOC647979	-2.7	647979	---
204864_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-2.7	3572	5q11
242320_at	FOXO3A	IMAGE:4769230, mRNA	-2.7	---	---
203717_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-2.7	1803	2q24.3
202158_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	-2.7	10659	10p13
242467_at	CSNK1A1	Transcribed locus	-2.7	---	---
1552717_s_at	CEP170	centrosomal protein 170kDa	-2.7	645455	1q44
204508_s_at	CA12	carbonic anhydrase XII	-2.7	771	15q22
227260_at	ANKRD10	Ankyrin repeat domain 10	-2.7	55608	13q34
222816_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	-2.63	54877	18q21.33
210807_s_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-2.63	9194	12q13
243963_at	SDCCAG8	Serologically defined colon cancer antigen 8	-2.63	10806	1q43-q44
241897_at	RBPMS	---	-2.63	---	---
222846_at	RAB8B	RAB8B, member RAS oncogene family	-2.63	51762	15q22.2
1552670_a_at	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	-2.63	79660	8p23.1
204612_at	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-2.63	5569	8q21.12
239227_at	EXT1	---	-2.63	---	---
230229_at	DLG1	Discs, large homolog 1 (Drosophila)	-2.63	1739	3q29

213998_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-2.63	10521	22q13.1
224829_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	-2.63	80315	5q21
229831_at	CNTN3	contactin 3 (plasmacytoma associated)	-2.63	5067	3p26
217523_at	CD44	CD44 molecule (Indian blood group)	-2.63	960	11p13
238563_at	ABI1	Transcribed locus	-2.63	---	---
235927_at	---	---	-2.63	---	---
206108_s_at	SFRS6	splicing factor, arginine/serine-rich 6	-2.56	6431	20q12-q13.1
204326_x_at	MT1X	metallothionein 1X	-2.56	4501	16q13
212859_x_at	MT1E	metallothionein 1E	-2.56	4493	16q13
233219_at	MKLN1	FLJ13365	-2.56	---	---
226210_s_at	MEG3	maternally expressed 3	-2.56	55384	14q32
212196_at	IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	-2.56	3572	5q11
235060_at	DKFZp547E087	hypothetical gene LOC283846	-2.56	283846	18p11.21
227259_at	CD47	CD47 molecule	-2.56	961	3q13.1-q13.2
213158_at	---	IMAGE:4214654, mRNA	-2.56	---	---
212758_s_at	ZEB1	zinc finger E-box binding homeobox 1	-2.5	6935	10p11.2
232528_at	UBE2E3	FLJ11226	-2.5	---	---
238883_at	THRAP2	Transcribed locus	-2.5	---	---
228483_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	-2.5	51616	Xq13.1-q21.1
1556416_s_at	SEC31L1	Full length insert cDNA clone ZD37D10	-2.5	---	---
207177_at	PTGFR	prostaglandin F receptor (FP)	-2.5	5737	1p31.1
236752_at	PKP4	Transcribed locus	-2.5	---	---
239597_at	PAN3	---	-2.5	---	---
212214_at	OPA1	optic atrophy 1 (autosomal dominant)	-2.5	4976	3q28-q29 3q28-q29
208368_s_at	BRC A2	breast cancer 2, early onset	-2.5	675	13q12.3
212286_at	ANKRD12	ankyrin repeat domain 12	-2.5	23253	18p11.22
214895_s_at	ADAM10	ADAM metalloproteinase domain 10	-2.5	102	15q2 15q22
242853_at	---	Transcribed locus	-2.5	---	---
234036_x_at	---	FLJ21384	-2.5	---	---
229858_at	---	FLJ12024	-2.5	---	---
222600_s_at	UBA6	ubiquitin-like modifier activating enzyme 6	-2.44	55236	4q13.2
226625_at	TGFBR3	Transforming growth factor, beta receptor III	-2.44	7049	1p33-p32
203789_s_at	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	-2.44	10512	7q21-q31
1556049_at	RTN4	reticulon 4	-2.44	57142	2p16.3
1560271_at	PTBP2	CDNA clone IMAGE:4797534	-2.44	---	---
213517_at	PCBP2	poly(rC) binding protein 2	-2.44	5094	12q13.12-q13.13
235067_at	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	-2.44	4289	7q32
226211_at	MEG3	maternally expressed 3	-2.44	55384	14q32
1556425_a_at	LOC284219	hypothetical protein LOC284219	-2.44	284219	18p11.22
214453_s_at	IFI44	interferon-induced protein 44	-2.44	10561	1p31.1
1552921_a_at	FIGNL1	figetin-like 1	-2.44	63979	7p12.2
210839_s_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	-2.44	5168	8q24.1
235592_at	ELL2	FLJ36210	-2.44	---	---
225656_at	EFHC1	EF-hand domain (C-terminal) containing 1	-2.44	114327	6p12.3
205046_at	CENPE	centromere protein E, 312kDa	-2.44	1062	4q24-q25
211814_s_at	CCNE2	cyclin E2	-2.44	9134	8q22.1
230127_at	---	Transcribed locus	-2.44	---	---
215287_at	---	ELISC-1	-2.44	---	---
218149_s_at	ZNF395	zinc finger protein 395	-2.38	55893	8p21.1
201295_s_at	WSB1	---	-2.38	---	---
209897_s_at	SLIT2	slit homolog 2 (Drosophila)	-2.38	9353	4p15.2
218000_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.38	22822	12q15

236907_at	PABPC1	FLJ25706	-2.38	---	---
225752_at	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	-2.38	123606	15q11.2
223494_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	-2.38	10724	10q24.1-q24.3
241681_at	MBNL1	Transcribed locus	-2.38	---	---
232356_at	KIAA0143	FLJ13539	-2.38	---	---
208814_at	HSPA4	Heat shock 70kDa protein 4	-2.38	3308	5q31.1-q31.2
207387_s_at	GK	glycerol kinase	-2.38	2710	Xp21.3
242665_at	FMNL2	formin-like 2	-2.38	114793	2q23.3
224999_at	EGFR	Placenta mRNA, clone PL45, partial sequence	-2.38	---	---
237290_at	DDAH1	Transcribed locus	-2.38	---	---
201487_at	CTSC	cathepsin C	-2.38	1075	11q14.1-q14.3
212746_s_at	CEP170	centrosomal protein 170kDa	-2.38	9859	1q44
239413_at	CEP152	centrosomal protein 152kDa	-2.38	22995	15q21.1
235244_at	CCDC58	coiled-coil domain containing 58	-2.38	131076	3q21.1
215867_x_at	CA12	carbonic anhydrase XII	-2.38	771	15q22
1558105_a_at	---	Homo sapiens, Similar to LOC169932, clone IMAGE:4499203, mRNA	-2.38	---	---
229824_at	---	FLJ45325	-2.38	---	---
210875_s_at	ZEB1	zinc finger E-box binding homeobox 1	-2.33	6935	10p11.2
231899_at	ZC3H12C	zinc finger CCCH-type containing 12C	-2.33	85463	11q22.3
233595_at	USP34	ubiquitin specific peptidase 34	-2.33	9736	2p15
235652_at	SCML1	CDNA FLJ37623 fis, clone BRCOC2014013	-2.33	---	---
226310_at	RICTOR	rapamycin-insensitive companion of mTOR	-2.33	253260	5p13.1
225946_at	RASSF8	Ras association (RalGDS/AF-6) domain family 8	-2.33	11228	12p12.3
241970_at	PVRL3	Transcribed locus	-2.33	---	---
212629_s_at	PKN2	protein kinase N2	-2.33	5586	1p22.2
212582_at	OSBPL8	oxysterol binding protein-like 8	-2.33	114882	12q14
1567224_at	HMGA2	high mobility group AT-hook 2	-2.33	8091	12q15
226568_at	FAM102B	family with sequence similarity 102, member B	-2.33	284611	1p13.3
237310_at	EXT1	Transcribed locus	-2.33	---	---
240593_x_at	CAMK2D	Transcribed locus	-2.33	---	---
233112_at	C9orf150	CDNA FLJ10263 fis, clone HEMBB1000991	-2.33	---	---
209006_s_at	C1orf63	chromosome 1 open reading frame 63	-2.33	57035	1p36.13-p35.1
244033_at	C14orf145	chromosome 14 open reading frame 145	-2.33	145508	14q31.1
1555326_a_at	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	-2.33	8754	8p11.23
202604_x_at	ADAM10	ADAM metallopeptidase domain 10	-2.33	102	15q21 15q22
202342_s_at	TRIM2	tripartite motif-containing 2	-2.27	23321	4q31.3
236545_at	PPP3CA	Transcribed locus	-2.27	---	---
204887_s_at	PLK4	polo-like kinase 4 (Drosophila)	-2.27	10733	4q28
241425_at	NUPL1	Nucleoporin like 1	-2.27	9818	13q12.13
213328_at	NEK1	NIMA (never in mitosis gene a)-related kinase 1	-2.27	4750	4q33
226520_at	MLR2	Primary neuroblastoma cDNA, clone:Nbla11485	-2.27	---	---
212188_at	KCTD12	potassium channel tetramerisation domain containing 12	-2.27	115207	13q22.3
206864_s_at	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	-2.27	8739	12q24.22
208025_s_at	HMGA2	high mobility group AT-hook 2	-2.27	8091	12q15
213895_at	EMP1	epithelial membrane protein 1	-2.27	2012	12p12.3
219469_at	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	-2.27	79659	11q21-q22.1
212253_x_at	DST	dystonin	-2.27	667	6p12.1
210735_s_at	CA12	carbonic anhydrase XII	-2.27	771	15q22
210896_s_at	ASPH	aspartate beta-hydroxylase	-2.27	444	8q12.1
230099_at	---	Transcribed locus	-2.27	---	---
235716_at	---	Transcribed locus	-2.27	---	---
228850_s_at	---	---	-2.27	---	---

242343_x_at	ZNF518	---	-2.22	---	---
216228_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	-2.22	11169	14q22.3
234994_at	TMEM200A	transmembrane protein 200A	-2.22	114801	6q23.1
227891_s_at	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	-2.22	8148	17q11.1-q11.2
204240_s_at	SMC2	structural maintenance of chromosomes 2	-2.22	10592	9q31.1
213649_at	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	-2.22	6432	2p22.1
227533_at	RALGPS2	Transcribed locus	-2.22	---	---
238706_at	PAPD4	PAP associated domain containing 4	-2.22	167153	5q14.1
236472_at	OSBPL9	Transcribed locus	-2.22	---	---
212585_at	OSBPL8	oxysterol binding protein-like 8	-2.22	114882	12q14
202599_s_at	NRIP1	nuclear receptor interacting protein 1	-2.22	8204	21q11.2
210756_s_at	NOTCH2	Notch homolog 2 (Drosophila)	-2.22	4853	1p13-p11
243857_at	MORF4L2	Mortality factor 4 like 2	-2.22	9643	Xq22
215177_s_at	ITGA6	integrin, alpha 6	-2.22	3655	2q31.1
224840_at	FKBP5	FK506 binding protein 5	-2.22	2289	6p21.3-p21.2
241457_at	FBXL7	Transcribed locus	-2.22	---	---
232264_at	EDD1	CDNA FLJ12142 fis, clone MAMMA1000356	-2.22	---	---
235236_at	DOCK2	FLJ31436	-2.22	---	---
235341_at	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	-2.22	5611	13q32
214164_x_at	CA12	carbonic anhydrase XII	-2.22	771	15q22
226630_at	C14orf106	chromosome 14 open reading frame 106	-2.22	55320	14q21.3
229694_at	BRWD2	bromodomain and WD repeat domain containing 2	-2.22	55717	10q26
235028_at	---	FLJ42313	-2.22	---	---
231862_at	---	CDNA clone IMAGE:4842353	-2.22	---	---
227501_at	WSB1	Transcribed locus	-2.17	---	---
202316_x_at	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	-2.17	10277	1p36.3
208944_at	TGFR2	transforming growth factor, beta receptor II (70/80kDa)	-2.17	7048	3p22
228370_at	SNRPN	Small nuclear ribonucleoprotein polypeptide N	-2.17	6638	15q11.2
206376_at	SLC6A15	solute carrier family 6, member 15	-2.17	55117	12q21.3
241786_at	PPP3R1	Transcribed locus	-2.17	---	---
214753_at	PFAAP5	Phosphonoformate immuno-associated protein 5	-2.17	10443	13q13.1
242865_at	NPTN	---	-2.17	---	---
208003_s_at	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	-2.17	10725	16q22.1
205018_s_at	MBNL2	muscleblind-like 2 (Drosophila)	-2.17	10150	13q32.1
1557987_at	LOC653786	otoancorin pseudogene	-2.17	653786	16p12.1
211930_at	HNRPA3	heterogeneous nuclear ribonucleoprotein A3	-2.17	220988	2q31.2
226184_at	FMNL2	formin-like 2	-2.17	114793	2q23.3
226432_at	ETNK1	ethanolamine kinase 1	-2.17	55500	12p12.1
220386_s_at	EML4	echinoderm microtubule associated protein like 4	-2.17	27436	2p22-p21
220342_x_at	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	-2.17	80267	1q24-q25
228033_at	E2F7	E2F transcription factor 7	-2.17	144455	12q21.2
232898_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-2.17	1601	5p13
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	-2.17	948	7q11.2
203963_at	CA12	carbonic anhydrase XII	-2.17	771	15q22
205808_at	ASPH	aspartate beta-hydroxylase	-2.17	444	8q12.1
216266_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-2.17	10565	8q13
228314_at	---	FLJ37485	-2.17	---	---
224549_x_at	---	---	-2.17	---	---
212368_at	ZNF292	zinc finger protein 292	-2.13	23036	6q15
1558733_at	ZBTB38	zinc finger and BTB domain containing 38	-2.13	253461	3q23
240383_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-2.13	7323	4q24
201645_at	TNC	tenascin C (hexabrachion)	-2.13	3371	9q33

212994_at	THOC2	THO complex 2	-2.13	57187	Xq25-q26.3
204731_at	TGFBR3	transforming growth factor, beta receptor III	-2.13	7049	1p33-p32
233300_at	TAS2R14	CDNA FLJ11548 fis, clone HEMBA1002944	-2.13	---	---
222088_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-2.13	6515	12p13.3
207057_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-2.13	9194	12q13
202127_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-2.13	8899	6p25.2
208995_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	-2.13	9360	2q31.1
205729_at	OSMR	oncostatin M receptor	-2.13	9180	5p13.1
207108_s_at	NIPBL	Nipped-B homolog (Drosophila)	-2.13	25836	5p13.2
235879_at	MBNL1	Muscleblind-like (Drosophila)	-2.13	4154	3q25
242471_at	LOC647135	Clone HLS_IMAGE_238756 mRNA sequence	-2.13	---	---
226561_at	LOC285086	hypothetical protein LOC285086	-2.13	285086	2q36.3
231866_at	LNPEP	leucyl/cystinyl aminopeptidase	-2.13	4012	5q15
232935_at	LHFP	Primary neuroblastoma cDNA, clone:Nbla03614, full insert sequence	-2.13	---	---
203285_s_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	-2.13	9653	1p31.1-p22.1
214093_s_at	FUBP1	far upstream element (FUSE) binding protein 1	-2.13	8880	1p31.1
231576_at	ETNK1	Transcribed locus	-2.13	---	---
206710_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	-2.13	23136	18p11.32
224911_s_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	-2.13	131566	3q12.1 3
202157_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	-2.13	10659	10p13
239629_at	FLAR	CASP8 and FADD-like apoptosis regulator	-2.13	8837	2q33-q34
208859_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	-2.13	546	Xq13.1-q21.1
224797_at	ARRDC3	arrestin domain containing 3	-2.13	57561	5q14.3
203526_s_at	APC	adenomatous polyposis coli	-2.13	324	5q21-q22
212289_at	ANKRD12	ankyrin repeat domain 12	-2.13	23253	18p11.22
229334_at	---	Transcribed locus	-2.13	---	---
230003_at	---	Transcribed locus	-2.13	---	---
233506_at	---	Full length insert cDNA clone ZB81B12	-2.13	---	---
218396_at	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	-2.08	54832	15q22.2
226035_at	USP31	ubiquitin specific peptidase 31	-2.08	57478	16p12.1
227256_at	USP31	ubiquitin specific peptidase 31	-2.08	57478	16p12.1
242673_at	UBE3C	Transcribed locus	-2.08	---	---
201730_s_at	TPR	translocated promoter region (to activated MET oncogene)	-2.08	7175	1q25
214600_at	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	-2.08	7003	11p15.2
227454_at	TAOK1	TAO kinase 1	-2.08	57551	17q11.2
230165_at	SGOL2	shugoshin-like 2 (S. pombe)	-2.08	151246	2q33.1
227224_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-2.08	55103	1q25.2
235484_at	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-2.08	375743	9q21.11
230270_at	PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	-2.08	55119	1p13.3
222719_s_at	PDGFC	platelet derived growth factor C	-2.08	56034	4q32
212298_at	NRP1	neuropilin 1	-2.08	8829	10p12
204475_at	MMP1	matrix metalloproteinase 1 (interstitial collagenase)	-2.08	4312	11q22.3
244414_at	MAML2	mastermind-like 2	-2.08	84441	11q21
233518_at	LSP1	CDNA FLJ11493 fis, clone HEMBA1001940	-2.08	---	---
225176_at	LNPEP	CDNA FLJ42149 fis, clone THYMU1000692	-2.08	---	---
242366_at	KIAA0701	Homo sapiens, clone IMAGE:3858719, mRNA	-2.08	---	---
210261_at	KCNK2	potassium channel, subfamily K, member 2	-2.08	3776	1q41
225115_at	HIPK2	homeodomain interacting protein kinase 2	-2.08	28996	7q32-q34
225116_at	HIPK2	homeodomain interacting protein kinase 2	-2.08	28996	7q32-q34
227350_at	HELLS	CDNA FLJ11381 fis, clone HEMBA1000501	-2.08	---	---
242890_at	HELLS	CDNA FLJ34225 fis, clone FCBBF3023372	-2.08	---	---
227059_at	GPC6	Glypican 6	-2.08	10082	13q32

1555996_s_at	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	-2.08	1974	3q28
213295_at	CYLD	cyldromatosis (turban tumor syndrome)	-2.08	1540	16q12.1
1556007_s_at	CSNK1A1	Casein kinase 1, alpha 1	-2.08	1452	5q32
201732_s_at	CLCN3	chloride channel 3	-2.08	1182	4q33
207719_x_at	CEP170	centrosomal protein 170kDa	-2.08	9859	1q44
225919_s_at	C9orf72	chromosome 9 open reading frame 72	-2.08	203228	9p21.2
217936_at	ARHGAP5	Rho GTPase activating protein 5	-2.08	394	14q12
210962_s_at	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	-2.08	10142	7q21-q22
243249_at	ACIN1	Transcribed locus	-2.08	---	---
226550_at	---	Homo sapiens, Similar to LOC169932, clone IMAGE:4499203, mRNA	-2.08	---	---
241906_at	ZNF708	---	-2.04	---	---
219062_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	-2.04	54877	18q21.33
219221_at	ZBTB38	zinc finger and BTB domain containing 38	-2.04	253461	3q23
205383_s_at	ZBTB20	zinc finger and BTB domain containing 20	-2.04	26137	3q13.2
223324_s_at	TRPM7	transient receptor potential cation channel, subfamily M, member 7	-2.04	54822	15q21
209257_s_at	SMC3	structural maintenance of chromosomes 3	-2.04	9126	10q25
202498_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-2.04	6515	12p13.3
227176_at	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	-2.04	114134	12q12
209681_at	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-2.04	10560	1q23.3
218273_s_at	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	-2.04	54704	8q22.1
232615_at	PDE4DIP	CDNA: FLJ22765 fis, clone KAIA1180	-2.04	---	---
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	-2.04	9975	3p24.2
225997_at	MOBK1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)	-2.04	92597	4q13.3
224558_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-2.04	378938	11q13.1
225575_at	LIFR	leukemia inhibitory factor receptor alpha	-2.04	3977	5p13-p12
212779_at	KIAA1109	KIAA1109	-2.04	84162	4q27
211959_at	IGFBP5	insulin-like growth factor binding protein 5	-2.04	3488	2q33-q36
220794_at	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	-2.04	64388	1q43
215203_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	-2.04	2803	3p22-p21.3
213212_x_at	FLJ40113	hypothetical protein LOC161527	-2.04	161527	15q25.2
225290_at	ETNK1	ethanolamine kinase 1	-2.04	55500	12p12.1
239719_at	CD109	CD109 molecule	-2.04	135228	6q13
226713_at	CCDC50	coiled-coil domain containing 50	-2.04	152137	3q28
228323_at	CASC5	cancer susceptibility candidate 5	-2.04	57082	15q14
231793_s_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-2.04	817	4q26
228728_at	C7orf58	chromosome 7 open reading frame 58	-2.04	79974	7q31.31
239151_at	BMS1P5	BMS1 pseudogene 5	-2.04	399761	10q11.22
241986_at	BMPER	BMP binding endothelial regulator	-2.04	168667	7p14.3
208703_s_at	APLP2	amyloid beta (A4) precursor-like protein 2	-2.04	334	11q23-q25 11q24
229307_at	ANKRD28	ankyrin repeat domain 28	-2.04	23243	3p24.3
234997_x_at	---	CDNA clone IMAGE:4794941	-2.04	---	---
206874_s_at	---	---	-2.04	---	---
221727_at	---	---	-2.04	---	---
227620_at	---	---	-2.04	---	---
201294_s_at	WSB1	WD repeat and SOCS box-containing 1	-2	26118	17q11.1
212577_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	-2	23347	18p11.32
222837_s_at	NARG1	NMDA receptor regulated 1	-2	80155	4q31.1
225160_x_at	MGC5370	hypothetical protein MGC5370	-2	84825	12q14.3
1554154_at	GDAP2	ganglioside induced differentiation associated protein 2	-2	54834	1p12
235791_x_at	CHD1	chromodomain helicase DNA binding protein 1	-2	1105	5q15-q21
226545_at	CD109	CD109 molecule	-2	135228	6q13
215198_s_at	CALD1	caldesmon 1	-2	800	7q33

210858_x_at	ATM	ataxia telangiectasia mutated	-2	472	11q22-q23
218659_at	ASXL2	additional sex combs like 2 (Drosophila)	-2	55252	2p24.1
202955_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-2	10565	8q13
202760_s_at	AKAP2	A kinase (PRKA) anchor protein 2	-2	11217	9q31-q33
242629_at	---	Transcribed locus	-2	---	---
230175_s_at	---	---	-2	---	---
226074_at	PPM1M	protein phosphatase 1M (PP2C domain containing)	2.01	132160	3p21.1
202150_s_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	2.01	4739	6p25-p24
204112_s_at	HNMT	histamine N-methyltransferase	2.01	3176	2q22.1
213170_at	GPX7	glutathione peroxidase 7	2.01	2882	1p32
212154_at	SDC2	syndecan 2	2.02	6383	8q22-q23
227219_x_at	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	2.02	84557	20cen-q13
205462_s_at	HPCAL1	hippocalcin-like 1	2.02	3241	2p25.1
224719_s_at	C12orf57	chromosome 12 open reading frame 57	2.02	113246	12p13.31
225314_at	OCIAD2	OCIA domain containing 2	2.03	132299	4p12
210319_x_at	MSX2	msh homeobox 2	2.03	4488	5q34-q35
227655_at	FLJ38512	FLJ38512	2.03	---	---
219785_s_at	FBXO31	F-box protein 31	2.03	79791	16q24.2
203417_at	MFAP2	microfibrillar-associated protein 2	2.04	4237	1p36.1-p35
229874_x_at	LOC729604	hypothetical protein LOC729604	2.04	729604	1p36.13
209759_s_at	DCI	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	2.04	1632	16p13.3
225894_at	SYNPO2	synaptopodin 2	2.06	171024	4q26
226674_at	TMEM58	transmembrane protein 58	2.07	149345	1q32.1
209651_at	TGFB11	transforming growth factor beta 1 induced transcript 1	2.07	7041	16p11.2
230963_at	EMX2OS	empty spiracles homeobox 2 opposite strand	2.07	196047	10q26.1
202720_at	TES	testis derived transcript (3 LIM domains)	2.08	26136	7q31.2
201397_at	PHGDH	phosphoglycerate dehydrogenase	2.08	26227	1p12
201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	2.08	3115	6p21.3
204400_at	EFS	embryonal Fyn-associated substrate	2.08	10278	14q11.2-q12
219729_at	PRRX2	paired related homeobox 2	2.09	51450	9q34.1
222379_at	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	2.09	23704	2q36.3
235173_at	hCG_1806964	hCG1806964	2.09	401093	3q25.1
206039_at	RAB33A	RAB33A, member RAS oncogene family	2.1	9363	Xq25
219806_s_at	C11orf75	chromosome 11 open reading frame 75	2.1	56935	11q13.3-q23.3
225895_at	SYNPO2	synaptopodin 2	2.11	171024	4q26
231559_at	NNMT	Nicotinamide N-methyltransferase	2.11	4837	11q23.1
227850_x_at	CDC42EP5	CDC42 effector protein (Rho GTPase binding) 5	2.11	148170	19q13.42
226434_at	C7orf47	chromosome 7 open reading frame 47	2.12	221908	7q22.1
220230_s_at	CYB5R2	cytochrome b5 reductase 2	2.13	51700	11p15.4
214293_at	Septin 11	Septin 11	2.14	55752	4q21.1
206969_at	KRT34	keratin 34	2.14	3885	17q12-q21
204929_s_at	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	2.15	10791	2p11.2
219215_s_at	SLC39A4	solute carrier family 39 (zinc transporter), member 4	2.15	55630	8q24.3
1555851_s_at	SEPW1	selenoprotein W, 1	2.15	6415	19q13.3
216268_s_at	JAG1	jagged 1 (Alagille syndrome)	2.15	182	20p12.1-p11.23
213260_at	FOXC1	forkhead box C1	2.16	2296	6p25
235666_at	---	Transcribed locus	2.16	---	---
210880_s_at	EFS	embryonal Fyn-associated substrate	2.18	10278	14q11.2-q12
202196_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	2.18	27122	11p15.2
230508_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	2.18	27122	11p15.2
203395_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	2.2	3280	3q28-q29
209917_s_at	TP53AP1	TP53 activated protein 1	2.21	11257	7q21.1

1598_g_at	GAS6	growth arrest-specific 6	2.21	2621	13q34
200706_s_at	LITAF	lipopolysaccharide-induced TNF factor	2.22	9516	16p13.13
209293_x_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	2.22	3400	6p22-p21
224378_x_at	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	2.24	84557	20cen-q13
214265_at	ITGA8	integrin, alpha 8	2.24	8516	10p13
205824_at	HSPB2	heat shock 27kDa protein 2	2.24	3316	11q22-q23
205555_s_at	MSX2	msh homeobox 2	2.25	4488	5q34-q35
202177_at	GAS6	growth arrest-specific 6	2.25	2621	13q34
208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	2.26	9124	10q22-q26.3
242888_at	PRRT3	Transcribed locus, strongly similar to NP_997234.2 hypothetical protein LOC285368	2.29	---	---
241440_at	FLJ30375	---	2.3	---	---
204015_s_at	DUSP4	dual specificity phosphatase 4	2.33	1846	8p12-p11
227372_s_at	BAIAP2L1	BAI1-associated protein 2-like 1	2.33	55971	7q21.3
225767_at	---	---	2.36	---	---
221127_s_at	RIG	regulated in glioma	2.37	10530	11p15.1
223292_s_at	MRPS15	mitochondrial ribosomal protein S15	2.37	64960	1p35-p34.1
226504_at	FAM109B	family with sequence similarity 109, member B	2.37	150368	22q13.2
1554819_a_at	ITGA11	integrin, alpha 11	2.38	22801	15q23
213747_at	---	---	2.38	---	---
1555480_a_at	FBLIM1	filamin binding LIM protein 1	2.39	54751	1p36.21
212848_s_at	C9orf3	chromosome 9 open reading frame 3	2.4	84909	9q22.32
204079_at	TPST2	tyrosylprotein sulfotransferase 2	2.41	8459	22q12.1
201194_at	SEPW1	selenoprotein W, 1	2.42	6415	19q13.3
212807_s_at	SORT1	sortilin 1	2.43	6272	1p21.3-p13.1
222450_at	TMEPAI	transmembrane, prostate androgen induced RNA	2.44	56937	20q13.31-q13.33
207076_s_at	ASS1	argininosuccinate synthetase 1	2.45	445	9q34.1
206117_at	TPM1	tropomyosin 1 (alpha)	2.47	7168	15q22.1
227262_at	HAPLN3	hyaluronan and proteoglycan link protein 3	2.49	145864	15q26.1
219310_at	C20orf39	chromosome 20 open reading frame 39	2.49	79953	20p11.21
225016_at	APCDD1	adenomatosis polyposis coli down-regulated 1	2.52	147495	18p11.22
223734_at	OSAP	ovary-specific acidic protein	2.53	84709	4q31.1
229872_s_at	LOC642441	hypothetical LOC642441	2.54	642441	1q21.1
228737_at	TOX2	TOX high mobility group box family member 2	2.55	84969	20q13.12
227959_at	---	Transcribed locus, weakly similar to XP_001113311.1 PREDICTED: hypothetical protein [Macaca mulatta]	2.55	---	---
223499_at	C1QTNF5	C1q and tumor necrosis factor related protein 5	2.58	114902	11q23.3
202149_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	2.6	4739	6p25-p24
204044_at	QPRT	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	2.64	23475	16p11.2
209292_at	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	2.65	3400	6p22-p21
204255_s_at	VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor	2.66	7421	12q13.11
229693_at	LOC388335	similar to RIKEN cDNA A730055C05 gene	2.68	388335	17p13.1
203394_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	2.74	3280	3q28-q29
207030_s_at	CSRP2	cysteine and glycine-rich protein 2	2.75	1466	12q21.1
221900_at	COL8A2	collagen, type VIII, alpha 2	2.78	1296	1p34.2
231183_s_at	JAG1	Jagged 1 (Alagille syndrome)	2.81	182	20p12.1-p11.23
211126_s_at	CSRP2	cysteine and glycine-rich protein 2	2.85	1466	12q21.1
219270_at	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	2.89	79094	15q15.1
209291_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	2.92	3400	6p22-p21
236640_at	LOC399959	Hypothetical gene supported by BX647608	2.98	399959	11q24.1
213942_at	MEGF6	multiple EGF-like-domains 6	2.99	1953	1p36.3
205992_s_at	IL15	interleukin 15	2.99	3600	4q31
202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	3.02	3485	2q33-q34
211538_s_at	HSPA2	heat shock 70kDa protein 2	3.05	3306	14q24.1

225056_at	SIPA1L2	signal-induced proliferation-associated 1 like 2	3.07	57568	1q42.2
228400_at	SHROOM3	shroom family member 3	3.07	57619	4q21.1
57588_at	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	3.08	57419	20p13
210372_s_at	TPD52L1	tumor protein D52-like 1	3.29	7164	6q22-q23
222899_at	ITGA11	integrin, alpha 11	3.37	22801	15q23
1558048_x_at	---	---	3.56	---	---
224550_s_at	MRV11	murine retrovirus integration site 1 homolog	3.63	10335	11p15
226933_s_at	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	3.66	3400	6p22-p21
209343_at	EFHD1	EF-hand domain family, member D1	3.66	80303	2q37.1
209167_at	GPM6B	glycoprotein M6B	3.71	2824	Xp22.2
207302_at	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	3.78	6445	13q12
240382_at	DSP	Clone IMAGE:110436 mRNA sequence	3.88	---	---
225548_at	SHROOM3	shroom family member 3	3.93	57619	4q21.1
205048_s_at	PSPH	phosphoserine phosphatase	3.93	5723	7p15.2-p15.1
229566_at	LOC645638	similar to WDNM1-like protein	3.94	645638	17q23.1
203126_at	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	3.96	3613	18p11.2
205132_at	ACTC1	actin, alpha, cardiac muscle 1	3.98	70	15q11-q14
203786_s_at	TPD52L1	tumor protein D52-like 1	3.99	7164	6q22-q23
227099_s_at	LOC387763	hypothetical LOC387763	4.23	387763	11p11.2
219090_at	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	4.25	57419	20p13
214027_x_at	DES	desmin	4.42	1674	2q35
203766_s_at	LMOD1	leiomodulin 1 (smooth muscle)	4.52	25802	1q32
211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	4.52	3113	6p21.3
227347_x_at	HES4	hairy and enhancer of split 4 (Drosophila)	4.56	57801	1p36.33
229296_at	FLJ34873	FLJ34873	4.6	---	---
219478_at	WFDC1	WAP four-disulfide core domain 1	5.02	58189	16q24.3
209170_s_at	GPM6B	glycoprotein M6B	5.06	2824	Xp22.2
237206_at	MYOCD	myocardin	5.29	93649	17p11.2
229479_at	LOC646324	Transcribed locus	5.49	---	---
203868_s_at	VCAM1	vascular cell adhesion molecule 1	5.68	7412	1p32-p31
229339_at	---	Transcribed locus	5.79	---	---
230784_at	PRAC	small nuclear protein PRAC	6.02	84366	17q21
202222_s_at	DES	desmin	6.57	1674	2q35
227006_at	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	6.9	94274	19q13.1
203951_at	CNN1	calponin 1, basic, smooth muscle	11.45	1264	19p13.2-p13.1
203924_at	GSTA1	glutathione S-transferase A1	13.55	2938	6p12.1
209948_at	KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	21.52	3779	5q34

MS

Probe Set ID	Gene Symbol	Gene Title	Fold ch	Entrez Gene	Chromosomal Location
1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-7.69	5743	1q25.2-q25.3
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-7.14	5743	1q25.2-q25.3
208719_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-3.57	10521	22q13.1
209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	-3.12	6696	4q21-q25
203887_s_at	THBD	thrombomodulin	-2.86	7056	20p11.2
201578_at	PODXL	podocalyxin-like	-2.86	5420	7q32-q33
203888_at	THBD	thrombomodulin	-2.63	7056	20p11.2
232174_at	FLJ21635	FLJ21635	-2.56	---	---
219759_at	ERAP2	endoplasmic reticulum aminopeptidase 2	-2.5	64167	5q15
208581_x_at	MT1X	metallothionein 1X	-2.5	4501	16q13
238320_at	TncRNA	trophoblast-derived noncoding RNA	-2.44	283131	11q13.1

235236_at	DOCK2	FLJ31436	-2.44	---	---
212859_x_at	MT1E	metallothionein 1E	-2.38	4493	16q13
212185_x_at	MT2A	metallothionein 2A	-2.27	4502	16q13
206461_x_at	MT1H	metallothionein 1H	-2.27	4496	16q13
237290_at	DDAH1	Transcribed locus	-2.22	---	---
227487_s_at	SERPINE2	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	-2.22	5270	2q33-q35
216336_x_at	MT1E/MT1M	metallothionein 1E/metallothionein 1M	-2.17	4493	16q13
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	-2.17	9693	4q32.1
211456_x_at	MT1P2	metallothionein 1 pseudogene 2	-2.13	645745	1q43
210735_s_at	CA12	carbonic anhydrase XII	-2.13	771	15q22
204326_x_at	MT1X	metallothionein 1X	-2.13	4501	16q13
241435_at	AA702930	AA702930	-2.04		
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	-2.04	10253	13q31.1
202434_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	-2.04	1545	2p21
1566482_at	DKFZp313L2229	DKFZp313L2229	-2.04	---	---
227404_s_at	EGR1	Early growth response 1	-2	1958	5q31.1
203180_at	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-2	220	15q26.3
208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	2	9124	10q22-q26.3
227674_at	ZNF585A	zinc finger protein 585A	2.05	199704	19q13.12
226196_s_at	C14orf179	chromosome 14 open reading frame 179	2.07	112752	14q24.3
229874_x_at	LOC729604	LOC729604	2.08	---	---
204929_s_at	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	2.11	10791	2p11.2
226195_at	C14orf179	chromosome 14 open reading frame 179	2.13	112752	14q24.3
220230_s_at	CYB5R2	cytochrome b5 reductase 2	2.14	51700	11p15.4
214293_at	SEPT11	Septin 11	2.16	55752	4q21.1
222001_x_at	FAM91A2	family with sequence similarity 91, member A2	2.19	57234	1q21.1
205872_x_at	PDE4DIP	phosphodiesterase 4D interacting protein (myomegalin)	2.28	9659	1q12
223305_at	MGC13379	HSPC244	2.29	51259	11q13.1
228235_at	MGC16121	hypothetical protein MGC16121	2.49	84848	Xq26.3
207076_s_at	ASS1	argininosuccinate synthetase 1	2.74	445	9q34.1
206932_at	CH25H	cholesterol 25-hydroxylase	2.81	9023	10q23
204112_s_at	HNMT	histamine N-methyltransferase	2.81	3176	2q22.1
205992_s_at	IL15	interleukin 15	2.9	3600	4q31
211732_x_at	HNMT	histamine N-methyltransferase	3.11	3176	2q22.1
236640_at	LOC399959	Hypothetical gene supported by BX647608	3.25	399959	11q24.1
228400_at	SHROOM3	shroom family member 3	3.48	57619	4q21.1
225548_at	SHROOM3	shroom family member 3	4.03	57619	4q21.1
218332_at	BEX1	brain expressed, X-linked 1	4.23	55859	Xq21-q23
203126_at	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	4.28	3613	18p11.2
205439_at	GSTT2	glutathione S-transferase theta 2	6.88	2953	22q11.2
203001_s_at	STMN2	stathmin-like 2	8.7	11075	8q21.13

SCS

Probe Set ID	Gene Symbol	Gene Title	Fold ch	Entrez Gene	Chromosomal Location
227314_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-5.56	3673	5q23-q31
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-5	4883	5p14-p13
205032_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-4.76	3673	5q23-q31
201578_at	PODXL	podocalyxin-like	-4.55	5420	7q32-q33
219054_at	C5orf23	chromosome 5 open reading frame 23	-3.33	79614	5p13.3
228399_at	OSR1	odd-skipped related 1 (Drosophila)	-3.33	130497	2p24.1

212859_x_at	MT1E	metallothionein 1E	-3.23	4493	16q13
203887_s_at	THBD	thrombomodulin	-3.03	7056	20p11.2
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	-2.94	10253	13q31.1
210310_s_at	FGF5	fibroblast growth factor 5	-2.94	2250	4q21
215177_s_at	ITGA6	integrin, alpha 6	-2.94	3655	2q31.1
203888_at	THBD	thrombomodulin	-2.86	7056	20p11.2
210311_at	FGF5	fibroblast growth factor 5	-2.86	2250	4q21
204475_at	MMP1	matrix metalloproteinase 1 (interstitial collagenase)	-2.78	4312	11q22.3
217999_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.7	22822	12q15
208378_x_at	FGF5	fibroblast growth factor 5	-2.63	2250	4q21
217998_at	LOC652993	pleckstrin homology-like domain, family A, member 1	-2.63	22822	12q15
218000_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.63	22822	12q15
238178_at	---	Transcribed locus	-2.63	---	---
206298_at	ARHGAP22	Rho GTPase activating protein 22	-2.56	58504	10q11.22
217997_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.5	22822	12q15
209189_at	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	-2.44	2353	14q24.3
216336_x_at	MT1E/MT1M	metallothionein 1E/metallothionein 1M	-2.44	4499	16q13
229824_at	BC042431	FLJ45325 fis, clone BRHIP3006717	-2.44	---	---
236834_at	SCFD2	sec1 family domain containing 2	-2.44	152579	4q12
229011_at	---	Transcribed locus	-2.33	---	---
201976_s_at	MYO10	myosin X	-2.17	4651	5p15.1-p14.3
203186_s_at	S100A4	S100 calcium binding protein A4	-2.17	6275	1q21
213865_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	-2.17	131566	3q12.1 3
217996_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.17	22822	12q15
222889_at	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	-2.17	64858	1p13.2
230973_at	SH2D5	SH2 domain containing 5	-2.13	400745	1p36.12
1552921_a_at	FIGNL1	figetin-like 1	-2.08	63979	7p12.2
207334_s_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	-2.08	7048	3p22
209457_at	DUSP5	dual specificity phosphatase 5	-2.04	1847	10q25
225173_at	ARHGAP18	Rho GTPase activating protein 18	-2.04	93663	6q22.33
225842_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.04	22822	12q15
241986_at	BMPER	BMP binding endothelial regulator	-2.04	168667	7p14.3
208025_s_at	HMG2	high mobility group AT-hook 2	-2	8091	12q15
232183_at	SERAC1	serine active site containing 1	2.05	84947	6q25.3
229872_s_at	LOC642441	hypothetical LOC642441	2.1	642441	1q21.1
202238_s_at	NNMT	nicotinamide N-methyltransferase	2.19	4837	11q23.1
219806_s_at	C11orf75	chromosome 11 open reading frame 75	2.24	56935	11q13.3-q23.3
227550_at	LOC143381	hypothetical protein LOC143381	2.29	143381	10q26.11
231987_at	LOC728264	hypothetical protein LOC728264	2.46	728264	5q33.1
213942_at	MEGF6	multiple EGF-like-domains 6	2.56	1953	1p36.3
241769_at	---	Transcribed locus	2.6	---	---
228772_at	HNMT	histamine N-methyltransferase	3.09	3176	2q22.1
211732_x_at	HNMT	histamine N-methyltransferase	3.37	3176	2q22.1
222899_at	ITGA11	integrin, alpha 11	3.78	22801	15q23
203786_s_at	TPD52L1	tumor protein D52-like 1	3.95	7164	6q22-q23
204984_at	GPC4	glypican 4	4.05	2239	Xq26.1
206101_at	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	4.17	1842	9q22.3
228235_at	MGC16121	hypothetical protein MGC16121	4.79	84848	Xq26.3
229296_at	---	FLJ34873	5.92	---	---
203001_s_at	STMN2	stathmin-like 2	12.04	11075	8q21.13